HYBRID

ESCAIDE

European Scientific Conference on Applied Infectious Disease Epidemiology

22-24 November 2023

in Barcelona & online

#ESCAIDE 2023

ABSTRACT BOOK

ESCAIDE

ecdc

EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

About ESCAIDE

The European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) is an annual conference which aims at strengthening the prevention and control of communicable disease through the sharing of knowledge, experience and contacts. It also provides opportunities for further professional development for fellows and students.

ESCAIDE is composed of a broad programme of sessions. The scientific content of the Conference primarily consists of plenary sessions, and oral and poster abstract presentations, which form a platform for the sharing of scientific advances.

Foreword

A very warm welcome to ESCAIDE 2023! For the second year in a row, the conference is held as a hybrid event, both in Barcelona and online. I hope you will find this edition both exciting and gratifying, and that you will be able to grow your personal and professional networks through the variety of in-person and online interactive opportunities on offer.

Similar to last year's edition, the hybrid format aims to promote sustainability and accessibility, by bringing the content of the conference to a broader audience. The success of ESCAIDE 2022, which brought the conference to more participants than ever before, has paved the way for a more accessible and interactive ESCAIDE. All conference participants can benefit from the many interactive features available through the online platform, which I invite you all to explore and make use of during the conference and even after it has ended.

One of the hallmarks of ESCAIDE has always been its scientific programme, built on the presentation of relevant, high-quality abstracts that are submitted by professionals working in the field of Public Health across Europe and the world. I would like to thank the record number of authors who have taken the time to submit their work to ESCAIDE in order to share their experiences with others. These abstract presentation sessions would also not be possible without the dedication of our team of expert reviewers who contribute to the selection process, as well as the moderators who ensure the sessions run smoothly.

I would like to take this opportunity to express my great appreciation to my colleagues on the Scientific Committee as well as to all of our speakers and presenters, who have put together an especially engaging and thought-provoking plenary programme this year. I hope the diverse and complementary topics of this year's plenary sessions will inspire us to broaden our perspectives and learn from different areas in order to help us prepare for future Public Health challenges.

The conference opens with Plenary A, which seeks to revisit the concept of 'prevention' for communicable diseases, drawing on lessons learned from different disease areas. The keynote session (Plenary B) focuses on digital transformation and the rise in popularity of Artificial Intelligence, and what it means for the future of Public Health. Plenary C explores the potential benefits and limitations of wastewater surveillance in preventing and controlling infectious diseases. Plenary D addresses the increasingly relevant topic of One Health and how global collaboration is needed to tackle current and future health challenges. The conference concludes with Plenary E, a reflection on the way forward for the Public Health workforce in the post-COVID-19 reality.

My thanks also go out to our colleagues in Spain, who have so gracefully hosted us in Barcelona. Their support has been invaluable in making us feel welcome in this city. The buzz and vibrancy of Barcelona have certainly permeated into the excitement we have felt in the many months of preparation that have preceded the conference.

Finally, on a personal note, this will be my last ESCAIDE before my retirement. It has been both a pleasure and an honour to be a part of these events over so many years, and to watch the conference evolve into its current iteration. I wish you all a fruitful and enjoyable conference, and hope it will serve to inspire you and renew your commitment to your work.

Mike Catchpole
Chair, ESCAIDE Scientific Committee

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General programme

CET time zone	DAY 1 - 22 November	
08:00-09:00	REGISTRATION LEVEL 0 AND WELCOME COFFEE LEVEL 2	
09:00-09:25	**Opening ceremony** AUDITORIUM 1	
09:25-10:45	PLENARY SESSION A AUDITORIUM 1 **Broadening the horizon: Revisiting the concept of 'prevention' for communicable diseases** **Chaired by the ESCAIDE Scientific Committee members:** *John Kinsman* (ECDC) *and Petronille Bogaert* (European Commission) **Speakers:** *Kateřina Šédová* (Loono, Czech Republic), *Emilie Karafillakis* (University of Antwerp, Belgium), *Hanna Tolonen* (THL, Finland)	
10:45-11:15	COFFEE BREAK LEVEL 2	
11:15-12:45	FIRESIDE SESSION 1 AUDITORIUM 1 **Surveillance in action: strategies, challenges, and innovations**	FIRESIDE SESSION 2 AUDITORIUM 2 **COVID-19 Vaccination: Assessing effectiveness**
12:45-14:00	LUNCH BREAK LEVEL 0	12:45-13:15 **Refresh and recharge session** Follow the science: follow the song LOUNGE ROOM
		12:50-13:50 **Side session 1:** Career Compass AUDITORIUM 2 **Moderated by:** *Alma Tostmann and Jane Whelan* **Speakers:** *Michael Edelstein* (Bar-ilan University, Israel), *Nadine Zeitlmann* (RKI, Germany), *Patrick Keating* (MSF), *Giovanna Jaramillo-Gutierrez* (Milan and Associates), *Sabine Dittrich* (Deggendorf Institute of Technology, Germany*)*
14:00-15:30	FIRESIDE SESSION 3 AUDITORIUM 1 **Threats and outbreaks of food and water borne diseases**	FIRESIDE SESSION 4 AUDITORIUM 2 **Sexually and community acquired infections, including HIV**
15:45-16:30	POSTER TOUR 1 | POSTER TOUR 2 POSTER TOUR 3 | POSTER TOUR 4 POSTER TOUR 5 | POSTER TOUR 6 POSTER TOUR 7 | POSTER TOUR 8 POSTER AREA	15:45-16:45 AUDITORIUM 2 **Side session 2:** Social Sciences Session: *The history of infectious disease pandemics in Europe: what are the lessons for prevention and control measures* **Moderated by:** *John Paget* (Nivel, Netherlands) **Speakers:** *Donatella Lippi* (University of Florence), *Peter Spreeuwenberg* (Nivel), *Lone Simonsen* (Roskilde University), *Jon Bilbatua* (ECDC)
16:30-17:00	COFFEE BREAK LEVEL 2	
17:00-18:15	PLENARY SESSION B AUDITORIUM 1 **Digital transformation and Artificial Intelligence** **Chaired by the ESCAIDE Scientific Committee members:** *Mike Catchpole (*ECDC) *and Chikwe Ihekweazu* (WHO) **Keynote speaker:** *John Brownstein* (Harvard Medical School, Canada), *Joanna Goodey* (European Union Agency for Fundamental Rights)	
18:15-18:30	DAILY WRAP-UP AUDITORIUM 1	
18:30-20:00	NETWORKING EVENT LEVEL 0	

DAY 2 - 23 November

CET time zone		
08:00-09:00	REGISTRATION **LEVEL 0** AND WELCOME COFFEE **LEVEL 2**	
09:00-10:30	PLENARY SESSION C **AUDITORIUM 1** **Wastewater surveillance: a magic bullet or just one piece of the puzzle?** **Chaired by the ESCAIDE Scientific Committee members:** *Jacobo Mendioroz* (Public Health Agency of Catalonia, Spain) *and Henriette de Valk (*Santé Publique France) **Keynote speaker:** *Paul Griffiths (*EMCDDA), *Marta Vargha* (National Center for Public Health and Pharmacy, Hungary) *and Marion Koopmans* (Erasmus MC, Netherlands)	
10:30-11:00	COFFEE BREAK **LEVEL 2**	
11:00-12:30	FIRESIDE SESSION 5 **AUDITORIUM 1** **Disease Surveillance: trends, outcomes and patterns**	FIRESIDE SESSION 6 **AUDITORIUM 2** **Health promotion and disease prevention**
12:30-13:45	LUNCH BREAK **LEVEL 0**	12:35-13:35 **Side session 3:** New initiatives on integrated surveillance under the European Health Union and the SCBTH regulation **AUDITORIUM 2**
		12:30-13:45 **EAN General Assembly (closed event)** **AUDITORIUM 3**
13:45-15:15	***Eurosurveillance* Seminar:** Changing urban environments and impact on infectious diseases epidemiology, surveillance, prevention and control. **AUDITORIUM 1** **Moderated by:** *Henriette de Valk* (Santé Publique France) **Speakers:** *Gerjon Ikink* (ECDC) *and Florence Fournet* (Institute of Research for Development, France)	FIRESIDE SESSION 7 **AUDITORIUM 2** **Respiratory infections**
15:30-16:15	POSTER TOUR 9 | POSTER TOUR 10 POSTER TOUR 11 | POSTER TOUR 12 POSTER TOUR 13 | POSTER TOUR 14 POSTER TOUR 15 | POSTER TOUR 16 **POSTER AREA**	15:30-16:30 **Side session 4:** Risk communication, community engagement and infodemic management (RCCE-IM) can save lives: success stories **AUDITORIUM 2** **Moderated by:** *Cristiana Salvi* (WHO Regional Office for Europe) *and Laura Woodward* (UK Health Security Agency) **Speakers:** *Richard Amlôt* (UK Health Security Agency), *Dilek Aslan* (Hacettepe University, Turkey), *Audra Diers-Lawson* (Kristiania University College, Norway), *Aizhana Dzhumalieva (*American University of Central Asia, Kyrgyzstan), *Rui Gaspar* (Catholic University of Portugal), *Fatjona Kamberi* (University of Vlora "Ismail Qemali", Albania)
16:15-16:45	COFFEE BREAK **LEVEL 2**	
16:45-18:15	PLENARY SESSION D **AUDITORIUM 1** **One Health: Tackling global health challenges together** **Chaired by the ESCAIDE Scientific Committee members:** *Mircea Ioan Popa* (Carol Davila University of Medicine and Pharmacy, Romania), *Carmen Varela Santos* (ECDC) and *Ágnes Hajdu* (National Center for Public Health and Pharmacy, Hungary) **Speakers:** *Greg Martin* (Health Protection Surveillance Centre, Ireland), *Karen Saylors* (Labyrinth Global Health, USA), *Stef Bronzwaer* (EFSA), *Sandra Gallina* (European Commission)	
18:15-18:30	DAILY WRAP-UP **AUDITORIUM 1**	
18:30-20:00	BARCAMP **AUDITORIUM 2**	

CET time zone	**DAY 3** - *24 November*	
08:00-09:00	REGISTRATION LEVEL 0 AND WELCOME COFFEE LEVEL 2	
09:00-10:30	PLENARY SESSION E AUDITORIUM 1 **Post-pandemic Public Health workforce** **Chaired by the ESCAIDE Scientific Committee members:** *Stine Nielsen* (EPIET Alumni Network) *and Adam Roth* (ECDC) **Speakers:** *Lucy Easthope* (Durham University, UK), *Katarzyna Czabanowska* (Maastricht University, the Netherlands), *Giorgio Grossi* (Karolinska Insitutet, Sweden)	
10:30-11:00	COFFEE BREAK LEVEL 2	
11:00-12:30	FIRESIDE SESSION 8 AUDITORIUM 1 **Healthcare-associated infections**	FIRESIDE SESSION 9 AUDITORIUM 2 **Global health**
12:30-13:45	LUNCH BREAK LEVEL 0	12:30-13:00 **Refresh and recharge session** Follow the science: follow the song LOUNGE ROOM
		12:35-13:35 **Side session 5:** #OutbreakAlert An unknown disease has been reported in…": technological advances taking us from local headlines to public health intelligence AUDITORIUM 2 **Moderated by:** *Vicky Lefevre* (ECDC) *and Philip Abdelmalik* (WHO Health Emergencies Programme*)* **Speakers:** *Luigi Spagnolo* (JRC, EC), *Gianfranco Spiteri* (ECDC), *Mercy Kyeng* (Africa Centres for Disease Control and Prevention)
		12:45-15:00 **Side session 6:** Escape room AUDITORIUM 3
13:45-15:15	FIRESIDE SESSION 10 AUDITORIUM 1 **Modelling, biostatistics, and health informatics**	FIRESIDE SESSION 11 AUDITORIUM 2 **Late breakers**
15:30-16:15	POSTER TOUR 17 | POSTER TOUR 18 POSTER TOUR 19 | POSTER TOUR 20 POSTER TOUR 21 | POSTER TOUR 22 POSTER TOUR 23 | POSTER TOUR 24 POSTER AREA	**Side session 7:** Preparedness session: Are we "PRET" for the next pandemic? AUDITORIUM 2 **Moderated by:** *Hannah Lewis* (Global Influenza Program, WHO) **Speakers:** *Gina Samaan* (Pandemic Preparedness Global Platforms, WHO), *Isabel Bergeri* (Global Influenza Program, WHO)
16:15-16:30	FINAL WRAP-UP AUDITORIUM 1	
16:30-16:45	CLOSING CEREMONY AND AWARDS AUDITORIUM 1	
16:45-17:00	GOODBYE *MERIENDA* LEVEL 2	

NOTE: This is a provisional programme and sessions may change. The final programme will be published closer to the conference dates.

FIRESIDE SESSIONS PROGRAMME

CET time zone

DAY 1 - *22 November 2023*

11:15-12:45

FIRESIDE SESSION 1

Surveillance in action: strategies, challenges, and innovations

moderated by Gianfranco Spiteri

a. Tracking dynamics of SARS-CoV-2 variants in Catalonia (Spain) through wastewater surveillance, *Albert Carcereny Sánchez*

b. A Qualitative Study to Investigate National Perspectives and Needs for Cross-border Contact Tracing in Europe, *Olivia Lewis*

c. Combining human health, food, weather, and land-use data in the investigation of a Shiga-toxin producing E. coli (STEC) O157 outbreak in the UK; a potential novel One Health surveillance approach, *Neil Cunningham*

d. National weekly epidemiological teleconferences – a successful tool for early warning and public health service communication within the COVID-19 crisis, *Nadine Zeitlmann*

e. Whole Genome Sequencing supports epidemiological investigation of community-based Clostridioides difficile clusters, *Israa Mohammed*

f. Sampling schedules for children and characterising non-travel cases of typhoid and paratyphoid: Evidence for actions, *Amoolya Vusirikala*

FIRESIDE SESSION 2

COVID-19 Vaccination: Assessing effectiveness

moderated by Marta Valenciano

a. Effectiveness and durability of a fourth COVID-19 vaccine dose against severe outcomes among older individuals in Norway: A population-based cohort study, *Melanie Stecher*

b. Effectiveness of COVID-19 vaccine boosters in individuals ≥80 years by number of doses and time since the booster using electronic health registries, VEBIS multi-country study, June 2022-January 2023, *Mario Fontán-Vela*

c. Effectiveness of mRNA bivalent vaccines against symptomatic SARS-CoV-2 infection at primary care level in the EU/EEA (VEBIS), September 2022–March 2023, *Charlotte Lanièce Delaunay*

d. Bivalent mRNA booster vaccine effectiveness against COVID-19 hospitalizations and deaths in Portugal using an electronic health records cohort, September 2022 to February 2023, *Ausenda Machado*

e Effectiveness of second BNT162b2 mRNA booster doses in protecting against SARS-CoV-2 infection during the Omicron sub-variant waves; the UK SIREN study June 2022 to March 2023, *Victoria Hall*

14:00-15:30

FIRESIDE SESSION 3

Threats and outbreaks of food and water borne diseases

moderated by Patricia Garvey

a. Cross-border sharing of food isolates solved an outbreak with invasive Listeria monocytogenes infection in ready-to-eat cold-cut meat, Denmark 2022, *Laura Espenhain*

b. Water supply system as the source of the largest Cryptosporidium outbreak recorded in France, November-December 2019, *Ramalli Lauriane*

c. Shiga toxin-producing Escherichia coli O103 outbreak linked to unpasteurised brie-style cheese: case-control study using a market research panel, *Eleanor Blakey*

d. An outbreak of Escherichia coli O157:H7 in Wales associated with a visit to an open farm in England, *Colin Griffiths*

e. The role and limitations of routine Cryptosporidium subtyping in Cryptosporidium surveillance in Sweden, *Hilde De Clerck*

f. Reduction in Salmonella notifications following introduction of COVID-19 control measures, Ireland, 2015-20212, *Charlotte Salgaard Nielsen*

FIRESIDE SESSION 4

Sexually and community acquired infections, including HIV

moderated by Irena Klavs

a. Questioning Risk Compensation: Pre-exposure Prophylaxis (PrEP) and Sexually Transmitted Infections Among Men who have Sex with Men in Denmark, *Sebastian von Schreeb*

b. Association between HIV status and risk of SARS-CoV-2 breakthrough infection and subsequent hospitalisation after COVID-19 vaccination in Italy (January – October 2021), *Alberto Mateo Urdiales*

c. Reduction in the risk of mpoxv infection after MVA-BN vaccination in individuals on HIV pre-exposure prophylaxis: a Spanish cohort study, *Mario Fontán-Vela*

d. Prevalence of Mpox-specific antibodies in sera collected between January – September 2022 in England: A cross-sectional seroprevalence study, *Ash Otter*

e. Less is more – strict control measures obstructed efficient contact tracing during the 2022 mpox outbreak in the Netherlands, *Diederik Brandwagt*

f. Factors associated with non-initiation of antiretroviral therapy among adults newly diagnosed with HIV in Andijan, Uzbekistan, 2018-2021, *Shokhruh Usmanov* *

** Remote presentation*

CET time zone

DAY 2 - *23 November 2023*

11:00-12:30

FIRESIDE SESSION 5

Disease Surveillance: trends, outcomes and patterns

moderated by Agnès Lepoutre

a. Impact of the closure of day-cares and schools in response to the COVID-19 pandemic on European adults' work-life balance, European Union 2020-2022, *Ettore Severi*

b. Transferring inpatients between wards drives large nosocomial COVID-19 outbreaks, Wales, United Kingdom, 2020-22: a matched case-control study using routine and enhanced surveillance data, *Rachel Merrick*

c. Impact of COVID-19 pandemic on incidence and mortality of Clostridioides difficile infection in Wales, UK, *Rubeshkumar Polani Chandrasekar*

d. Epidemiology of persons with repeat episodes of Clostridioides difficile in Wales, United Kingdom, April 2015- March 2022, *Rubeshkumar Polani Chandrasekar*

e. Using surveillance data to evaluate the risk of severe outcomes of COVID-19 during the 2022/2023 winter in Sweden – did the autumn booster among people 65 years and older make a difference?, *Emma Löf*

f. How did the number of healthcare associated infection outbreaks with bacterial pathogens develop during the SARS-CoV-2 pandemic? – Descriptive analysis of surveillance data in Germany, 2017–2022, *Jan M Stratil* *

FIRESIDE SESSION 6

Health promotion and disease prevention

moderated by Petronille Bogaert

a. Establishing infodemic management in Germany: a framework for social listening and integrated analysis to report infodemic insights at the national public health institute, *Sonia Boender*

b. Hygiene assessment in day care centres using the Infection Risk Scan (IRIS), the Netherlands, *E.M. den Boogert*

c. Frameworks to support evidence-informed decision-making from a public health perspective and its application in infectious disease prevention and control: A scoping review, *Pablo Alonso-Coello*

d. Invitation and reminders for shingles vaccination improves uptake among patients registered with a GP. A cross-sectional survey of General Practices in Wales, 2022, *Frances Rowley*

e. Perceived barriers and facilitators to infection prevention and control in Dutch residential care facilities for people with intellectual and developmental disabilities: a cross-sectional study, *Famke Houben*

f. Public considerations about implementing non-pharmaceutical interventions to manage a novel COVID-19 epidemic, *Sophie Kemper*

13:45-15:15

FIRESIDE SESSION 7

Respiratory infections

moderated by Piotr Kramarz

a. Vaccine effectiveness against influenza A(H3N2), A(H1N1)pdm09 and B: Results from the 2022–23 season European VEBIS primary care multicentre study, *Marine Maurel*

b. 2022/23 seasonal vaccine effectiveness against hospitalised influenza A: pooled results from 7 countries participating in the European Vaccine Effectiveness, Burden and Impact Studies (VEBIS) project, *Jennifer Howard*

c. Varicella zoster as a risk factor for invasive Group A Streptococcal infection in children aged 6 months to 5 years, a prospective case control study in the Netherlands, *Ilse Hazelhorst*

d. Factors associated with mortality from invasive group A Streptococcus infection, England, 2015-2023, *Oliver McManus*

e. Factors associated with unfavorable tuberculosis treatment outcomes, Almaty, Kazakhstan, 2018-2021, *Malika Gabdullina*

f. Influenza and Covid-19 vaccine effectiveness against associated hospital admission and death among individuals over 65 years in Norway: a population-based cohort study, 3 October 2022 to 20 June 2023, *Hinta Meijerink*

* *Remote presentation*

CET time zone

DAY 3 - *24 November 2023*

11:00-12:30

FIRESIDE SESSION 8

Healthcare-associated infections

moderated by Ágnes Hajdu

a. Incidence of healthcare-associated infections in Greek long-term care facility residents, May-December 2022 (GR-H4LS), *Lida Politi*

b. Outbreak of iatrogenic botulism post intragastric botulinum neurotoxin treatment for obesity – travel-associated cases in Germany, *Christina Frank*

c. Update: Disability-adjusted life-years and attributable deaths caused by bloodstream infections due to vancomycin-resistant Enterococcus faecium in Germany, 2015-2021, *Simon Brinkwirth*

d. Genotypic and phenotypic antimicrobial resistance in Clostridioides difficile in the overall Irish population, 2022, *Lieke Brouwer*

e. Healthcare-associated hepatitis B and C transmission to patients in the EU/EEA and UK: a systematic review of reported outbreaks between 2006 and 2021, *Jasleen Singh*

f. Waterborne outbreak of Mycobacterium abscessus in a UK specialist heart and lung hospital: patients, mitigations and implications, *Ellen Heinsbroek*

FIRESIDE SESSION 9

Global health

moderated by John Kinsman

a. Antenatal care-based molecular surveillance of malaria in Mozambique, *Nanna Brokhattingen*

b. Investigation of an aseptic meningitis outbreak in Hebron district, West Bank, 2022, *Ayah Tuffaha*

c. Cholera outbreaks: the need to connect epidemiology to systems-level interventions – Municipality of Caraga, Philippines, 2021, *Ian Christian Gonzales*

d. Distribution of Rickettsia species among hospitalized cases and ticks in Pavlodar region, Kazakhstan, 2019, *Yekaterina Bumburidi*

e. Prevalence and determinants of depression among healthcare workers during the COVID-19 pandemic in Khujand, Tajikistan, 2022, *Jamila Silemonshoeva*

13:45-15:15

FIRESIDE SESSION 10

Modelling, biostatistics, and health informatics

moderated by Rene Niehus

a. Environmental factors associated with Escherichia coli concentration at freshwater beaches in Lake Winnipeg, Manitoba, Canada, *Binyam Desta*

b. SARS-CoV-2 transmission patterns in educational settings, *Carla Molina Grané*

c. Risk factors associated with COVID-19 outbreak intensity in Canada: a negative binomial analysis, *Demy Dam*

d. Modelling the incidence and prevalence of chronic hepatitis C among people who inject drugs in Norway to monitor progress towards elimination, *Robert Whittaker*

e. Estimating the effect of the South Africa flightban in November 2021 on the SARS-CoV-2 Omicron outbreak in the Netherlands: A modelling study, *Elke Wynberg* *

f. Impact of the 2023 autumn COVID-19 vaccination campaign by vaccine coverage and level of immunity waning: an agent-based simulation study between August 2023 and June 2024, *David E. Singh* *

FIRESIDE SESSION 11

Late breakers

moderated by Barbara Albiger

a. Iatrogenic botulism, an example from Turkiye, *Zeynep Ozge Ozguler*

b. HIV-cases in Germany in the context of the Ukrainian refugee reception: Description of patient characteristics, transmission routes and infection stages, March 2022 – June 2023, *Klara Röbl*

c. Enhanced surveillance for diphtheria amongst asylum seekers arriving by small boat to England, July-September, 2023: challenges in implementation and outcomes, *Teresa Cullip*

d. Investigating avian influenza transmission to humans from infected animals in England: interim results of an enhanced surveillance programme, *Paula Blomquist*

e. Salmonella Enteritidis restaurant outbreak investigation using till receipt data provides further evidence for eggs as source in widespread international cluster, England, March to April 2023, *Lucy Findlater*

f. Re-emergence of Crimean-Congo Hemorrhagic Fever in North Macedonia, 2023, *Dragan Kochinski* *

** Remote presentation*

POSTER TOURS PROGRAMME

DAY 1 - *22 November 2023* 15:45-16:30 *CET time zone*

POSTER TOUR 1

COVID-19: Surveillance

moderated by Justine Schaeffer

a. Impact of the COVID-19 pandemic on the reporting of infectious diseases in the EU/EEA, 2012-2021, *Carlos Carvalho*

b. Characterisation of SARS-CoV-2 reinfections detected through successive variant waves in the SIREN UK healthcare worker study, June 2020 to March 2023, *Katie Munro*

c. Risk factors associated with COVID-19-related death during the Omicron period in North Macedonia, 2022, *Katerina Kirkovik Kolevska*

d. A case-case study design using national surveillance data underlines the role of immunocompromise among vaccinated COVID-19 cases requiring critical care in Ireland in 2021, *David Kelly*

e. The participatory surveillance system GrippeWeb helps to date and quantify changes in sensitivity of COVID-19 incidence in national notifiable disease surveillance data in Germany, *Anna Loenenbach*

f. Results from WHO GISRS Global External Quality Assessment Programme (EQAP) 2020-2022 for molecular detection of SARS-CoV-2, *Saira Hussain**

POSTER TOUR 2

Food- and waterborne diseases

moderated by Pawel Stefanoff

a. Assessing Giardiasis incidence in travellers for various destination countries and regions using surveillance and travel data, Germany, 2014–2019, *Mirko Faber*

b. Risk factors for household transmission of Shigella during an outbreak in Tunisia, July-November 2022, *Emna Mziou*

c. Foodbook 2.0: Highlights from the Canadian food, water and animal exposure study, *Katharine Fagan-Garcia*

d. Molecular detection of Shiga toxin-producing Escherichia coli (STEC) in water using a sensitive and rapid water-based filtration method, *Zina Alfahl **

POSTER TOUR 3

COVID-19: Vaccination

moderated by Jane Whelan

a. COVID-19 vaccination in Spain - a success story, *Ana Fernandez Dueñas*

b. Additional benefit of a second booster dose against COVID-19 hospitalization. A case-control study with data from sentinel SARI surveillance in Spain, *Clara Mazagatos*

c. Temporal changes to case fatality risk of COVID-19 following vaccination in England: a national surveillance study, *Florence Halford*

d. Pre-existing chronic conditions and COVID-19 vaccination uptake, *Mary Barker*

e. Reactogenicity of heterologous boosting with Bimervax (PHH-1V, HIPRA) against SARS-CoV-2: differences upon previous infection and prime-vaccination regime. Results of a phase 3 clinical trial, *Salomé de Cambra Florensa*

f. Impact of the Health on Wheels Intervention on COVID-19 vaccination in Guatemala, *Evelyn Balsells **

POSTER TOUR 4

Antimicrobial resistance

moderated by Anna Machowska

a. Extended-spectrum beta-lactamase producing E. coli causing urinary tract infections in Iceland. Analysis of epidemiology and risk factors in 2012-2021, *Anna Margrét Halldórsdóttir*

b. Changes in the epidemiology of carbapenem-resistant Acinetobacter spp. before and during the COVID-19-pandemic, Germany, January 2017 – December 2021, *Jonathan Hans Josef Baum*

c. Antimicrobial resistance in Greece: data from the Greek Electronic System for the Surveillance of Antimicrobial Resistance – WHONET-Greece, 2018 to 2022, *Michalis Polemis*

d. Epidemiology and antimicrobial resistance of neisseria gonorrhoeae in Catalonia,2018-2021, *Mercè Herrero Garcia*

e. Investigation of genomic clusters of NDM-1-producing Klebsiella pneumoniae in Germany suggests geographically broad spread in Ukraine and nosocomial transmission in Germany, 2022, *Mirco Sandfort*

f. Consumption of antibiotics in response to invasive group A streptococcus outbreak and changed clinical guidelines in England, winter 2022, *Emma Budd*

** Remote presentation*

POSTER TOUR 5

COVID-19: Burden of disease

moderated by Charlotte Hammer

a. Household transmission of the omicron variant of SARS-CoV-2 – Results from the DigiHero study, *Bianca Klee*

b. Importance of socioeconomic status for COVID-19 outcomes in urban Italy during the vaccine rollout, January - November 2021, *Emmanouil Alexandros Fotakis*

c. Timely detection of excess mortality attributable to COVID-19 in Europe compared to officially reported COVID-19 deaths: Estimates from 26 countries in the EuroMOMO network, *Sarah Kristine Nørgaard*

d. COVID19 and influenza attributable mortality during the COVID19 pandemic in 31 European countries, *Jens Nielsen*

e. Predictors of COVID-19 vaccination uptake among health care workers, in Albania, 2023, *Anisa Xhaferi*

f. COVID-19 knowledge and attitude towards COVID-19 among students and faculty of medical universities, Kazakhstan, February-March 2021, *Ulyana Kirpicheva*

POSTER TOUR 6

Tuberculosis

moderated by Veronica Cristea

a. Active tuberculosis screening among the displaced population fleeing Ukraine, France, February to October 2022, *Jean-Paul Guthmann*

b. Trends in Tuberculosis in Cyprus: analysis of surveillance data from 2011 to 2021, *Annalisa Quattrocchi*

c. Effectiveness of preventive treatment for latent tuberculosis infection and its determinants in real-world settings: A retrospective cohort study in Korea, 2015-2018, *Da Seul Kim*

d. Low sensitivity of the Tuberculosis surveillance system: a capture-recapture study, Tunis, Tunisia, 2022, *Ines Cherif*

e. Evaluation of the implementation of the change to the BCG immunisation programme in England, *Koren Jones*

f. Epidemiological investigations informed a TB screening event for the homeless population in Boston, England, *Mona Dave*

POSTER TOUR 7

HIV, STIs and viral hepatitis: Surveillance

moderated by Esther Kukielka Zunzunegui

a. A statistical method to estimate the number of duplicate entries in statutory infectious disease surveillance in the absence of personal identifiers: Example of hepatitis B in Germany, 2017-2022, *Anja Schoeps*

b. Task Force for the rapid response to the outbreak of severe acute hepatitis of unknown aetiology in children in Portugal in 2022, *Berta Grau-Pujol*

c. Spatial epidemiology of genital herpes simplex in Korea: Clustering and Bayesian spatial regression analysis for its determinants, *Joonsu Jang*

d. Mpox outbreak in France: the association between reported sexual activity and epidemiological characteristics of male cases aged 15 years or older, 2022, *Catarina Krug*

e. Predictors of repeat testing and repeat infectious syphilis in men who have sex with men with a history of syphilis in the Netherlands, *Laura Kayaert*

POSTER TOUR 8

COVID-19: vaccine effectiveness

moderated by Nina Rodic

a. COVID-19 vaccine effectiveness by number of doses received in a multicentre test-negative design study at primary care level in Europe (VEBIS), *Charlotte Lanièce Delaunay*

b. Relative effectiveness of any COVID-19 vaccine booster doses against Omicron SARS-CoV-2 infections in an ECDC multi-centre healthcare worker cohort (VEBIS study), December 2021–March 2023, *Camelia Savulescu*

c. Estimating vaccine effectiveness against COVID-19 using related sick leaves as an indicator: A nationwide population-based cohort study, Norway, July 2021 – December 2022, *Hinta Meijerink*

d. Estimation of COVID-19 vaccine effectiveness against severe outcomes among adults hospitalized for severe acute respiratory infections in Albania, July 2022-March 2023, *Jonilda Sulo*

e. Three reference groups for estimating the effectiveness of the most recent COVID-19 vaccination dose, Vaccine Effectiveness Burden and Impact Studies (VEBIS), December 2021–February 2023, *Liliana Antunes*

f. Duration of COVID-19 vaccine effectiveness against Omicron and its sub-variants by dose: a systematic review, *Anurima Baidya*

DAY 2 - *23 November 2023* 15:30-16:15 *CET time zone*

POSTER TOUR 9

Emerging diseases

moderated by Justine Schaeffer

a. Citizen science as an effective tool to detect the tiger mosquito (Aedes albopictus) in Belgium, *Javiera Rebolledo*

b. Elevated neuroinvasive Toscana Virus incidence in Italy during 2022: an emerging public health threat?, *Emmanouil Alexandros Fotakis*

c. Acute hepatitis of unknown aetiology: examining the North-East England Cohort, *Emer Cullen*

d. Hay exposure as a risk factor associated with the spread of Crimean-Congo Hemorrhagic fever (CCHF), Georgia, 2022, *Levan Liluashvili*

e. Aetiology of Acute Undifferentiated Febrile Illness (AUFI) at a tertiary care centre in Eastern Uttar Pradesh, India, *Vishwa Deepak Tiwari*

f. Fatal Streptococcus pyogenes cases in Europe and Turkey, a case series including autopsy data, *Veroniek Saegeman**

POSTER TOUR 10

Foodborne disease outbreak investigations

moderated by Margaret Fitzgerald

a. Foodborne outbreak investigation in a Public High School in Cinfães, Northern Region of Portugal, February 2023, *Davy Fernandes*

b. Outbreak of Salmonella Typhimurium linked to Swedish rocket salad, Sweden, September-November 2022, *Karolina Fischerström*

c. Shigella flexneri outbreak linked to a takeaway in South Wales, February 2023: a case-control study, *Amy Plimmer*

d. A Foodborne Outbreak of B. cereus associated with Consumption of Bonito Fish, in a Factory, Gebze, Kocaeli, Türkiye, January 2023, *Nurhayat Gürbüz-Adem*

e. Gastroenteritis outbreak at a delivery restaurant, Talgar, Kazakhstan, 2023, *Feruza Ablimitova*

POSTER TOUR 11

Late breakers I

moderated by Ettore Amato

a. A pseudo-outbreak of Bordetella parapertussis centred on a hospital in France, revealing contamination of nasopharyngeal swabs, July 2023, *David Kelly*

b. Attitude towards antibiotic prophylaxis among household contacts of patients with invasive Group A Streptococcal (iGAS) disease and its impact on the incidence of iGAS among contacts in the Netherland, *Henriëtte ter Waarbeek*

c. Measuring the impact of sequential guest bedroom bookings and the effectiveness of interventions in a large, prolonged norovirus outbreak at an allinclusive resort in England, May-June 2023, *Rebecca Hams*

d. National wastewater-based surveillance in Belgium of SARS-CoV-2 variants in summer 2023, *Raphael Janssens*

e. A nosocomial outbreak of invasive Group A Streptococcus infection during a national upsurge in incidence in Ireland, *Cliodhna Ni Bhuachalla* *

f. High prevalence of toxigenic Corynebacterium diphtheriae in wounds of refugees arriving in the Netherlands in June and July 2023, *Dimphey Van Meijeren* *

POSTER TOUR 12

One Health, global health and climate change

moderated by Anna Machowska

a. Effect of seawater temperature on incidence of severe Vibrio spp infections in Norway, 2014-2018, *Beatriz Valcarcel*

b. SARS-CoV-2 in lions, gorilla's and zookeepers in the Rotterdam zoo: a one health investigation, *Aimée Tjon-A-Tsien*

c. Climate change and public health – stepping up to the challenge of the Asian tiger mosquito in Baden-Wuerttemberg, Germany, *Maylin Meincke*

d. Mosquito-borne virus preparedness and response: a stakeholder network analysis for the Netherlands, *Pauline Amber de Best*

** Remote presentation*

POSTER TOUR 13

Genome sequencing in surveillance and outbreak investigations

moderated by Andreas Hoefer

a. Whole genome sequencing versus PCR ribotyping for investigation of Clostridioides difficile – infection, prevention and control impacts, *Victoria Daniel*

b. Increase of Group A Streptococcus (GAS) infections in Austria in 2023 - a genome-based characterization of invasive and non-invasive Streptococcus pyogenes isolates, *Maria João Cardoso*

c. A multi-serotype Salmonella public house outbreak (2020-2023) identified through Whole Genome Sequencing (WGS) in the Midlands, UK, *Daniel Blackman*

d. Multi-country outbreak of Salmonella Senftenberg linked to cherry tomatoes, 2022 to 2023, *Laura Giese*

e. Consumer purchase data facilitated identification of fish patties as the source of an invasive Listeria monocytogenes outbreak, Denmark 2022, *Pernille Kold Munch*

f. Molecular epidemiology of TB in Ireland over 10 years reveals a heterogeneous population and over-estimation of transmission events using traditional genotyping methods, *Emma Roycroft**

POSTER TOUR 14

Implementation science and vaccine preventable diseases

moderated by Jane Whelan

a. Vaccine effectiveness using the 23-valent pneumococcal polysaccharide vaccine against invasive pneumococcal disease in those ≥65 years old: Estimating effectiveness over time and stratified by age, *Katrine Finderup Nielsen*

b. Knowledge, attitudes and practices (KAP) towards pneumococcal infection and vaccination among primary health care physicians, Ukraine, 2021, *Oksana Artemchuk*

c. Effectiveness of the 23-valent pneumococcal polysaccharide vaccine against invasive pneumococcal disease and serotype specific disease aimed at those ≥65 years of age, *Lise Birk Nielsen*

d. Maternal and infant immunity against pertussis in Norway, *Margrethe Greve-Isdahl*

e. Measles and Rubella immune status from serological cross-sectional surveys in 1995-1996, 2006-2007 and 2016-2017 in The Netherlands, *Tom Woudenberg*

f. Low seroprotection against diphtheria and tetanus in Lao adolescents, *Lisa Hefele **

POSTER TOUR 15

Mpox: surveillance and outbreak investigations

moderated by Silvia Funke

a. Global epidemiology of the multicounty monkeypox outbreak, 2022-23, *Ana Hoxha*

b. Monkeypox outbreak surveillance based on emergency department visits, *Bernadette Verrat*

c. In-action evaluation of surveillance processes of mpox in EU/EEA, 2022, *Xanthi Andrianou*

d. Household mpox transmission: estimating the secondary attack rate and factors associated with transmission within households in the UK mpox outbreak between May and November 2022, *Charlotte Anderson*

e. Effectiveness of historical childhood smallpox vaccination against mpox: estimation using the screening method on surveillance data from countries in Europe, 2022-2023, *Soledad Colombe*

f. Investigation of a suspected case of monkey pox, Iboke, health district of Tabou, Côte d'Ivoire, July 2022, *Kalifa Coulibaly*

POSTER TOUR 16

COVID-19 and other respiratory diseases

moderated by Maximilian Riess

a. Real-world evaluation of daily self-administered lateral flow tests for SARS-CoV2 for contacts of COVID-19 cases, *Nicola Love **

b. How the COVID pandemic and physical distancing measures implemented impacted on the social contacts and mixing patterns in Norway? Insights from a panel study, April to September 2020, *Lamprini Veneti*

c. Characterisation of serological correlates of protection against SARS-CoV-2 throughout the pandemic within the UK-based SIREN study, *Ana Atti*

d. Severity assessment of Acute Respiratory infections during the pandemic seasons 2019/2020- 2022/23 in Germany, *Tanja Jung-Sendzik*

e. Annual Burden of Hospitalized Influenza in Albania, 2009/2010 – 2021, *Artan Simaku*

** Remote presentation*

DAY 3 - 24 November 2023 15:30-16:15 *CET time zone*

POSTER TOUR 17

Modelling, biostatistics, and health informatics

moderated by Gaetano Marrone

a. Malaria spatial genomics to infer connectivity, importation and transmission flow of Plasmodium falciparum in Mozambique, *Arnau Pujol*

b. Modelling COVID-19 outbreaks and response options in the 30 EU/EEA countries: Insights from continuous model development and reflections for winter 2023-2024, *Rene Niehus*

c. Causal relationships between human mobility and the spread of Covid19 in Spain, *Camila Pontes*

d. A spatio-temporal predictive model inferring the year-to-year probability of occurrence of TBE human cases in Europe, *Francesca Dagostin*

e. Studying time-evolution of age-specific differences in susceptibility to SARS-CoV-2 infection based on social contact data, *Nicolas Franco*

f. A novel approach to analyzing seasonal patterns in epidemics using a higher-dimensional state space, *Lenka Pribylova*

POSTER TOUR 18

Surveillance in action: strategies, challenges, and innovations

moderated by Esther Kukielka Zunzunegui

a. Implementing a subnational family-doctor-based respiratory disease surveillance system in Baden-Wuerttemberg, Germany, 2022, *Juliana Klein*

b. Improving Compliance of Village Health Centers to the Mandatory Reporting of Notifiable Diseases in the Municipality of Itogon, Province of Benguet, Philippines, 2022, *Rossan Balisto*

c. Nationwide system for early warning and monitoring of nosocomial outbreaks of (highly resistant) microorganisms in the Netherlands: characteristics of outbreaks in 2012-2021, *Sjoukje Woudt*

d. Enhancing Respiratory Infection Monitoring in Albania: The Role of Integrated Surveillance Information System, *Kujtim Mersini*

e. The StopptCOVID Study: Analysing the Effectiveness of Non-Pharmaceutical Interventions in Germany Across Three Waves, *Andreas Hicketier*

f. Using passive samplers in sewage to monitor a hepatitis A outbreak at an Amsterdam school, *Maarten de Jong*

POSTER TOUR 19

Insights on vaccination

moderated by Nina Rodic

a. Evaluating the hepatitis B vaccination impact in the Republic of Moldova – a nationwide representative serosurvey of children born in 2013, *Michael Brandl*

b. Outcomes of post-exposure vaccination prophylaxis for Mpox in paediatric contacts during 2022 outbreak in Catalonia, *Blanca Borras-Bermejo*

c. Taking stock of vaccine hesitancy, associated characteristics and moral values among Dutch parents, *Daphne Bussink-Voorend*

d. Impact of under-reporting on vaccine effectiveness estimates derived from retrospective cohort studies: a simulation study, *Chiara Sacco*

e. Effectiveness of control interventions during a large meningococcal C outbreak in Tuscany, Italy, *Giorgio Guzzetta* *

f. Knowledge, attitudes and practices of influenza vaccination among healthcare workers in Bitola, Republic of North Macedonia, *Svetlana Popovska Kljuseva* *

POSTER TOUR 20

Waterborne outbreaks and related interventions

moderated by Margaret Fitzgerald

a. Community waterborne outbreak due to Salmonella Bovismorbificans, Greece, August 2022, *Lida Politi*

b. Cholera: back to the basics of community sanitation - an outbreak in the Municipality of Manay, Philippines, 2021, *Ian Christian Gonzales*

c. A Waterborne Outbreak of Hemolytic Uremic Syndrome (HUS) caused by Verotoxigenic E. Coli O104:H4 after Feast of Sacrifice in Turkiye, *Burak Kurt*

d. Waterborne outbreak in Bilecik, Türkiye, February 2022, *Tugba Baltaci*

e. A large outbreak of Hepatitis A Outbreak in a northern community in Canada 2021-2022: Public Health Interventions and Immunisation in a Remote Context, *Yassen Tcholakov*

f. Investigation and characterisation of a cholera outbreak in Lebanon after three decades cholera-free, 2022, *Abass Jouny*

** Remote presentation*

POSTER TOUR 21

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

moderated by Silvia Funke

a. Measurement of Population-Level Measles Immunity in Ontario, Canada Using Serology Data Linked to Health Administrative Data, *Archchun Ariyarajah*

b. 20 years of MERIN (Meningitis and Encephalitis Registry in Lower Saxony and Bremen) – design and main results of a syndromic surveillance system, *Mareike Wollenweber*

c. Local increase of serogroup B invasive meningococcal disease caused by an emerging strain, Auvergne-Rhône-Alpes region, France, 2021-2022, *Alexandra Thabuis*

d. Varicella burden in Portugal from 2013 to 2022: implications of the COVID-19 pandemic in a context of a missing varicella vaccine recommendation, *Berta Grau-Pujol*

e. Genomic characterization, antimicrobial susceptibility and vaccine reactivity to 4CMenB of Neisseria meningitidis producing invasive meningococcal disease in Spain, *Josep Roca*

f. Insufficient access to diagnosis hampers surveillance of invasive meningococcal disease in the Republic of Moldova, *Veaceslav Gutu*

POSTER TOUR 22

Infectious diseases and at risk populations

moderated by Charlotte Hammer

a. Socioeconomical inequalities in the incidence of bacteraemias in England: a national surveillance and data linkage study, *Andrea Mazzella*

b. Group B Streptococcus maternal colonization and neonatal sepsis in Belgium between 2012 and 2021: a description of the epidemiological situation, *Zsofia Bognar*

c. An outbreak of invasive Group A Streptoccocus in a residential care facility in the North-East of Ireland, *Ciara Carroll*

d. STEC clearance times in children and risk of transmission in childcare setting remain unchanged despite increase in detected non-O157 cases in England, *Amoolya Vusirikala*

e. Impact of COVID-19 on thirty-day all-cause mortality associated with Gram-negative Bacteraemia in England, *Taimoor Hasan*

f. Preparing long-term care facilities for future pandemics – a systematic review on the effectiveness of non-pharmacological interventions against viral, respiratory pathogens with pandemic potential, *Jan M Stratil **

POSTER TOUR 23

Late breakers II

moderated by Pawel Stefanoff

a. Ongoing mumps genotype G outbreak among primary school children, June September 2023, The Hague, The Netherlands, *Kevin Wassing*

b. Triangulated phylodynamic-spatio-temporal analysis of A/H5N1 outbreak in cats in Poland during spring/summer 2023, *Andrzej Jarynowski*

c. Ongoing multidrug-resistant tuberculosis outbreak among the African immigrant population from 2019 to 2023 in Bilbao, Spain, *Camille Jacqueline*

d. Epidemiologically independent and genetically distinct dengue local transmission events in Italy, summer 2023, *Flavia Riccardo*

e. Application of MALDI-MS and Machine Learning for detection of SARS-CoV-2 and non-COVID acute respiratory infections, *Irina Kadyrova*

f. The evolving relationship between SARS-CoV-2 cases and wastewater concentrations in Luxembourg from lockdown in 2020 until autumn in 2023, *Joël Mossong*

POSTER TOUR 24

Surveillance methods and tools

moderated by Andreas Hoefer

a. Implementation of primary health care surveillance in Malta: a data completion evaluation, *Ariana Wijermans*

b. Using artificial intelligence to improve epidemic intelligence processes: development and impact measurement of R templates for validating and summarising public health threats, *Laura Espinosa*

c. Extracting Contextual Information about Infectious Diseases from Electronic Case Notes for Situational Awareness, *Mark Drakesmith **

d. Evalution of a newly implemented electronic reporting system for notifiable diseases in Denmark, *Sidsel Skou Voss*

e. Development and validation of syndromic surveillance for gastrointestinal infections in emergency departments: a novel tool that complements existing surveillance, Germany, January 2019 – August 2022, *Jonathan Baum*

f. Development of Acute Respiratory Illness (ARI) surveillance through sentinel pharmacies: a Welsh pilot, *Frances Rowley*

** Remote presentation*

TABLE OF CONTENTS

PLENARY SESSIONS

Plenary sessions at ESCAIDE aim to provide an opportunity to discuss public health challenges and scientific advances, bringing together experts in cross-cutting fields to enable evidence from infectious disease research and epidemiology to be translated into improvements in public health.

The content of plenaries is proposed by the ESCAIDE Scientific Committee (11 cross-field members), who invite high level speakers to discuss and tackle topics of significant current importance in infectious disease and public health, deliver inspiring presentations and address questions from the audience. There are five plenary sessions at ESCAIDE 2023, chaired by the ESCAIDE Scientific Committee. The format of each varies from panel discussions, interviews and debates.

Scientific committee

Mike Catchpole

Sweden

Chief Scientist, European Centre for Disease Prevention and Control (ECDC)
Chair of the ESCAIDE Scientific Committee

Mike Catchpole is the Chief Scientist at ECDC. As Head of the Scientific Methods and Standards Unit, he is responsible for driving the scientific agenda and overseeing the quality of the scientific outputs of the Centre. Prior to joining ECDC in 2014, he was the Director of Public Health England's national Centre for Infectious Disease Surveillance and Control. He is a medical doctor with over 20 years of experience working in infectious disease epidemiology at national and international levels and was chair of the EPIET Steering Committee for six years, prior to the oversight passing to ECDC. His main research interests have been in the fields of sexual health, major incident and disaster response, and medical information systems.

Mircea Ioan Popa

Romania

Microbiology Professor
Carol Davila University of Medicine and Pharmacy

Mircea Ioan Popa is Microbiology Professor at Carol Davila University of Medicine and Pharmacy, since 1991. He has been working in the Cantacuzino National Medico-Military Institute for Research and Development since 2018; however he has been working for Cantacuzino Institute since 1997. He successfully completed the Applied Epidemiology Introductory Course (CDC, Atlanta and Emory University, 1999) and the EPIET Introductory Course (2001). He was appointed as a member of the Standing Committee of the Regional Committee for Europe (SCRC, 2000-2001). He coordinated the catch-up campaign to prevent measles and rubella (2.1 million people vaccinated, 1998-1999). Dr Popa initiated (2000) the PHARE Project (Strengthening of Communicable Diseases Surveillance on Laboratory Issues; Europe Aid/113121/D/SV/RO 0107.14), co-financed by the Romanian Ministry of Health. He worked with WHO EMRO in Afghanistan (2002-2003) and acted as the National Microbiology Focal Point in relation with ECDC (2007-2009), Director of Preventive Medicine Department (1997-1999), General Director for Public Health (1999-2001), and Co-Chair of the National Commission on Epidemiology (2005-2006), within the Romanian Ministry of Health. General Director of Cantacuzino Institute (2017-2018). He has been authored/co-authored more than 150 publications in national/international peer-reviewed journals and several chapters in national/international books. He obtained his PhD in 1998 and Master of Management in Social Services and Healthcare in 2001.

Petronille Bogaert

Belgium

Policy Officer, DG SANTE, European Commission

Petronille is Policy Officer in the Health Security Unit in DG SANTE at the European Commission. She is working on prevention, preparedness and response planning. Previously at Sciensano, she was project researcher and head of unit EU health information systems. Her work primarily focussed on European research projects in the area of population health information and the re-use of health data. She coordinated the Population Health Information Research Infrastructure (PHIRI) and was working on the Joint Action Towards the European Health Data Space, EHDS2 Pilot, HERA-IT, BY-COVID and Healthy Cloud. She is a graduate from a double European Master of Public Health. She also holds a Bachelor's and Master's in Biomedical Sciences and has a PhD on the European perspective to support health information systems. She is president of the EUPHA Public health monitoring and reporting.

Adam Roth

Sweden

Head of Fellowship Programme, Public Health Training
European Centre for Disease Prevention and Control (ECDC)

Adam Roth is a medical doctor (M.D.) specialized in Clinical Bacteriology and Virology and an associate professor with a PhD in epidemiology. He has several years of experience from running research and public health projects in low-, middle- and high income countries, as well as in developing epidemiology training in the Pacific Region. Prior to joining ECDC as Head of Fellowship Programme, Adam headed the Unit for Vaccination Programmes at the Public Health Agency of Sweden.

Stine Nielsen

Denmark

Vice-president, EPIET Alumni Network (EAN)

Stine Nielsen is the vice-president of the EPIET Alumni Network which brings together more than 600 European field epidemiologists and public health microbiologists. She has a MSc in public health sciences from Copenhagen University and a promotion (dr.rer.medic) from the Charité university in Berlin. She has worked mainly on HIV and viral hepatitis focusing mostly on increasing access to health and harm reduction services for people who use drugs. She worked at WHO/Europe (2004-2008) and the Robert Koch Institute (2008-2015). From 2015-2022 she was a home-based consultant in Madrid working for Epiconcept and others. Since August 2022, she is a senior epidemiologist in the Department of Infectious Disease Epidemiology and Prevention at Statens Serum Institut (SSI) in Denmark. Stine is active on Twitter as @StineNielsenEPI.

John Kinsman

Sweden

Expert Social and Behaviour Change
European Centre for Disease Prevention and Control (ECDC)

John Kinsman has conducted social and behaviour change research since 1996, including on the social determinants of health, health system strengthening, public health emergency preparedness, and the prevention and control of diseases such as HIV/AIDS, Ebola, Zika and poliomyelitis. He joined ECDC in 2019, working initially on promoting vaccination acceptance and the prevention of antibiotic resistance in the EU, but with a focus on COVID-19 during the pandemic. COVID-19-related projects have included addressing pandemic fatigue, supporting socially vulnerable populations, promoting vaccination, and countering online vaccination misinformation. John gained his PhD in medical anthropology at the University of Amsterdam in 2008, and was Associate Professor in Global Health at Umeå University in Sweden from 2013 until he joined ECDC.

Luísa Peixe

Portugal

Professor of Bacteriology, University of Porto

Luísa Peixe has a degree in Pharmaceutical Sciences and doctorate in Microbiology. During her career as Professor of Bacteriology at the Faculty of Pharmacy of the University of Porto (FFUP), Portugal (1987- present) she has conducted research on antimicrobial resistance on different clinically relevant bacteria, with a One Health approach. This is done to understand the ecology, drivers and evolution of bacteria, as well as to help improve their detection and control. As the effectiveness of standard antimicrobial treatments in urinary tract infections has vastly diminished, her research team has been investigating the role of the urinary microbiome in urinary tract health and disease. Currently, she is Director of Department of Biological Sciences at FFUP and has published over 200 publications in international peer-reviewed journals. She holds several positions in national and international institutions in connection with her expertise in clinical bacteriology and antimicrobial resistance. These include the Biological Hazards Panel at the European Food Safety Authority (EFSA), the Qualitative Presumption of Safety Working Group at EFSA and the Joint Programming Initiative on Antimicrobial Resistance (JPIAMR) Scientific Board.

Chikwe Ihekweazu

Germany

Assistant Director-General
Health Emergency Intelligence, WHO

Chikwe Ihekweazu is the Assistant Director General at the World Health Organization (WHO) for Surveillance and Health Emergency Intelligence and leads the WHO Hub for Pandemic and Epidemic Intelligence, based in Berlin, Germany. Previously, Dr Ihekweazu was the first Director General of the Nigeria Centre for Disease Control (NCDC), which he led July 2016 - October 2021, building it from a small unit to a leading public health agency in Africa. He acted as Interim Director of the West Africa Regional Centre for Surveillance and Disease Control through 2017. Dr Ihekweazu trained as an infectious disease epidemiologist and has over 25 years' experience working in senior public health and leadership positions in national public health institutes including NCDC, South African National Institute for Communicable Diseases, the UK's Health Protection Agency, and Germany's Robert Koch Institute. Dr Ihekweazu has led several short-term engagements for WHO, mainly building surveillance systems and responding to major infectious disease outbreaks. He was part of the first WHO COVID-19 international mission to China. Dr Ihekweazu is a graduate of the College of Medicine, University of Nigeria and has a Masters in Public Health from the Heinrich-Heine University, Dusseldorf, Germany. In 2003, he was awarded a Fellowship for the European Programme for Intervention Epidemiology Training and subsequently completed his Public Health specialisation in the UK. He has over one hundred publications in medical peer review journals, mostly focused on the epidemiology of infectious diseases. Dr Ihekweazu is on the board of the NGOs: African Society of Laboratory Medicine, Child Health and Mortality Prevention Surveillance, Public Health Foundation of Nigeria, Health Watch Foundation, Society for Family Health, Education as a Vaccine, and the Africa Policy Advisory Board of ONE. He was a TED Fellow and co-founded and delivered the TEDxEuston event from 2009 to 2019.

Jet (Henriette) de Valk

France

Head of Unit, Foodborne, Vectorborne and Zoonotic Infections Unit
Santé Publique France

Jet (Henriette) de Valk is a medical doctor and infectious diseases epidemiologist at the French National Public Health Agency (Santé Publique France). As the head of the Foodborne, Vectorborne and Zoonotic Infections Unit she is in charge of surveillance, outbreak investigations and applied research. She is actively involved in European networking activities for surveillance of infectious diseases, as a national representative in supranational surveillance networks, as a member of the coordination group of the Vectorborne and Emerging Diseases network of the European Centre for Disease Prevention and Control (ECDC) and as supervisor in the European Programme for Intervention Epidemiology Training. She recently worked on guidelines for surveillance of emerging arboviruses, on the disease burden of foodborne intestinal infectious diseases and on whole genome sequencing for surveillance. She is serving on the national committee nominating the National Reference Centres (laboratories) for infectious agents in France and in Belgium. Jet graduated from the University of Leyden in the Netherlands, the London school of Hygiene and Tropical Medicine in the United Kingdom and the Institut for Tropical Medicine in Antwerp, Belgium and is an alumnus of The European Programme for Intervention Epidemiology Training. Prior to coming to the Santé Publique France she worked for the NGO Médecins Sans Frontières (Doctors Without Borders) in emergency relief programmes in Sudan, Uganda and Mali, for the German Technical Cooperation (GTZ) in Cameroon and for the World Health Organization in Indonesia at the control programmes for diarrhoeal and respiratory infections.

Jacobo Mendioroz

Spain

Sub-director General, Surveillance and Response to Public Health Emergencies
Public Health Agency of Catalonia

Jacobo Mendioroz is a medical doctor (M.D.) specialist in Preventive Medicine and Public Health and has a master in Public Health from Pompeu Fabra University. In 2020, he was designated by the Catalan government as director of the COVID-19 response unit for the Health Department of Catalonia. Currently he is the Sub-director General of Surveillance and Response to Public Health Emergencies at the Public Health Agency of Catalonia. He started his career as a researcher on the field of epidemiology of congenital diseases for the Carlos III Health Institute (ISCIII) of Madrid. He also worked as field epidemiologist and researcher for the study of tropical diseases in Angola as part of the International Health Program (PROSICS) of the Catalan Health Institute (ICS). For the same institution, he worked at the Health Territorial Management of Central Catalonia as head of Health Data Managing Area and as scientific coordinator of the Research Support Unit for primary health care professionals. As a researcher, he has been studying epidemiology of both transmissible and non-transmissible diseases and, in the last years, medical information systems and delivery of health care. During this time, he reconciled his research interests both with technical support to the health management directions and as an emergency room M.D. both in hospitals and in primary health care centres of Catalonia.

Ágnes Hajdu

Hungary

Senior Adviso, Unit of Infection Control and Hospital Epidemiology
National Center for Public Health and Pharmacy

Ágnes Hajdu is a medical doctor, specialist in preventive medicine and public health, and EPIET alumna. For more than 15 years she has worked in the field of healthcare epidemiology and antimicrobial resistance (AMR). As a senior advisor in the Unit of Infection Control and Hospital Epidemiology at the National Public Health Center in Hungary, she has contributed to the development of national methodological guidances in infection prevention and control (IPC), coordination of surveillance modules of healthcare-associated infections, multidisciplinary investigations of nosocomial outbreaks, policy initiatives on IPC and AMR, and behavioural research on antimicrobial prescribing in primary care. She is a member of the Hungarian National Infection Control and Antibiotic Committee. She has a longstanding collaboration with the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization's Regional Office for Europe (WHO/Europe) through various national functions.

Plenary speakers

Plenary A: Broadening the horizon: Revisiting the concept of 'prevention' for communicable diseases

Emilie Karafillakis

Belgium

European research lead, Vaccine Confidence Project, University of Antwerp

Emilie Karafillakis is the European research lead at the Vaccine Confidence Project, based at the Vaccine and Infectious Disease Institute (VAXINFECTIO) of the University of Antwerp in Belgium and at the London School of Hygiene & Tropical Medicine. With a background in public health, infectious disease control, and health systems and policies research, she has around 10 years of experience researching vaccine and health intervention confidence. As a social scientist, her work focuses on understanding individual and group beliefs, attitudes and confidence in health interventions and assess how these can influence public health control measures and health promotion strategies, including vaccination.
She holds a Master of Science in the Control of Infectious Diseases and a PhD on vaccine confidence from LSHTM.

Hanna Tolonen

Finland

Research Programme Director, Finnish Institute for Health and Welfare

Hanna Tolonen is the current Research, Development and Innovation Director at the Finnish Institute for Health and Welfare, where she is responsible for the RDI programme on population health and welfare monitoring and foresight. She is also an adjunct professor at the University of Eastern Finland. She has served as the vice-president of the European Public Health Association (EUPHA) section on Public Health Monitoring and Reporting since 2021. Her areas of expertise include the collection of population-based health information through health examination surveys, the evaluation of the impact of survey non-response, and enhancing the accessibility of health information for research both on a national and international level. She holds a master's degree in statistics and a PhD in public health and epidemiology.

Kateřina Šédová

Czech Republic

Physician, CEO, Loono, Faculty Hospital Bukova

Katerina graduated from the First Faculty of Medicine at Charles University in Prague. During her studies, she spent a semester at Harvard Medical School. In 2014, after her own cancer experience, she founded the NGO Loono, with the mission of saving millions of lives. Loono raises health literacy in NCDs and participates in policy-making regarding prevention and health. Thanks to her contribution to the field of prevention, she was listed in 30 under 30 by Forbes Magazine, received the EU Commission Health Award for Cancer Prevention Campaign and the Czechs of The Year 2016 Prize. In 2020 she was one of the most active members of the Smart Quarantine project, which created the entire ecosystem for monitoring people who have tested positive for COVID-19. In 2021, Ernst and Young named her The Social Entrepreneur of the Year. In 2022 she founded the Cancer Care Coordinators Project at Faculty Hospital Bulovka (the first ever in Czechia). She currently works as an internal medicine resident with the intention to specialise in preventive healthcare later in her career. Katerina is passionate about projects with a positive impact on society, which is a board member of other non-profits and mentors other social leaders a lot.

Plenary B: Digital transformation and Artificial Intelligence

John Brownstein

Canada

Chief Innovation Officer, Professor, Boston Children's Hospital, Harvard Medical School

John Brownstein, PhD is Professor of Biomedical Informatics at Harvard Medical School and is the Chief Innovation Officer of Boston Children’s Hospital. He also directs the Computational Epidemiology Lab and the Innovation and Digital Health Accelerator both at Boston Children’s. He was trained as an epidemiologist at Yale University. Overall, his work aims to have translational impact on the surveillance, control and prevention of disease. He has been at the forefront of the development and application of data mining and citizen science to public health.

In addition to research achievements, this translational impact comes from playing an advisory role to numerous agencies on real-time public health surveillance including HHS, DHS, CDC, IOM, WHO and the White House. He was awarded the Presidential Early Career Award for Scientists and Engineers, the highest honour bestowed by the United States government to outstanding scientists and the Lagrange Prize for international achievements in complexity sciences and an Emmy for his contributions to medical reporting during the covid-19 pandemic.

Dr. Brownstein is also the co-founder of digital health companies Epidemico and Circulation and an ABC Medical News Contributor.

Joanna Goodey

Austria

Head of Unit - Justice, Digital and Migration
European Union Agency for Fundamental Rights

Jo Goodey (PhD) is Head of research for 'Justice, Digital and Migration' at the European Union Agency for Fundamental Rights (FRA). She is responsible for overseeing the Agency's EU-wide research and activities in the field of Artificial Intelligence with respect to fundamental rights, which ranges from work on online content moderation through to the use of remote biometric identifiers. Among other roles, in 2019 she chaired the EU Agencies' Network on Scientific Advice, and in the same period was a member of the European Commission's High Level Expert Group on Artificial Intelligence. Prior to joining FRA, she was a research fellow at the United Nations Office on Drugs and Crime, and in the 1990s held lectureships in criminology and criminal justice at the Universities of Sheffield and Leeds in the UK. In the 1990s-early 2000s she was also a regular study fellow at the Max Planck Institute for the study of Crime, Security and Law in Freiburg. She is the author of an academic textbook on victims of crime, and has published widely in academic journals, as well as several book chapters, on a range of criminological and fundamental rights-related themes.

Plenary C: Wastewater surveillance: A magic bullet or just one piece of the puzzle?

Paul Griffiths

Portugal

Scientific Director, European Monitoring Centre for Drugs and Drug Addiction (EMCDDA)

Paul Griffiths is the current Scientific Director of the European Monitoring Centre for Drugs and Drug Addiction. He has been active in in the drugs field for over 30 years. Prior to 1999, he worked as a researcher and research manager based at the National Addiction Centre in London. From 2000, his activities have focused on the international monitoring of drug use, working first for the United Nations Office on Drugs and Crime, in Vienna, (UNODC).
Paul joined the EMCDDA in 2002, as head of the epidemiology unit and was appointed Scientific Director in 2010. In his current role he is responsible for the overall coordination of the EMCDDA scientific work. He holds an honorary position as a Visiting Senior Lecturer in the Department of Addictions, Institute of Psychiatry, King's College London.

Márta Vargha

Hungary

Head, Water Hygiene Department, National Center for Public Health and Pharmacy

Márta Vargha is a chief counsellor at the National Center for Public Health and Pharmacy, Hungary, responsible for water hygiene.

Her team works on drinking and bathing water quality, covering all aspect from research to regulation. The laboratory developed and operates the national wastewater surveillance programme. Marta is a microbiologist by training, holding a PhD in environmental science.

Her main research interests are emerging risks in water and the prevention of water related disease. She is the head of the WHO Collaborating Centre for Environmental Risk Management and the current chair of the WHO EURO/UNECE Protocol on Water and Health.

She has been member of the Guideline development group for the WHO interim guidance on Environmental surveillance for SARS-COV-2 to complement public health surveillance and the Guidelines for Recreational Water Quality.

Marion Koopmans

Netherlands

Head, Department of Viroscience, Erasmus Medical Centre

Prof Koopmans is director of the Department of Viroscience at Erasmus Medical Centre in the Netherlands, the WHO collaborating centre for Emerging Infectious Diseases, scientific director for Emerging Infectious Diseases of the Netherlands Centre for One Health (NCOH) and scientific director of the Pandemic and Disaster Preparedness Centre in Rotterdam/Delft, the Netherlands.

Her research focuses on emerging infections with special emphasis on unravelling pathways of disease emergence and spread at the human animal interface. Creating global networks to fight infectious diseases systematically and on a large scale is a common thread in Koopmans' work.

She coordinates the EU funded consortium VEO, which develops a risk based innovative early warning surveillance in a One Health context, and is deputy coordinator of a recently awarded HERA funded network of centres of excellence for EID research preparedness. In 2021, Koopmans founded the Pandemic and Disaster Preparedness Centre PDPC, a research centre with a focus on the occurrence and prevention of pandemics and climate-related disasters, combining expertise from technical, bio-medical, environmental and social sciences. During the corona crisis in the Netherlands in 2020, Koopmans was a member of the Outbreak Management Team that advised the national government on measures to stop the spread of SARS-CoV-2.

Plenary D: One Health: Tackling global health challenges together

Greg Martin

Ireland

Director, Health Protection Surveillance Centre
National Health Protection Service

Greg Martin is the Director of the Health Protection Surveillance Centre in Ireland and has a diverse background in global health. He trained as a medical doctor in South Africa, with a specialisation in public health. He has since worked with organisations such as the WHO, UNITAID, and the Clinton Health Access Initiative.

He runs the Global Health YouTube channel with almost 150K subscribers where he discusses threats and opportunities, including pandemic responses, antimicrobial resistance, and the impact of climate change. He is the editor-in-chief of the Globalization and Health journal and is a founding director of Wellola, a company which provides Electronic Health Records software and patient portals.

Karen Saylors

United States

CEO and Co-founder, Labyrinth Global Health

As CEO and Co-Founder of Labyrinth Global Health, Inc., Karen Saylors, PhD, has worked in the international public health field for over a decade and has spent many years living in Africa establishing global surveillance networks, working with partners to improve Global Health policy on infectious disease detection, response, prevention, and control. At Labyrinth, Dr. Saylors specialises in studies that aim to understand and mitigate biological and behavioural risk of disease transmission. After working with Médecins Sans Frontières on neglected tropical disease impact in Cameroon, she has remained focused in Central and West Africa and continues to work with local partners to expand laboratory and surveillance networks throughout the region.

Dr. Saylors has also worked with Oxford University Clinical Trials Network in Vietnam on zoonotic disease surveillance research and continues to coordinate with regional partners in SE Asia on mitigating the impact of emerging outbreaks in animal and human populations at high-risk interfaces, such as live animal markets. As a lead scientist for Labyrinth, Dr. Saylors has an energetic commitment to multilateral research, coordinating international programs through the Company's offices in DRC, Sierra Leone, Ukraine, Turkey, Azerbaijan, Georgia, and the US.

Sandra Gallina

Belgium

Director-General, Health and Food Safety, European Commission

Sandra Gallina joined the European Commission in 1988. She is today Director General for HEALTH & FOOD SAFETY. Before joining DG SANTE, between 2018 and 2020 she was Deputy Director General for TRADE. Between 2014 and 2018 she was Director for DG TRADE Directorate D "Sustainable Development; Economic Partnership Agreements - African, Caribbean and Pacific; Agri-food and Fisheries".

Sandra Gallina was also the EU chief negotiator for the EU-MERCOSUR Free Trade Agreement. Between 2001 and 2009 she was the EU Lead Negotiator for Non-Agricultural Market Access in the WTO Doha Round and in that capacity, she defined and presented EU policy for the Doha Development Agenda on non-agricultural market access negotiations. Before joining DG TRADE, she worked in the Directorate General for Taxation and Customs Union (DG TAXUD) at the end of the 1990s.

Stef Bronzwaer

Italy

Research Coordinator, European Food Safety Agency (EFSA)

Stef Bronzwaer is a medical doctor who currently serves as a Research Coordinator at the European Food Safety Authority (EFSA) in Parma, Italy. His domains of expertise include scientific cooperation and liaison, antimicrobial resistance surveillance, research, communicable diseases and food safety. He has previously worked in the Infectious Disease Unit of the Istituto Superiore di Sanità in Rome, Italy, and in the Department of Infectious Disease Epidemiology of the National Institute for Public Health and the Environment (RIVM) in the Netherlands, where he helped establish the European Antimicrobial Resistance Surveillance System (EARSS). Before he joined EFSA in 2006, he worked at the European Commission in Luxembourg where he held responsibility for the proper functioning and coherence of a number of European surveillance networks on communicable diseases and followed the implementation of the Community strategy against antimicrobial resistance.

Plenary E:
Post-pandemic public health workforce

Lucy Easthope

United Kingdom

Professor in Practice of Risk and Hazard, Durham University

Lucy Easthope is a UK expert and adviser on emergency planning and disaster recovery. She is a Professor in Practice of Risk and Hazard at the University of Durham, and co-founder of the After Disaster Network at the university. She is also Professor in Mass Fatalities and Pandemics at the Centre for Death and Society at the University of Bath, a researcher at the Joint Centre for Disaster Research at Massey University and a member of the UK Cabinet Office National Risk Assessment Behavioural Science Expert Group.

She is the author of *When the Dust Settles: Stories of Love, Loss and Hope from an Expert in Disaster* and *The Recovery Myth: The Plans and Situated Realities of Post-Disaster Response*.

Katarzyna Czabanowska

Netherlands

Professor in Public Health Leadership and Workforce Development
Maastricht University

Prof. Dr. habil. Katarzyna (Kasia) Czabanowska is a professor of Public Health Leadership and Workforce Development and Head of the Department of International Health, Care and Public Health Research Institute (CAPHRI), Maastricht University, the Netherlands, Honorary Member of the UK Faculty of Public Health.

Her research involves leadership development, leadership competencies for public health and health-related disciplines, capacity building in public health, including competency and training needs assessment, design of training programmes, competency-based education and systematic development of competency frameworks for public health and health workforce, public health workforce development and planning including professionalization.

She is a Past President of the Association of the Schools of Public Health in the European Region (ASPHER), and a lead author of the WHO-ASPHER Competency Framework and the Road Map to Professionalizing the Public Health Workforce in the European Region. She is an academic Board Member of the Studio Europa at Maastricht University; visiting professor at the Institute of Public Health Jagiellonian University, Krakow, Poland, and adjunct professor at the Richard Fairbanks School of Public Health, Indiana University, US.

Giorgio Grossi

Sweden

Behavioural Scientist, Psychotherapist, Karolinska Institutet,
The Virtual Stress Clinic

Giorgio Grossi is a behavioural scientist and associate professor in Medical Psychology with a degree from the Department of Psychology of Stockholm University. He has a background as a researcher and conducted his doctoral thesis on stress among the unemployed. In 2000 he began work as a researcher in the Stress Clinic Project at the Institute for Psychosocial Medicine. He trained further as a licensed psychotherapist with a specialty cognitive behavioural therapy (CBT), in Uppsala and at the Karolinska Institutet, where he is also an associate professor. He is the author of several books in Swedish and, presently, he is the director of the newly established Virtual Stress Clinic (Virtuella Stressmottagningen).

Plenary summaries

Plenary A:
Broadening the horizon: Revisiting the concept of ‘prevention’ for communicable diseases

Day 1 - Wednesday 22 November, 9:15-10:45

This session aims to reflect on the scope of the concept of ‘prevention’ and its complexities, as well as how it relates to preparedness. The audience will hear from a diverse panel of experts about the challenges, potentials and lessons learned from different disease areas – including non-communicable diseases – and the application and relevance of social and behavioural sciences in communicable disease prevention. The session will also explore the role of Public Health professionals in defining and addressing diverse prevention needs in different population groups, as well as the role of community engagement in communicable disease prevention.

Chairs: Petronille Bogaert (European Commission) and John Kinsman (ECDC)
Speakers: Kateřina Šédová (Loono, Czech Republic), Emilie Karafillakis (University of Antwerp, Belgium), Hanna Tolonen (THL, Finland)

Plenary B:
Digital transformation and Artificial Intelligence

Day 1 - Wednesday 22 November, 17:00-18:15

Keynote session
The rise in popularity of Artificial Intelligence presents many opportunities and challenges for communicable disease surveillance and preparedness. In this session the audience will hear about the risks and benefits of digital health technologies, and what this digital transformation entails for the Public Health workforce and their work in accessing scientific information, assessing situations and making decisions.

Chairs: Chikwe Ihekweazu (WHO) and Mike Catchpole (ECDC)
Keynote speaker: John Brownstein (Harvard Medical School, Boston Children's Hospital, USA), Joanna Goodey (European Union Agency for Fundamental Rights)

Plenary C:
Wastewater surveillance: a magic bullet or just one piece of the puzzle?

Day 2 - Thursday 23 November, 9:00-10:30

Wastewater surveillance is a promising approach to gathering information about the health of a population, and has gained attention during the COVID-19 pandemic as a potential tool for public health decision-making. This session will explore the potential benefits and limitations of wastewater surveillance, along with the lessons learned from recent experiences for different agents and populations. Experts will discuss wastewater surveillance as one piece of the puzzle, its feasibility and its possible contributions to for future surveillance of a broader range of biological markers in different settings.

Chairs: Jacobo Mendioroz (Public Health Agency of Catalonia) and Henriette de Valk (Santé Publique France)
Speakers: Marta Vargha (National Center for Public Health and Pharmacy, Hungary), Marion Koopmans (Erasmus MC Department of Viroscience, the Netherlands), Paul Griffiths (EMCDDA)

Plenary D:
One Health: Tackling global health challenges together

Day 2 - Thursday 23 November, 16:45-18:15

One Health collaboration is widely supported and invested in to tackle global health challenges affecting humans, animals, plants and the environment. However, implementation of One Health approaches is still not commonplace in many countries given the lack of tradition, collaboration mechanisms, resources or awareness. The session aims to review current achievements and possible future directions and priorities of One Health initiatives and actions, with an emphasis on international collaboration and antimicrobial resistance.

Chairs: Mircea Ioan Popa (Carol Davila University of Medicine and Pharmacy, Romania), Carmen Varela Santos (ECDC) and Agnes Hajdu (National Center for Public Health and Pharmacy, Hungary)
Speakers: Greg Martin (Health Protection Surveillance Centre, Ireland), Karen Saylors (Labyrinth Global Health, USA), Stef Bronzwaer (EFSA), Sandra Gallina (European Commission)

Plenary E:
Post-pandemic Public Health workforce

Day 3 - Friday 24 November, 9:00-10:30

The COVID-19 pandemic has had a profound impact on the Public Health workforce and their work environment, leaving many professionals overwhelmed and fatigued. How can we address the post-disaster recovery, learn from our experiences and set new priorities to ensure an effective and healthy Public Health workforce? The panel of experts will examine the way forward for Public Health professionals in the post-pandemic reality through a lens of disaster recovery, defining the leadership and skills-mix needed to face the ongoing and future changes. They will discuss how individuals and organisations can address work-life balance and mental wellbeing in rapidly changing environments.

Chairs: Stine Nielsen (EPIET Alumni Network) and Adam Roth (ECDC)
Speakers: Lucy Easthope (Durham University, UK), Katarzyna Czabanowska (Maastricht University, the Netherlands), Giorgio Grossi (Karolinska Institutet, Sweden)

Abstract presentations

This year, we received a remarkable number of nearly 900 abstract submissions, encompassing both standard call and late breaker abstracts. Out of these, around 260 were selected for inclusion in the program, spanning a wide array of topics in applied infectious disease research and epidemiology, thereby enhancing the diversity and richness of the conference content. These accepted abstracts have been allocated to poster sessions and oral presentations, ensuring a comprehensive distribution across different conference themes.

This abstract book has been produced using author's supplied copy. The information provided in each abstract is the responsibility of the author(s).

Oral presentations – fireside sessions

A fireside session is a moderated Q&A where the presenters are given the opportunity to discuss their work and answer questions from the audience.

During the session, each presenter has 15 minutes to discuss their work, which includes a short presentation by the speaker (~7 min), a moderator-led discussion (~5 min) and questions from the audience (~2 min).

Poster presentations – poster tours

Poster tours provide a platform to highlight recent research and developments across various fields. These sessions foster networking and potential collaborations between researchers, organisations, and interested attendees. Given the limited time, the primary objective is to facilitate initial connections, encouraging follow-up discussions and deeper engagement with the authors post-session.

During a poster tour session, each presenter has 7 minutes to discuss their work, which includes a short presentation by the speaker (~2 min), a moderator-led discussion with the audience (~5 min).

Online-only posters

Online-only posters will be displayed in the virtual poster exhibition on the online conference platform, and the abstracts will be listed in the abstract book. However, due to time and venue capacity limitations, there will not be the opportunity to give a verbal presentation of the poster, but participants are encouraged to view the posters online and can post comments and questions for authors to respond to.

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Abstract reviewers

The Scientific Committee warmly thanks the reviewers of the abstracts submitted for ESCAIDE 2023.

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Bulgaria
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Hungary
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Antonietta Filia
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Netherlands
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Poland
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Romania
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Sweden
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Zimbabwe
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ECDC
Adam Roth
Aikaterini Mougkou
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Fireside sessions

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

Tracking dynamics of SARS-CoV-2 variants in Catalonia (Spain) through wastewater surveillance

A. Carcereny Sánchez [1]
D. Garcia-Pedemonte [2], M. Costafreda [3], C. Fuentes [4], A. Bosch [5], S. Guix [6], R. Pintó [7]

[1] Institute of Nutrition and Food Safety (INSA) | Enteric Virus Laboratory, University of Barcelona (UB)
[2, 3, 4, 5, 6, 7] Enteric Virus Laboratory, University of Barcelona (UB) | Institute of Nutrition and Food Safety (INSA)

BACKGROUND

Since the early beginning of the SARS-CoV-2 pandemic, wastewater-based epidemiology has proven to be a useful complementary tool to clinical surveillance. In wastewater, both the amount of circulating virus and the occurrence of variants can be monitored using PCR and NGS techniques. Our study aimed at tracking the dynamics of SARS-CoV-2 variants at the population level through wastewater analysis, to identify factors that may be related with the dominance of a given variant over a previous one.

METHODS

Variants from Alpha to Omicron BA.5, were weekly monitored using duplex RT-qPCR assays targeting signature indels of each variant. NGS was performed monthly to validate the RT-qPCR results and, especially from Omicron BA.1 onwards, to estimate proportions of different circulating sublineages. The ability of each emerging variant to replace the previously dominant one was estimated by calculating its outcompetition rate (OR) using duplex RT-qPCR data. The variant entry ratio (ER), the diversity of the receptor variant swarms (Shannon entropy, SE), and the herd immunity were also estimated.

RESULTS

Significant differences were found between the OR of the different variants, being Delta and Omicron BA.1 the fastest ones. A multi-correlation study was performed between the OR, the variant ER, the SE, and the herd immunity. The OR showed significant positive correlations with the variant ER and herd immunity, and negative correlation with the SE. The variant ER negatively correlated with the SE and herd immunity, while these two latter parameters showed a strong positive correlation.

CONCLUSIONS

Overall, wastewater surveillance not only enables to monitor SARS-CoV-2 evolution in the population, but also allows for a deeper analysis of different factors that may play a key role in virus behaviour.

Keywords: SARS-CoV-2, Wastewater-based Epidemiological Monitoring, Population Dynamics, Outcompetition Rate
ABSTRACT ID: 289
PRESENTED BY: Albert Carcereny Sánchez, Spain / acarcereny@ub.edu

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

A Qualitative Study to Investigate National Perspectives and Needs for Cross-border Contact Tracing in Europe

O. Lewis [1]
T. Cesuroglu [2], A. van der Meer [3], R. Baron [4], I. Mogami [5], J. Hansen [6], M. Kirwan [7], C. Swaan [8], M. Stein [9]

[1] The Dutch National Institute for Public Health and the Environment (RIVM) | Vrije Universiteit (VU) Amsterdam
[2, 3, 8, 9] The Dutch National Institute for Public Health and the Environment (RIVM)
[4, 5, 6] Netherlands Institute for Health Services Research (NIVEL)
[7] The Royal College of Surgeons in Ireland (RSCI)

BACKGROUND
The COVID-19 pandemic required countries to conduct high volumes of cross-border contact tracing (CT). This study investigated countries' perspectives on national and international level barriers or facilitators that can be used to enhance (future) cross-border CT in Europe.

METHODS
Semi-structured interviews were conducted online with nine EU/EEA countries and two non-EU/EEA countries, exploring COVID-19 experiences, subsequent developments and future plans for national and international cross-border CT systems, practices, digital tools, governance, and legislation. To validate findings and further explore the barriers and facilitators to implementation, two webinars were conducted with participants from EU/EEA countries. Data analysis involved open coding and thematic analysis.

RESULTS
During peak times of COVID-19, most interviewed countries experienced: a lack of internationally standardised definitions of CT data, a lack of knowledge regarding other EU/EEA countries' CT definitions, practices and needs, a lack of standardised practice for collecting CT data from airlines, a lack of national and international CT digitalisation and a lack of standardised use of existing EU digital tools for collecting and sharing CT data; all impacting timeliness and efficiency of cross-border CT. The webinars confirmed standardisation, digitalisation and coordination as major issues and revealed additional considerations and suggestions, such as to improve evidence regarding the effectiveness of CT that can support more coordinated and standardised CT across borders.

CONCLUSIONS
There is a need for: more in-depth and standardised cross-border CT guidance and definitions for EU/EEA countries, improved digitalisation of CT, standardised protocols, practices and/or systems for obtaining passenger data from airlines, structuring and coordinated use of EU digital CT tools, evidence in support of the effectiveness of cross-border CT and lastly opportunities for EU/EEA countries to share CT knowledge and practices.

Keywords: Contact tracing, Cross-border, COVID-19, Digital technologies for contact tracing, Governance of contact tracing, Pandemic preparedness
ABSTRACT ID: 685

PRESENTED BY: Olivia Lewis, Netherlands / Lewis.oliviac@gmail.com

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

Combining human health, food, weather, and land-use data in the investigation of a Shiga-toxin producing E. coli (STEC) O157 outbreak in the UK; a potential novel One Health surveillance approach

N. Cuningham [1]
B. Eggen [2], R. Close [3], S. Williams [4], C. Gathumbi [5], A. Hoban [6], C. Stocker [7], A. Douglas [8], T. Potter [9], J. Wild [10], S. Balasegaram [11], G. Leonardi [12], L. Larkin [13], C. Jenkins [14], S. Hopkins [15]
[1, 2, 3, 4, 6, 8, 11, 12, 13, 14, 15] UK Health Security Agency
[5, 7, 9, 10] Food Standards Agency

BACKGROUND
In late August and September 2022, a substantial increase in the number of presumptive Shiga-toxin producing E. coli (STEC) O157 laboratory referrals to the reference laboratory of the UK Health Security Agency (UKHSA) was observed. A national level investigation was initiated, and a multi-disciplinary Incident Management Team (IMT) was established to investigate the cause of the increase, including if weather could have played a role.

METHODS
Whole genome sequencing was used to identify outbreak cases of STEC 0157. Food exposure information and a food chain investigation was used to identify the likely outbreak source. Analysis of weather and rainfall data identified likely candidate weather events that may have led to amplification contamination by a foodborne pathogen. Land use data was analysed to identify areas of land used to grow vegetables and salad for human consumption.

RESULTS
259 confirmed (STEC) O157 t5.5294 cases reported throughout the UK, in all regions in England and across all four countries. The majority of cases interviewed highlighted consuming salad products at food service establishments. One particular grower was directly or indirectly linked to all other growers, and consequently, linked to the food service establishments. Weather and land use data revealed two isolated and unusual heavy precipitation events at the location of the grower of interest in an otherwise drought-like situation, corroborated by land-use data indicating an area of land used to grow salad for human consumption.

CONCLUSIONS
Climate and weather effects could have far reaching implications for food safety through pathogen amplification and we propose that a combination of weather data and land-use data could in some circumstances form the basis of a OneHealth early warning surveillance system for foodborne pathogen outbreaks.

Keywords: One Health, Climate Change, Surveillance, Weather, STEC, E Coli, Food safety, Foodborne
ABSTRACT ID: 415
PRESENTED BY: Neil Cunningham, United Kingdom / neilcunningham001@gmail.com

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

National weekly epidemiological teleconferences – a successful tool for early warning and public health service communication within the COVID-19 crisis

N. Zeitlmann [1]
C. Siffczyk [2], R. Biallas [3], I. Muecke [4], U. Rexroth [5], M. an der Heiden [6], (GROUP) EpiLag Working Group
[1, 2, 3, 4, 5, 6] Robert Koch Institute, Berlin

BACKGROUND
EpiLag (established 2019) is a weekly telephone conference between the Robert Koch Institute (RKI) and the 16 German federal state health authorities. It aims to inform on and discuss current infectious disease events (international, national, subnational) and related other topics. EpiLag has voluntary participation and reporting of topics and constitutes a useful, highly-appreciated communication tool inside the public health service (PHS) (past evaluations). We analysed EpiLag's performance during COVID-19.

METHODS
We extracted data from EpiLag monitoring databases (Excel) from 01/01/2020 to 31/12/2022 and performed descriptive analysis on participation and frequency of selected COVID-19-related topics (outbreaks, surveillance) while highlighting different periods of the pandemic.

RESULTS
From 2020-2022, 153 EpiLag conferences were held with an average weekly participation of 97%. Between 09/04/2020 and 28/05/2020 (first COVID-19 wave) EpiLag's frequency was increased to twice a week. COVID-19 was first reported in EpiLag on 07.01.2023 as an international event in China and EpiLag sent out first guidance documents (case definitions, contact tracing) for the PHS two weeks later. Before the first wave occurred in Germany, EpiLag had already discussed 8 reports on small (suspected) COVID-19 outbreaks from subnational levels (2020-2022: 207 reports). However, during the crisis that followed, COVID-19-related surveillance became the most frequent discussion topic each week (2020-2022: 305 reports).

CONCLUSIONS
Before the first COVID-19 wave started in Germany, EpiLag provided epidemic intelligence and fulfilled early warning/preparedness functions for the PHS. Later, inside the crisis management, EpiLag was essential to maintain regular time-efficient exchange on topics and challenges most relevant to the subnational PHS. Also, the frequency could be adapted flexibly to its participants' needs. We highly recommend other countries (or sectors) to implement routine tools like EpiLag inside their PHS.

Keywords: Epidemic intelligence, Early warning, Event-based surveillance, Preparedness, Communication tool, Pandemic
ABSTRACT ID: 794
PRESENTED BY: Nadine Zeitlmann, Germany / zeitlmannn@rki.de

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

Whole Genome Sequencing supports epidemiological investigation of community-based Clostridioides difficile clusters

I. Mohammed [1]
A. Plimmer [2], M. Morgan [3], C. McKerr [4], M. Perry [5], T. Morris [6]
[1, 2, 3, 4, 5, 6] Public Health Wales

BACKGROUND
Clostridioides difficile causes significant morbidity and mortality worldwide. Spore production facilitates environmental persistence and gut carriage variable incubation periods, making transmission events difficult to ascertain. Cases are often diagnosed in healthcare settings and apportioned as hospital-acquired, but C. difficile is increasingly recognised as causing diarrhoea in the community. C. difficile isolates are routinely tested by the Anaerobe Reference Unit using whole-genome sequencing (WGS). We evaluate the use of WGS in supporting community-based cluster investigations.

METHODS
We defined genetic clusters as >2 persons with toxin positive or negative C. difficile isolates, with a genome difference of <2 single nucleotide polymorphisms (SNPs). We extracted hospital admissions and residential addresses for patients in genetic clusters between Jun 2020-May 2022, to determine epidemiological links and likely transmission event locations (hospital/community). Where we identified epidemiological links, we notified infection prevention and control (IPC teams).

RESULTS
We identified four community-based clusters with genetic and epidemiological links. Cases per cluster ranged from two to six and were geographically close or linked by family contact. Two clusters were in community care facilities, with approximately one-year time lag between first and last known case. Investigations suggest transmission occurred indirectly via the environment or due to breaches in IPC practices. Control measures were implemented by IPC teams for care home clusters.

CONCLUSIONS
WGS supports epidemiological surveillance of community-based C. difficile clusters, including identifying clusters unlikely to be found using traditional epidemiological methods. Our findings demonstrate the invaluable insights into community transmission that can be obtained from routine integration of genomic and epidemiological data.

Keywords: Clostridioides difficile, Genomics, Epidemiologic Methods, Diarrhea
ABSTRACT ID: 468
PRESENTED BY: Israa Mohammed, United Kingdom / israa.Mohammed@wales.nhs.uk

FIRESIDE SESSION 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Gianfranco Spiteri

Abstract

Sampling schedules for children and characterising non-travel cases of typhoid and paratyphoid: Evidence for action

A. Vusirikala [1]
K. Grineviciute [2], R. Manuel [3], S. Balasegaram [4]

[1] UK FETP Fellow UK Health Security Agency
[2, 3, 4] UK Health Security Agency Health Protection Operations

BACKGROUND
Children with enteric fever aged <6 years are considered high risk for secondary transmission. Current English guidance recommends three consecutive negative clearance samples 48 hours apart (previously a week apart), before return to school/childcare, and one screening sample for contacts. Microbiological follow-up is labour intensive for public health teams and disruptive to families and children's education. We audited compliance of clearance schedule and sample positivity to assess whether sampling could be reduced, to inform revision of guidelines.

METHODS
We extracted case clearance and contact data for confirmed cases aged <6 years attending childcare settings in England between 2017-2022, from the public health case management system. Compliance was the proportion of cases submitting at least 3 samples.

RESULTS
We identified 124 confirmed enteric fever cases aged <6 years; 82 (66%) had clearance information. 75/82 cases submitted at least 3 eligible stool samples (91% compliance). 18/75 (24%) cases had at least one of their first three samples positive, of which 5 cases (7% overall) tested positive following two negative clearance samples. 13/75 (17%) cases required > five samples to achieve the clearance criteria. 27/130 contacts screened (21%) had positive samples.

CONCLUSIONS
High compliance and 75% of cases achieving clearance after three samples supports the current schedule with a 48-hour interval. We recommend keeping three samples as reducing screening could mean 7% of cases return whilst potentially infectious. We suggest emphasising to families possible delayed return to education for almost quarter of cases. Contact screening as per guidance should continue, given the yield. One third of cases had missing data; efforts are required to improve systematic recording of clearance and screening information to enable accurate evaluation of guidance.

Keywords: Clearance, Enteric fever, Children, Return to school
ABSTRACT ID: 272

PRESENTED BY: Amoolya Vusirikala, United Kingdom / amoolyav@gmail.com

FIRESIDE SESSION 2
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

COVID-19 Vaccination: Assessing effectiveness

MODERATOR
Marta Valenciano

Abstract

Effectiveness and durability of a fourth COVID-19 vaccine dose against severe outcomes among older individuals in Norway: A population-based cohort study

M. Stecher [1]
A. Kristoffersen [2], K. Li [3], S. Andersen [4], H. Meijerink [5], J. Starrfelt [6]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Department of Infection Control and Vaccines, Norwegian Institute of Public Health, EPIET
[2] Department of Method Development and Analytics, Norwegian Institute of Public Health
[3, 4, 5] Department of Infection Control and Vaccines, Norwegian Institute of Public Health
[6] Department of Infection Control and Preparedness, Norwegian Institute of Public Health

BACKGROUND
The effectiveness of the monovalent coronavirus disease 2019 (COVID-19) vaccines is weakening during the predominant Omicron period. Therefore, the new bivalent vaccines become recently available. Our objective was to assess the effectiveness of a fourth dose (monovalent or bivalent vaccine) compared to a third dose among older individuals.

METHODS
We conducted a population-based cohort study in Norway from 01/07/2022 to 15/01/2023, including individuals ≥75 years of age. Cox-proportional hazard models were used to estimate vaccine effectiveness on severe COVID-19 related outcomes (hospitalization, intensive care unit admission, death) and all-cause mortality. We compared fourth-dose recipients with either a monovalent or bivalent vaccine (Wuhan/BA.1 or Wuhan/BA.4-5), to individuals who received the third-dose >24 weeks ago. Vaccine status was included as a time-varying covariate and models were adjusted for age, sex, region of residence, COVID-19 severity risk group, and long-term care facility residence status.

RESULTS
A total of 408,073 individuals were included. We identified an additional protective effect against COVID-19 associated mortality, with estimates for the bivalent Wuhan/BA.1 vaccine (adjusted hazard ratio (aHR)=0.08, 95% CI=0.02-0.32) relative to the bivalent Wuhan/BA.4-5 (aHR=0.27, 95% CI=0.14-0.56) and a monovalent dose (aHR=0.34, 95% CI=0.26-0.45) 2-9 weeks after vaccination. The increased protective effect waned after 17 weeks with no added protection compared to a third dose after 33 weeks. We observed similar patterns for all-cause mortality and for other severe COVID-19 outcomes.

CONCLUSIONS
The waning protective effect of a fourth dose suggests that the timely administration of the fifth dose is important to maintain protection against severe COVID-19. Therefore, public health authorities should consider recommending a fifth dose for individuals aged 75 years and older if more than six months have passed since the fourth dose.

Keywords: SARS-CoV-2, Omicron, Real-world evidence, Mortality, Bivalent vaccine, Monovalent vaccine
ABSTRACT ID: 201
PRESENTED BY: Melanie Stecher, Norway / melanie.stecher@fhi.no

FIRESIDE SESSION 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

COVID-19 Vaccination: Assessing effectiveness

MODERATOR
Marta Valenciano

Abstract

Effectiveness of COVID-19 vaccine boosters in individuals ≥80 years by number of doses and time since the booster using electronic health registries, VEBIS multi-country study, June 2022-January 2023

M. Fontán-Vela [1]
A. Santís [2], I. Kislaya [3], B. Nunes [4], H. Emborg [5], K. Nielsen [6], C. Hansen [7], I. Martínez-Baz [8], J. Castilla [9], T. Braeye [10], I. Van Evercooren [11], H. Meijerink [12], J. Starrfelt [13], S. Bacci [14], N. Nicolay [15], A. Nardone [16], S. Monge [17]

[1] Centro Nacional de Epidemiología (Instituto de Salud Carlos III)
[2, 16] Epidemiology Department, EpiConcept, París, France
[3, 4] Instituto Nacional de Saúde Doutor Ricardo Jorge (INSA), Lisbon, Portugal
[5, 6, 7] Statens Serum Institut (SSI), Copenhagen, Denmark
[8, 9] Instituto de Salud Pública y Laboral de Navarra (ISPLN), Pamplona, Navarre, Spain
[10, 11] Epidemiology of infectious diseases, Sciensano, Brussels, Belgium
[12, 13] Norwegian Institute of Public Health (NIPH), Oslo, Norway
[14, 15] Vaccine preventable diseases and Immunisation, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[17] Instituto de Salud Carlos III (ISCIII), Madrid, Spain | CIBER on Infectious Diseases

BACKGROUND
COVID-19 vaccination campaigns currently target vulnerable groups. An ECDC-funded multi-country study aimed to estimate monthly COVID-19 vaccine effectiveness (CVE) of booster doses against hospitalisation due to COVID-19 in individuals ≥80-years-old using electronic health registries (EHR) from Belgium, Denmark, Spain (Navarre), Norway and Portugal between June 2022 - January 2023.

METHODS
Using linked EHR and a common protocol, each country selected community-dwelling residents aged ≥80-years-old and estimated each month CVE for an 8-week-observation-period. Cox regression was used to estimate CVE [(1-hazard ratio)*100] for first, second and third booster adjusted for age, sex, region, comorbidities and socioeconomic status, overall and by time since the booster (<12, 12-24, >24-weeks). We pooled country-specific CVE using random-effects meta-analysis.

RESULTS
The study population included 28-32 million people depending on the month. Over the study period, pooled CVE of first booster >24-weeks (vs primary vaccination) varied between 28%-42%. CVE of second booster (vs primary vaccination) administered <12-weeks fluctuated between 60%-79%, and between 30-67% after 12-24-weeks. No second-booster effect was observed >24-weeks. CVE of third booster (vs primary vaccination) administered <12-weeks decreased from 71% to 53% between October-November22 and December22-January23, and it was 41% when administered between 12-24-weeks (in December22-January23). The overall effect of each additional dose was 34%-62% for the second booster (vs. first booster) and 13%-54% for the third booster (vs. second booster).

CONCLUSIONS
Our results support the recommendation to administer periodic boosters to maintain adequate protection against hospitalisation due to COVID-19 in ≥80-year-olds. This EHR-based multi-country approach provide timely and robust CVE estimates for decision-making purpose at EU-level. Part of the CVE fluctuation may be attributed to diverse vaccination schedule rollout across participating countries.

Keywords: COVID-19, Vaccine effectiveness, Booster doses, Electronic health records, Hospitalisation, Multicentre study
ABSTRACT ID: 264
PRESENTED BY: Mario Fontán-Vela, Spain / mario.fontan@isciii.es

FIRESIDE SESSION 2
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

COVID-19 Vaccination: Assessing effectiveness

MODERATOR
Marta Valenciano

Abstract

Effectiveness of mRNA bivalent vaccines against symptomatic SARS-CoV-2 infection at primary care level in the EU/EEA (VEBIS, September 2022–March 2023

C. Lanièce Delaunay [1]

C. Mazagatos [2], G. Túri [3], F. Dijkstra [4], V. Gómez [5], L. Goerlitz [6], L. Domegan [7], N. Sève [8], M. Ilic [9], I. Martinez-Baz [10], M. Lazar [11], A. Carnahan [12], M. Maurel [13], A. Melo [14], G. Pérez-Gimeno [15], B. Oroszi [16], A. Meijer [17], N. Verdasca [18], R. Dürrwald [19], J. O'Donnell [20], V. Enouf [21], S. Kurecic Filipovic [22], C. Trobajo-Sanmartín [23], O. Timnea [24], N. Latorre-Margalef [25], S. Bacci [26], M. Kaczmarek [27], E. Kissling [28], (GROUP) European primary care vaccine effectiveness group

[1] Epiconcept, Paris, France
[2, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25] National Centre of Epidemiology, CIBERESP, Carlos III Health Institute, Madrid, Spain
[3] National Laboratory for Health Security, Epidemiology and Surveillance Centre, Semmelweis University, Budapest, Hungary
[4] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[5] Instituto Nacional de Saúde Dr. Ricardo Jorge, Lisbon, Portugal
[6] Robert Koch Institut, Berlin, Germany
[7] Health Service Executive-Health Protection Surveillance Centre, Dublin, Ireland
[8] INSERM, Sorbonne Université, Institut Pierre Louis d'épidémiologie et de Santé Publique (IPLESP UMRS 1136), Paris, France
[9] Croatian Institute of Public Health (CIPH), Zagreb, Croatia
[10] Instituto de Salud Pública de Navarra – IdiSNA – CIBERESP, Pamplona, Spain
[11] Cantacuzino National Military Medical Institute for Research and Development, Bucharest, Romania
[12] The Public Health Agency of Sweden, Stockholm, Sweden
[13, 28] Epiconcept, Paris, France
[21] CNR des virus des infections respiratoires, WHO National Influenza Centre, Institut Pasteur, Paris, France
[26, 27] European Centre for Disease Prevention and Control, Stockholm, Sweden

BACKGROUND

In September 2022, the European Medicines Agency authorised COVID-19 mRNA bivalent vaccines. We conducted a multicentre test-negative study at primary care level in 10 European countries (VEBIS) to estimate bivalent vaccine effectiveness (VE) against symptomatic SARS-CoV-2 infection caused by Omicron variants during September 2022–March 2023.

METHODS

Cases were SARS-CoV-2 RT-PCR positive and controls were negative patients presenting to primary care with an acute respiratory infection. We estimated first and second booster VE in age-specific target groups for vaccination, using logistic regression adjusting for site, age, sex, chronic conditions and onset date. We measured VE by time since last vaccination and age group, using unvaccinated as the reference group.

RESULTS

We included 275 cases and 1,682 controls in first booster analyses (age ≥18 years), and 353 cases and 2,498 controls in second booster analyses (age ≥50 years). First booster VE was 36% (95% confidence interval [95%CI]: -6–64%) overall; 36% (95%CI: -32–73%) and 41% (95%CI: -24–74%) for ages <50 and ≥50 years, respectively. For those with onset <3 months and ≥3 months after booster dose, VE was 54% (95%CI: 11–79%) and -7% (95%CI: -118–53%), respectively. Second booster VE among those aged ≥50 years was 22% (95%CI: -14–46%) overall; 26% (95%CI: -13–51%) and 0% (95%CI: -73%–41%) <3 months and ≥3 months after vaccination, respectively.

CONCLUSIONS

Our results suggest moderate protection of bivalent mRNA boosters against symptomatic infection with Omicron variants at primary care level within three months post-vaccination. Results should be interpreted with caution due to the limited sample size. Further research is needed to explore VE of bivalent mRNA boosters including during periods of recombinant Omicron variant circulation.

Keywords: COVID-19, SARS-CoV-2, Vaccines, Primary Health Care
ABSTRACT ID: 316
PRESENTED BY: Charlotte Lanièce Delaunay, France / c.laniece@epiconcept.fr

FIRESIDE SESSION 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

COVID-19 Vaccination: Assessing effectiveness

MODERATOR
Marta Valenciano

Abstract

Bivalent mRNA booster vaccine effectiveness against COVID-19 hospitalizations and deaths in Portugal using an electronic health records cohort, September 2022 to February 2023.

A. Machado [1]
I. Kislay [2], S. Magalhães [3], A. Rodrigues [4], R. Franco [5], P. Pinto Leite [6], C. Matias Dias [7], B. Nunes [8]

[1] Instituto Nacional de Saude Doutor Ricardo Jorge
[2] Instituto Nacional de Saude Doutor Ricardo Jorge | Bernhard Nocht Institute for Tropical Medicine
[3, 5] Serviços Partilhados do Ministério da Saúde
[4, 7, 8] Instituto Nacional de Saude Doutor Ricardo Jorge
[6] Direção Geral da Saúde

BACKGROUND
In Portugal, bivalent COVID-19 vaccine booster was recommended for those with primary COVID-19 vaccination, starting on September 2022. This study aims to estimate the mRNA bivalent vaccine effectiveness (VE) against COVID-19 hospitalization and death on the Portuguese population aged 65 and more years.

METHODS
A population-based cohort of those eligible for COVID-19 bivalent booster was established using a deterministic data linkage of electronics health records and followed-up from September 2022 to February 2023. The outcomes included hospitalization with COVID-19 as primary diagnosis and a COVID-19-related death defined as all-cause death with a positive RT-PCR test within the previous 30 days. Individuals were considered vaccinated 14 days following a bivalent mRNA COVID-19 vaccine uptake. COVID-19 bivalent VE was estimated as one minus the confounder adjusted hazard ratio of bivalent vaccine vs. no bivalent vaccine, for each outcome, estimated by time-dependent Cox regression with time dependent vaccine exposure.

RESULTS
In the ≥80 year-olds, bivalent VE was 54.4% (95%CI: 47.0 to 60.7) and 62.6% (95%CI: 57.6 to 67.0), against COVID-19-related hospitalisation and death, respectively. In the 65-79 year-old, bivalent VE was 70.4% (95%CI: 63.6 to 76.0) against hospitalisation and 76.5% (95%CI: 71.4 to 80.7) against death.

CONCLUSIONS
In a population with a high risk of SARS-CoV-2 complications, we observed moderate to high bivalent VE estimates against severe COVID-19. The lower VE observed in the ≥80 year-olds should be interpreted in light of the reference group used for the estimation, i.e., individuals with high vaccine coverage (both primary series and recent boosters. Further analysis will be developed considering different reference groups and time since last booster. Finally, continuous evaluation of bivalent VE over time will be conducted to evaluate potential effectiveness decay.

Keywords: COVID-19, Vaccine effectiveness, Bivalent vaccine, Hospitalizations, Death
ABSTRACT ID: 768
PRESENTED BY: Ausenda Machado, Portugal / ausenda.machado@insa.min-saude.pt

FIRESIDE SESSION 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
11:15-12:45

COVID-19 Vaccination: Assessing effectiveness

MODERATOR
Marta Valenciano

Abstract

Effectiveness of second BNT162b2 mRNA booster doses in protecting against SARS-CoV-2 infection during the Omicron sub-variant waves; the UK SIREN study June 2022 to March 2023

V. Hall [1]
P. Kirwan [2], S. Foulkes [3], F. Insalata [4], A. Presanis [5], A. Charlett [6], D. De Angelis [7], S. Hopkins [8], (GROUP) SIREN Study Group

[1] UK Health Security Agency
[2, 7] MRC-Biostatistics Unit, University of Cambridge | UK Health Security Agency
[3, 6, 8] UK Health Security Agency
[4] UK Health Security Agency | Imperial College London
[5] MRC-Biostatistics Unit, University of Cambridge

BACKGROUND
In the current COVID-19 pandemic multiple factors have the potential to effect protection against infection e.g., vaccination dose and prior infection. The SIREN study has tracked protection over time throughout the vaccination roll-out in the United Kingdom (UK). For this analysis we investigated the effectiveness of the second booster-dose and previous infection against SARS-CoV-2 infection in our cohort of fortnightly PCR-tested healthcare workers.

METHODS
SIREN is a UK-wide multicentre prospective cohort study with data on demographics, vaccination, SARS-CoV-2 infection history, and symptoms. A multi-state model was used to estimate relative vaccine effectiveness from the second booster-dose against the circulating Omicron variants (BA.4, BA.5, and various sub-variants) by previous infection status, controlling for measured confounders and interval-censored PCR testing. Symptomatic vs. asymptomatic infections were described by prior infection and vaccination status.

RESULTS
We included 12,782 participants, with a total of 2,540 infections during analysis time (01/06/2022-31/03/2023). Among previously uninfected participants, second booster-dose vaccines provided 34% (95%CI 21-44%) additional protection. Booster vaccines were marginally effective for those with a WT/Alpha/Delta-period infection (17%, 95%CI -1-31%), and not estimated to be effective among those with a recent (Omicron BA.1/BA.2 period) infection (-20%, 95%CI -53-6%). There were possible indications of waning of protection within 6 months, with further analysis ongoing. Symptomatic infections differed according to prior variant, however booster-doses had little impact on the presence of symptoms.

CONCLUSIONS
The second booster-dose provided protection for those with no history of COVID-19, with limited additional benefit of vaccination estimated for those already substantially protected against infection by their recent exposure. Our findings demonstrate the complexity of protection during the pandemic and the importance of continued monitoring and analysis in subgroups with varied infection and vaccination history.

Keywords: COVID-19, Vaccines, Vaccine effectiveness, Cohort studies, Immunity
ABSTRACT ID: 787
PRESENTED BY: Victoria Hall, United Kingdom / victoria.hall@ukhsa.gov.uk

FIRESIDE SESSION 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

Cross-border sharing of food isolates solved an outbreak with invasive Listeria monocytogenes infection in ready-to-eat cold-cut meat, Denmark 2022

L. Espenhain [1]
S. Schjørring [2], A. R. Larsen [3], C. Thougaard Vester [4], P. Leekitcharoenphon [5], M. Sandberg [6], S. Ethelberg [7], L. Müller [8], E. Møller Nielsen [9]

[1, 2, 7, 8, 9] Statens Serum Institut
[3, 4] Danish Veterinary and Food Administration
[5, 6] National Food Institute, Technical University of Denmark

BACKGROUND
Listeriosis is a severe foodborne infection caused by Listeria monocytogenes. During late spring 2022, a concerning rise in number of listeriosis patients was observed, including several clusters based on whole genome sequencing (WGS). Here we describe the investigation.

METHODS
Outbreak cases were defined based on core genome multilocus sequence types. We did hypothesis-generating interviews, traceback-investigations, intensified food- and environmental sampling, and compared sequences. Food business operators were encouraged to have focus on own-checks, and relevant international authorities were informed.

RESULTS
We identified 10 outbreak cases aged 55–84 years. Nine fell ill from mid-April to July 2022. No other countries reported similar cases. All (nine) interviewed cases reported consumption of ready-to-eat cold-cut meat (9/9 'rullepølse' and 8/9 sliced ham). A general traceback on cold-cut meat identified four suppliers with production on six locations in two countries. Sampling was done on three production sites in Denmark and no L. monocytogenes matching the type seen in patients was identified. Traceback for 'rullepølse' identified one common production site, outside of Denmark. On this site, L. monocytogenes was identified in the production environment and in an own-check sample from 'rullepølse'. The company made a recall and shared the isolates with the Danish Veterinary and Food Administration for comparison. The sequences matched the outbreak strain.

CONCLUSIONS
This investigation underlines the importance of involvement of food business operators at an early stage during outbreak investigation and the power of using WGS for surveillance, which can be of use to other European countries. Even though interviews showed a strong indication of a cold-cut product, the microbiological evidence could not have been established without collaboration from the company and the outbreak would likely have continued.

Keywords: Listeria monocytogenes, Whole Genome Sequencing, Ready-To-Eat Meals, Epidemiology, Infectious disease outbreaks
ABSTRACT ID: 486
PRESENTED BY: Laura Espenhain, Denmark / laes@ssi.dk

FIRESIDE SESSION 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

Water supply system as the source of the largest Cryptosporidium outbreak recorded in France, November-December 2019

L. Ramalli [1]
P. Chaud [2], P. Malfait [3], J. Raibaut [4], S. Joubert [5], A. François [6], F. Chereau [7], D. Costa [8], S. Valot [9], L. Favennec [10], F. Dalle [11]

[1, 2, 3] Santé publique France, regional office of the French national public health agency in Provence-Alpes-Côte d'Azur and Corsica. F-94415 Saint-Maurice, France
[4] Regional health authority of Provence Alpes Côte d'Azur, Nice, France
[5, 6] Microbiology laboratory Bioesterel, Mouans Sartoux, France
[7] Santé publique France, the French national public health agency. F-94415 Saint-Maurice, France
[8, 10] CNR Cryptosporidium, microsporidia and other digestive protozoa – coordinating center CHU Rouen, Rouen, France
[9, 11] Collaborator CNR - LE Cryptosporidioses, CHU Dijon, Dijon, France

BACKGROUND
On November 13th 2019, the national reference centre for Cryptosporidium notified the national institute of public health of an increase of cryptosporidium infections in the South of France. We investigated the outbreak to identify the source, estimate the magnitude and implement control measures.

METHODS
We defined a laboratory confirmed case of cryptosporidiosis as a person presenting symptoms of gastroenteritis between October 1st and December 31st 2019 with a positive PCR for Cryptosporidium species in stool samples. We asked laboratories and hospitals in the area to report confirmed cases and interviewed them with a standardized questionnaire. The reference laboratory typed all strains and genotyped a random subset. Approximately 300 samples from the water supply system underwent bacterial, parasitological and virological analysis. We conducted a cross-sectional study by telephone in the area to estimate the point-prevalence of gastroenteritis.

RESULTS
We interviewed 137 confirmed cases with symptom onset between October 15th and December 6th 2019. Consumption of tap water was the sole common exposure among cases, all of whom shared the same water supply system. Between November 27th and March 23rd cryptosporidium oocysts were isolated 18 times in this water supply. Among 48 clinical isolates genotyped, 75% were C.parvum IIdA22G1. This subtype was also isolated in water samples along with four other subtypes. The cross sectional-study estimated a point-prevalence of declared gastroenteritis of 21.5% in the area, with 13,369 ill inhabitants attributed to this outbreak.

CONCLUSIONS
This is the largest Cryptosporidium outbreak ever described in France. Investigations rapidly identified a water supply system serving approximatively 90,000 inhabitants as the source of this outbreak. Water consumption restrictions were applied until ultraviolet and ultrafiltration were implemented on the water system.

Keywords: Waterborne Diseases, Cryptosporidium, Infectious Disease Outbreaks, Cross-sectional study, Gastroenteritis, France
ABSTRACT ID: 46
PRESENTED BY: Ramalli Lauriane, France / lauriane.ramalli@santepubliquefrance.fr

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FIRESIDE SESSION 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

Shiga toxin-producing Escherichia coli O103 outbreak linked to unpasteurised brie-style cheese: case-control study using a market research panel

E. Blakey [1]
R. Elson [2], S. Balasegaram [3], N. Verlander [4], Y. Chan [5], A. Douglas [6], A. Simpson [7], R. Smith [8], C. Williams [9], E. Heinsbroek [10]

[1, 2, 3, 4, 5, 6, 7, 10] UK Health Security Agency

[8, 9] Public Health Wales

BACKGROUND
In July 2022, a genetically linked and geographically dispersed cluster of twelve cases of Shiga toxin-producing Escherichia coli (STEC) O103 was detected by the UK Health Security Agency using whole genome sequencing. Descriptive analysis of food history questionnaires identified cheese (particularly an unpasteurised brie-style cheese) and mixed salad leaves as potential vehicles. A case-control study was implemented to investigate exposure to these products and support public health actions.

METHODS
Case food history information was collected by telephone. Two controls for each case were recruited using a market research panel, frequency-matched on region, socioeconomic status and age group. Controls self-completed an online questionnaire focusing on dairy product and salad leave consumption. Univariable and multivariable analyses were undertaken using Firth Logistic Regression. Concurrently, the production of the brie-style cheese was investigated, including microbiological sampling of the product and the implicated dairy farm.

RESULTS
Twelve cases (10/12 resident in England, 2/12 in Wales, 58% female, age range 8-88 years) and twenty-four controls were included in the analysis. The brie-style cheese of interest was significantly associated with illness in the multivariable analysis (OR 108, 95% confidence interval: 3.6-206). No other food items were associated with illness. Sample results for the cheese products and implicated dairy herd identified the presence of stx genes and STEC respectively, but did not identify the outbreak strain.

CONCLUSIONS
The case-control study results provided key evidence for the brie-style cheese as the source of this outbreak in the absence of microbiological results; hygiene processes at the producer were reviewed and milk used for production was pasteurised. The use of a market research panel was rapid and efficient in recruiting controls and should be considered in future epidemiological investigations.

Keywords: E. coli, Epidemiology, Statistical analysis, Unpasteurised dairy product, Market research
ABSTRACT ID: 506
PRESENTED BY: Eleanor Blakey, United Kingdom / eleanor.blakey@ukhsa.gov.uk

FIRESIDE SESSION 3
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

An outbreak of Escherichia coli O157:H7 in Wales associated with a visit to an open farm in England

C. Griffiths [1]
J. Crocker [2], A. Nelson [3], C. Jenkins [4], A. Gjini [5]

[1, 2, 5] North Wales Health Protection Team, Health Protection Division, Public Health Wales
[3] Communicable Disease Surveillance Centre, Public Health Wales
[4] Gastro and Food Safety (One Health) Division, UK Health Security Agency

BACKGROUND
In the summer of 2022, an increase in Escherichia coli O157 cases was observed in North Wales. Investigations were initiated to describe and understand the increase; leading to the detection of the cluster of E. coli O157:H7 cases described here.

METHODS
Descriptive epidemiology of laboratory confirmed cases was performed, including detailed exposure information as well as whole genome sequencing (WGS) of isolates. Faecal and environmental samples were also collected from the suspected source of the cluster.

RESULTS
In August 2022, Whole Genome Sequencing (WGS) identified a cluster (t5.6781) of three E. coli O157:H7 cases with no obvious direct epidemiological links between them. Analysis of exposure histories identified an exposure in common, as all three cases had visited the same open farm during their incubation period and within 48 hours of each other. In November 2022, WGS identified three E. coli O157:H7 cases within the same household that were gnomically indistinguishable from the August cases (at the 0 Single Nucleotide Polymorphism [SNP] level). An asymptomatic case in the November cluster reported a visit to the same open farm as the August cases. Investigations by partner agencies at the farm revealed a single isolate from a pig pen with the identical WGS (at 0 SNP level) as the six human cases in the t5.6781 cluster. No other cases in the UK had this SNP address (at the 5 SNP level).

CONCLUSIONS
This investigation highlights the power of WGS when combined with rigorous descriptive epidemiology to link cases separated both temporally and geographically. This incident further underscores the importance of effective control measures at open farms to prevent the transmission of infection to the visitors.

Keywords: Disease Outbreaks, Farms, Escherichia coli O157
ABSTRACT ID: 634
PRESENTED BY: Colin Griffiths, United Kingdom / colin.griffiths4@wales.nhs.uk

FIRESIDE SESSION 3
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

The role and limitations of routine Cryptosporidium subtyping in Cryptosporidium surveillance in Sweden

H. De Clerck [1]
A. Hansen [2], I. Bujila [3], M. Rehn [4]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Public Health Agency of Sweden (PHAS), Solna, Sweden, EPIET
[2, 3, 4] Public Health Agency of Sweden (PHAS), Solna, Sweden

BACKGROUND
Cryptosporidiosis is the most reported domestic parasitic diarrhoeal disease in humans in Sweden. The disease mainly spreads through contaminated food, water or animal contact. The Swedish Cryptosporidium surveillance program consists of an epidemiological component based on mandatory notification of cases to health authorities, and a microbiological component, including subtyping of Cryptosporidium-positive human samples using the gp60 genetic marker. The primary objective of the microbiological surveillance is to map circulating Cryptosporidium-subtypes in the country, though subtyping may also contribute to outbreak investigation. We evaluated the representativeness and timeliness of the Cryptosporidium microbiological surveillance component to, as needed, suggest adaptations to the program to increase its usefulness in outbreak investigation.

METHODS
We conducted descriptive analysis on Cryptosporidium-specific laboratory data from the Swedish national electronic case-reporting system from 2018-2022. Representativeness was evaluated by assessing regional differences in the proportion of cases subtyped. Timeliness was evaluated by computing turn-around-times (TAT) between sampling and obtaining a subtyping result, in total and by region.

RESULTS
A total of 3680 laboratory-confirmed Cryptosporidium cases were reported in Sweden between 2018 and 2022, of which 2641 (72%) were domestic. Of the domestic cases 1050 (40%) were sent for subtyping, varying between regions from 0-74%. The median TAT among 1041 domestic cases with available data was 20 days (IQR: 12-37 days), varying between regions from 12 to 54 days.

CONCLUSIONS
The varying proportion of samples sent for subtyping across regions and rather long TAT suggests that gp60-subtyping can only play a limited role in outbreak investigation. A planned survey, exploring involved laboratories' working methods and algorithms, aiming to identify reasons for the delays and varying representativeness, may allow improvement of the system.

Keywords: Cryptosporidium, Surveillance, Infectious disease outbreaks, Molecular typing, Scandinavia
ABSTRACT ID: 309
PRESENTED BY: Hilde De Clerck, Sweden / hilde.declerck@gmail.com

FIRESIDE SESSION 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Threats and outbreaks of food and water borne diseases

MODERATOR
Patricia Garvey

Abstract

Reduction in Salmonella notifications following introduction of COVID-19 control measures, Ireland, 2015-2021

C. Nielsen [1]
A. Colgan [2], P. McKeown [3], P. Garvey [4]

[1] Health Service Executive (HSE) - Health Protection Surveillance Centre (HPSC), Dublin, Ireland, EPIET ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4] Health Service Executive (HSE) - Health Protection Surveillance Centre (HPSC), Dublin, Ireland

BACKGROUND
On 12-03-2020, nationwide restrictions were introduced in Ireland to reduce the spread of SARS-CoV-2, affecting travel, social activities and workplaces. Internationally, implemented pandemic control measures have been associated with a change in the reported incidence of infectious diseases other than COVID-19. We assessed if Salmonella notification rates changed in Ireland following the introduction of pandemic restrictions.

METHODS
We conducted an interrupted timeseries analysis using negative binomial regression modelling of weekly case counts of laboratory-confirmed Salmonella notifications from 2015-2021. Modelling accounted for secular trend, seasonality, and the interruption as a binary variable distinguishing the periods before and after 12-03-2020. We investigated differences in hospital admission, serotypes, and age groups.

RESULTS
From 2015-2021, there were 1,978 Salmonella notifications, of which 343 were notified after 12-03-2020. After adjusting for underlying trend and seasonality, we observed a 54% (95% CI 45-62%) reduction in notified Salmonella cases after 12-03-2020. Notifications of hospitalised cases reduced by 47% (95% CI 32-59%). The reduction in notifications was greater for S. Enteritidis [73% (95% CI 60-82%)] than for S. Typhimurium [59% (95% CI 39-72%)], and for 20-44-year-olds [68% (95% CI 56-76%)] compared to younger [42% (95% CI 23-57%)] and older age groups [51% (95% CI 34-63%)].

CONCLUSIONS
Pandemic restrictions appear to have reduced Salmonella notification rates, as well as impacted on COVID-19 incidence. Considering known Salmonella risk factors in Ireland, the larger reduction in certain subgroups (S. Enteritidis and younger adults) is likely related to a greater impact of pandemic restrictions on foreign travel and eating out in these groups. These analyses may prove useful in supporting public health messages to limit salmonellosis in the future.

Keywords: Epidemiology, Gastroenteritis, Salmonellosis, Time Series, COVID-19 Pandemic
ABSTRACT ID: 160
PRESENTED BY: Charlotte Salgaard Nielsen, Ireland / charlottesalgaardnielsen@hotmail.com

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Questioning Risk Compensation: Pre-exposure Prophylaxis (PrEP) and Sexually Transmitted Infections Among Men who have Sex with Men in Denmark

S. von Schreeb [1]
K. Melbardis Jørgensen [2], L. Holm Harritshøj [3], F. Boëtius Hertz [4], S. Lunding [5], M. Glindvad Ahlström [6], J. Gerstoft [7], L. Nørregaard Nielsen [8], G. Kronborg [9], F. Neess Engsig [10]

[1] Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen | Department of Infectious Diseases, Copenhagen University Hospital – Amager and Hvidovre, Copenhagen
[2] Department of Clinical Microbiology, Copenhagen University Hospital - Amager and Hvidovre, Copenhagen
[3] Department of Clinical Immunology, Copenhagen University Hospital - Rigshospitalet, Copenhagen
[4] Department of Clinical Microbiology, Copenhagen University Hospital - Rigshospitalet, Copenhagen
[5] Department of Internal Medicine, Copenhagen University Hospital – Herlev and Gentofte, Copenhagen
[6] Department of Clinical Microbiology, Copenhagen University Hospital - Herlev and Gentofte, Copenhagen
[7] Department of Infectious Diseases, Copenhagen University Hospital - Rigshospitalet, Copenhagen
[8] Department of Pulmonary and Infectious Diseases, Copenhagen University Hospital – North Zealand Hospital, Copenhagen
[9, 10] Department of Infectious Diseases, Copenhagen University Hospital – Amager and Hvidovre, Copenhagen

BACKGROUND
Pre-exposure prophylaxis (PrEP) currently provides HIV protection to millions of people worldwide. The controversy over whether PrEP leads to sexual risk compensation is a central challenge to the extension of programs globally. The current study, conducted in Denmark, aims to investigate the magnitude and timing of the association between PrEP-use and the incidence of chlamydia, gonorrhea, and syphilis.

METHODS
PrEP-users in the capital region of Denmark were included between January 2019 and June 2022. Incidence rate ratios (IRR) for sexually transmitted infections (STI) pre and post PrEP initiation were calculated, adjusting for testing frequency and age. In a subanalysis, IRR were stratified by age groups and anatomical site of infections. Weekly STI incidence rates were plotted to determine when they began to rise, aligning with individual PrEP start dates.

RESULTS
Totally 1326 participants enrolled (99.7 % med), with a median age of 35 years (interquartile range 29-44). The incidence rate increase from 35.3 to 81.2 STIs per 100.000 person years, before and on PrEP, respectively. The adjusted IRR was 1.35 [1.18-1.56]. STI-specific adjusted IRR were: chlamydia 1.23 [1.03-1.48], gonorrhea 1.24 [1.04 - 1.47] and syphilis 1.15 [0.76 - 1.72]. Anatomical sites subanalysis found an adjusted IRR of 1.26 [1.01-1.56] for rectal chlamydia and 0.66 [0.45-0.96] for genital gonorrhea. No significant age difference was found. The increases in STI incidence rates began 10-20 weeks prior to PrEP initiation.

CONCLUSIONS
The current study found a 35 % increase in STI incidence rate associated with PrEP use. However, the rise preceded PrEP initiation, which questions the common assumption that PrEP causes sexual risk-taking through risk compensation. Rather, the data indicate that PrEP is administered when it is most needed.

Keywords: Pre-exposure prophylaxis, HIV, Chlamydia, Gonorrhea, Syphilis, Risk compensation
ABSTRACT ID: 643
PRESENTED BY: Sebastian von Schreeb, Denmark / sebastianvonschreeb@gmail.com

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Association between HIV status and risk of SARS-CoV-2 breakthrough infection and subsequent hospitalisation after COVID-19 vaccination in Italy (January – October 2021)

A. Mateo Urdiales [1]
F. Mayer [2], M. Fabiani [3], S. Spila Alegiani [4], C. Morciano [5], M. Cutillo [6], C. Sacco [7], D. Petrone [8], A. Bella [9], F. Riccardo [10], M. Del Manso [11], P. Pezzotti [12], M. Massari [13]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13] Istituto Superiore di Sanità

BACKGROUND

There is evidence that mRNA COVID-19 vaccines prevent SARS-CoV-2 infection and severe COVID-19. However, people with immune dysfunction may have a lower immunological response following vaccination. This study aims to estimate the risk of infection and severe COVID-19 in vaccinated people according to HIV status.

METHODS

We conducted a cohort study emulating a clinical trial. A distributed analyses tool, TheShinISS, was used linking data from vaccination, COVID-19 surveillance, hospital and pharmacological registries of four Italian regions, from January to October 2021. We selected immunocompetent adults vaccinated with mRNA vaccines without previous SARS-CoV-2 infection. We matched every vaccinated person living with HIV (PLWH) with one person without HIV (PLWoH) by sex, age, region, week of vaccination, vaccination type and propensity score, estimated from all available information on co-morbidities and drugs prescribed. We used Kaplan-Meier estimators to calculate the relative risk (RR) of infection and subsequent hospitalisation in PLWH and in PLWoH.

RESULTS

We included 85,606 participants, half of which were PLWH. Maximum period of follow up, since first dose, was 270 days. Overall, we didn't observe differences in the risk of breakthrough infection in the period 0-139 days post-first dose in PLWH compared with PLWoH (RR:1.12;95% confidence interval (CI):0.92-1.38), whereas we observed a lower risk of breakthrough infection in the period 140-270 days post first dose in PLWH (RR:0.59;95%CI:0.36-0.92). Overall, we did not find differences in the risk of hospitalisation in PLWH compared to PLWoH (RR:0.89;95%CI: 0.37-2.83).

CONCLUSIONS

In Italy, where the vast majority of PLWH are on antiretroviral therapy, we did not observe differences in the risk of breakthrough infection or subsequent hospitalisation after mRNA vaccination in the HIV positive population.

Keywords: COVID-19, HIV, Effectiveness, Vaccination
ABSTRACT ID: 711
PRESENTED BY: Alberto Mateo Urdiales, Italy / amateo250@hotmail.com

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Reduction in the risk of mpoxv infection after MVA-BN vaccination in individuals on HIV pre-exposure prophylaxis: a Spanish cohort study

M. Fontán-Vela [1]
(GROUP) MPOX-VE study group

[1] Centro Nacional de Epidemiología (Instituto de Salud Carlos III)

BACKGROUND
With over 7,500 cases notified since April 2022, Spain has experienced the highest incidence of mpox in Europe. From July 12th onwards, the Modified Vaccinia Ankara-Bavaria Nordic (MVA-BN) smallpox vaccine was offered as pre-exposure prophylaxis for individuals at high-risk of mpox, including those receiving HIV-PrEP. Our aim was to assess the effectiveness of at least one-dose of MVA-BN vaccine pre-exposure against mpox infection in persons on HIV-PrEP.

METHODS
We conducted a national retrospective cohort study between July 12th and December 12th, 2022. Individuals ≥18 years, receiving HIV-PrEP as of July 12th and with no previous mpox infection or vaccination were eligible. On each day, we matched individuals receiving a first dose of MVA-BN vaccine and unvaccinated controls of the same age group and region. We estimated risk of infection using a Kaplan-Meier estimator and calculated risk ratios (RR) and vaccine effectiveness (VE=1-RR).

RESULTS
We included 5,660 matched pairs, with a median follow-up of 62 days (interquartile range 24-97). Mpox cumulative incidence (per 1,000) was 5.6 (25 cases) in non-vaccinated and 3.5 (18 cases) in vaccinated; last case occurred at 63 and 17 days after enrolment, respectively. No effect was found during days 0-6 post-vaccination (RR 1.38; 95% confidence interval (CI): 0.54-4.33), but VE was 65% in ≥7 days (RR 0.35; CI:0.12-0.77) and 79% in ≥14 days (RR 0.21; CI:0.00-0.67) after vaccination.

CONCLUSIONS
At least one dose of MVA-BN vaccine offered protection against mpox in a high-risk population. Because the incidence of mpox was decreasing when the vaccination campaign began, we can only assess its effectiveness shortly after vaccination. Further studies need to assess the VE of a second dose and the duration of protection over time.

Keywords: Mpox, Vaccine effectiveness, Monkeypox, MVA-BN
ABSTRACT ID: 340
PRESENTED BY: Mario Fontán-Vela, Spain / mario.fontan@isciii.es

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Prevalence of Mpox-specific antibodies in sera collected between January – September 2022 in England: A cross-sectional seroprevalence study

A. Otter [1]
H. Fifer [2], M. Yung [3], R. Pitt [4], I. Everall [5], S. Jones [6], T. Rampling [7], H. Mohammed [8], J. Saunders [9], (GROUP) UKHSA Mpox serosurveillance group

[1] Emerging Pathogen Serology, UK Health Security Agency
[2, 3, 4, 5, 8, 9] UK Health Security Agency, London
[6, 7] UK Health Security Agency, Porton Down

BACKGROUND
Between 6 May 2022 and 19 December 2022 there were 3,404 confirmed cases of Mpox infection in England, predominantly among gay, bisexual, and other men who have sex with men (GBMSM). We measured the sero-prevalence of poxvirus antibodies in sera collected before the first identified case to determine when infections first appeared in England, and from sera collected later in 2022, to measure the extent of undiagnosed Mpox infection.

METHODS
We collected residual sera from men in London and Southeast England having confirmatory syphilis testing (before Mpox-outbreak as a proxy for high-risk) January-May 2022 (before Mpox outbreak), and from adults attending sexual health services (SHS) in London and Manchester May-September 2022 (during Mpox-outbreak). Two different ELISAs were utilised, one that detects pan-poxvirus antibodies, and a differential assay using the MPXV A27 antigen, which is absent from IMVANEX vaccine, detecting only those with prior Mpox-infection, or historical Smallpox vaccination (aged ›51).

RESULTS
In total, 3,482 samples from individuals were tested; 797 from men sampled between January-May 2022 and 2,685 from individuals attending SHS May-September 2022. 858 individuals (24.65%) demonstrated poxvirus antigen reactivity, whilst 120 individuals (3.45%) were also positive on the differential assay. All positive samples prior to the Mpox-outbreak (n=22) were from men aged ›51, suggesting antibody reactivity due to historical Smallpox vaccination.

CONCLUSIONS
We did not find any evidence of Mpox-specific antibodies in this sample of high-risk men prior to identification of the Mpox outbreak in England. The low Mpox seroprevalence amongst SHS attendees may reflect very little undiagnosed infection, or sampling bias. Linkage to national STI data surveillance is ongoing and will allow further analysis of the latter to determine seroprevalence within sub-populations of GBMSM.

Keywords: Mpox, Monkeypox, Serosurveillance, Vaccination, GBMSM, IMVANEX
ABSTRACT ID: 65
PRESENTED BY: Ash Otter, United Kingdom / ashley.otter@ukhsa.gov.uk

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Less is more – strict control measures obstructed efficient contact tracing during the 2022 mpox outbreak in the Netherlands

D. Brandwagt [1]
M. te Wierik [2], E. Op de Coul [3], E. Franz [4], P. Hintaran [5], H. Götz [6], G. van Rijckevorsel [7], T. Leenstra [8]

[1, 2, 3, 4, 8] National Institute for Public Health and the Environment (RIVM)
[5] Public Health Service Utrecht region
[6] Public Health Service Rotterdam - Rijnmond
[7] Public Health Service Amsterdam

BACKGROUND
On 20 May 2022, the first cases of mpox were reported in the Netherlands. Considered a public health threat, mpox was classified as a group A notifiable disease, the highest level possible. This classification required immediate notification of all suspected cases, and allowed strict control measures, including isolation of cases and a 21-day quarantine period for high-risk contacts. Post-exposure vaccination was offered to all high-risk contacts.In June, regional public health services requested a policy change. Cases were sometimes reluctant to disclose their contacts, due to the impact of the quarantine measure. These contacts could therefore not be reached for vaccination. Furthermore, quarantine of health care workers classified as high-risk contacts was regarded disproportional.

METHODS
Analyzing data on transmission routes from the Netherlands and other European countries disclosed that intensive physical (sexual) contact or contact with broken skin or mucous membranes were the main routes of transmission during this outbreak. The quarantine measure was replaced by behavioral advices, including sexual restraint, on the 22nd of June. To monitor the effect of this change, we compared the proportion of cases that reported contacts and the contact-to-case-ratio in the period before and after 22 June.

RESULTS
The proportion of contacts disclosed by cases increased from 68% (127/186) to 94% (961/1023) in the 12 weeks since the policy change. The contact-to-case-ratio increased from 4.3 to 4.7, this mainly concerned non-high-risk contacts, as the proportion of high-risk contacts decreased from 51 to 25%.

CONCLUSIONS
Releasing quarantine for high-risk contacts increased the number of reported contacts, although mainly non-high-risk contacts. For future outbreaks, factors that could negatively affect compliance of control measures, should be taken into account and discussed with behavioral experts.

Keywords: Monkeypox, Policy, Quarantine, Communicable Disease Control, Prevention & control
ABSTRACT ID: 203
PRESENTED BY: Diederik Brandwagt, Netherlands / diederik.brandwagt@rivm.nl

FIRESIDE SESSION 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
14:00-15:30

Sexually and community acquired infections, including HIV

MODERATOR
Irena Klavs

Abstract

Factors associated with non-initiation of antiretroviral therapy among adults newly diagnosed with HIV in Andijan, Uzbekistan, 2018-2021

S. Usmanov[1]

R. Horth[2], A. Denebayeva[3], B. Asfendiyarov Kazakh National Medical University, A[4], F. Nasirova[5], D. Nabirova[6]

[1] Central Asia Field Epidemiology Training Program | Andizhan region Center for Prevention and Control of AIDS, HIV Center, Uzbekistan | Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[2, 6] U.S. Centers for Disease Control and Prevention, Central Asia Office, Almaty, Kazakhstan | Central Asia Field Epidemiology Training Program | Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[3] Central Asia Field Epidemiology Training Program | Almaty City Center for Prevention and Control of AIDS, HIV Center, Kazakhstan | Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[4] Sanitary and Epidemiological Welfare and Public Health Committee Tashkent, Uzbekistan
[5] Andizhan State Medical Institute, Andizhan, Uzbekistan

BACKGROUND

Immediate uptake of antiretroviral therapy (ART) by people newly diagnosed with HIV reduces morbidity and viral transmission. Since 2018, in Uzbekistan, people newly diagnosed with HIV are immediately offered ART, but just over half of people living with HIV are estimated to be on ART. To reach global targets, we assessed factors associated with ART non-initiation.

METHODS

We conducted a retrospective cohort study among all people ≥18 years of age newly diagnosed with HIV in Andijan Region AIDS Center between January 1, 2018, and June 31, 2021. We analyzed sociodemographic and behavioral factors associated with non-initiation of ART, defined as not having initiated ART by December 31, 2021. Using multivariate Poisson regression, we calculated adjusted risk ratios (RR) and 95% confidence intervals [CI].

RESULTS

From 2018 to 2021 in Andijan Province, 1,098 people were newly diagnosed with HIV, of which 113 (10.3%) did not initiate ART. Participants were mostly 30-49 years old (49%), male (56%), married (46%), and with secondary education (74%). Also, 39% and 31% had HIV clinical stage I and II, respectively. Risk for non-initiation was higher among people with secondary education (ARR=8.6 [95%CI=1.2–60.9]) compared to higher education, with multiple partners (RR=2.7 [95%CI=1.5-5.0]), with disease stage I (ARR=3.3 [95%CI=2.0–5.2]) and stage II (ARR=4.4 [95%CI=2.8–7.0]). People with sexual partners living with HIV had higher risk of non-initiation (ARR=1.8 [95%CI=1.2–2.9]) than people with partners without HIV. Being single was associated with reduced risk of non-initiation (ARR=0.1 [95%CI=0.03–0.3]).

CONCLUSIONS

People with multiple partners and with partners living with HIV should be prioritized for ART initiation support. Increased risk of non-initiation among people in earlier disease stages points to the need for interventions to increase awareness of test-and-start among providers.

Keywords: HIV, Antiretroviral therapy (ART), Non-initiation, Uzbekistan
ABSTRACT ID: 369
PRESENTED BY: Shokhruh Usmanov, Uzbekistan / Shohrux1718@gmail.com

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patterns

MODERATOR
Agnès Lepoutre

Abstract

Impact of the closure of day-cares and schools in response to the COVID-19 pandemic on European adults' work-life balance, European Union 2020-2022

E. Severi [1]
G. Marrone [2], F. Innocenti [3], M. Hyland [4], V. Toffolutti [5], M. Anzillotti [6], B. Prasse [7], F. Sandmann [8], T. Karki [9], M. heloury [10], A. Romani [11], M. Mascherini [12]

[1, 2, 3, 7, 8, 9, 10, 11] ECDC
[4, 6, 12] Eurofound
[5] Universitá Bocconi | Queen Mary University of London

BACKGROUND
The scientific evidence on the impact of educational setting closures on adults' work-life balance (WLB) during the COVID-19 pandemic in Europe is scarce. Our objective was to study associations between educational setting closures and WLB among adults living in the 27 EU countries from March-2020 to May-2022.

METHODS
We used logistic regression models on matched data from the "ECDC-JRC Response Measures Database" and the Eurofound Survey "Living, Working and COVID-19" to assess associations between educational setting closures and five binary outcomes defining work-anxiety, and work-life and life-work conflicts. All models were adjusted for respondent sociodemographic factors (gender, age-group, education, living with partner, living with children, teleworking, area of residence, EU-geographical region), stay-at-home policies in place and seven-day average COVID-19 deaths.

RESULTS
We analysed 118,927 responses from workers from five survey-rounds. At least 60% of them were female, highly educated, living with a partner or childless. Educational setting closures were associated with increased worker's anxiety about their job (odds ratio-OR 1.08, 95% confidence interval-95%CI 1.04-1.11 - for primary schools), a decrease in their work-family conflicts (OR 0.59, 95%CI 0.57-0.61 for primary schools on work-household conflicts) and a non-significant impact on their family-work conflicts. Adults living with children aged <12 years had larger negative impact on their work-anxiety and on family-work conflicts, resulting in decreased work-dedicated time and work-concentration due to family responsibilities. Teleworkers were associated with worse life-work conflicts; however, non-teleworkers were more likely to suffer from work-anxiety out of work.

CONCLUSIONS
Educational setting closures have an impact on European adults' WLB. Authorities planning such intervention should consider social protection policies for people with children <12 years and teleworkers to perform their work without damage to their work-life balance.

Keywords: COVID-19, Work-Life Balance, European Union, Schools, Non-pharmaceutical interventions
ABSTRACT ID: 176
PRESENTED BY: Ettore Severi, Sweden / ettore.severi@ecdc.europa.eu

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patterns

MODERATOR
Agnès Lepoutre

Abstract

Transferring inpatients between wards drives large nosocomial COVID-19 outbreaks, Wales, United Kingdom, 2020-22: a matched case-control study using routine and enhanced surveillance data

R. Merrick [1]
C. McKerr [2], J. Song [3], J. Beer [4], K. Donnelly [5], A. Ledgerton [6], R. Gerrard [7], M. Morgan [8], C. Williams [9], N. Craine [10]

[1] UK Field Epidemiology Training Programme (UK-FETP) | UK Health Security Agency (UKHSA)
Public Health Wales (PHW)
[2, 3, 4, 9, 10] Public Health Wales (PHW)
[5, 6, 7] Betsi Cadwaladr University Health Board (BCUHB)
[8] Public Health Wales (PHW) | UK Health Security Agency (UKHSA)

BACKGROUND
Undetected SARS-CoV-2 infection in healthcare settings can facilitate onwards transmission to vulnerable individuals. As the role of hospital environments, staffing, and inpatient mix in disease spread is unclear, we measured associations between ward characteristics and large COVID-19 outbreaks to inform mitigations.

METHODS
We compared wards with large (case-wards) and small (control-wards) outbreaks in three acute hospitals. Case-wards were adult medical/surgical wards with ≥10 healthcare associated COVID-19 (HCA-C19) inpatients (positive PCR ≥8 days post-admission) within rolling 14-day periods, between 01/04/2020-30/04/2022. Control-wards were equivalents with 2-9 HCA-C19 inpatients. Demographic and laboratory information were extracted from routine surveillance data. Hospital staff provided ward-level structural (number of beds, toilets, isolation cubicles), operational (number of staff, community admissions, discharges, internal inpatient transfers) and clinical specialty information. Continuous data were aggregated fortnightly and analysed as binary variables according to median values. Case-wards were compared with two control-wards matched on outbreak start date (± 14 days) to calculate odds ratios (OR) and 95% confidence intervals (95%CI) using univariable and conditional multivariable logistic regression.

RESULTS
From 170 outbreaks (median: 5 inpatients, IQR: 2-9), we identified 35 case-wards. Community admissions were lower in case-wards vs. control-wards (5 vs. 10 median admissions, $p<0.01$, respectively), whereas transfers between wards within the same hospital were higher (58 vs. 29 median transfers, $p<0.01$, respectively). After adjustment, wards with higher numbers of transfers were 9 times more likely to experience a large outbreak (≥35 vs. <35 transfers; 95%CI: 2.5-33).

CONCLUSIONS
Large outbreaks were associated with high numbers of transfers into a ward in the preceding fortnight. We recommend safely minimising patient movements, such as by asking clinicians to record the rationale for transfer, to reduce the likelihood of undetected transmission.

Keywords: COVID-19, SARS-CoV-2, Nosocomial, Case-control, Wales, Outbreak
ABSTRACT ID: 218
PRESENTED BY: Rachel Merrick, United Kingdom / rachel.merrick@wales.nhs.uk

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patterns

MODERATOR
Agnès Lepoutre

Abstract

Impact of COVID-19 pandemic on incidence and mortality of Clostridioides difficile infection in Wales, UK

R. Polani Chandrasekar [1]
J. Beer [2], V. McClure [3], M. Morgan [4]
[1, 2, 3, 4] Public Health Wales NHS Trust

BACKGROUND
Clostridioides difficile infection (CDI) is a significant public health concern and is increasing in Wales; the COVID-19 pandemic may have impacted its occurrence. We aimed to compare CDI epidemiology between the pre-pandemic and pandemic periods to better interpret surveillance trends.

METHODS
We compared CDI incidence and mortality between the immediate pre-pandemic (01/01/2019-26/02/2020) and pandemic (27/02/2020-31/12/2021) periods, and between pandemic waves (Wave-1: 27/02/2020-26/07/2020; Wave-2: 27/07/2020-16/05/2021; Wave-3: 17/05/2021-31/12/2021). We extracted test results from the laboratory information system and death dates from patient administration systems. CDI was defined as a positive toxin enzyme immunoassay. Mortality was death from any cause within 28 days of positive test. We used annualized population denominators to account for different time period lengths. We used the Wilson method to compute 95% confidence intervals (95%CI) and Z-score and Chi-square tests to test significance.

RESULTS
Of 2752 CDI cases, 943 (34%) and 1809 (66%) were from the pre-pandemic and pandemic periods, respectively. Incidence per 100,000 population was significantly higher in the pandemic period (31.0; 95%CI: 29.6-32.4 vs 25.9; 95%CI: 24.3-27.6, Z= 4.47, p<0.001). There was no difference in mortality between the pandemic (12.2%; 95%CI: 10.7%-13.7%) and pre-pandemic periods (13.0%; 95%CI: 11.0%-15.3%, Z= -0.67, p=0.5). Within the pandemic period, incidence per 100,000 population was significantly higher in Wave-3 (38.0; 95%CI: 35.3-40.7) compared to Wave-1 (26.2, 95%CI: 23.4-28.9) and Wave-2 (27.9, 95%CI: 25.9-30.0; X2= 49.16; p<0.001) but mortality was not different.

CONCLUSIONS
We found higher CDI incidence during the pandemic compared to the immediate pre-pandemic period, particularly in Wave 3. This is potentially from increased prescribing or the impact of SARS-CoV-2 virus on gut microbiomes. No impact on severity was identified. Further investigation into exposures of identified cases is recommended.

Keywords: COVID-19, Clostridiodes difficile, SARS-CoV-2, Disease Surveillance
ABSTRACT ID: 698
PRESENTED BY: Rubeshkumar Polani Chandrasekar, United Kingdom / rubesh.polanichandrasekar@wales.nhs.uk

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patterns

MODERATOR
Agnès Lepoutre

Abstract

Epidemiology of persons with repeat episodes of Clostridioides difficile in Wales, United Kingdom, April 2015- March 2022

R. Polani Chandrasekar [1]
N. Craine [2], M. Morgan [3], V. McClure [4], C. McKerr [5]
[1, 2, 3, 4, 5] Public Health Wales NHS Trust

BACKGROUND

Clostridioides difficile infection (CDI) causes substantial morbidity and mortality in Wales; repeat infections, from relapse or new infections, are a known issue. We aimed to quantify repeat episodes and describe patients with them, to support infection prevention and treatment.

METHODS

We extracted CDI tests from April 2015-March 2022 from the laboratory information system. We identified individuals with multiple episodes by matching on NHS numbers and excluded repeats within 28 days as duplicates. We categorised repeats as relapses of the original infection (29-84 days post original infection) and recurrences i.e. new infections (>84 days). We described and compared individuals with single episodes and repeats by demographics and location of specimen collection, using chi-square test/chi-square test for linear trend.

RESULTS

We analysed 18,821 episodes in 15,092 individuals. More than 80% (12,507/15,092) of individuals had only one episode within the timeframe; 17% (2,585/15,092) had repeat episodes (3729), with a median of one repeat (range: 1-10). Of repeat episodes, 59% (2209/3729) were relapses and 41% (1520/3729) recurrences. Individuals with repeats were significantly older (X2 for trend= 10.57, $p<0.001$). A higher proportion of first samples were taken in non-inpatient locations in persons with repeats, than in those with single episodes (47% vs 41%, X2= 32.65, $p<0.001$).

CONCLUSIONS

One in five episodes were repeats, contributing substantially to the CDI burden and impacting patient quality of life. Most repeat episodes were likely relapses of the original infection; incorporating genomic data would support better distinction of relapses from new infections to support identification and prevention of treatment failures. The substantial burden of repeat episodes in patients first diagnosed outside of secondary care settings warrants attention to clinical management of CDI in these settings.

Keywords: Clostridioides difficile, Healthcare infections, Disease surveillance, Emerging infections
ABSTRACT ID: 704
PRESENTED BY: Rubeshkumar Polani Chandrasekar, United Kingdom / rubesh.polanichandrasekar@wales.nhs.uk

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patternss

MODERATOR
Agnès Lepoutre

Abstract

Using surveillance data to evaluate the risk of severe outcomes of COVID-19 during the 2022/2023 winter in Sweden – did the autumn booster among people 65 years and older make a difference?

E. Löf [1]
M. Rehn [2], A. Ohlson [3], A. Carnahan [4], V. Bergfeldt [5], R. Brodin [6], M. Jansson Mörk [7]
[1, 2, 3, 4, 5, 6, 7] Public Health Agency of Sweden

BACKGROUND
During the autumn 2022 in Sweden, people 65 years or older were recommended a booster-dose of vaccine against COVID-19. In the 2022/2023 winter there was a large peak of COVID-19 transmission in the community. We evaluated the risk of severe COVID-19 outcomes during the winter peak for those that received a booster-dose during autumn, were vaccinated earlier or were unvaccinated.

METHODS
We used COVID-19 surveillance data and national registries to categorize COVID-19-cases 65 years and older and corresponding population denominators into vaccinated or unvaccinated. The vaccinated group was further categorized into recent-boosted or earlier-boosted depending on if the last dose was given within five months or more before COVID-19 confirmation. People receiving home care or living in care homes were omitted. Severe outcomes among COVID-19 cases were hospitalisation, intensive care (IC), or death, reported during week 47 2022 to week 2 2023. We calculated incidence rates of severe outcomes and compared between groups using incidence rate ratios (IRR) with 95-percent confidence intervals (CI).

RESULTS
The recent-booster group had lower risk for hospitalisation compared to the unvaccinated group (IRR 0.35 95% CI 0.30-0.40), IC (IRR 0.25 95% CI 0.16-0.39) and death (IRR 0.26 95% CI 0.20-0.34) and compared to the earlier-boosted group; hospitalisation (IRR 0.65 95% CI 0.59-0.71), IC (IRR 0.60 95% CI 0.43-0.84) and death (IRR 0.51 95% CI 0.42-0.61).

CONCLUSIONS
These results suggest that the recommended autumn booster-dose protected against severe outcomes of COVID-19 during the 2022/2023 winter peak and supports future boosters timed before seasonal peaks. Surveillance data can be used for rapid analysis to catch changed patterns in risk of severe outcomes of disease among vaccinated to target further actions in a timely manner.

Keywords: COVID-19, Vaccine, Surveillance, Disease severity
ABSTRACT ID: 649
PRESENTED BY: Emma Löf, Sweden / emma.k.lof@gmail.com

FIRESIDE SESSION 5

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Disease Surveillance: trends, outcomes and patternss

MODERATOR
Agnès Lepoutre

Abstract

How did the number of healthcare associated infection outbreaks with bacterial pathogens develop during the SARS-CoV-2 pandemic? – Descriptive analysis of surveillance data in Germany, 2017–2022

S. Jan M [1]
B. Suwono [2], S. Haller [3]

[1] European Programme for Intervention Epidemiology Training, European Centre for Disease Prevention and Control, Solna, Sweden | Unit of Healthcare-associated Infections, Surveillance of Antibiotic Resistance and Consumption, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
[2, 3] Unit of Healthcare-associated Infections, Surveillance of Antibiotic Resistance and Consumption, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND
Healthcare-associated infections (HAIs) contribute significantly to global disease burden. It was assumed that HAI burden may increase (e.g., higher antibiotic use) and decrease (e.g., increased hygiene measures) during the SARS-CoV-2-pandemic. We compare outbreaks with bacterial pathogens in German inpatient healthcare institutions before and during the SARS-CoV-2 pandemic.

METHODS
We descriptively analyze German national-level surveillance data of HAI outbreaks reported electronically by local public health authorities. We compare the frequency of outbreaks, cases, deaths, and diagnosis-to-reporting delay as an indicator for reporting-bias for a pre-pandemic (2017–2019) and a pandemic period (2020–2022), stratified by pathogen and year.

RESULTS
Prior to the pandemic, the reported number of bacterial HAI outbreaks decreased from 160 (2017) to 133 (2019). During the pandemic, we observed a decline, ranging from n=87 (2020) to n=101 (2021). In the pre-pandemic period, the mean case fatality ratio ranged from 6.4% (2019) to 9.5% (2017). In the pandemic period, we observed a pronounced increase to 15.0% (2021) and 12.3% (2022). The overall number of reported deaths was higher during (n=234) compared to before the pandemic period (n=175). Klebsiella spp., Enterococcus spp., and Acinetobacter spp. accounted for 82% of these deaths during the pandemic, compared to pre-pandemic 59%. The median diagnosis-to-reporting delay was slightly lower prior compared to during the pandemic period (5–7 vs. 5–9 days).

CONCLUSIONS
Our findings suggest that during the SARS-CoV-2-pandemic, more severe and fatal bacterial HAI outbreaks occurred; as changes in the reporting-bias indicator were slight and cannot explain the increase in total number of deaths. We will further assess contributing factors as changes in hospital-admission and testing. Preparedness strategies ought to include measures to interrupt transmission of bacterial HAI during pandemics.

Keywords: SARS-CoV-2, Healthcare Associated Infections, Cross infection, Drug Resistance, Bacterial, Bacterial Infections
ABSTRACT ID: 622
PRESENTED BY: Stratil Jan M, Germany / stratilj@rki.de

FIRESIDE SESSION 6
DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Establishing infodemic management in Germany: a framework for social listening and integrated analysis to report infodemic insights at the national public health institute

S. Boender [1]
P. Schneider [2], C. Houareau [3], S. Wehrli [4], T. Purnat [5], A. Ishizumi 6, E. Wilhelm [7], C. Voegeli [8], L. Wieler[9], C. Leuker [10]

[1, 2, 10] Robert Koch Institute, Risk Communication Unit, Berlin
[3] Robert Koch Institute, Department for Infectious Disease Epidemiology, Berlin
[4] Robert Koch Institute, Centre for Artificial Intelligence in Public Health Research, Berlin
[5, 6] World Health Organization, Department of Pandemic and Epidemic Preparedness and Prevention, Health Emergencies Programme, Geneva
[7] Visiting Fellow, Brown University School of Public Health Information Futures Lab, Providence, RI
[8] Centers for Disease Control and Prevention, Atlanta, GA
[9] Robert Koch Institute, Berlin | Digital Global Public Health, Hasso Plattner Institute, University of Potsdam, Potsdam

BACKGROUND
To address the need for establishing infodemic management functions at Germany's national public health institute (Robert Koch Institute; RKI), we explored and assessed available data sources, developed a social listening and integrated analysis framework, and defined when infodemic management functions would activate during emergencies. We aimed to establish a framework for social listening and integrated analysis for public health in the German context, using international examples and technical guidance documents for infodemic management.

METHODS
We 1) identified (potentially) available data sources for social listening and integrated analysis; 2) assessed these data sources for their suitability and usefulness for integrated analysis, and assessed their data protection requirement; 3) developed a framework and workflow to combine social listening and integrated analysis to report back actionable infodemic insights for public health communications by the RKI and stakeholders; 4) defined criteria for activating integrated analysis structures in case of a specific health event or emergency.

RESULTS
We included and assessed 16 out of the 42 identified and assessed data sources for social listening and integrated analysis at RKI, which fall into three categories: social media and online listening data, RKI-specific data, and infodemic insights. Most data sources can be analysed on a weekly basis to detect current trends and narratives and to inform a timely response through reporting insights that include a risk assessment and scalar judgements of the different narratives and themes.

CONCLUSIONS
We established a framework for social listening and integrated analysis to report actionable infodemic insights to establish and operationalise infodemic management at RKI, which can serve as a roadmap for others. Ultimately, once operational, these activities will inform better and targeted public health communication.

Keywords: Infodemic, Social listening, Infodemiology, Misinformation, Integrated analysis, Infodemic insights
ABSTRACT ID: 32
PRESENTED BY: Sonia Boender, Germany / sboender@ggd.amsterdam.nl

FIRESIDE SESSION 6

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Hygiene assessment in day care centres using the Infection Risk Scan (IRIS), the Netherlands

E. den Boogert[1]
I. Willemsen[2], K. Wannée-de Smalen[3], R. Baggen[4], M. Broeren[5], A. van Gurp[6], C. den Heijer[7], J. van den Heuvel[8], P. Jansingh[9], E. Musters[10], R. Stoop[11], M. Theunissen[12], L. Tromp[13], A. Rietveld[14], J. Hautvast[15]

[1] Department of Infectious Disease Control, Municipal Public health service Hart voor Brabant, 's-Hertogenbosch, The Netherlands
[2, 11] Contrain – Infection Control Coach, Breda, The Netherlands
[3, 8, 14] Department of Infectious Disease Control, Municipal Public health service Hart voor Brabant, 's-Hertogenbosch, The Netherlands
[4, 12] Department of Sexual Health, Infectious Diseases and Environmental Health, South Limburg Public Health Service, PO Box 33, 6400 AA Heerlen, The Netherlands
[5, 9] Department of general health care, Municipal Public health service Limburg-Noord, Venlo, The Netherlands.
[6] Department of Infectious Disease Control, Municipal Public health service West-Brabant, Breda, The Netherlands
[7] Department of Sexual Health, Infectious Diseases and Environmental Health, South Limburg Public Health Service, PO Box 33, 6400 AA Heerlen, The Netherlands | Department of Social Medicine, Care and Public Health Research Institute (CAPHRI), Faculty of Health, Medicine and Life Sciences, Maastricht University, PO box 616, 6200 MD Maastricht, The Netherlands
[10] Department of Infectious Disease Control, Municipal Public health service Zeeland, PO box 345, 4460 AS Goes, The Netherlands
[13] Department of Infectious Disease Control, Municipal Public health service Brabant-Zuidoost, Eindhoven, The Netherlands
[15] Radboud university medical center, Radboud Institute for Health Sciences, Department of Primary and Community care, Nijmegen, The Netherlands

BACKGROUND

Infectious diseases, such as gastroenteritis and influenza-like illnesses, have a higher incidence among children attending day care centres (DCCs) than children who don't. We investigated infection prevention practices (IPP) in DCCs to better understand the hygiene status and possibilities for interventions.

METHODS

Through a cross-sectional design we assessed IPP in 28 DCCs from Dec 2022-April 2023. DCCs were selected in six Public Health Service (PHS) regions. IPP was measured using the Infection Risk Scan (IRIS), which consists of objective and reproducible measurements: observation of hand hygiene performance and personal hygiene of DCC staff and children; presence of infection prevention preconditions; and assessment of environmental contamination measured by adenosine triphosphate (ATP) reporting Relative Light Units (RLU). PHS professionals were trained to assess IPP at DCCs to ensure standardized implementation.

RESULTS

Twenty-eight DCCs with 92 child groups were included. The IRIS demonstrated that in 73.9% of the 92 groups DCC staff wore rings, 69.6% wore bracelets and/or watches and 76.1% wore long sleeves during activities e.g. changing diapers and preparing food. Overall, children washed hands after playing outside (79.3%), after going to the toilet (54.4%) and before eating food (71.7%). Of all child groups 72.9% had children sized toilets, and 73.9% had children sized handwashing facilities. Of 1305 ATP measurements 401 (30.1%) items were considered clean (<1,000 RLU), 337 (25.8%) intermediate (≥1,000 <3,000 RLU), 309 (23.7%) contaminated (≥3,000 and <10,000 RLU) and 258 (19.8%) extremely contaminated (≥10,000 RLU).

CONCLUSIONS

These preliminary findings show that various IPP aspects at DCCs did not meet the standards set by the IRIS expert group. DCCs can use these results to improve basic hygiene and increase awareness of relevant hygiene points.

Keywords: Child Day Care Centres, Infection Control, Risk factors, Netherlands
ABSTRACT ID: 480
PRESENTED BY: E.M. den Boogert, Netherlands / e.den.boogert@ggdhvb.nl

FIRESIDE SESSION 6

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Frameworks to support evidence-informed decision-making from a public health perspective and its application in infectious disease prevention and control: A scoping review

J. Bracchiglione [1]
Y. Song [2], B. Albiger [3], H. Gomes [4], J. Meneses-Echavez [5], D. Rigau [6], P. Alonso-Coello [7]

[1] Iberoamerican Cochrane Centre (CCIb) - Biomedical Research Institute Sant Pau (IIB Sant Pau), Barcelona, Spain
Centro de Investigación Biomédica en Red de Epidemiología y Salud Pública (CIBERESP), Spain
[2, 6] Iberoamerican Cochrane Centre (CCIb) - Biomedical Research Institute Sant Pau (IIB Sant Pau), Barcelona, Spain
[3, 4] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[5] Norwegian Institute of Public Health, Oslo, Norway
[7] Iberoamerican Cochrane Centre (CCIb) - Biomedical Research Institute Sant Pau (IIB Sant Pau), Barcelona, Spain
Centro de Investigación Biomédica en Red de Epidemiología y Salud Pública (CIBERESP), Barcelona, Spain

BACKGROUND

Evidence-to-Decision (EtD) frameworks guide decision-making processes by explicitly considering several criteria. EtD frameworks with a public health (PH) perspective and their application in the infectious diseases' field have not been systematically reviewed. We aim to identify and describe EtD frameworks from a PH perspective, including examples and experience of use, in the infectious diseases field.

METHODS

We conducted a scoping review. We included documents describing structured processes for moving from evidence to decisions at the health system or PH level on behalf of a population. We also identified examples and experiences of their use in the infectious diseases field. We searched MEDLINE and Health System Evidence (2013-2023). We reviewed the websites of 60 institutions, conducted citation searches, and surveyed key stakeholders. Pairs of reviewers selected the studies and extracted the following data: frameworks' scope, target audience and setting, categories of decisions, methods for development, definition of 'evidence', and decision-making criteria. We also described the identified examples, barriers, and facilitators.

RESULTS

Preliminarily, we have identified 21 EtD frameworks. GRADE-EtD and WHO-INTEGRATE were the most cited frameworks, with the former being the most common in infectious diseases. Users of both the GRADE-EtD and WHO-INTEGRATE frameworks value the structured processes and transparency, but sometimes have concerns about the wording or how to assess specific criteria. We have found no description of experience using other frameworks yet.

CONCLUSIONS

This scoping review will guide panels in selecting the most suitable framework for making decisions from a PH perspective and further inform methodological research on decision-making processes from a PH perspective.

Keywords: Health Policy, Decision Making, Guidelines as Topic, Evidence-Based Medicine, Public Health
ABSTRACT ID: 666
PRESENTED BY: Pablo Alonso-Coello, Spain / palonso@santpau.cat

FIRESIDE SESSION 6

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Invitation and reminders for shingles vaccination improves uptake among patients registered with a GP. A cross-sectional survey of General Practices in Wales, 2022

F. Rowley [1]
C. Howard [2], N. Meredith [3], J. Song [4], A. Barassa-Blanco [5], S. Cottrell [6]

[1] UKFETP | Public Health Wales | UK Health Security Agency
[2, 3, 4, 6] Public Health Wales
[5] UK Health Security Agency

BACKGROUND
In 2013, shingles vaccination was introduced in Wales as a routine immunisation programme for older adults. National policy does not mandate invitation for this vaccination. We surveyed General Practices (GPs) to investigate if invitations and reminders are associated with higher uptake of shingles vaccine.

METHODS
Using data from GPs, we calculated GP-level shingles vaccine uptake between 01/07/2021 and 31/06/2022 for registered patients aged 70-84 years. We distributed an online survey via email to all GPs in Wales investigating whether practices sent invites and reminders for vaccination.We used linear regression to calculate coefficients and 95%CI to measure associations between invitations and vaccine uptake, adjusting for key demographics, with a multi-level component to account for similarities between GPs within the same health board.

RESULTS
Survey response rate was 37% (143/384). Median vaccine uptake for responding GPs was 57% (IQR 50-68%) compared to 58% (IQR 48-68%) nationally. GPs inviting all eligible patients (n=95) had a 9% (95%CI 6-13%) higher vaccination uptake compared to those inviting none or some (n=48, p<0.001).Of GPs sending invitations, those who reminded all patients (n=42) had a 6% (95%CI 1-11%, p=0.02) higher uptake compared to those that reminded none (n=30), GPs reminding some patients had no statistical difference (95%CI -0.2-9%, p=0.06).

CONCLUSIONS
Not all GPs in Wales invite for shingles vaccination. GPs inviting and reminding all eligible patients for shingles vaccination have a higher uptake compared to those inviting and reminding only some or none. We recommend national vaccine policy should mandate vaccine invitation for shingles in GPs.

Keywords: Aged, Multivariate Analysis, Herpes Zoster, Vaccination, Cross-Sectional Studies
ABSTRACT ID: 137
PRESENTED BY: Frances Rowley, United Kingdom / frances.rowley@wales.nhs.uk

FIRESIDE SESSION 6

DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Perceived barriers and facilitators to infection prevention and control in Dutch residential care facilities for people with intellectual and developmental disabilities: a cross-sectional study

F. Houben [1]
C. den Heijer [2], N. Dukers-Muijrers [3], C. Hoebe [4]
[1, 2, 3, 4] Public Health Service South Limburg

BACKGROUND

Adequate implementation of infection prevention and control (IPC) in residential care facilities (RCFs) for people with intellectual and developmental disabilities (IDDs) is crucial to safeguard this vulnerable population. We aimed to identify perceived barriers and facilitators to IPC among professionals working in these settings, along with recommendations to improve IPC, to inform targeted intervention development.

METHODS

An online questionnaire was administered to 323 professionals from 16 Dutch RCFs (March 2021-March 2022). Perceived barriers and facilitators (on the guideline, client, interpersonal, organisational, and broader environment/policy level) were measured on a 5-point Likert scale (totally disagree-totally agree), for which 'agree' and 'totally agree' responses were classified as barriers/facilitators. Recommendations were assessed using a 5-point Likert scale (not at all helpful-extremely helpful), supplemented by an open-ended question. Barriers, facilitators, and recommendations were analysed by descriptive statistics. Open answers to recommendations were analysed using thematic coding.

RESULTS

Barriers included the client group (e.g., lack of IPC awareness) (63%), dilemmas between IPC and culture of domesticity (42%), high work pressure (39%) and abundance of guidelines/protocols (33%). Facilitators were perceived social support (90%), procedural clarity of guidelines (83%), and organisational sense of urgency (74%). Main recommendations included clear IPC policies and regulations (86%), a practical IPC guideline (84%), and structural education and training programmes (especially aimed at new employees) (85%), while professionals also emphasised the need for IPC improvement efforts to be tailored to the local care context and involve clients and their relatives.

CONCLUSIONS

IPC improvement strategies in disability care settings should aim to involve clients (and relatives), develop a practical and context-specific IPC guideline, encourage social support among colleagues through peer coaching, reduce workload, and create an IPC culture within the organisation.

Keywords: COVID-19, Infection Control, Long-term care, Intellectual Disability, Developmental disability, Cross-Sectional Studies
ABSTRACT ID: 70
PRESENTED BY: Famke Houben, Netherlands / famke.houben@ggdzl.nl

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FIRESIDE SESSION 6
DAY 2 – THURSDAY 23 NOVEMBER 2023
11:00-12:30

Health promotion and disease prevention

MODERATOR
Petronille Bogaert

Abstract

Public considerations about implementing non-pharmaceutical interventions to manage a novel COVID-19 epidemic

S. Kemper [1]
M. de Vries [2], E. de Weger [3], M. Bongers [4], F. Kupper [5], A. Timen [6]

[1] Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands | Athena Institute, Faculty of Science, VU University Amsterdam, Amsterdam, The Netherlands
[2, 4] Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[3, 5] Athena Institute, Faculty of Science, VU University Amsterdam, Amsterdam, The Netherland
[6] Department of Primary and Community Care, Radboud University Medical Center, Nijmegen, The Netherlands Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands | Athena Institute, Faculty of Science, VU University Amsterdam, Amsterdam, The Netherlands.

BACKGROUND
In the future, new variants of the SARS-CoV-2 virus might emerge and cause outbreaks. When these occur, implementing non-pharmaceutical interventions (NPIs) could protect the health of citizens. Currently, decision-making regarding NPIs is mainly executed by experts and governments, even though numerous institutions have emphasized the importance of engaging public views in pandemic response. Therefore, in this study, the public perspective regarding the implementation of NPIs is elucidated.

METHODS
In May 2023, a live deliberative mini-public (DMP) of 2.5 hours with 44 participants was executed in the Netherlands. A diverse group of citizens convened and deliberated in groups about their considerations when implementing NPIs during a hypothetical outbreak of a new SARS-CoV-2 variant. The participants were asked to act as decision-makers and were briefed by experts in pandemic response. The group deliberations during the DMP were thematically analysed.

RESULTS
Participants found it important to implement NPIs early on to prevent exceeding healthcare capacity, long-term mental health issues, educational deficits, and bankruptcies. Simultaneously, participants emphasized that the public support for NPIs should be considered, and participants shared how this could remain high. Furthermore, participants wanted to give citizens personal responsibility and freedom in making their own assessment regarding which NPIs to take and how much risk citizens are willing to accept. Also, participants needed the government to be more reflective regarding improvements in pandemic responses and to generate more focus on long-term strategies.

CONCLUSIONS
The gathered public considerations about NPIs might be beneficial to integrate in pandemic responses, to create policies that ultimately better align with public values. Moreover, DMPs seem a promising method to yield public needs, values and preferences about implementing NPIs, such as prevention, freedom and autonomy.

Keywords: COVID-19, Public participation, Policy-making, Public health, Communicable disease control
ABSTRACT ID: 854
PRESENTED BY: Sophie Kemper, Netherlands / sophie.kemper@rivm.nl

FIRESIDE SESSION 7

DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45 - 15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

Vaccine effectiveness against influenza A(H3N2), A(H1N1)pdm09 and B: Results from the 2022–23 season European VEBIS primary care multicentre study

M. Maurel [1]

F. Pozo [2], L. Goerlitz [3], I. Martínez-Baz [4], M. de Lange [5], N. Latorre-Margalef [6], M. Mihai [7], G. Pérez-Gimeno [8], J. Horváth [9], A. Machado [10], L. Domegan [11], M. Ilic [12], N. Sève [13], R. Dürrwald [14], J. Castilla [15], A. Meijer [16], T. Samuelsson-Hagey [17], M. Lazar [18], C. Mazagatos [19], G. Turi [20], R. Guiomar [21], J. O'Donnell [22], V. Visekruna Vucina [23], A. Falchi [24], S. Bacci [25], M. Kaczmarek [26], E. Kissling [27], (GROUP) European primary care vaccine effectiveness group

[1] Epidemiology Department, Epiconcept, Paris, France
[2, 14, 15, 16, 17, 18, 20, 22] Instituto de Salud Carlos III, Madrid, Spain
[3] Robert Koch Institut, Berlin, Germany
[4] Instituto de Salud Pública de Navarra - IdiSNA - CIBERESP, Pamplona, Spain
[5] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[6] Microbiology Department, The Public Health Agency of Sweden (PHAS)
[7] Cantacuzino National Military Medical Institute for Research and Development, Bucharest, Romania
[8] tional Centre of Epidemiology, CIBERESP, Carlos III Health Institute. Madrid, Spain
[9] National Laboratory for Health Security, Epidemiology and Surveillance Centre, Semmelweis University, Budapest, Hungary
[10] Department of Epidemiology, National Institute of Health Doutor Ricardo Jorge
[11] Health Service Executive- Health Protection Surveillance Centre, Dublin, Ireland
[12, 23] Croatian Institute of Public Health (CIPH), Zagreb, Croatia
[13] INSERM, Sorbonne Université, Institut Pierre Louis d'épidémiologie et de Santé Publique (IPLESP UMRS 1136), Paris, France
[19] National Centre of Epidemiology, CIBERESP, Carlos III Health Institute. Madrid, Spain
[21] Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge
[24] Laboratoire de Virologie, Université de Corse-Inserm, Corte, France
[25, 26] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[27] Epidemiology Department, Epiconcept, Paris, France

BACKGROUND

In 2022–23, the VEBIS primary care network conducted a multicentre test-negative case-control study in 10 European countries to measure influenza vaccine effectiveness (IVE) against influenza A(H3N2), A(H1N1)pdm09 and B.

METHODS

General practitioners swabbed patients presenting with acute respiratory infection or influenza-like illness, collecting information on demographics, vaccination and clinical characteristics. Cases were RT-PCR positive for influenza viruses A(H3N2), A(H1N1)pdm09 or B; controls were negative for any influenza virus. Using logistic regression, we calculated IVE as (1-odds ratio of vaccination)*100, adjusting for study site, age, sex, symptom onset date, and presence of chronic conditions. We estimated IVE overall and by age group, sample size permitting.

RESULTS

From September 2022 to April 2023, we included 30,827 patients; 3,764 were positive for influenza A(H3N2), 1,420 for A(H1N1)pdm09 and 2,907 for influenza B.Overall IVE against influenza A(H3N2) was 37% (95%CI: 26–47). It was 56% (95%CI: 34–71), 35% (95%CI: 19–48) and 26% (95%CI: -2–46) among those aged 0–14, 15–64 and ≥65 years, respectively.Overall IVE against influenza A(H1N1)pdm09 was 44% (95%CI: 31–54). It was 52% (95%CI: 18–74), 50% (95%CI: 35–62) and 29% (95%CI: -9–53) among those aged 0–14, 15–64 and ≥65 years, respectively.Overall IVE against influenza B was 76% (95%CI: 68–82). It was 83% (95%CI: 72–90) and 74% (95%CI: 63–82) among those aged 0–14 and 15–64 years, respectively.

CONCLUSIONS

The 2022–23 IVE results indicated that vaccination reduced the risk of primary care attended influenza B by 76%. Influenza A vaccine components halved the risk in children and provided limited protection for older adults. We plan to estimate (sub)clade-specific IVE to better understand differences by time and age.

Keywords: Influenza, Influenza vaccine, Vaccine effectiveness, Multicentre study, Case control studies, Test-negative design
ABSTRACT ID: 317

PRESENTED BY: Marine Maurel, France / m.maurel@epiconcept.fr

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DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45-15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

2022/23 seasonal vaccine effectiveness against hospitalised influenza A: pooled results from 7 countries participating in the European Vaccine Effectiveness, Burden and Impact Studies (VEBIS) project

A. Rose [1]
F. Pozo [2], I. Martínez-Baz [3], C. Mazagatos [4], S. Abela [5], BELSARI-Net [6], G. Petrovic [7], M. Lazar [8], M. Kuliese [9], R. Dürrwald [10], J. Horváth [11], J. O'Donnell [12], A. Machado [13], J. Howard [14], S. Bacci [15], J. Castilla [16], M. Lozano Álvarez [17], G. Xuereb [18], I. Tabain [19], S. Popovici [20], F. Majauskaite [21], K. Tolksdorf [22], B. Oroszi [23], L. Domegan [24], C. Henriques [25], R. Li [26], N. Nicolay [27], (GROUP) ECDC VEBIS Hospital study team

[1] Epiconcept, Paris
[2, 18] National Centre for Microbiology, Institute of Health Carlos III, Madrid
[3, 16] Instituto de Salud Pública de Navarra (IdiSNA), CIBERESP, Pamplona
[4] National Centre of Epidemiology, CIBERESP, Carlos III Health Institute, Madrid
[5] Infectious Disease Prevention and Control Unit IDCU), Health Promotion and Disease Prevention, Msida
[6] Sciensano, Brussels
[7, 19] Croatian Institute of Public Health, Zagreb
[8] Cantacuzino National Military-Medical Institute for Research and Development, Bucharest
[9] Department of Infectious Diseases, Lithuanian University of Health Sciences, Kaunas
[10] National Reference Centre for Influenza, Robert Koch Institute, Berlin
[11, 23] National Laboratory for Health Security, Epidemiology and Surveillance Centre, Semmelweis University, Budapest
[12, 24] HSE-Health Protection Surveillance Centre (HPSC), Dublin
[13, 25] Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisbon
[14, 26] Epiconcept, Paris
[15, 27] European Centre for Disease Prevention and Control, Stockholm
[17] National Centre of Epidemiology, Carlos III Health Institute, Madrid
[20] National Centre for Communicable Diseases Surveillance and Control, Institute of Public Health, Bucharest
[21] Clinic of Infectious Diseases and Dermatovenerology, Institute of Clinical Medicine, Medical Faculty, Vilnius University, Vilnius
[22] Department for Infectious Disease Epidemiology, Respiratory Infections Unit, Robert Koch Institute, Berlin

BACKGROUND

In the 2022/23 season, influenza A(H1N1)pdm09, A(H3N2) and B viruses co-circulated in Europe. We aimed to measure influenza vaccine effectiveness (IVE) against hospitalisation with laboratory-confirmed influenza A overall and by subtype for this season, through the VEBIS multicentre project.

METHODS

Hospital teams swabbed patients admitted with severe acute respiratory infection (SARI) ≤7 days before symptom onset, collecting information on demographics, influenza vaccination, chronic conditions and RT-PCR results. We defined cases as SARI patients RT-PCR positive for influenza A (sub)types; controls as those RT-PCR negative for any influenza virus. We estimated IVE using logistic regression, adjusting for study site, swab date, age and chronic condition.

RESULTS

Between October 2022 and April 2023, we included 796 influenza A cases and 4,962 controls from 41 hospitals in seven countries. Most cases (375; 47%) were influenza A(H3N2); 246 (31%) were A(H1N1)pdm09, 175 (22%) A (unsubtyped). Seasonal influenza vaccination coverage was 38% for cases (n=300); 48% for controls (n=2,372). IVE against 2022/23 seasonal influenza A overall (all ages) was 21% (95%CI: 4–35). For those in influenza vaccine target groups (IVTGs), all-A influenza IVE was 25% (7–40). Low vaccine coverage in some younger age-groups made VE estimates in these groups difficult to interpret. For 18–64 years, IVE against influenza A(H1N1) pdm09 was 20% (95%CI: -106–69). For ≥65 years, IVE against influenza A(H3N2) and A(H1N1)pdm09 was 24% (95%CI: -32–57) and 44% (2–68), respectively; for those in IVTGs, IVE was 25% (95%CI: -25–55) and 41% (1–65), respectively.

CONCLUSIONS

Our results suggest protection during the 2022/23 influenza season against hospitalisation with influenza A for one-in-five to two-in-five influenza-vaccinated adult SARI patients, depending on age-group and subtype.

Keywords: Influenza, Vaccine effectiveness, Hospital, Europe

ABSTRACT ID: 671

PRESENTED BY: Jennifer Howard, France / j.howard@epiconcept.fr

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DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45-15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

Varicella zoster as a risk factor for invasive Group A Streptococcal infection in children aged 6 months to 5 years, a prospective case control study in the Netherlands

I. Hazelhorst [1]
K. van Ewijk [2], L. Wielders [3], M. te Wierik [4], S. Hahne [5], H. de Melker [6], M. Knol [7], B. de Gier [8]

[1, 2] RIVM | ECDC | EPIET
[3, 4, 5, 6, 7, 8] RIVM

BACKGROUND

In 2022, an increase of invasive Group A Streptococcal infection (iGAS) cases was observed in the Netherlands, compared to pre-COVID years 2016-2019. Among children aged 0-5 years, there was a sevenfold increase, including 9 reported fatalities among 42 cases. In consequence, all iGAS manifestations became notifiable by 2023 and post-exposure prophylaxis was indicated for household contacts. We aimed to quantify varicella zoster as a risk factor for iGAS in children aged 6 months to 5 years.

METHODS

We conducted a prospective case-control study between February and May 2023. We used data of notified iGAS cases, defined as invasive disease with GAS cultured from a normally sterile site. Parents of controls were recruited from the general population via social media. Whenever a case was notified, we invited 10 controls, matched on sex and birthyear, to complete an online questionnaire on exposure to varicella zoster in the past 4 weeks. Conditional logistic regression was performed to estimate odds ratios (OR) of exposures.

RESULTS

We included 50 cases; 26 (52%) males and 24 (48%) females. Of 500 invited controls, 300 responded to the questionnaire (response rate 60%), with a median of 5 controls per case (interquartile range 4,5 – 7) of whom 160 (53%) were male and 140 (47%) female. A varicella zoster infection prior to date of onset was reported in 8% (n=4) of cases and 1% (n=3) of controls (OR: 24.2, 95% CI: 2,68-218).

CONCLUSIONS

Varicella zoster infection has been found to increase the risk of iGAS. There might be a benefit to extending post-exposure prophylaxis for any contact of iGAS with varicella zoster infection.

Keywords: Case-control study, Varicella zoster, Risk factor, Children, Streptococcal disease, Netherlands
ABSTRACT ID: 667
PRESENTED BY: Ilse Hazelhorst, Netherlands / ilse.hazelhorst@rivm.nl ail

FIRESIDE SESSION 7
DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45 - 15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

Factors associated with mortality from invasive group A Streptococcus infection, England, 2015-2023

O. McManus [1]
R. Guy [2], T. Lamagni [3], P. Crook [4], C. Brown [5], C. Jarvis [6], C. Byers [7], A. Graham [8], T. Ma [9], F. Halford [10], P. Blomquist [11], E. Heinsbroek [12]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12] UK Health Security Agency

BACKGROUND
In 2022/23, an unprecedented number of invasive group A Streptococcus (iGAS) cases occurred in England, with a high number of deaths. To inform the UK Health Security Agency's incident response, we investigated factors associated with death to assess whether these fully explained the high case-fatality rate (CFR) in 2022/23.

METHODS
We extracted information on laboratory-confirmed iGAS cases (samples from sterile sites) and associated deaths (within 7 days of sample, or post-mortem samples) from England's laboratory reporting system and National Health Service data, from January 2015 to March 2023. Using logistic regression, we examined associations between death and age, sex, respiratory viral co-infection (-14 to +7 days from iGAS sample), emm type, socioeconomic status, season, iGAS year (weeks 37–36), and ethnicity.

RESULTS
In 2022/23 the crude iGAS CFR was 14.1% (328/2,326), compared to 11.5% (1,754/15,222) in 2015–2021/22. Factors independently associated with increased mortality included viral co-infection (odds ratio 2.37, 95% confidence interval 1.98–2.83), emm1 (1.84, 95% CI 1.63–2.07) and 12 (1.30, 95% CI 1.08–1.56), female sex (1.11, 95% CI 1.01–1.22), and season (1.36, 95% CI 1.18–1.58 for winter vs summer). Mortality was lowest for young adults (20–29 years) compared to other age groups, and for people of non-British white ethnicity compared to white-British people (0.54, 95% CI 0.37–0.77). Mortality was consistent for other ethnicities and across deprivation levels. After adjustment for these factors, 2022/23 was not associated with additional higher mortality.

CONCLUSIONS
We identified several factors associated with increased iGAS mortality, which explained the high CFR seen in 2022/23. Surveillance of emm type distribution and concurrent respiratory viral activity is key for early risk assessment of future iGAS waves.

Keywords: Streptococcus pyogenes, Epidemiology, Public health, Epidemiological Models, Mortality, Communicable Diseases
ABSTRACT ID: 577
PRESENTED BY: Oliver McManus, United Kingdom / oliver.mcmanus@ukhsa.gov.uk

FIRESIDE SESSION 7

DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45 - 15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

Factors associated with unfavorable tuberculosis treatment outcomes, Almaty, Kazakhstan, 2018-2021

M. Gabdullina [1]
P. Dzhazybekova [2], G. Amanova [3], R. Horth [4], D. Nabirova [5]

[1] Central Asia Field Epidemiology Training Program |
National Scientific Center of Phthisiopulmonology Asfendiyarov Kazakh National Medical University
[2, 5] National Scientific Center of Phthisiopulmonology
[3] Central Asia Field Epidemiology Training Program
Scientific and Practical Center for Sanitary and Epidemiological Expertise and Monitoring
[4] US Centers for Disease Control and Prevention
Central Asia Field Epidemiology Training Program
Asfendiyarov Kazakh National Medical University

BACKGROUND
The COVID-19 pandemic negatively influenced timely TB detection, diagnosis, and treatment around the world. We aimed to assess the impact of the COVID-19 pandemic on TB treatment outcomes in Almaty, and to determine factors associated with unfavorable TB treatment outcomes before (2018-2019) and during the pandemic (2020-2021).

METHODS
We conducted a retrospective cohort study among newly diagnosed drug-sensitive TB patients >18 years old who initiated treatment from 2018-2021 in Almaty. We abstracted data from the national TB registry. Unfavorable treatment outcomes included: ineffective treatment, death, loss for follow-up, results not evaluated, and transferred for treatment with second-line anti-TB drugs. We used multivariate Poisson regression to calculate adjusted relative risk [aRR] and 95% confidence intervals [95%CI].

RESULTS
Among 1548 study participants, average age was 43 years (range 18-93) and 52% were male. A higher proportion of people had unfavorable treatment outcomes during the pandemic (2020-21) than before the pandemic (2018-19) (20% vs 11%, respectively, and aRR=1.8; CI: 1.4-2.2). Among those with unsuccessful outcomes, 1% were lost to follow-up, 3% had treatment failures, and 9% died. Risk factors for unfavorable treatment outcomes were: being male (aRR=1.4, 95%CI=1.1-1.8), having HIV (aRR=2.4, 95%CI=1.8-3.3), having drinking disorder (aRR=2.3, 95%CI=1.6-3.3) and experiencing homelessness (aRR=2.6, 95%CI=1.5-4.3). Protective factors for unfavorable treatment outcomes were: being 18-39 years old (aRR=0.4, 95%CI=0.3-0.6), 40-59 years old (aRR=0.6, 95%CI=0.4-0.8), and being student (aRR=0.1, 95%CI=0.02-0.9).

CONCLUSIONS
The COVID-19 pandemic was associated with unfavorable treatment outcomes for people newly diagnosed with drug-sensitive tuberculosis in Almaty, Kazakhstan. People with lower social stability were at increased risk. Results point to the need for improved continuity of care for TB treatment for people at increased risk of unfavorable outcomes, especially during disease outbreaks and pandemics.

Keywords: Tuberculosis, COVID-19, Pandemic, Kazakhstan, HIV
ABSTRACT ID: 367
PRESENTED BY: Malika Gabdullina, Kazakhstan / gabdullina.malika@gmail.com

FIRESIDE SESSION 7

DAY 2 – THURSDAY 23 NOVEMBER 2023
13:45-15:15

Respiratory infections

MODERATOR
Piotr Kramarz

Abstract

Influenza and Covid-19 vaccine effectiveness against associated hospital admission and death among individuals over 65 years in Norway: a population-based cohort study, 3 October 2022 to 20 June 2023

E. Seppälä [1]
J. Dahl [2], L. Veneti [3], K. Rydland [4], B. Klüwer [5], A. Rohringer [6], H. Meijerink [7]
[1] Norwegian Institute of Public Health
[2, 3, 4, 5, 6, 7] Norwegian Institute of Public Health

BACKGROUND
Co-circulation of influenza virus and SARS-CoV-2 can lead to double epidemics and increased pressure on health systems. Little data is available on the performance of influenza and Covid-19 vaccines during intense co-circulation of these viruses. We estimated the adjusted vaccine effectiveness (aVE) of influenza and Covid-19 vaccines against severe disease in elderly in the 2022-2023 season in Norway when influenza and Covid-19 peaked simultaneously.

METHODS
In this cohort study, we included register data on all individuals ≥65 years, living in Norway. Using Cox proportional hazard models, we estimated aVE (95% confidence interval) of influenza and Covid-19 vaccines against hospitalisation and death associated with laboratory confirmed influenza and Covid-19, respectively, between 3 October 2022 and 20 June 2023. Vaccine status was included as a time-varying covariate and all models were adjusted for potential confounders (age, sex, resident county, birth country, education, medical risk group and the other vaccine).

RESULTS
We identified 2429 influenza-associated hospitalisations and 176 deaths, alongside 5837 Covid-19-associated hospitalisations and 621 deaths. The aVE against influenza-associated hospitalisation was highest in the first three months after vaccination; compared to unvaccinated, the aVE was 32% (23%-40%) among 65-79-year-olds and 39% (29%-48%) among ≥80-year-olds. The aVE against influenza-associated death was not significant. Similarly, the highest aVE against Covid-19-associated hospitalisation was 65% (61%-69%) among 65-79-year-olds and 54% (48%-60%) among ≥80-year-olds in the first three months after vaccination, compared to those vaccinated against Covid-19 ≥180 days ago. The aVE against Covid-19-associated death was 68% (48%-80%) and 78% (65%-86%) in these age groups, respectively.

CONCLUSIONS
Covid-19 and influenza vaccines reduced the risk of severe disease in the high-risk population. Ensuring high uptake of both vaccines could thus limit the overall health care burden.

Keywords: Vaccine effectiveness, COVID-19 Vaccines, Influenza Vaccines, COVID-19, Human influenza, Hospitalization, Death, Cohort study, Norway
ABSTRACT ID: 882
PRESENTED BY: Hinta Meijerink, Norway / hinta.meijerink@fhi.no

FIRESIDE SESSION 8

FRIDAY 24 NOVEMBER 2023
11:00-12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Incidence of healthcare-associated infections in Greek long-term care facility residents, May-December 2022 (GR-H4LS)

C. Kavakioti [1]
D. Krystallaki [2], S. Sypsa [3], D. Kalotychou [4], L. Politi [5], K. Mellou [6]

[1, 2, 3, 4] National Public Health Organization, Athens, Greece
[5] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden | Department of Microbial Resistance and Infections in Health Care Settings, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[6] Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece

BACKGROUND
The burden of healthcare-associated infections (HAIs) in elderly residents of long-term care facilities (LTCFs) in Greece remains elusive. This study aimed to estimate HAI incidence among residents and identify possible risk factors.

METHODS
A prospective pilot study using ECDC H4LS protocol was conducted. A cohort of 250 residents of 4 LTCFs (convenience sample) was followed up during May-December 2022. HAI incidence (number of infections/1000 resident-days) and infection duration were recorded. LTCFs' and residents' characteristics (e.g., total beds, infection control indicators, demographics, medical conditions) were recorded at start and end of the study period. Microbiological information was retrieved from available laboratory testing. Univariate and logistic regression analysis were performed to identify potential risk factors for HAI.

RESULTS
Median resident age was 86 years (IQR: 11) and 76.4% were female. HAI incidence was 1.1 infection/1000 resident-days (51/45,903) and median duration was 6 days (IQR: 4). Of the 51 recorded HAIs, 20 were SARS-CoV-2 infections (39.2%) in 2 LTCF clusters, 8 urinary tract infections (UTIs, 15.7%), 7 upper and 5 lower respiratory tract infections (13.7% and 9.8%, respectively), 5 skin/soft tissue infections (9.8%) and 3 gastrointestinal (5.9%) including one C. difficile infection (1.9%). Laboratory data were available for 6 UTIs; only E. coli was identified. Resistance to third generation cephalosporins was reported for 16.7%(1/6) of tested isolates; all were susceptible to carbapenems. HAI acquisition was associated with higher age (b=1.05, p-value=0.041). Residing in a LTCF with functionally independent residents was protective (b=0.79, p-value=0.019).

CONCLUSIONS
This study was the first effort to quantify the HAI burden in this vulnerable population. Subsequent studies are needed to further understand AMR burden and compliance to infection control measures in LTCFs to support public health interventions.

Keywords: Infections, Long-term care facilities, Incidence, COVID-19, HAIs, Resident
ABSTRACT ID: 76
PRESENTED BY: Lida Politi, Greece / l.politi@eody.gov.gr

FIRESIDE SESSION 8
DAY 3 – FRIDAY 24 NOVEMBER 2023
11:00-12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Outbreak of iatrogenic botulism post intragastric botulinum neurotoxin treatment for obesity – travel-associated cases in Germany

C. Frank [1]
M. B. Dorner [2] , H. Wilking [3], B. G. Dorner [4]
[1, 2,3, 4] RKI

BACKGROUND
Iatrogenic botulism (IB), caused by exposure to botulinum neurotoxin (BoNT) for medical or cosmetic purposes, is rare but serious. Minute toxin doses and lag-time hinder laboratory confirmation.

METHODS
Clinical botulism is legally notifiable in Germany. In early March 2023, Germany informed widely about travel associated cases of botulism following intragastric BoNT injection (IBNI) in Türkiye aimed at reducing obesity. We describe the epidemiological and laboratory investigation of the German cases, including active case finding off a list of IBNI recipients provided by Turkish authorities.

RESULTS
Thirty botulism cases post IBNI (29 treated in one hospital in Istanbul, 1 in an Izmir hospital) were notified in Germany in early 2023: 21 women and 9 men (all adults) with botulism symptom onset 18 January through 9 March, 0-12 days post IBNI. Twenty-two (73%) were hospitalized, 6/28 (21%) in intensive care, none died. In active case finding, the attack rate (symptomatic botulism) was 22/26 (85%) among all listed IBNI recipients. In 9 out of 12 cases with serum samples innovative endopeptidase assays detected minute traces of botulinum neurotoxin in serum taken up to 11 days after IBNI.

CONCLUSIONS
Zero to 24 (median 6.5) botulism cases were reported annually 2001-2022 in Germany, but no IB cases, rendering the 30 IB outbreak cases in 2023 highly unusual. In Türkiye, Switzerland, Austria, and France associated cases were also noted. Endopeptidase assays proved essential in laboratory confirmation. The exact mechanism, source or error resulting in IB after IBNI remains unclear, but likely involved an overdose. We consider IBNI in these cases causal. Potential risks associated with procedures such as IBNI need to be carefully balanced with expected benefits. Effectiveness of IBNI remains unclear.

Keywords: Botulism, Botulinum Toxins, Outbreak, Medical tourism, Iatrogenic
ABSTRACT ID: 62
PRESENTED BY: Christina Frank, Germany / frankc@rki.de

FIRESIDE SESSION 8

DAY 3 – FRIDAY 24 NOVEMBER 2023
11:00-12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Update: Disability-adjusted life-years and attributable deaths caused by bloodstream infections due to vancomycin-resistant Enterococcus faecium in Germany, 2015-2021

S. Brinkwirth [1]
I. Noll [2], M. Feig [3], T. Eckmanns [4], S. Haller [5], N. Willrich [6]

[1] Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany and European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Unit 37: Healthcare-Associated Infections, Surveillance of Antibiotic Resistance and Consumption, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[2, 4, 5, 6] Unit 37: Healthcare-Associated Infections, Surveillance of Antibiotic Resistance and Consumption, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
3 Unit IT4: Development, Department of Methods Development, Research Infrastructure and Information Technology, Robert Koch Institute, Berlin, Germany

BACKGROUND

In Germany, we detected an increasing spread of vancomycin-resistant Enterococcus faecium (VREfm) bloodstream infections (BSIs). This study aims to analyse the burden of VREfm-BSIs in disability-adjusted life years (DALYs) and attributable deaths from 2015 to 2021 in order to quantify this emerging public health issue.

METHODS

We analysed routine diagnostic data from the voluntary laboratory-based Antibiotic Resistance Surveillance (ARS) system to estimate the incidence of VREfm-BSIs per 100,000 inhabitants (inhabitants). A reported VREfm isolate in blood culture was classified as a proxy of BSI. Incidence was estimated based on the number of isolates (n = 4,488) and the proportion of hospitals covered in ARS in the respective year (range: 21% to 39%). The incidences were entered into the Burden of Communicable Disease in Europe toolkit to estimate associated DALYs per inhabitants and attributable deaths with 95% uncertainty intervals (UI), stratified by age and sex.

RESULTS

The DALYs per inhabitants due to VREfm-BSIs increased from 8.3 (95%UI: 7.2-9.5) in 2015 to 17.9 (95%UI: 16.7-19.3) in 2021. The estimated attributable deaths increased from 263 (95%UI: 230-300; 0.32/inhabitants) in 2015 to 625 (95%UI: 587-667; 0.75/inhabitants) in 2021. The most affected age category are the 65-69-year-olds, while infants were most affected in the age categories under 30 years. The VREfm-BSI burden was higher in males compared to females (68% vs. 32%).

CONCLUSIONS

Our results emphasise the increasing burden, particularly in older hospitalised males and infants. We recommend continuous and comprehensive surveillance of VREfm to monitor the development and spread over time. Furthermore, the burden quantification of other BSI-causing pathogens is necessary to assess and compare the impacts of different (resistant) pathogens.

Keywords: Enterococcus faecium, VRE, VREfm, AMR, DALYs, Burden of Disease
ABSTRACT ID: 541
PRESENTED BY: Simon Brinkwirth, Germany / brinkwirths@rki.de

FIRESIDE SESSION 8
DAY 3 – FRIDAY 24 NOVEMBER 2023
11:00-12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Genotypic and phenotypic antimicrobial resistance in Clostridioides difficile in the overall Irish population, 2022

L. Brouwer [1]
A. Carroll [2], E. McNamara [3]
[1, 2, 3] Public Health Laboratory, HSE, Dublin, Ireland

BACKGROUND
Infection with Clostridioides difficile (C. difficile) usually occurs after antibiotic treatment for other infections and can cause gastro-intestinal disorders of variable severity. C. difficile is resistant against a wide spectrum of antibiotics. Correlation between genotypic markers and phenotypic antimicrobial resistance (AMR) is not well defined, requiring costly and time-consuming phenotypical analyses. The aim of this study is to assess the correlation between genotypic and phenotypic resistance in C. difficile isolates from Public Health Laboratory in Ireland (2022) to identify antibiotics for which phenotypic resistance can be predicted from genetic indicators.

METHODS
A total of 99 C. difficile isolates were phenotypically characterized for resistance to cefoxitin, clindamycin, moxifloxacin, tetracycline, vancomycin, metronidazole and imipenem using ANAERO3 Sensititre plates, and to rifampicin using E-tests. The genomes were screened for point mutations and antibiotic resistance genes using BioNumerics.

RESULTS
We found high rates of resistance (>90%) for cefoxitin, intermediate rates (10% - 60%) for moxifloxacin, clindamycin and tetracycline and low rates (<10%) for imipenem, metronidazole, vancomycin and rifampicin. The majority of the isolates did not contain genetic markers for the last 4 antibiotics (88% – 100%). All isolates contained genetic markers for cefoxitin resistance. For moxifloxacin and tetracycline, correlations between genotypic and phenotypic AMR were high, with accuracies of 95% and 87%, respectively. The accuracy for clindamycin was 60%.

CONCLUSIONS
Our data suggests that phenotypic resistance against moxifloxacin and tetracycline in C. difficile may be predicted from genetic indicators, while this is not the case for clindamycin. For the other five antibiotics, larger datasets are needed to determine the correlation between phenotypical resistance and genetic markers to allow for implementation of less time-consuming and costly phenotypic testing.

Keywords: Clostridioides difficile, Drug Resistance Microbial, Genetic Association Studies, Genotype, Phenotype
ABSTRACT ID: 200
PRESENTED BY: Lieke Brouwer, Ireland / lieke.brouwer@hse.ie

FIRESIDE SESSION 8
DAY 3 – FRIDAY 24 NOVEMBER 2023
11:00 - 12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Healthcare-associated hepatitis B and C transmission to patients in the EU/EEA and UK: a systematic review of reported outbreaks between 2006 and 2021

J. Singh [1]
E. Duffell [2], S. Stoitsova [3], K. Zakrzewska [4], L. Henszel [5], M. Rosinska [6]

[1] European Centre for Disease Prevention and Control (ECDC) | UK Health Security Agency (UKHSA)
[2] European Centre for Disease Prevention and Control (ECDC)
[3] European Programme for Intervention Epidemiology Training (EPIET) | National Institute of Public Health NIH, National Research Institute, Poland
[4, 5, 6] National Institute of Public Health NIH, National Research Institute, Poland

BACKGROUND
Healthcare-associated transmission was the second most common transmission route for hepatitis B (HBV) and hepatitis C (HCV) in 2006-2012 European surveillance data, but the true burden is unclear due to data quality issues. We carried out a systematic review of published literature on healthcare-associated transmission of HBV or HCV to gain a fuller understanding of the epidemiological situation and identify higher-risk settings.

METHODS
We searched the PubMed and EMBASE databases over the period January 2006 to September 2021, for publications reporting transmission events after 2000 in the EU/EEA and UK related to a healthcare setting or procedure. We collected data on the country, number of patients, setting type and route of transmission for each event.

RESULTS
We identified 91 nosocomial transmission events (43 HBV and 48 HBC) in the literature reported from 16 EU/EEA countries and the UK between 2006 and 2021, resulting in a total of 442 infections. Most events were reported from Italy (7 HBV; 12 HCV), Germany (8 HBV; 5 HCV) and the UK (8 HBV; 5 HCV). The most common settings reported included ‘multi-settings’ for events involving blood products (21%), dialysis units (18%), inpatient wards (14%), nursing homes (11%) and haematology/oncology units (11%). A breach of infection prevention control (IPC) precautions was the most commonly reported risk factor (30% of studies) followed by contamination of blood products (26%).

CONCLUSIONS
Healthcare-associated transmission of HBV and HCV continues to occur in a range of healthcare settings across EU/EEA countries, although the true extent cannot be fully determined due to under-reporting and publication bias. Strict IPC precautions should be implemented across all healthcare settings and surveillance systems strengthened to improve reporting of nosocomial infections across the EU.

Keywords: Hepatitis B, Hepatitis C, Healthcare-associated, Transmission route
ABSTRACT ID: 240
PRESENTED BY: Jasleen Singh, United Kingdom / jasleen.singh@nhs.net

FIRESIDE SESSION 8
DAY 3 – FRIDAY 24 NOVEMBER 2023
11:00 - 12:30

Healthcare-associated infections

MODERATOR
Ágnes Hajdu

Abstract

Waterborne outbreak of Mycobacterium abscessus in a UK specialist heart and lung hospital: patients, mitigations and implications.

E. Heinsbroek [1]
I. Roddick [2], U. Hill [3], O. Allen [4], A. Selby [5], D. Allen [6], K. Randall [7], R. Puleston [8], M. Reacher [9], S. Kapadia [10], J. Hoffmann [11], L. Lambourne [12], D. Edwards [13], C. Brown [14], E. Robinson [15], I. Smith [16]
[1, 2, 8, 9, 10, 11, 12, 13, 14, 15] UK Health Security Agency
[3, 4, 5, 6, 7, 16] Royal Papworth Hospital, England

BACKGROUND
A cardiothoracic hospital in England relocated to a new building in May 2019. Three months later two cases of Mycobacterium abscessus were identified post lung transplantation, an infection not previously seen in such patients, triggering an outbreak investigation. Further cases were subsequently identified; investigations identified the hospital water as the most probable source and various mitigations were introduced.

METHODS
Isolates from patients, water and environmental samples identified an outbreak strain by whole genome sequencing. We used hospital admission data to describe attack rates of the strain by patient diagnostic group and calculate the incidence rate of the outbreak strain before and after control measure implementation.

RESULTS
Of 43,756 patients admitted between May 2019 and October 2022, there were 54 new cases of Mycobacterium abscessus. An outbreak strain identified in seven water samples and one environmental sample matched the results for 35 patients (57% male, age 17-82 years). Attack rates of the outbreak strain were highest in lung transplant (9/225: 4.0%) and cystic fibrosis (CF) patients (10/379; 2.6%); cases were also identified in bronchiectasis (13/1704: 0.8%), interstitial lung disease (1/1283: 0.08%), thoracic surgery (1/1809, 0.06%) and cardiac surgery (1/5136: 0.02%) patients. Despite being clinically at risk, there were no cases among heart transplant recipients or patients with other cardiorespiratory diagnoses. After implementation of wide-ranging control measures (e.g. tap and shower filter installation, biocide implementation), the incidence reduced from 17.1 to 2.5 per 100,000 bed-days (p=0.001).

CONCLUSIONS
Patients undergoing lung transplantation were particularly at risk for acquisition of the waterborne outbreak strain followed by patients with CF and bronchiectasis. Extra surveillance and awareness of the potential risks, particularly in new hospital water systems, is required to avoid future outbreaks.

Keywords: Mycobacterium abscessus, Health Care Associated Infections, Waterborne Diseases, Lung Diseases, Immunocompromised Patient, Hospital Design and Construction
ABSTRACT ID: 781
PRESENTED BY: Ellen Heinsbroek, United Kingdom / ellen.heinsbroek@ukhsa.gov.uk

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FIRESIDE SESSION 9

FRIDAY 24 NOVEMBER
11:00 - 12:30

Global health

MODERATOR
John Kinsman

Abstract

Antenatal care-based molecular surveillance of malaria in Mozambique

N. Brokhattingen [1]
A. Pujol [2], G. Matambisso [3], H. Mbeve [4], P. Cístero [5], S. Maculuve [6], B. Cuna [7], C. Melembe [8], N. Ndimande [9], C. da Silva [10], E. Vickers [11], H. Munguambe [12], J. Montaña [13], L. Nhamussua [14], W. Simone [15], L. Quintó [16], A. Chidimatembue [17], H. Martí-Soler [18], B. Galatas [19], C. Guinovart [20], E. Rovira-Vallbona [21], F. Saúte [22], P. Aide [23], A. Aranda-Díaz [24], B. Greenhouse [25], E. Macete [26], A. Mayor [27]

[1, 2, 5, 13, 14, 15, 17, 18, 20, 21, 22, 23] ISGlobal, Hospital Clínic - Universitat de Barcelona, Barcelona
[3, 4, 6, 7, 8, 9, 10, 12] Centro de Investigação em Saúde de Manhiça (CISM), Maputo
[11] EPPIcenter Research Program, Division of HIV, Infectious Diseases, and Global Medicine, Department of Medicine, University of California, San Francisco, California, USA
Chan Zuckerberg Biohub, San Francisco, California
[16, 19] ISGlobal, Hospital Clínic - Universitat de Barcelona, Barcelon
Centro de Investigação em Saúde de Manhiça (CISM), Maputo
[24, 25] EPPIcenter Research Program, Division of HIV, Infectious Diseases, and Global Medicine, Department of Medicine, University of California, San Francisco, California
Chan Zuckerberg Biohub, San Francisco, California
[26] National Institute of Health, Ministry of Health, Maputo
Centro de Investigação em Saúde de Manhiça (CISM), Maputo
[27] ISGlobal, Hospital Clínic - Universitat de Barcelona, Barcelona
Centro de Investigação em Saúde de Manhiça (CISM), Maputo
Spanish Consortium for Research in Epidemiology and Public Health (CIBERESP), Madrid
Department of Physiologica l Sciences, Faculty of Medicine, Universidade Eduardo Mondlane, Maputo

BACKGROUND
Pregnant women attending their first antenatal care (ANC) visit might be a convenient and cost-effective sentinel population for malaria molecular surveillance in sub-Saharan Africa. However, their representability relative to the community remains to be established.

METHODS
Dried blood spots (DBS) were obtained from 8,910 women attending ANC in southern Mozambique in 2016-2019. Plasmodium falciparum (Pf) was detected using quantitative polymerase chain reaction, and anti-Pf antibodies were measured in a multiplex bead immunoassay. 414 Pf-positive DBS were also amplicon-sequenced targeting loci of interest. Trends in Pf positivity rates and prevalence of drug resistance markers in women were compared with those observed in children from community-based surveys using linear regression, Pearson correlation coefficient (PCC), and Z test of proportions.

RESULTS
Pf positivity rates in pregnant women were highly correlated with those in the community regardless of HIV status and gravidity (PCC>0.8), but with a 2-3 month time lag. However, at rapid diagnostic test-detection levels (<100 parasites/µl) for multigravid women in a moderate-transmission setting, correlation was lower (PCC=0.61). Seroprevalence of antibodies against VAR2CSA (DBL3-4 domains), indicating recent infection in pregnancy, also showed high correlation with community Pf positivity trends (PCC=0.74). Similar prevalence of drug resistance was observed at ANC and among children.

CONCLUSIONS

Pregnant women at their first ANC visit could be a valuable sentinel population, mirroring malaria trends in the community, including prevalence of drug resistance. However, ANC trends lag 2-3 months behind, and detectability depends on gravidity when transmission is high, indicating that immunity plays a role. On the other hand, pregnancy-specific VAR2CSA antibodies could be exploited in serosurveillance to improve sensitivity to detect trends.

Keywords: Malaria, Surveillance, Pregnancy, Genomics, Serology
ABSTRACT ID: 49

PRESENTED BY: Nanna Brokhattingen, Spain / nanna.brokhattingen@gmail.com

FIRESIDE SESSION 9

FRIDAY 24 NOVEMBER
11:00 - 12:30

Global health

MODERATOR
John Kinsman

Abstract

Investigation of an aseptic meningitis outbreak in Hebron district, West Bank, 2022

A. Tuffaha [1]
S. Assad [2]

[1] Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden | Palestinian Ministry of Health, West Bank, Palestine
[2] Palestinian Ministry of Health, West Bank, Palestine

BACKGROUND
The burden of aseptic meningitis has been largely overlooked in the West Bank due to the COVID-19 pandemic. Since August 2022, a significant increase in aseptic meningitis cases of unknown aetiology was observed in Hebron. We conducted an outbreak investigation to characterize cases and their clinical outcomes, identify aetiologic causes of illness, and recommend containment measures.

METHODS
Confirmed cases were defined as fever and/or meningeal symptoms in Hebron since 1 August 2022, with cerebrospinal fluid pleocytosis and no evidence of bacterial or fungal infection in lab tests. Door-to-door and hospital-based active case finding was conducted with inter-locality preventive health department cooperation. Cases were investigated to obtain information on demographics, clinical and laboratory results, vaccination status, exposure history, and any close contacts. [EWJ1] Cerebrospinal fluid samples were sent for laboratory investigation.

RESULTS
From 1 August to 31 December 2022, 122 cases of aseptic meningitis were identified. Among these, 47% (n=57) were under 1 year of age, and 37% (n=45) were aged 1-4 years. 93% (n=114) of cases required hospitalization. Common symptoms included fever (98%), vomiting (45%), and headache (31%). No exposure to meningitis, mumps, or measles contacts was reported. Five cases tested positive for enterovirus and one for cytomegalovirus, while the remaining were negative for common viral pathogens. Poliovirus testing was unavailable.

CONCLUSIONS
This outbreak emphasizes the importance of improving continuous surveillance and the need for more comprehensive laboratory tests to determine viral aetiologies. The negative laboratory results indicate the possibility of a new or emerging viral pathogen, meriting further investigation. Future epidemiological analyses of risk factors for aseptic meningitis in the West Bank is crucial for improving prevention and control of similar outbreaks in the future.

Keywords: Outbreak, Aseptic meningitis, Bacterial meningitis, Enterovirus, Cytomegalovirus
ABSTRACT ID: 380
PRESENTED BY: Ayah Tuffaha, Palestine / ayahtuffaha231@yahoo.com

FIRESIDE SESSION 9

FRIDAY 24 NOVEMBER
11:00 - 12:30

Global health

MODERATOR
John Kinsman

Abstract

Cholera outbreaks: the need to connect epidemiology to systems-level interventions – Municipality of Caraga, Philippines, 2021

I. Gonzales [1]
K. Gecosala [2], R. Martinez [3], A. Segarra [4]

[1] Department of Health | Epidemiology Bureau | Philippine Field Epidemiology Training Program
[2, 3, 4] Department of Health | Epidemiology Bureau | Philippines

BACKGROUND
On 1 November 2021, a clustering of diarrhea cases was reported in Caraga, Davao Oriental. Continued increase in cases prompted a field investigation to determine the existence of an outbreak, source and mode of transmission, and risk factors.

METHODS
A descriptive study followed by a 1:1 matched case-control study was conducted. A case was defined as a previously well individual from Caraga who had acute watery diarrhea between 2 October to 10 November 2021. Controls were age- and sex-matched well individuals from the same municipality. We conducted records review, active case finding, and key informant interviews. We collected stool and water samples for testing.

RESULTS
Prior data identified 65 acute watery diarrhea cases in the same period. We identified 45 cases which started on 2 October and peaked by 26 October after weeks of persistent rain. Santiago Village had 30 cases with an attack rate of 11.28 per 1,000 population. The main water source were untreated springs which was positive for E. coli on rapid testing. One case was positive for Cholera. Having a household member with diarrhea (OR 14.29, 95% CI 1.73–640), finding fecal material around the water source (OR 10.24, 95% CI 1.20–468), and drinking untreated water (OR 4.44, 95% CI 1.27–16.70) were identified risk factors.

CONCLUSIONS
There was a Cholera outbreak in Santiago Village, Caraga. Poor sanitation practices were identified factors. We recommended stronger health education, access to water treatment options, and infection prevention protocols when caring for ill household members. Though cases initially declined, a larger outbreak occurred in January 2022 with a total of 667 cases. To prevent its recurrence, systems-level improvements such as investing in water systems must be done.

Keywords: Cholera, Sanitation, Disease outbreak, Case-control study
ABSTRACT ID: 396
PRESENTED BY: Ian Christian Gonzales, Philippines / icagonzales@doh.gov.ph

FIRESIDE SESSION 9

FRIDAY 24 NOVEMBER
11:00 - 12:30

Global health

MODERATOR
John Kinsman

Abstract

Distribution of Rickettsia species among hospitalized cases and ticks in Pavlodar region, Kazakhstan, 2019

Y. Bumburidi [1]
D. Berezovskiy [2], B. Zhakipbayeva [3], R. Horth [4], Y. Ostapchuk [5], Z. Berdygulova [6], G. Zemtsova [7], W. Nicholson [8], Z. Shapiyeva [9]

[1, 2, 3, 4] CDC Kazakhstan
[5, 6] Branch of National Center of Biotechnology of the Ministry of Health
[7, 8] CDC Atlanta
[9] Scientific Practical Center for Sanitary-Epidemiological Expertise and Monitoring, National Center for Public Healthcare, Ministry of Health, Almaty, Kazakhstan

BACKGROUND

Spotted Fever Group Rickettsioses (SFGR) is a group of neglected, life-threatening zoonotic diseases caused by closely related bacteria spread primarily by ticks. Little is known about SFGR incidence and distribution of Rickettsiae species in Kazakhstan. This knowledge can help inform SFGR prevention and treatment efforts.

METHODS

We conducted sentinel surveillance from April to October 2019 in six hospitals in the Pavlodar region. Samples, including skin lesions and two serum samples at the acute stage (AS) and convalescent stage (CS), were collected from consenting patients with SFRG symptoms. We classified participants as having acute SFGR if they had either: (1) positive PCR, or (2) a four-fold increase in IFA IgG titers from AS to CS samples, or (3) IgG titers (≥1:64) in an AS sample. We also collected ticks using dragging or flagging of vegetation and tested them using real-time PCR.

RESULTS

Of 105 people enrolled, 69% had acute SFGR. Incidence rates per 100,000 population at sentinel sites ranged from 7 to 50. R. sibirica (40%), R. raoultii (39%), and R. slovaca (7%) were identified in participants. R. raoultii and R. spp were identified in 9% of Dermacentor reticulatus ticks (n=610) and 7% of Dermacentor marginatus ticks (n=349). R. sibirica was identified in 1% of D. marginatus ticks.

CONCLUSIONS

There was a two-fold increase in cases detected through active surveillance during our study than reported in previous years (105 in 2019 compared to 54 in 2018 and 40 in 2017). R. sibirica and R. raoultii are the dominant strains associated with SFGR in Pavlodar and are also found in ticks. Improved disease detection and regular testing of humans and ticks in areas with SFGR cases is needed.

Keywords: Spotted Fever Group Rickettsioses, Tick-borne diseases, Kazakhstan, Rickettsia sibirica, Rickettsia slovaca, Rickettsia raoultii
ABSTRACT ID: 279
PRESENTED BY: Yekaterina Bumburidi, Kazakhstan / hnz6@cdc.gov

FIRESIDE SESSION 9

FRIDAY 24 NOVEMBER
11:00 - 12:30

Global health

MODERATOR
John Kinsman

Abstract

Prevalence and determinants of depression among healthcare workers during the COVID-19 pandemic in Khujand, Tajikistan, 2022

J. Silemonshoeva [1]
R. Horth [2], Z. Tilloeva [3], N. Jafarov [4], S. Zikriyarova [5], D. Nabirova [6]

[1] Central Asia Field Epidemiology Training Program
Kazakhstan National Medical University named after S.D. Asfendiyarov
[2, 6] U.S. Centers for Disease Control and Prevention, Central Asia Office |
Central Asia Field Epidemiology Training Program
Kazakhstan National Medical University named after S.D. Asfendiyarov
[3] Municipal Disinfection Station, Dushanbe, Tajikistan | Central Asia Field Epidemiology Training Program
[4] Tajik Research Institute of Preventive Medicine | Ministry of Health and Social Protection of Tajikistan
[5] Kazakhstan National Medical University named after S.D. Asfendiyarov

BACKGROUND
Healthcare workers experienced substantial work overload and stress during the COVID-19 response. Increase in prevalence of mental health conditions among healthcare workers have been reported globally. To inform program planning, we aimed to determine prevalence of depression, associated factors, and care gap among healthcare workers.

METHODS
We conducted a cross-sectional study of all healthcare providers (physicians, nurses, and nurse assistants) working from July to August 2022 in three COVID-19 referral hospitals and three polyclinics in Khujand city, Tajikistan. We systematically sampled every fifth provider. Depression was assessed with the Hospital Anxiety and Depression Scale. We used multivariable logistic regression with random effect of hospital to identify factors associated with depression.

RESULTS
Among 400 healthcare workers, 277 (69%) had depression (Table 1). Half (44%) no longer enjoyed the things they used to. Prevalence of depression was significantly higher ($p<0.01$) among females than males (71% vs 59%), nurses than physicians (77% vs 56%). Among providers with depression, 20% had received professional services, 32% had taken a vacation, 32% had severe COVID-19, and 53% experienced frequent respiratory issues, and 56% felt people avoided them because of work. In multivariable analysis depression was associated with being a nurse (adjusted odds ratio [aOR]=3.5; 95% confidence ratio [CI]: 1.7-7.2), having had severe COVID-19 disease (aOR=4.0; 95%CI=1.4-11.8) and having felt that people avoided them because of work (aOR=1.6; 95%CI=1.0-2.6).. Providers who used respirators >3 hours had lower odds of depression (aOR=0.4; 95%CI=0.2-0.9).

CONCLUSIONS
We found high prevalence of depression among healthcare workers in Khujand city, Tajikistan. Timely screening and increase in supportive services is needed. These services should be offered to all providers, and especially targeted towards those with prior severe COVID-19 disease and nurses.

Keywords: Depression, COVID-19, Medical staff, Tajikistan, Stress
ABSTRACT ID: 362
PRESENTED BY: Jamila Silemonshoeva, Tajikistan / jamilasilemonshoeva@gmail.com

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45 - 15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

Environmental factors associated with Escherichia coli concentration at freshwater beaches in Lake Winnipeg, Manitoba, Canada

B. Desta [1]
J. Sanchez [2], C. Heasley [3], I. Young [4], J. Tustin [5]
[1, 2, 3, 4, 5] School of Occupational and Public Health, Toronto Metropolitan University

BACKGROUND
At some public beaches, routine monitoring of beach water quality using fecal indicator bacteria is conducted to evaluate the risk of recreational water illness. Results from water sample analysis can take over 24h, which may no longer accurately reflect current water quality conditions. This study aimed to assess which combination of environmental factors best predicts fecal contamination (E. coli) levels at two of the most popular beaches on Lake Winnipeg, Manitoba (Gimli and Grand), by linking water quality data and publicly available environmental data from 2007 to 2021.

METHODS
We developed separate mixed effects models for each beach for two outcomes, linear (continuous log-transformed E. coli concentration) and categorical (200 CFU/100 ml threshold), to explore differences in the predictors of E. coli concentrations and exceedances of the provincial health risk threshold, respectively.

RESULTS
For both beaches, we identified clustering of the E. coli outcomes by year, suggesting year-specific variation. We also determined that extreme weather days, with higher levels of rainfall in the preceding 48 h, previous day average air temperature, and previous day E. coli concentration could result in a higher probability of E. coli threshold exceedances or higher concentrations in the water bodies. In Grand beach, we identified that days with lower average UV levels in the previous 24 h and antecedent dry days could result in a higher probability of E. coli threshold exceedances or higher concentrations.

CONCLUSIONS
The findings can inform possible trends in other freshwater settings and help develop real-time recreational water quality predictive models to allow more accurate beach management decisions and warrant enhancement of beach monitoring programs for extreme weather events as part of the climate change preparedness efforts.

Keywords: Fecal indicator bacteria, Escherichia coli, Recreational water, Environmental factors, Water quality, Manitoba

ABSTRACT ID: 725
PRESENTED BY: Binyam Desta, Canada / binyam.desta@torontomu.ca

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

SARS-CoV-2 transmission patterns in educational settings

C. Molina Grané [1]
P. Mancuso [2], M. Vicentini [3], F. Venturelli [4], O. Djuric [5], M. Manica [6], G. Guzzetta [7], V. Marziano [8], A. Zardini [9], V. d'Andrea [10], F. Trentini [11], E. Bisaccia [12], E. Larosa [13], S. Cilloni [14], M. Cassinadri [15], P. Pezzotti [16], M. Ajelli [17], P. Giorgi Rossi [18], S. Merler [19], P. Poletti [20]

[1] Center for Health Emergencies, Bruno Kessler Foundation, Trento, Italy
Department of Mathematics, University of Trento, Trento, Italy
[2, 3, 4, 18] Epidemiology Unit, Azienda Unità Sanitaria Locale – IRCCS di Reggio Emilia, Reggio Emilia, Italy
[5] Epidemiology Unit, Azienda Unità Sanitaria Locale – IRCCS di Reggio Emilia, Reggio Emilia, Italy
Department of Biomedical, Metabolic and Neural Sciences, Centre for Environmental, Nutritional and Genetic Epidemiology (CREAGEN), Public Health Unit, University of Modena and Reggio Emilia, Reggio Emilia, Italy
[6, 7, 8, 9, 10, 19, 20] Center for Health Emergencies, Bruno Kessler Foundation, Trento, Italy
[11] Center for Health Emergencies, Bruno Kessler Foundation, Trento, Italy
Dondena Centre for Research on Social Dynamics and Public Policy, Bocconi University, Milan, Italy
[12, 13, 14, 15] Public Health Unit, Azienda Unità Sanitaria Locale – IRCCS di Reggio Emilia, Reggio Emilia, Italy
[16] Department of Infectious Diseases, Istituto Superiore di Sanità, Rome, Italy
[17] Laboratory for Computational Epidemiology and Public Health, Department of Epidemiology and Biostatistics, Indiana University School of Public Health, Bloomington, IN, USA

BACKGROUND

Different monitoring and control policies were implemented in schools to minimize the SARS-CoV-2 spread. However, transmission in schools has been hard to quantify due to the large proportion of asymptomatic carriers in young individuals and the heterogeneous ability of monitoring systems in tracking infections in educational settings.

METHODS

We provide quantitative estimates of SARS-CoV-2 transmission in school, by applying a Bayesian approach to reconstruct the transmission chains between infections ascertained during 87 school outbreak investigations conducted between March and April 2021 in Italy. The developed model exploits the temporal information on SARS-CoV-2 infections recorded in the data to probabilistically identify, for every case, the likely source of infection (from outside the school or from a specific school contact).

RESULTS

We found that 46.1% (95%CrI: 37.7-54.1%) of infections among school attendees were caused by school contacts. The mean number of secondary cases infected at school by a positive individual during in-person education was estimated to be 0.36 (95%CrI: 0.28-0.43), with marked heterogeneity across individuals. A higher mean number of secondary cases (0.54, 95%CrI: 0.25-0.83) was found for infected individuals who attended school for at least 6 days before being isolated or quarantined. Under the policy of reactive quarantines, 71.5% (95%CrI: 65.9-78.0%) of students and school personnel who tested positive during in-person education did not cause any secondary infection at school.

CONCLUSIONS

Our findings quantified the contribution of school transmission to the spread of SARS-CoV-2 in young individuals, which are key to designing adequate surveillance and control protocols. Results suggest that identifying positive cases within 5 days after exposure to their infector could reduce by at least 30% onward transmission in school.

Keywords: COVID-19, School, Children, Transmission chain reconstruction, Surveillance, Transmission model
ABSTRACT ID: 212
PRESENTED BY: Carla Molina Grané, Italy / cmolinagrane@fbk.eu

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45 - 15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

Risk factors associated with COVID-19 outbreak intensity in Canada: a negative binomial analysis

D. Dam [1]

M. Chen [2], E. Rees [3], B. Cheng [4], L. Sukkarieh [5], E. McGill [6], Y. Tehami [7], A. Bellos [8], J. Edwin [9], K. Patterson [10]

[1, 2, 3, 4, 5, 6, 7, 8, 9, 10] Public Health Agency of Canada (PHAC), Ottawa, Canada

BACKGROUND
COVID-19 outbreaks have disproportionately impacted high-risk individuals and settings. There is limited research examining factors associated with the size, duration, and intensity of outbreaks to inform prevention and control strategies. Our study aims to assess for associations between outbreak intensity, setting, and regional population risk factors.

METHODS
This analysis used 2021 outbreak data from the Canadian COVID-19 Outbreak Surveillance System and includes seven provinces/territories, representing 93% of the Canadian population. Outbreak intensity was defined as the number of outbreak-associated cases divided by outbreak duration. Descriptive analyses were conducted to assess COVID-19 outbreak intensity trends. A fixed-effect negative binomial model was used to assess the association between various factors (e.g., setting, vaccination, population at risk) and outbreak intensity.

RESULTS
The longest outbreaks occurred in long-term care facilities (LTCF) (median = 20 days), followed by correctional facilities (median = 17 days) which also reported the largest outbreaks (mean = 56 cases). All settings had significantly less intense outbreaks compared to correctional facilities (reference), by a notable margin. LTCF and childcare centres had the second highest intensity (intensity ratio = 0.39 [95% CI: 0.34-0.44]) while schools had the lowest (intensity ratio: 0.31 [95% CI: 0.28-0.35]). Vaccination coverage with at least 1 dose was associated with reduced outbreak intensity. Outbreak intensity increased following the introduction of the more transmissible and immuno-evasive Omicron variant in December 2021.

CONCLUSIONS
COVID-19 had a devastating impact on congregate living settings, particularly in correctional facilities and LTCF. Findings from this study highlight the importance of vaccination in mitigating outbreaks and reducing outbreak intensity, especially in vulnerable populations living in high-risk settings. Finally, this analysis demonstrated the utility of assessing outbreak intensity for pathogens of outbreak potential.

Keywords: Canada, COVID-19, Outbreaks, Surveillance, Statistical model, Risk factors
ABSTRACT ID: 664
PRESENTED BY: Demy Dam, Canada / demy.dam8@gmail.com

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45 - 15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

Modelling the incidence and prevalence of chronic hepatitis C among people who inject drugs in Norway to monitor progress towards elimination

R. Whittaker [1]
J. Eriksson Midtbø [2], H. Kløvstad [3]
[1, 2, 3] Norwegian Institute of Public Health

BACKGROUND
In Norway, the hepatitis C epidemic is concentrated among people who inject drugs (PWID). In line with the global health strategy, Norway aims to eliminate hepatitis C as a public health threat. The global incidence targets are an 80% relative decrease compared to 2015, or an absolute incidence <2 per 100 PWID. We generated bespoke modelled estimates of the incidence and prevalence of hepatitis C among PWID in Norway to monitor progress towards this elimination target.

METHODS
We built a stochastic compartmental model to simulate the incidence and prevalence of hepatitis C among PWID from 1972 until 2022, with projections until 2030. The model was implemented in the mcstate framework. We modelled active and ex-PWID populations separately. To inform the model we utilised data from different national data sources, literature and expert opinion, including prevalence studies among PWID in Norway, the coverage of harm reduction measures, and national treatment prescriptions. Transmission of hepatitis C was only assumed among active PWID.

RESULTS
The model estimated 20 (95% confidence interval (CI): 6–78) new infections among active PWID in 2022, 0.25 per 100 active PWID (95%CI: 0.07–1.00) and an 89% relative decrease in the point estimate compared to 2015 (n=184, 95%CI: 155–210). The model estimated that the prevalence of chronic infections in this group will fall below 5% in 2027. The estimated prevalence among all PWID populations in 2022 was 1,839 chronic infections (95%CI: 296–5,038).

CONCLUSIONS
Results suggest that Norway has achieved the global incidence targets for the elimination of hepatitis C among PWID. This provides a clear example of the feasibility of elimination in a setting with high coverage of harm reduction measures and treatment freely available for all infected.

Keywords: Hepatitis C, Public Health Surveillance, Disease Elimination, Epidemiological Models, Norway
ABSTRACT ID: 186
PRESENTED BY: Robert Whittaker, Norway / robert.whittaker@fhi.no

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45 - 15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

Estimating the effect of the South Africa flight ban in November 2021 on the SARS-CoV-2 Omicron outbreak in the Netherlands: A modelling study

E. Wynberg [1]
R. Bavalia [2], S. Lee [3], V. Eijrond [4], L. Coffeng [5], S. de Vlas [6], B. Kolen [7], A. Schreijer [8], (GROUP) Omicron Flight Ban Study Group

[1] Pandemic and Disaster Preparedness Centre, Erasmus Medical Center, Rotterdam, the Netherlands
* Joint first author
[2] Pandemic and Disaster Preparedness Centre, Erasmus Medical Center, Rotterdam, the Netherlands
* Joint first author
[3] Department of Values, Technology and Innovation, Delft University of Technology, Delft, the Netherlands
[4, 8] Pandemic and Disaster Preparedness Centre, Erasmus Medical Center, Rotterdam, the Netherlands
[5, 6] Department of Public Health, Erasmus MC, University Medical Center Rotterdam, the Netherlands
[7] Pandemic and Disaster Preparedness Centre, Erasmus Medical Center, Rotterdam, the Netherlands
Department of Values, Technology and Innovation, Delft University of Technology, Delft, the Netherlands

BACKGROUND

Governments occasionally used travel bans during the COVID-19 pandemic to prevent importation of new variants of concern (VoC). In the Netherlands, direct flights from South African countries were banned from 26 November 2021 to combat the introduction of Omicron (B.1.1.529). We evaluated the effect of this flight ban on subsequent Omicron infections in the Netherlands.

METHODS

Using an SIR model, we assessed the impact of the flight ban, its timing and the proportion of indirectly-imported cases on days to 10,000 secondary Omicron infections. We defined the flight ban as a complete halt in direct flights, while passengers arriving via indirect routes were unaffected. We incorporated best estimates of real-world epidemiological parameters in our model, including daily importation rates of Omicron from South Africa (using South African surveillance data and test results of passengers travelling on 26 November) and Re of Omicron in the Netherlands (nationally estimated at 1.3 at that time).

RESULTS

We scaled our model input to 15 directly-imported Omicron cases on 26 November 2021 (61/624 incoming passengers tested positive; 14/16 sequenceable samples showed infection with Omicron). Our model indicated the flight ban resulted in a 23-day delay (97 vs. 74 days) in reaching 10,000 Omicron cases without indirect importation, with an additional 3-day delay if initiated 1 day earlier. However, if indirect imports were incorporated at 20% of the direct importation rate, only a 10-day delay remained and initiating the flight ban 1 day sooner no longer resulted in additional time gained.

CONCLUSIONS

Our model indicates the Dutch flight ban delayed the outbreak of Omicron, buying extra time for outbreak preparations. However, importation via indirect travel routes limited the flight ban's effect.

Keywords: COVID-19, SARS-CoV-2, Public health, Modelling, Outbreak
ABSTRACT ID: 442
PRESENTED BY: Elke Wynberg, Netherlands / e.wynberg@erasmusmc.nl

FIRESIDE SESSION 10

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45 - 15:15

Modelling, biostatistics, and health informatics

MODERATOR
Rene Niehus

Abstract

Impact of the 2023 autumn COVID-19 vaccination campaign by vaccine coverage and level of immunity waning: an agent-based simulation study between August 2023 and June 2024

D. E. Singh [1]
A. Cublier Martinez [2], M. Marinescu [3], J. Carretero [4], D. Gomez-Barroso [5], C. Delgado Sanz [6], S. Monge Corella [7], C. Olmedo Luceron [8], A. Limia Sanchez [9]

[1] Universidad Carlos III de Madrid
[2, 4] Universidad Carlos III de Madrid
[3] Barcelona Supercomputing Center
[5, 6, 7] Centro Nacional de Epidemiología. Instituto de Salud Carlos III|CIBER en Epidemiología y Salud Pública (CIBERESP)
[8, 9] Área de Vacunas. Subdirección General de Promoción de la Salud y Prevención. Dirección General de Salud Pública. Ministerio de Sanidad

BACKGROUND
Simulating alternative COVID-19 vaccine rollout scenarios and their impact on COVID-19 burden can help decision-makers to define the most appropriate vaccination policies. Within the ECDC European Scenario Hub Round 5 different scenarios for the vaccination of 60+ year-olds were specified for the 2023 autumn vaccination campaign, depending on the coverage and level of waning immunity. Our aim is to estimate averted infections, hospitalisations and deaths under these scenarios, between August 2023 and June 2024.

METHODS
We used EpiGraph, an epidemiologic agent-based simulator, to connect various models that reproduce the environment where the infection occurs: a highly detailed social model, an epidemic model, and a vaccination model. Both natural and vaccination-induced immunities are subjected to waning. Data were from the sentinel respiratory virus surveillance in Spain.

RESULTS
Eight scenarios [1] were simulated for an 8-month simulation horizon starting on 1st August 2023. The vaccination of individuals aged 60+, compared to not vaccinating this group, does not reduce the cumulative number of infections but reduces the total hospital admissions between 4% and 19%, and the total number of deaths between 7% and 35%, with the impact increasing with increasing vaccination coverage and immunity waning. When we only consider the elderly population, the maximum reduction in hospitalization and deaths is 33% and 38%, respectively.[1] https://github.com/covid19-forecast-hub-europe/covid19-scenario-hub-europe/wiki/Round-5.

CONCLUSIONS
The impact of the upcoming autumn COVID-19 vaccination campaign will be low in reducing overall infections but higher for severe infections. The vaccination of 60+ year-olds, even if the coverage is reduced, is crucial to minimize hospitalizations and fatalities on this population. This work was submitted to ECDC's Round 5 on August 20th. Round 5 results are communicated to the HERA and NITAGs groups.

Keywords: Modelling, Biostatistics, Health informatics, COVID-19
ABSTRACT ID: 930
PRESENTED BY: David E. Singh, Spain / dexposit@inf.uc3m.es

FIRESIDE SESSION 11
DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

Iatrogenic botulism, an example from Turkiye

Z. Ozguler [1]
[1] Communicable Diseases and Early Warning Department, General Directorate of Public Health, Ankara, Turkiye

BACKGROUND
As the Early Warning and Response team, we received several notifications via National Poison Center, the IHR NFPs and Provincial Health Centers on botulism cases. We assessed the situation as an acute health threat and initiated investigation.

METHODS
We started multistakeholder risk communication and reached cases who had symptoms after receiving an intragastric injection of botulinum neurotoxin type A (BoNT/A) in health center A. We collected data on the cases retrospectively from hospital records and interviewed cases when possible. We also planned out a new indicator-based surveillance system to catch new iatrogenic botulism cases.

RESULTS
Between 24.01.2023 and 03.03.2023, 519 individuals (female:85.5%) received gastric injections and 74 had symptoms between 21.02.2003 and 27.03.2023. All individuals were reported to be injected with the same dose of the same brand. Maximum days reported as the incubation period was 38 days and minimum was on the same day of the procedure (mean=7.5days +/-6.8). Mean weight of the cases was 91.7kg (+/-20,3) and mean age was 35.4 (+/-9.6). Most common symptoms were fatigue (58.7%), sight problems (54.7%) followed by dysphagia (%56), and dyspnea (52%). Six of the patients received Botulinum Antitoxin Heptavalent. Multi-stakeholder meetings were held to evaluate current case detection mechanisms and a new ICD code was introduced to reggsitry systems. We built a real-time indicator-based surveillance system.

CONCLUSIONS
Intragastric usage of botulinum toxin is not recommended for weight control by the Ministry of Health; public announcements were made about the issue. Involving the Medicines and Medical Devices Agency and the General Directorate of Health Services has enabled multidirectional investigations. Combined results led us to think the problem may be about the doses and the usage of the BoNT/A.

Keywords: Botulism, Outbreaks, Surveillance, Iatrogenic diseases
ABSTRACT ID: 967
PRESENTED BY: Zeynep Ozge Ozguler, Turkey / zeynepozgemd@gmail.com

FIRESIDE SESSION 11

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

HIV-cases in Germany in the context of the Ukrainian refugee reception: Description of patient characteristics, transmission routes and infection stages, March 2022 – June 2023

K. Röbl [1]
M. Friebe 2, C. Kollan 3, U. Marcus 4, B. Gunsenheimer-Bartmeyer 5

[1] Department of Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany|Postgraduate Training for Applied Epidemiology (PAE), Robert Koch-Institute, Berlin, Germany|ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5] Department of Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany

BACKGROUND
Since the ongoing Russian invasion, more than one million people from Ukraine – a country with high Human Immunodeficiency Virus (HIV)-prevalence – have fled to Germany. We aimed to analyse the proportion of newly notified HIV-cases in Germany linked to Ukraine and characterise those People Living with HIV/AIDS (PLWH) to better understand their care needs.

METHODS
We descriptively analysed German routine HIV-surveillance data from 03/2022-06/2023 regarding links to Ukraine (i.e. country of infection or origin) in terms of gender and age distribution, stage of infection according to CD4-cell counts, and transmission routes in comparison to cases without link to Ukraine.

RESULTS
Of 5,688 newly notified HIV-cases, 2,601 (46%) had information on country of origin or infection, of which 1,101 (42%) were Ukraine-related (monthly proportions between 26-59% and remaining high up to 06/2023 (41%)). Ukraine-related cases were more often female (61%) and younger (mean age: 38.4y) than others (15%, 40.7y). Of 1,647 cases with information on CD4-cell counts, Ukraine-related cases showed higher CD4-cell counts (57% >500/µl; 18% <200/µl) compared to others (27% >500/µl; 35% <200/µl). Heterosexual contact, followed by intravenous drug use, were the most likely transmission routes among Ukraine-related women (83%, 10%) and men (52%, 27%), and women without link to Ukraine (66%, 12%), whereas among men without link to Ukraine, sex between men (MSM) was most frequently stated (84%).

CONCLUSIONS
Ukraine-related PLWH – still constituting a substantial proportion of HIV-cases in 2023 – require German health policy attention. Higher CD4-cell counts point towards a higher proportion of already known and treated HIV-infections, which will be further investigated by analysing viral loads. To ensure their continuous treatment, Ukrainian refugees must have rapid access to healthcare and antiviral therapy.

Keywords: HIV, Ukraine, Germany, Policy
ABSTRACT ID: 870
PRESENTED BY: Klara Röbl, Germany / roeblk@rki.de

FIRESIDE SESSION 11

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

Enhanced surveillance for diphtheria amongst asylum seekers arriving by small boat to England, July-September, 2023: challenges in implementation and outcomes

T. Cullip [1]
A. Shah [2], K. Wrenn [3], P. Blomquist [4], S. Thompson [5], D. Litt [6], R. Cordery [7], (GROUP) DAISIES Team

[1] UKHSA
[2, 3, 4, 5, 6, 7] UKHSA

BACKGROUND
Since November 2022, asylum seekers (AS) arriving by small boat to England have been offered diphtheria-containing vaccine and antibiotic prophylaxis. The UK is the only country reported to have made this offer, prompted by an increase in toxigenic diphtheria cases in this population and challenges with individual-level case and contact management. We describe enhanced surveillance subsequently undertaken amongst unaccompanied asylum-seeking children (UASC) in temporary hotels, to ascertain toxigenic diphtheria prevalence.

METHODS
Newly-arrived UASC in three hotels were recruited by on-site nurses. All consenting participants without current antibiotic therapy received a throat swab and wound swab (if wound present). Demographic, clinical, travel and vaccination information were collected. Swabs were tested for toxigenic C. diphtheriae, C. ulcerans and C. pseudotuberculosis.

RESULTS
From 4 July-5 September 2023, 210 UASC were recruited. 94% were male (n=197) and ages ranged from 13-18 years (median:15 years). Of 157 UASC with reported country of birth, most were born in Afghanistan (36%, n=57), Sudan (16%, n=25), and Iran (13%, n=20). None reported previous diphtheria vaccination. We identified 2 toxigenic C. diphtheriae cases in throat swabs (prevalence: 1% (95% CI: 0.12%-3.4%)). Three participants reported symptoms at recruitment, including one case.

CONCLUSIONS
Our observed toxigenic diphtheria prevalence is higher than the estimated background prevalence in the UK, (<0.04%), despite the mostly asymptomatic sampling. Travel and vaccination history were challenging to collect due to lack of knowledge and disclosure hesitancy, but many UASC originate from countries with interrupted vaccination programmes. These findings suggest the need for continued prophylaxis and vaccination in this cohort and ongoing enhanced surveillance expanded to adult asylum seekers to inform guidance in the wider AS population, in the context of evolving antibiotic resistant strains.

Keywords: Diphtheria, Asylum seekers, Prevalence, Corynebacterium, Vaccines
ABSTRACT ID: 949
PRESENTED BY: Teresa Cullip, United Kingdom / teresa.cullip@ukhsa.gov.uk

FIRESIDE SESSION 11
DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

Investigating avian influenza transmission to humans from infected animals in England: interim results of an enhanced surveillance programme

P. Blomquist [1]
O. Olufon [2], N. Bray [3], C. Byers [4], N. Cunningham [5], F. Halford 6, C. Inzoungou-Massanga [7], M. Pietzsch [8], J. Singh [9], N. Machin [10], S. Hopkins [11], M. Chand [12], D. Kumar [13], R. Puleston [14]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14] UKHSA

BACKGROUND
In response to an ongoing influenza A(H5N1) epidemic in birds in England and globally, the UK Health Security Agency (UKHSA) launched an enhanced surveillance programme in England in March 2023. It aims to investigate the risk of avian influenza infection and risk factors among persons working with infected animals. We provide interim results as of September 13, 2023.

METHODS
The Animal and Plant Health Agency notified the UKHSA Rapid Investigation Team of avian influenza outbreaks. We recruited exposed persons over 18 years at infected premises (IPs) during culling operations. Consenting persons self-administered a nose/throat swab under observation, were interviewed about exposures, and were requested to self-administer tests 2, 5, and 8 days later. £100 e-vouchers were given for returning all samples. If an individual received a positive H5 PCR result, UKHSA collected blood samples for serology promptly and 21 days later, and offered £100 compensation per day of isolation.

RESULTS
We recruited 164 persons from eleven IPs, among 259 exposed persons (63% uptake). Ten sites were bird farms, >50% in the North of England. 75% of participants were culling staff (n=123), 17%(n=27) farm workers, and 9%(n=14) had other roles. 565 samples were returned, and 80% of participants completed all four tests. We identified two persons with plausible asymptomatic infection: 1.2% positivity (95%CI 0.15%-4.3%). Both were involved in culling wearing personal protective equipment. Two further individuals were identified with transient contamination.

CONCLUSIONS
We identified two H5 cases out of 164 exposure events, with relatively high study uptake and testing adherence. This is similar to previous surveillance in England, which identified one detection among 120 exposed. Continued surveillance will enhance the robustness of estimates and improve assessments of pandemic potential.

Keywords: Avian influenza, Zoonotic infection, Transmission risk
ABSTRACT ID: 950
PRESENTED BY: Paula Blomquist, United Kingdom / paula.blomquist@ukhsa.gov.uk

FIRESIDE SESSION 11

DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

Salmonella Enteritidis restaurant outbreak investigation using till receipt data provides further evidence for eggs as source in widespread international cluster, England, March to April 2023

L. Findlater [1]
A. Vusirikala [2], H. Benson [3], L. Reeve [4], M. Pietzsch [5], O. Olufon [6], E. Matthews [7], A. Hoban [8], A. Painset [9], L. Larkin [10], S. Weir [11], S. Balasegaram [12], E. Heinsbroek [13], (GROUP) Incident Management Team
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13] UK Health Security Agency

BACKGROUND
Since 2014, Europe has seen an internationally distributed 10-single nucleotide polymorphism (SNP) cluster of Salmonella Enteritidis, associated with chicken or egg consumption. We identified a 5-SNP sub-cluster in England, with sporadic cases since July 2022, and a restaurant outbreak identified in April 2023. We aimed to define common exposures for cases in the 5-SNP cluster to determine the likely source of infection.

METHODS
Confirmed cases had laboratory-confirmed S. Enteritidis infection belonging to the 5-SNP cluster (Enterobase cgMLST HC2_316378) between 1 March 2023 and 31 May 2023. Confirmed cases were categorised as having known, unknown, or no exposure to the restaurant of interest. Probable cases had gastroenteritis and dined at the restaurant between 1 March and 1 April 2023.Restaurant-linked cases were interviewed using a bespoke menu-based questionnaire; for cases not linked to the restaurant, a trawling questionnaire was used. We used restaurant till receipt data to calculate attack rates and odds ratios for specific menu items and grouped menu items with common ingredients.

RESULTS
Overall, there were 65 cases: 25 confirmed and 18 probable cases linked to the restaurant, 10 confirmed cases with unknown restaurant attendance, and 12 confirmed cases with no restaurant attendance. Consumption of restaurant dishes containing chicken or egg was associated with becoming a case (odds ratios 2.92 (95% CI 1.17-7.27) and 4.38 (2.06-9.31) respectively). Food chain investigations identified that eggs imported from Poland were used at the restaurant and consumed by two cases without restaurant attendance.

CONCLUSIONS
This restaurant outbreak provided an opportunity to elucidate potentially implicated food chains in a wider international cluster. Epidemiological and ongoing food chain investigations suggest imported eggs from Poland as the likely source of this outbreak.

Keywords: Salmonella Enteritidis, Whole genome sequencing, Outbreaks, Restaurants, Epidemiology
ABSTRACT ID: 871
PRESENTED BY: Lucy Findlater, United Kingdom / lucy.findlater@ukhsa.gov.uk

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FIRESIDE SESSION 11
DAY 3 – FRIDAY 24 NOVEMBER 2023
13:45-15:15

Late breakers

MODERATOR
Barbara Albiger

Abstract

Re-emergence of Crimean-Congo Hemorrhagic Fever in North Macedonia, 2023

D. Kochinski [1]
K. Kjirkovikj Kolevska [2], E. Pollozhan [3], K. Stavridis [4], G. Kuzmanovska [5], S. Zhivkova [6], L. Imeri [7], B. Trajkova [8], B. Todorovski [9], G. Boshevska [10], E. Jancheska [11], S. Memeti [12]

[1] Institute of Public Health, North Macedonia | Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[2, 3, 4] Institute of Public Health, North Macedonia | Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[5, 10, 11] Institute of Public Health, North Macedonia
[6] Center for Public Health Shtip
[7] Center for Public Health Skopje
[8, 9] Center for Public Health Veles
[12] Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden | Institute of Public Health, North Macedonia

BACKGROUND
Crimean-Congo hemorrhagic fever (CCHF) is a widespread tick-borne disease with case-fatality reaching up to 40%. CCHF is endemic in Africa, the Balkans, the Middle East, and Asia. The first described outbreak in North Macedonia occurred in 1971 with 13 reported cases and two deaths in the region of Tetovo. A single case was also detected in 2010 in Skopje region. We investigated re-emerging cases in 2023, 13 years after the last detected case.

METHODS
Diagnosis was performed by ELISA in serum (IgM and IgG) and by RT-PCR. Cases and contacts were classified according to WHO guidance. For all cases, demographic, occupational, clinical presentation, history of contact with animals and ticks, travel history, and close contacts were recorded using a structured questionnaire.

RESULTS
Between 27.07-13.08.2023, 3 CCHF cases were detected in North Macedonia, aged 27-47 years, from 3 regions (Shtip, Skopje, Veles). Cases' professions were farmer, paramedic, and welder. Clinical presentation including hemorrhagic syndrome varied from mild (n=2) to severe (n=1). All 3 cases were hospitalized and isolated; one of them died. Exposure data suggested a tick bite for the first and human-to-human nosocomial transmission for the second (linked) case. For the third case, the mode of transmission was not clear. Cases had no travel history abroad. Overall, 96 close contacts were identified and classified as high- (n=8), medium- (n=44), or low-risk (n=44). High- and medium-risk contacts were monitored for 14 days.

CONCLUSIONS
The re-emergence of CCHF in North Macedonia underscores the need for increased vigilance, and a One Health approach including enhanced surveillance of human and animal cases, vectors, and health promotion activities to minimize the risk in the population.

Keywords: CCHF, North Macedonia, Re-emergence, Ticks
ABSTRACT ID: 881
PRESENTED BY: Dragan Kochinski, North Macedonia / dragan.kocinski@gmail.com

Poster tours

POSTER TOUR 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

Impact of the COVID-19 pandemic on the reporting of infectious diseases in the EU/EEA, 2012-2021

C. Carvalho [1]
L. Alves de Sousa [2] , J. Gomes Dias [3] , A. Torres [4] , B. Ciancio [5], J. Beauté [6]
[1, 2, 3, 4, 5, 6] European Centre for Disease Prevention and Control (ECDC)

BACKGROUND
Changes in population behaviour and in health systems' capacity during the COVID-19 pandemic may have impacted the occurrence and reporting of infectious diseases. We assessed whether and to what extent this occurred in EU/EEA countries to inform strengthening of surveillance capacity.

METHODS
We analysed numbers of cases reported to ECDC by EU/EEA countries in 2012-2021 by disease and group of diseases (emerging and vector-borne, food and water-borne, sexually transmitted and blood-borne, and respiratory-transmitted) excluding those with annual totals of less than 100 cases in 2012-2019. We used interrupted time series analysis to determine if significant changes occurred in the pandemic period (2020-2021) compared with the pre-pandemic period.

RESULTS
In 2012-2021, 6.2 million cases of 32 infectious diseases were reported to ECDC by 30 EU/EEA countries. The number of reported cases decreased by 25% in 2020 and 17% in 2021, mostly for respiratory diseases (-61% and -83%, respectively) and less for other groups (-20% in 2020 and -8% in 2021). Biggest decreases were observed for rubella and measles (-92% and -78% in 2020, -96% and -99% in 2021, respectively). Notifications of Legionnaires' disease, gonorrhoea, and tick-borne encephalitis increased by 27 and 62%, 18 and 41%, and 43 and 12% in 2020 and 2021, respectively.

CONCLUSIONS
During the COVID-19 pandemic, the number of cases of infectious diseases reported to ECDC decreased overall and for most diseases. The impact was much greater and sustained for respiratory diseases, which might be partially explained by COVID-19 non-pharmaceutical interventions, but under-diagnosis and under-notification might have also played a role for most diseases. Resilient routine surveillance systems are essential to avoid overlooking public health threats, especially when healthcare resources are strained such as during pandemics.

Keywords: COVID-19 pandemic, Infectious diseases, Public health surveillance, European Union
ABSTRACT ID: 80
PRESENTED BY: Carlos Carvalho, Sweden / carlos.carvalho@ecdc.europa.eu

POSTER TOUR 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

Characterisation of SARS-CoV-2 reinfections detected through successive variant waves in the SIREN UK healthcare worker study, June 2020 to March 2023

K. Munro[1]
A. Atti[2], J. Khawam[3], N. Kapirial[4], N. Hettiarachchi[5], O. Akinbami[6], A. Dunne[7], M. Cole[8], J. Islam[9], S. Hopkins[10], V. Hall[11], S. Foulkes[12]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12] UK Health Security Agency

BACKGROUND

As the COVID-19 pandemic has progressed, reinfections have become increasingly common. Reinfection is a key factor to consider when assessing disease burden. We aimed to characterise SARS-CoV-2 reinfections detected within SIREN since June 2020.

METHODS

We analysed data from SIREN, a large prospective cohort study with regular PCR and antibody testing. Reinfections were defined as: PCR positive infections >=90 days after a previous PCR positive or >=28 days after an antibody positive sample consistent with prior infection. Sequencing data was used to categorise primary infections by variant. Multi-variable logistic regression was used to compare characteristics of participants with repeat infections against those with only one infection.

RESULTS

By 31/03/2023, 4,828 reinfections were identified - 707 (14.6%) before Omicron; 2,652 (54.9%) during Omicron BA1/2; 1,469 (30.4%) other Omicron sub-variants.4,061 (91.6%) participants had two, 355 (8.0%) had three and 19 (0.4%) had four infections.2,801 (58.0%) reinfections were flagged from two PCR samples. Median time between infection episodes was 394 days overall (IQR: 252-562) – 428 days (IQR: 373-508) for Wildtype/Alpha primary infections; Delta (228 days; IQR: 156-369); Omicron (252 days; IQR: 168-331).Reinfections were more common among those aged 45-54yrs (aOR=1.58, 95%CI:1.28-1.95, p<0.001, ref=18-25yrs), the estates/porters staff-group (aOR=1.33, 95%CI:1.04-1.72, p=0.022, ref=Administrative), those working in inpatient wards (aOR=1.17, 95%CI:1.05-1.31, p=0.005, ref=office-based), the Black ethnic group (aOR=1.45, 95%CI:1.17-1.81, p=0.001, ref=White) and those with chronic respiratory conditions (aOR=1.13, 95%CI:1.03-1.25, p=0.014).

CONCLUSIONS

Time, variant and demographics/exposures all contribute to the likelihood of SARS-CoV-2 reinfection. SIREN is uniquely placed to contribute to our understanding of these factors – its scale, frequent testing and longevity allows increased opportunity for capturing reinfections. Regular serology also allows identification of reinfections where previous PCR data is unavailable.

Keywords: SARS-CoV-2, Reinfection, COVID-19, Monitoring, Cohort Study
ABSTRACT ID: 97
PRESENTED BY: Katie Munro, United Kingdom / katie.munro@ukhsa.gov.uk

POSTER TOUR 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

Risk factors associated with COVID-19-related death during the Omicron period in North Macedonia, 2022

K. Kirkovik Kolevska [1]
S. Memeti [2], K. Danis [3], I. Finci [4], E. Pollozhani [5], D. Kochinski [6], K. Stavridis [7]

[1] Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC) | Institute of Public Health, North Macedonia
[2] Institute of Public Health, North Macedonia | Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[3] Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC)
[4] World Health Organization, Regional Office for Europe, Denmark
[5, 6, 7] Institute of Public Health, North Macedonia | Mediterranean Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden

BACKGROUND
During the Omicron period (December 2021–December 2022), when COVID-19 vaccines were already available, over 1500 COVID-related deaths occurred in North Macedonia. We aimed to identify risk factors associated with COVID-19-related death during this period.

METHODS
Using the demographic, clinical and vaccination data obtained from the COVID-19 national surveillance database, we conducted a retrospective study among all persons with laboratory-confirmed SARS-CoV-2 infection during the Omicron-period, 6/12/2021–31/12/2022. We described COVID-19 cases using descriptive statistics, and we used multivariable logistic regression analysis to calculate adjusted odds ratios (aOR).

RESULTS
During the study period, 128,804 COVID-19 cases occured. The median age was 44 years (IQR:32-60); 26% were older than 60 years; 55% were female, 40% were unvaccinated, and 58% received at least two COVID-19 vaccine doses. Overall, 1,541 (case fatality:1.2%) deaths were registered. The median age was 76 (IQR: 69-82), 60% were male, 93% had at least one comorbidity and 60% were unvaccinated. Odds of death were higher in males (aOR=2.0; 95%CI=1.8–2.3), persons ≥60 years (aOR=13; 95%CI=10–15), persons with neurologic disease (aOR=9.8; 95%CI=8.4–12), carcinoma (aOR=6.0; 95%CI=4.5–7.3), kidney disease (aOR=5.3; 95%CI=4.2–6.8), cardiac disease (aOR=4.5; 95%CI=3.8–5.2), lung disease (aOR=2.7; 95%CI=2.3–3.3), diabetes (aOR=2.1; 95%CI=1.9–2.4). Compared with unvaccinated, odds of death were lower in those vaccinated with two doses (aOR=0.30; 95%CI=0.26–0.33) or ≥3doses (aOR=0.05; 95%CI=0.04–0.07).

CONCLUSIONS
Among SARS-CoV-2-infected persons in North Macedonia during an Omicron-predominant period, males, older persons, those with comorbidities, and unvaccinated persons had a higher risk of death. Targeting these high-risk groups for COVID-19 vaccination could help reduce mortality from COVID-19 in North Macedonia in the future.

Keywords: COVID-19, Omicron, Risk factors, COVID-19 related death
ABSTRACT ID: 554
PRESENTED BY: Katerina Kirkovik Kolevska, Republic of North Macedonia / kejtkkolevska@gmail.com

POSTER TOUR 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

A case-case study design using national surveillance data underlines the role of immunocompromise among vaccinated COVID-19 cases requiring critical care in Ireland in 2021

D. Kelly [1]
L. Marron [2], K. O'Donnell [3], R. Dwyer [4], M. Power [5], C. Migone [6], J. O'Donnell [7], C. Walsh [8]

[1, 2] Health Protection Surveillance Centre, Health Service Executive, Dublin, Ireland
National Immunisation Office, Health Service Executive, Dublin, Ireland
[3, 7] Health Protection Surveillance Centre, Health Service Executive, Dublin, Ireland
[4] National Office for Clinical Audit, RCSI, Dublin, Ireland
[5] National Clinical Programme for Critical Care Advisory Group, Health Service Executive, Ireland
[6] National Immunisation Office, Health Service Executive, Dublin, Ireland
[8] Health Research Institute and MACSI, University of Limerick, Ireland

BACKGROUND
During 2021 the proportion of cases admitted to critical care who had received 2-doses of a COVID-19 vaccine increased over time in Ireland. This observation has public health implications for vaccine confidence. A potential explanation is the reduced ability of the immunocompromised to produce an adequate and sustained immune response to vaccination. We aimed to measure the association between vaccination status of critical care patients and their underlying degree of immunocompromise.

METHODS
We analysed surveillance data from a national database of COVID-19 critical care admissions from 1 July to 29 October 2021. We employed a case-case study design to compare vaccinated versus unvaccinated COVID-19 cases by immunocompromise status. We used logistic regression analysis to estimate the odds ratio of immunocompromise among vaccinated COVID-19 cases in critical care compared to unvaccinated cases, stratified by age.

RESULTS
Among the 365 critical care COVID-19 patients included in the study, 38% (139/365) were fully vaccinated versus 62% (226/365) unvaccinated, while 28% (101/365) were immunocompromised. Vaccinated patients were significantly more likely to be aged over 65 years (60% versus 24%, $p<0.0001$), immunocompromised (57% versus 10%, $p<0.0001$), and admitted later in the study period (65% versus 56%, $p=0.03$) compared to unvaccinated. Vaccinated patients were significantly more likely to be highly immunocompromised compared to unvaccinated patients: age<65 (OR=57.0, 95% CI 17.7–183) and age >65 (OR=3.1, CI 1.1–8.8).

CONCLUSIONS
The findings demonstrate that immunocompromised patients are disproportionately represented among vaccinated critical care admissions, likely due to a suboptimal immune response to 2-doses of COVID-19 vaccination. This supports current recommendations for additional booster doses of COVID-19 vaccination for the immunocompromised to reduce the risk of critical care admission and relieve pressure on acute healthcare services.

Keywords: Immunocompromised Host, COVID-19 Vaccines, Critical care, Immunity, Ireland
ABSTRACT ID: 42
PRESENTED BY: David Kelly, Ireland / kellyd18@tcd.ie

POSTER TOUR 1
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

The participatory surveillance system GrippeWeb helps to date and quantify changes in sensitivity of COVID-19 incidence in national notifiable disease surveillance data in Germany

A. Loenenbach [1]
A. Lehfeld [2], K. Prahm [3], U. Preuß [4], S. Buda [5], R. Dürrwald [6], M. Diercke [7], U. Buchholz [8]

[1] Robert Koch Institute, Department of Infectious Disease Epidemiology, Respiratory Infections Unit, Berlin, Germany
[2, 3, 4, 5, 8] Robert Koch Institute, Department of Infectious Disease Epidemiology, Respiratory Infections Unit, Berlin, Germany
[6] Robert Koch Institute, Department of Infectious Diseases, Influenza Viruses and Other Respiratory Tract Viruses Unit, Berlin, Germany
[7] Robert Koch Institute, Department of Infectious Disease Epidemiology, Surveillance Unit, Berlin, Germany

BACKGROUND

During the COVID-19 pandemic the WHO followed the incidence of COVID-19 relying on notification data of laboratory confirmed cases. In Germany, notification data continuously assessed severe COVID-19 cases reliably, however, the sensitivity of the overall COVID-19-incidence decreased over time, but it was not clear when, and which events triggered it.

METHODS

We compared weekly incidence rates of nationally notified COVID-19 cases (≥15-year-olds) with two additional indicators stemming from the participatory surveillance system "GrippeWeb". GrippeWeb-indicator 1 (GWI1) used information from the sentinel virologic surveillance system (from calendar week (CW)10/2020), the second (GWI2) used information from GrippeWeb participants who reported positive SARS-CoV-2 tests (including self-tests) (from CW27/2022). Sensitivity was calculated as the ratio of the weekly incidence of notification data relative to that assessed by GWI1 and GWI2. We also gathered information on the timing of control measures, e.g. testing regulations and rules.

RESULTS

Between CW10/2020-CW21/2022, the overall course of the incidence rates of notification data was similar to GWI1. Since then, sensitivity of the notification data decreased linearly until CW1/2023 to about 50%, and decreased more rapidly (to about 12%) during CW2-17/2023. In contrast, GWI1 and GWI2 continued to show similar incidence rates. Around CW10-17/2022 regular testing at schools and workplaces stopped, and at the end of 2022 free citizen testing ceased.

CONCLUSIONS

The participatory surveillance system GrippeWeb was capable to pinpoint when notifiable data became less sensitive. In Germany we identified two sensitivity dents, by and large coinciding with the ending of rules and regulations leading to changed test behaviour. Transitioning from pandemic to endemic phase, surveillance systems, complementary to the notification system are increasingly important to confidently describe the epidemiological situation, particularly when measures are slowly relieved.

Keywords: COVID-19, Epidemiological Monitoring, Incidence, Surveillance, Pandemic Public Health and Social Measures
ABSTRACT ID: 465
PRESENTED BY: Anna Loenenbach, Germany / loenenbacha@rki.de

POSTER TOUR 1

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Surveillance

MODERATOR
Justine Schaeffer

Abstract

Results from WHO GISRS Global External Quality Assessment Programme (EQAP) 2020-2022 for molecular detection of SARS-CoV-2

S. Hussain [1]
A. Barakat [2], A. Guseinova [3], B. Herring [4], F. Inbanathan [5], J. Leite [6], J. Lo [7], J. Mendez Rico [8], K. Nahapetyan [9], P. Nguyen [10], D. Pereyaslov [11], M. Samaan [12], S. Wong [13], W. Zhang [14]

[1] WHO Global Influenza Programme, Geneva, Switzerland, WHO Collaborating Centre for Reference and Research on Influenza, Melbourne, Australia
[2] WHO Health Emergency Programme, World Health Organization Regional office for the Eastern Mediterranean, Cairo, Egypt
[3] WHO Regional office for Europe, World Health Organization
[4] WHO Health Emergency Programme, World Health Organization Regional Office for Africa
[5] WHO Health Emergency Programme, World Health Organization Regional office for South-East Asia
[6] Health Emergencies, Pan American Health Organization, World Health Organization Regional Office for the Americas
[7, 13] Centre for Health Protection, Department of Health, Hong Kong Special Administrative Region of China
[8] PAHO Health Emergencies, Pan American Health Organization, World Health Organization Regional Office for the Americas
[9] Regional Office for Europe, World Health Organization
[10] WHO Health Emergency Programme, World Health Organization Regional office for Western Pacific
[11, 12, 14] Global Influenza Programme, World Health Organization

BACKGROUND
In 2020, the External Quality Assessment Programme (EQAP) for the Detection of SARS-CoV-2 Virus by RT-PCR was rapidly launched to assess the proficiency of laboratories in the molecular detection of SARS-CoV-2, building on the existing WHO coordinated Global Influenza Surveillance and Response System (GISRS) EQAP.

METHODS
Since 2020, 291 laboratories from 189 countries, areas or territories in six WHO regions were invited to participate. Validated panels of virus samples containing SARS-CoV-2 wild type and variants of concern as well as human coronaviruses, were distributed to laboratories, accompanied by a survey to identify concerns in launching/implementing molecular detection.

RESULTS
Of the returned results, 94.8%, 80.1% and 96.1% of laboratories reported all correct results in 2020, 2021 and 2022, respectively. In most cases, further assay validation/sensitivity was required to reduce errors. Responses from the survey highlighted that the biggest concerns for implementing detection of SARS-CoV-2 were the need for specific staff training, insufficient extraction kits/reagents and primers/probes/testing reagents, and establishing procedures/guidelines/protocols on specimen collection/shipping/storage and standard virus detection methods. [NK1] In 2022, a larger proportion of respondents (12.8%) indicated that they had no major concerns about implementing detection of SARS-CoV-2. By 2022, ~30% and ~50% of laboratories reported detecting variants of concern by real-time RT-PCR and/or sequencing, respectively.

CONCLUSIONS

Our results indicate that laboratories are performing well in the molecular detection of SARS-CoV-2. In 2022, 93.6% of responding participant GISRS laboratories reported that both detection of SARS-CoV-2 and influenza are being implemented. Integrated sentinel surveillance of influenza and SARS-CoV-2 is now a primary objective of GISRS; the WHO GISRS EQAP is important to ensure and maintain quality assurance of laboratories and support countries in the molecular detection of SARS-CoV-2.

Keywords: SARS-CoV-2, WHO, Sentinel surveillance, Laboratories, RT-PCR
ABSTRACT ID: 837
PRESENTED BY: Saira Hussain, Australia /saira.hussain@influenzacentre.org

POSTER TOUR 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Food- and waterborne diseases

MODERATOR
Pawel Stefanoff

Abstract

Assessing Giardiasis incidence in travellers for various destination countries and regions using surveillance and travel data, Germany, 2014–2019

F. Hommes [1]
S. Behnke [2], A. Dörre [3], K. Stark [4], M. Faber [5]

[1] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 4 ,5] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[3] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Germany

BACKGROUND

Giardia duodenalis is a leading cause of gastroenteritis worldwide. In Europe, giardiasis is often associated with travel abroad. We aim to estimate the risk of giardiasis in travellers from Germany by destination country and region.

METHODS

We analysed travel-related giardiasis cases, their countries and regions of exposure and the age and sex distribution of cases reported in 2014–2019 in Germany. We defined a travel-related giardiasis case as a laboratory-confirmed symptomatic individual with outbound travel abroad within 3–25 days before symptom onset. Based on the number of reported cases per exposure country and UNWTO travel data for Germany, we calculated the number of travel-related giardiasis cases per 100,000 travellers, comparing the incidence in 2014–2016 and 2017–2019.

RESULTS

In 2014–2019, 21,172 giardiasis cases were reported in Germany, corresponding to an overall incidence of 4.3 per 100,000 population. Of all cases, 6,879 (32%) were travel-related with a median age of 34 (1st, 3rd Quartile: 25, 50), 51% were male. Southern Asia was the most frequently reported exposure region and had the highest incidence in travellers (64.1) in 2017–2019, followed by Latin America and the Caribbean (15.4) and Sub-Saharan Africa (12.9). The regional incidence in Europe ranged from 0.1 to 0.4 cases per 100,000 travellers. We observed statistically significant decreasing trends for Southern Asia and Sub-Saharan Africa. Latin America and the Caribbean was the only region with a statistically significant increasing trend.

CONCLUSIONS

Almost one-third of the giardiasis cases were travel-related. Giardiasis incidence differed more than 600-fold between regions. Decreasing trends in many regions might be due to improvements in food hygiene or travel conditions. Our results may inform medical consultation pre and post patient’s travel.

Keywords: Giardiasis, Travel-Related illness, Disease transmission, Surveillance

ABSTRACT ID: 41
PRESENTED BY: Mirko Faber, Germany / faberm@rki.de

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POSTER TOUR 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Food- and waterborne diseases

MODERATOR
Pawel Stefanoff

Abstract

Risk factors for household transmission of Shigella during an outbreak in Tunisia, July-November 2022

E. MZIOU [1]
S. Dhaouadi [2], A. Hechaichi [3], F. Ben Youssef [4], H. Letaief [5], S. Guermazi [6], M. Safer [7], S. Derouiche [8], L. Bouabid [9], S. Bouagtef [10], S. Elmili [11], M. Rebhi [12], N. Bouafif ep Ben Alaya [13]

[1] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET),
European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[2, 3, 5, 13] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET),
European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
Faculty of Medicine of Tunis, University Tunis El Manar, Tunis, Tunisia
[4, 8, 9, 10, 11] National Observatory of New and Emerging Diseases, Tunis, Tunisia
[6, 12] National Authority for the Sanitary Safety of Food Products, Tunisia
[7] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Faculty of Medicine of Tunis, University Tunis El Manar, Tunis, Tunisia

BACKGROUND
In July-November 2022, the National Observatory of New and Emerging Diseases in Tunisia received 320 alerts of Shigella Sonnei cases. Given the increase in the number of Shigellosis cases compared to previous years, an outbreak was declared on 5 November 2023. An investigation was conducted to identify risk factors for household transmission and to provide hygiene education to the community in affected households.

METHODS
We performed a cross-sectional epidemiological and sanitary survey of households with at least one laboratory-confirmed cases in December 2022-January 2023. We randomly selected households within reporting governorates. Field data-collection was done by trained investigation-teams. During household visits, we collected epidemiological data, environmental samples and provided sanitary education. Households with more than one infected person were labelled at-risk of further transmission. We conducted multivariable logistic regression to identify predictive factors of having multiple cases within a household (at-risk household).

RESULTS
Among 69 households surveyed, 40.6% (n=28) were classified as at-risk with multiple cases.Factors independently associated with this outcome were use of overflowing cesspools for wastewater disposal due to the absence of a public sanitation system (OR=8.9, 95%CI: 1.3-65.7, p=0.031), home-manipulation of diapers (OR=7.8, 95%CI: 1.1-68.0, p=0.050) and water interruption in the seven days preceding the case onset (OR=4.3, 95%CI: 1.2-16.4, p=0.033). All environmental samples (n=232, water, food, surfaces and footprints) were negative.

CONCLUSIONS
Summer 2022 was marked by frequent nationwide water interruptions; which further degrade sanitation conditions to favour propagation of water-borne germs, as underscored by our findings. To prevent within household transmission, our results helped inform sanitary education by promoting hand hygiene, improved diaper handling and household-waste management. We also recommended avoiding drinking from unknown or uncontrolled water sources.

Keywords: Shigella, Surveys and Questionnaires, Risk Factors, Tunisia
ABSTRACT ID: 244
PRESENTED BY: Emna Mziou, Tunisia / dremnamziou@gmail.com

POSTER TOUR 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Food- and waterborne diseases

MODERATOR
Pawel Stefanoff

Abstract

Foodbook 2.0: Highlights from the Canadian food, water and animal exposure study

M. Tooby [1]
[1] Public Health Agency of Canada

BACKGROUND

Foodbook provides population-level estimates of Canadian's exposure to potential sources of enteric illness. The second iteration of this study, Foodbook 2.0, uses expanded methods, including multiple modes of administration, and is being conducted in all Canadian provinces and territories from January to December 2023.Foodbook 2.0's primary objective is to provide updated population-level, seven-day food exposure data to compare to foods eaten by cases during a foodborne illness outbreak. The study will also support risk assessments and burden of illness estimates, to help target public health interventions to prevent illness, and inform food safety education initiatives.

METHODS

The survey collects data on food exposures, drinking and recreational water exposures, animal-related exposures, consumer food safety knowledge and practices, recent acute gastrointestinal illnesses, and demographic factors. Results will update and enhance data from Foodbook 1, conducted in 2014-2015, and establish consumption data on over 100 new exposures of interest, including high-risk foods.A mixed methods, telephone and online approach was selected in order to increase response rates. An estimated 20,000 Canadians across all provinces and territories will be interviewed over a twelve-month period.

RESULTS

Preliminary data are available and were analyzed to provide population-level estimates on food, water and animal exposures. Data has been compared to findings from Foodbook 1, illustrating that consumption of many foods has stayed consistent, with some 'trendier' foods being consumed more often.

CONCLUSIONS

Foodbook provides data to enhance response to enteric illness outbreaks and to inform additional Canada-wide, cross-disciplinary efforts to prevent and control disease. The presentation will describe the study, present preliminary results, and describe anticipated knowledge translation outputs. At the time of the presentation, further results will be available.

Keywords: Canadian, Foodborne, Survey, Outbreak
ABSTRACT ID: 43
PRESENTED BY: Katharine Fagan-Garcia, Canada / katharine.fagan-garcia@phac-aspc.gc.ca

POSTER TOUR 2

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Food- and waterborne diseases

MODERATOR
Pawel Stefanoff

Abstract

Molecular detection of Shiga toxin-producing Escherichia coli (STEC) in water using a sensitive and rapid water-based filtration method

Z. Alfahl [1]
L. O'Connor [2], K. Burgess [3], D. Morris [4], G. Miliotis [5], J. O'Dwyer [6], P. Hynds [7], L. Burke [8]

[1] Antimicrobial Resistance and Microbial Ecology Group, School of Medicine, University of Galway, Galway, Ireland
Centre for One Health, Ryan Institute, University of Galway, Galway, Ireland
[2] Centre for One Health, Ryan Institute, University of Galway, Galway, Ireland
Molecular Diagnostics Research Group, College of Science & Engineering, University of Galway, Ireland
[3] Teagasc Food Research Centre, Ashtown, Dublin, Ireland
[4, 5, 8] Antimicrobial Resistance and Microbial Ecology Group, School of Medicine, University of Galway, Galway, Ireland
Centre for One Health, Ryan Institute, University of Galway, Galway, Ireland
[6] School of Biological, Earth and Environmental Sciences, University College Cork, Cork, Ireland
Irish Centre for Research in Applied Geosciences (iCRAG), University College Dublin, Ireland
[7] Irish Centre for Research in Applied Geosciences (iCRAG), University College Dublin, Ireland
Environmental Sustainability and Health Institute, Technological University Dublin, Ireland

BACKGROUND
Infection with STEC can range from asymptomatic to Haemolytic Uraemic Syndrome, renal failure and death. Groundwater-derived drinking water is one of the main transmission routes for STEC, which has an infectious dose as low as 10 cells. This study aimed to develop a new sensitive, enrichment-free water filtration method to detect and enumerate STEC using quantitative real-time PCR (qPCR) and rapid Loop-mediated Isothermal Amplification (LAMP) technologies.

METHODS
Freshwater (n=10), groundwater wells (n=9) and drain (n=1) samples were collected from locations around Galway. Water samples (100 ml) were passed through a 0.22 µm filter and buffer was added to elute captured cells. An aliquot of the eluate was tested using qPCR assays to determine the copy numbers of STEC O157 and O26 serogroups. Shiga toxins (stx1, stx2) and E. coli (phoA) gene detection was performed using LAMP assays (turnaround time 30 minutes). Presence of STEC associated gene targets including eae and serogroups O103, O104, O111 and O145 was determined by real-time PCR.

RESULTS
Overall, 17/20 (85%) samples were O157 positive (mean 7.03x104 copies/reaction), while 16/20 (80%) samples were O26 positive (mean 9.30x104 copies/reaction). Shiga toxins (stx1, stx2) were detected in 13/20 (65%) and 7/20 (35%) samples; respectively, while E. coli (phoA) was found in 19/20 (95%) samples. Intimin (eae) and serogroups O103, O104, O111 and O145 were detected in 19 (95%), 5 (25%), 12 (60%), 10 (50%) and 8 (40%) samples, respectively.

CONCLUSIONS
We describe a novel, rapid method for detection of STEC contamination of water, with potential to be used to detect other waterborne pathogens. Findings indicate high rates of STEC serogroups and toxins in water.

Keywords: Shiga toxin-producing Escherichia coli, Molecular diagnostics, Loop-mediated Isothermal Amplification, Quantitative real-time PCR, Water filtration, Bacterial infections

ABSTRACT ID: 239
PRESENTED BY: Zina Alfahl, Ireland / zina.alfahl@universityofgalway.ie

POSTER TOUR 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

COVID-19 vaccination in Spain - a success story

A. Fernandez Dueñas [1]
C. Olmedo Lucerón [2], L. Sánchez-Cambronero Cejudo [3], S. Fernández Conde [4], E. Cantero Gudino [5], A. Limia Sánchez [6]

[1] Immunization Programme Area, General Directorate of Public Health, Ministry of Health, Spain
[2, 3, 4, 6] Immunization Programme Area, General Directorate of Public Health, Ministry of Health, Spain
[5] TRAGSATEC's technical assistance to the Ministry of Health

BACKGROUND
Spain was one of Europe's worst hit countries from the first COVID-19 wave in spring 2020. Despite having one of the highest coverage rates in Europe of vaccines included in the national immunization programme, national surveys conducted before availability of vaccines showed a COVID-19 vaccine hesitancy of 15-40% and an intention to vaccinate of only 30-40% of the population. This was mainly due to uncertainties regarding the pandemic and future vaccines. The objective is to describe the process to achieve one of the world's highest COVID-19 vaccine coverage.

METHODS
An internal assessment using quantitative and qualitative methodology of the COVID-19 vaccination strategy was conducted, including a survey to relevant stakeholders. A national binding agreement was reached to implement a single vaccination strategy and to develop the first national vaccination registry (REGVACU).

RESULTS
Immunisation coverage (fully vaccinated) was 92.6% in population over 12 years old. A multidisciplinary group coordinated from the Ministry of Health deployed innovative methods to follow the vaccination programme development at regional level and to enable proper vaccine rollout and sharing good practices. This was key for achieving the vaccination success. The overall impact of the pandemic on other immunisation programmes has been limited. For the first time, new tools and strategies were used to succeed in the COVID-19 vaccination strategy and overcome initial vaccine hesitancy. In addition, the registry has been a game changer in Spanish immunisation information system.

CONCLUSIONS
Overall, the COVID-19 vaccination programme was a success and vaccine confidence in Spanish population was reinforced. Nationwide equity was ensured despite decentralisation, heterogeneity and challenges faced. The high vaccination coverage reached in Spain contributed significantly to limit the impact in subsequent SARS-CoV-2 waves.

Keywords: Immunisation programs, Vaccines, COVID-19, Vaccine-preventable diseases
ABSTRACT ID: 296
PRESENTED BY: Ana Fernandez Dueñas, Spain / afernandezd@sanidad.gob.es

POSTER TOUR 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

Additional benefit of a second booster dose against COVID-19 hospitalization. A case-control study with data from sentinel SARI surveillance in Spain

C. Mazagatos [1]
G. Pérez-Gimeno [2], V. Sandonis [3], M. Lozano [4], C. Delgado-Sanz [5], A. Larrauri [6], (GROUP) SARI surveillance VE group in Spain

[1] National Centre of Epidemiology, Instituto de Salud Carlos III | CIBERESP
[2, 4] National Centre of Epidemiology, Instituto de Salud Carlos III
[3] National Centre of Microbiology, Instituto de Salud Carlos III
[5, 6] National Centre of Epidemiology, Instituto de Salud Carlos III | CIBERESP

BACKGROUND
Sentinel surveillance of severe acute respiratory infection (SARI) in Spain allows monitoring of COVID-19 and influenza, while providing a platform to monitor vaccine effectiveness (VE). During autumn 2022, people over 60 years in Spain were eligible for a second booster dose. We aimed to estimate the additional benefit of these booster doses in the Spanish population.

METHODS
SARI data from 22 sentinel hospitals was used. Patients were systematically tested for SARS-CoV-2 and included as cases (positives) or controls (negatives). We estimated relative VE of doses administered as of 26 September 2022 (second booster) compared to primary vaccination with or without first booster (PV), or primary vaccination with a first booster (FB). We computed VE by age group and time since vaccination, using logistic regression and adjusting for age, sex, hospital, chronic disease and onset date.

RESULTS
Between September 2022 and March 2023, 342 cases and 1867 controls were included, with a median age of 83 and 82 years, respectively. Relative VE (95% confidence interval) of the second booster over PV was 48% (31-61) in 60+ years, and 53% (33-68%) in 80+ years, and was 22% (-30-53) and 49% (5-73), respectively, four months after vaccination. Relative VE of the second booster over FB was 42% (21-57) in 60+ years and 44% (18-62) in 80+ years, and was 1% (-71-42) and 34% (-32-67), respectively, four months after vaccination.

CONCLUSIONS
VE with SARI data showed the additional benefit of second booster doses administered in Spain in autumn 2022 in persons previously vaccinated with either primary vaccination or primary vaccination and a first booster, while evidencing a decrease in protection with time since the second booster in the Spanish elderly population.

Keywords: COVID-19, Respiratory infections, Surveillance, Hospitalization, Vaccination, Vaccine effectiveness
ABSTRACT ID: 555
PRESENTED BY: Clara Mazagatos, Spain / cmazagatos@isciii.es

POSTER TOUR 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

Temporal changes to case fatality risk of COVID-19 following vaccination in England: a national surveillance study

F. Halford [1]
K. Yates [2], T. Clare [3], J. Lopez-Bernal [4], M. Kall [5], H. Allen [6]
[1, 2, 3, 4, 5, 6] UK Health Security Agency

BACKGROUND

Risk of death following SARS-CoV-2 infection has fallen during the pandemic, largely due to immunity from vaccination. In England, the timing and extent of this reduction varied due to staggered eligibility during the primary vaccination campaign, based on age and clinical risk group. Durability of protection is less well understood. We estimate case fatality risk (CFR) by vaccination status and time since last dose in adults aged >50 during a period of widespread community testing to better understand the impact of COVID-19 vaccination and duration of protection.

METHODS

SARS-CoV-2 cases diagnosed between May 2020 and February 2022, recorded by England's laboratory reporting system, were linked to vaccine records from National Immunisation Management System. CFR was calculated as the proportion of cases that died of COVID-19 per the death certificate, aggregated by week of specimen and stratified by 10-year age-band and vaccination status.

RESULTS

Overall, a reduction in CFR was observed for all age-bands, with a clear temporal link to when the age group became eligible for primary vaccination and then the first booster. CFR increased with age (0.27% 50-59 years; 1.16% 60-69; 4.72% 70-79; 16.34% 80+) and was highest in the unvaccinated - albeit a reduction was observed over time. The highest CFR was seen in the unvaccinated 80+ group prior to vaccination rollout (30.60%). CFR was consistently lowest in vaccinated populations within 6 months of last dose yet increased after over 6 months elapsed since last dose, across all age-bands.

CONCLUSIONS

COVID-19 CFR reduced following vaccination, with the lowest CFR seen across all age-bands when vaccinated up to 6 months prior to specimen date. This provides some evidence for continued booster doses in older age groups.

Keywords: COVID-19/epidemiology, COVID-19/mortality, Case fatality rate, Mortality/trends, Epidemiology, SARS-CoV-2
ABSTRACT ID: 345

PRESENTED BY: Florence Halford, United Kingdom / florence.halford@ukhsa.gov.uk

POSTER TOUR 3
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

Pre-existing chronic conditions and COVID-19 vaccination uptake

M. Barker [1]
K. Kõiv [2], I. Magnúsdóttir [3], H. Milbourn [4], B. Wang [5], X. Du [6], G. Murphy [7], H. Ask [8], R. Eek Brandlistuen [9], D. McCartney [10], O. Ebrahimi [11], O. Andreassen [12], K. Lehto [13], U. Valdimarsdóttir [14], F. Fang [15]

[1] Unit of Integrative Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden
[2, 13, 15] Estonian Genome Centre, Institute of Genomics, University of Tartu, Estonia
[3, 14] Center of Public Health Sciences, Faculty of Medicine, University of Iceland, Reykjavik, Iceland
[4, 10] University of Edinburgh, Edinburgh, Scotland
[5, 8, 9] Norwegian Institute of Public Health, Oslo, Norway
[6, 11, 12] University of Oslo, Oslo, Norway
[7] Unit of Integrative Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden

BACKGROUND

COVID-19 vaccination is especially important among high-risk groups for severe COVID-19 infection, such as individuals with mental or physical health conditions. Previous country-specific studies suggest swifter uptake among individuals with chronic physical conditions, while conflicting results have emerged for individuals with mental disorders. Our study aimed to explore the impact of pre-existing mental and physical conditions on COVID-19 vaccination uptake across seven cohort studies conducted in Sweden (Omtanke2020), Norway (Map-19, MoBa), Iceland (C-19 Resilience), Estonia (EstBB-C19, EstBB-EHR) and Scotland (CovidLife).

METHODS

Prior diagnoses of any chronic physical condition or mental disorder were used as the study exposures. The outcome was defined as uptake of the first dose of a COVID-19 vaccine by 30th September 2021. Each cohort conducted multivariable logistic regression models, which were pooled using random effects meta-analyses.

RESULTS

In total, 336,641 participants (65.0% female, mean age: 48.3 [Standard Deviation (SD): 2.8] years) were included in the study, 266,557 (79.2%) of whom received the first dose of a COVID-19 vaccination by 30th September 2021. Participants with a chronic physical condition had significantly higher odds of being vaccinated against COVID-19 (Odds Ratio [OR]: 1.33, 95% Confidence Interval [CI]: 1.02 to 1.74). However, those with a mental disorder had significantly lower odds of COVID-19 vaccination uptake (OR: 0.88, 95% CI: 0.78 to 0.99).

CONCLUSIONS

These findings support previous studies showing swifter uptake of COVID-19 vaccination among individuals with chronic physical conditions, whilst those with a history of mental disorders demonstrated lower uptake. These results are particularly concerning given the documented risks of adverse COVID-19 outcomes in this population, and are important for the development of current and future vaccination campaigns.

Keywords: COVID-19 Vaccines, Chronic Disease, Mental Health, Meta-Analysis
ABSTRACT ID: 2
PRESENTED BY: Mary Barker, Sweden / mary.barker@ki.se

POSTER TOUR 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

Reactogenicity of heterologous boosting with Bimervax (PHH-1V, HIPRA) against SARS-CoV-2: differences upon previous infection and prime-vaccination regime. Results of a phase 3 clinical trial

L. Ferrer Soler [1]
S. De Cambra Florensa [2], J. Corominas García [3], I. Güell Casellas [4], T. Prat Cabañas [5]

BACKGROUND
Bimervax (PHH-1V, HIPRA) is an adjuvanted bivalent recombinant protein vaccine based on the receptor binding domain of two SARS-CoV-2 variants, Beta and Alpha. PHH-1V has shown to be a safe and well tolerated vaccine when used as third and fourth dose in previously vaccinated individuals with Comirnaty (Pfizer/BioNTech).

METHODS
Phase III, open-label, uncontrolled, multicentre clinical trial (NCT05246137) in a cohort of volunteers (≥ 16 years) vaccinated with Comirnaty (Pfizer/BioNTech), Spikevax (Moderna), Vaxzevria (AstraZeneca) or Jcovden (Janssen), at least 3 months prior to administration of a booster dose with Bimervax. Solicited local and systemic reactions were assessed through Day 7 and unsolicited local and systemic adverse events through Day 28 after vaccination. Reactogenicity was analysed upon previous primary vaccination regimen and history of SARS-CoV-2 infection.

RESULTS
A total of 2,646 subjects were included. The median age was 34.4 years (16 to 85 years), 52.49% male and 43.54% had COVID-19 after primary vaccination. All of them completed day 14 post-vaccination and 86.96% experienced at least one adverse event, mostly of mild or moderate intensity. Most common adverse reactions were injection site pain (82.01%), fatigue (31.25%) and headache (30.88%). Subgroup analysis revealed no relevant differences in the safety and reactogenicity profile based on the primary vaccination regime or previous COVID-19 infection. There were no cases of severe COVID-19.

CONCLUSIONS
The PHH-1V vaccine was well tolerated and safe, regardless of the primary vaccination schedule received or previous SARS-CoV-2 infection. Heterologous booster with PHH-1V could be a safe and interesting strategy for upcoming vaccination campaigns in individuals already immunised with mRNA and/or vector vaccines.

Keywords: COVID-19, Vaccination, Recombinant protein, Booster
ABSTRACT ID: 586
PRESENTED BY: Salomé de Cambra Florensa, Spain / Salome.decambra@hipra.com

POSTER TOUR 3

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Vaccination

MODERATOR
Jane Whelan

Abstract

Impact of the Health on Wheels Intervention on COVID-19 vaccination in Guatemala

M. Rondy [1]

S. Reyes Leiva [2], M. Figueroa [3], K. Sum [4], E. Balsells [5], I. Fortín [6], M. Vicente Batz [7], K. Castellanos [8], C. Jarquín [9] M. Montenegro [10], E. Montúfar Velarde [11], L. Quezada [12]

[1] Pan American Health Organization Guatemala
[2, 4, 5, 6, 9, 12] Pan American Health Organization Guatemala
[3, 7, 8, 11] Ministry of Health and Wellness Guatemala
[10] OSAR Guatemala

BACKGROUND

By May 2022, after one year of COVID-19 vaccination in Guatemala, there were large differences in vaccine uptake between metropolitan and rural areas. An anthropological survey stressed the importance to include community leaders in outreach vaccination activities and to increase the promotion in local languages in rural areas. To address this need, the Ministry of Health (MOH) piloted the “Salud Sobre Ruedas” - “Health on Wheels” intervention (HoW), consisting of mobile vaccination brigades, supported by community facilitators chosen by local leaders and fluent in local languages.

METHODS

From August 1 to October 31 2022, HoW brigades visited 189 communities in 15 districts in the rural regions of Alta Verapaz. Communities were selected if 1-dose coverage was <30% by May 2022. Paper-based vaccination registries were maintained at the community level. To measure the impact, we compared the increase in COVID-19 1-dose vaccination coverage in the intervened (n=189) and non-intervened communities (n=190) in the same municipalities during the same period. Communities were classified as “vaccine hesitant” or “non-hesitant” if communities’ rejection of vaccination activities had been documented prior to the HoW intervention. Coverage was estimated at the community level and compared.

RESULTS

During the intervention, the increase in 1-dose COVID-19 vaccination coverage was 2.4 times higher in intervened versus non-intervened communities (19.7%, and 8.2% increase, respectively). Among intervened communities, the increase in vaccination coverage was 2.9 times higher in communities with a history of vaccination hesitancy compared with non-hesitant communities.

CONCLUSIONS

The HoW intervention doubled the increase in vaccination coverage against COVID-19 in intervened communities in rural areas of a region of Guatemala. The impact was higher in vaccine-hesitant communities. In 2023, the MOH adopted this intervention as an innovative model.

Keywords: Community participation, COVID-19, Vaccination, Vaccination Hesitancy, Vaccination Coverage
ABSTRACT ID: 798
PRESENTED BY: Evelyn Balsells, Guatemala / evebalsells03@gmail.com

POSTER TOUR 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Extended-spectrum beta-lactamase producing E. coli causing urinary tract infections in Iceland. Analysis of epidemiology and risk factors in 2012-2021

A. Halldórsdóttir [1]
B. Hrafnkelsson [2], K. Einarsdóttir [3], K. Kristinsson [4]

[1] Center for Health Security and Communicable Disease Control, Directorate of Health
[2] Faculty of Physical Sciences, University of Iceland
[3] Department of Public Health Sciences, University of Iceland
[4] Department of Clinical MIcrobiology, Landspitali University Hospital

BACKGROUND
The incidence of infections due to bacteria producing extended-spectrum β-lactamases (ESBL) has increased posing a threat to public health. The aim was to investigate the association of potential risk factors for urinary tract infections (UTI) caused by E. coli producing ESBL vs. not producing ESBL.

METHODS
This observational, case-control study includes a cohort of 27,747 patients (22,800 females and 4,947 males, 1207 cases and 26,540 controls) of all ages with UTI caused by E. coli in 2012 to 2021 according to urine cultures at the Department of Microbiology at Landspitali University Hospital, Iceland. Relevant patient data was obtained from national health and prescription medicines registers and connected using personal identification numbers. Logistic regression was used to calculate odds ratios (ORs) as a measure of association between ESBL and selected exposure variables.

RESULTS
The proportion of samples with ESBL-producing E. coli increased during the study period, from 2.6% in 2012 to 7.6% in 2021 ($p<0.001$). ESBL-positive strains were detected in 1207 individuals (4.4%), 905 females (4.0%) and 302 males (6.1%). The following risk factors were identified: Male sex, higher age, hospital-association, Charlson comorbidity index score ≥3, history of cystitis or hospitalization in the past year, and specific antibiotic or protein pumb inihibitors (PPIs) prescriptions in the past half year. The antibiotic associated with the highest risk was ciprofloxacin (OR 2.45). Risk factors varied between sex/age subgroups.

CONCLUSIONS
The prevalence of UTIs caused by ESBL-producing E. coli is increasing in Iceland. Among the strongest risk factors for ESBL production were antibiotic use, especially ciprofloxacin, and PPIs, both considered to be overprescribed. It´s important to promote the prudent use of these drugs in the future, by educating physicians and the public.

Keywords: Escherichia coli, Anti-Bacterial Agents, Urinary Tract Infections, Risk Factors, Beta-Lactamases
ABSTRACT ID: 188
PRESENTED BY: Anna Margrét Halldórsdóttir, Iceland / anna.m.halldorsdottir@landlaeknir.is

POSTER TOUR 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Changes in the epidemiology of carbapenem-resistant Acinetobacter spp. before and during the COVID-19-pandemic, Germany, January 2017 – December 2021

J. Baum [1]
M. Sandfort [2], F. Reichert [3], A. Dörre [4], T. Eckmanns [5], S. Haller [6]

[1] Robert Koch Institute (RKI), Department for Infectious Disease Epidemiology, Berlin, Germany | European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden | Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
[2, 3, 4, 5, 6] Robert Koch Institute (RKI), Department for Infectious Disease Epidemiology, Berlin, Germany

BACKGROUND
Carbapenem-resistant Acinetobacter spp. (CRA), often causing nosocomial outbreaks, are among WHO's priority pathogens with antimicrobial resistance (AMR). During the COVID-19-pandemic, EU countries and the USA showed heterogenous CRA-trends. We described and quantified changes in CRA-epidemiology in Germany before and during the COVID-19-pandemic.

METHODS
We included CRA notifications (01/2017-12/2021) from German statutory surveillance, fulfilling the case definition: infections or colonisations due to Acinetobacter spp. with carbapenemase-determinant or reduced carbapenem susceptibility. We described cases by sex, age-groups and infection/colonisation. To estimate counterfactual case numbers for pandemic years, we established a predictive model using time-series-regression of pre-pandemic case numbers (01/2017-12/2019). We compared estimated with observed annual case numbers to quantify changes, assessing significance via 95%-confidence-intervals. A second predictive model accounted for overall inpatient numbers in German hospitals (Federal Statistical Office data).

RESULTS
We included 3,250 CRA cases. Excluding missings, 67% (2,163/3,246) were male, 64% (1,416/2,204) colonised and most, i.e. 27% (868/3,247), were 60-79 years old. Time-series showed stable pre-pandemic CRA-trends and a pandemic decrease. Compared to modelled estimates (686), there was a significant 30% (95%CI: 19%-39%) decrease in observed cases in 2020 (480). In 2021, observed numbers (501) were 23% (8%-36%) lower than estimated (654). Adding the observed inpatient decrease (Δ≈13%) to the model, we still found 20% (8%-31%) reduction in 2020 and 12% (-6%-27%) in 2021.

CONCLUSIONS
We observed a strong decrease in CRA cases during the COVID-19-pandemic, even when accounting for fewer inpatients. Several factors, like intensified hygiene, fewer elective surgeries and fewer patient transfers during the COVID-19-pandemic may have contributed. Understanding CRA-epidemiology plus underlying factors improves antimicrobial stewardship and infection prevention and control at patient and population levels, particularly for a possible post-pandemic AMR rebound.

Keywords: Drug Resistance Microbial, Cross Infection, Public Health Surveillance, Acinetobacter, COVID-19, Pandemic
ABSTRACT ID: 720
PRESENTED BY: Jonathan Hans Josef Baum, Germany / jonathan.baum@fu-berlin.de

POSTER TOUR 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Antimicrobial resistance in Greece: data from the Greek Electronic System for the Surveillance of Antimicrobial Resistance – WHONET-Greece, 2018 to 2022

M. Polemis [1]
E. Theofili [2], A. Vatopoulos [3], K. Tryfinopoulou [4], (GROUP) WHONET-Greece study group

[1, 2, 4] Central Public Health Laboratory, National Public Health Organization, Athens, Greece
[3] Department of Public Health Policies, School of Public Health, University of West Attica, Athens, Greece

BACKGROUND

Antimicrobial resistance (AMR) changes over time and continuous monitoring provides insight on AMR levels to inform empirical treatment and public health action. Our aim was to survey AMR levels among key pathogens using data from the Greek Electronic System for the Surveillance of AMR (WHONET-Greece).

METHODS

We studied the routine susceptibility data of 142,605 isolates from hospitalised patients in 41, mainly tertiary hospitals participating in the WHONET-Greece AMR surveillance network for AMR levels for the period of January 2018 - December 2022. Only the first isolate per species from each patient was included. Hospital wards and intensive care units (ICUs) were analysed separately.

RESULTS

Rates of Klebsiella pneumoniae carbapenem resistance increased from 41.8% to 53.5% and from 75.5% to 83.5% in patients hospitalised in wards and ICU respectively from 2018 to 2022. In Acinetobacter baumannii, carbapenem, aminoglycosides and fluoroquinolones resistance was found in most cases over 90%. In Pseudomonas aeruginosa a sharp increase of carbapenem and aminoglycosides non-susceptibility was observed during 2022 after a rather stable trend during 2018-2021, reaching 60.4% and 44.7% in ICU and 39.9% and 30.9% in wards respectively. In Enterococcus faecium resistance to vancomycin increased from 31% in 2018 to 58.8% and 50.9% in 2022 in ICU and wards respectively, while methicillin resistance rates of Staphylococcus aureus remained stable during the study period in both wards and ICU at 37.5% on average.

CONCLUSION

High rates of resistance have been observed for K.pneumoniae, A.baumanni and E.faecium, while in P.aeruginosa the alarming increase of carbapenem and aminoglycoside resistance in 2022 needs further investigation. Continuous monitoring of the emergence and evolution of resistance to key antimicrobials over time constitutes a crucial AMR surveillance tool.

Keywords: Antimicrobial Drug Resistance, Public Health Surveillance, Greece, ICU Intensive Care Units
ABSTRACT ID: 748
PRESENTED BY: Michalis Polemis, Greece / m.polemis@eody.gov.gr

POSTER TOUR 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Epidemiology and antimicrobial resistance of neisseria gonorrhoeae in Catalonia, 2018-2021

M. Herrero Garcia [1]
S. Broner [2], G. Patsi [3], A. Martin [4], E. Lopez [5], V. González [6], J. Casabona [7], J. Mendioroz [8], P. Ciruela [9],
(GROUP) Working group at Microbiological Reporting System

[1, 2, 3, 4, 8] Subdirectorate General for Public Health Surveillance and Emergency Response
[5, 6, 7] Centre of Epidemiological Studies of HIV/AIDS and STI of Catalonia (CEEISCAT)
CIBER Epidemiologia y Salud Pública (CIBERESP), Instituto de Salud Carlos III
[9] Subdirectorate General for Public Health Surveillance and Emergency Response
CIBER Epidemiologia y Salud Pública (CIBERESP), Instituto de Salud Carlos III

BACKGROUND
Antimicrobial resistance data for Neisseria gonorrhoeae is globally sparse and resistant strains are emerging in Catalonia. We aim to describe epidemiological and antimicrobial resistance in patients infected with Neisseria gonorrhoeae, during the period from 2018 to 2021, using available antimicrobial susceptibility data.

METHODS
We retrospectively analyzed Neisseria gonorrhoeae, laboratory-confirmed cases notified to Catalonia's microbiological reporting system. Antibiotic susceptibility testing (azithromycin, cefixime, ceftriaxone, ciprofloxacin, penicillin, spectinomycin, and tetracycline) was assessed using clinical breakpoints published by the European Committee on Antimicrobial Susceptibility Testing. Incidence rates were calculated and proportions were compared using the x2 test or Fisher's exact test, and analysed using the Statistical Package for Social Sciences (SPSS 27.0).

RESULTS
A total of 20,044 confirmed cases of N. gonorrhoeae were notified. Incidence increased from 48.1 cases/100,000 person-years ($p < 0.001$) in 2018 to 90.1 in 2021, men having 4,23 times more infections than women (16,216 vs 3,831). Culture was available in 7,388 isolates (36.9%), of which, in 5,674 (76.8%) cases, the antimicrobial sensitivity was studied. Resistant strains were: ciprofloxacin (60.9%), tetracycline (33%), penicillin (22.4%) and azithromycin, (13.6%). Azithromycin resistance rose from 7.9% in 2018 to 19.4% in 2021 ($p < 0.001$). Only 1.4% (49/5,610 cases) were resistant to ceftriaxone. Six cases of N. gonorrhoeae presented multidrug-resistant to azithromycin and cefixime.

CONCLUSIONS
In Catalonia, 13.6% of the N. gonorrhoeae isolates were resistant to azithromycin in the 2018–2021 period. According to WHO, resistance above 5% indicates an alert to review treatment. In our study, culture was not enough performed or notified, and we need to raise awareness among clinicians and microbiologists, as culture is essential to monitor trends and prevent the spread of antimicrobial resistance.

Keywords: Neisseria gonorrhoeae, Multi-drug resistant, Ceftriaxone, Azithromycin, Antimicrobial resistance
ABSTRACT ID: 553
PRESENTED BY: Mercè Herrero Garcia, Spain / merce.herrerog@gencat.cat

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Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Investigation of genomic clusters of NDM-1-producing Klebsiella pneumoniae in Germany suggests geographically broad spread in Ukraine and nosocomial transmission in Germany, 2022

M. Sandfort [1]
J. Hans [2], M. Fischer [3], F. Reichert [4], M. Cremanns [5], J. Eisfeld [6], Y. Pfeifer [7], T. Eckmanns [8], G. Werner [9], S. Gatermann [10], S. Haller [11], N. Pfennigwerth [12]

[1] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
These authors share first authorship.
[2] German National Reference Centre for Multidrug-resistant Gram-negative Bacteria, Department of Medical Microbiology, Ruhr-University Bochum, Bochum, Germany | These authors share first authorship.
[3] Department of Infectious Diseases, Robert Koch Institute, Wernigerode, Germany
These authors share first authorship.
[4, 8] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[5, 6, 10] German National Reference Centre for Multidrug-resistant Gram-negative Bacteria, Department of Medical Microbiology, Ruhr-University Bochum, Bochum, Germany
[7, 9] Department of Infectious Diseases, Robert Koch Institute, Wernigerode, Germany
[11] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
These authors share senior authorship.
[12] German National Reference Centre for Multidrug-resistant Gram-negative Bacteria, Department of Medical Microbiology, Ruhr-University Bochum, Bochum, Germany | These authors share senior authorship.

BACKGROUND
Surveillance of notifiable carbapenem-resistant Enterobacterales (CRE) in Germany revealed an increase of carbapenemase NDM-1-producing Klebsiella pneumoniae in 2022, disproportionately affecting Ukrainian war-victims. We investigated genomic clusters to locate transmission.

METHODS
Among 200/330 NDM-1-producing K. pneumoniae isolates, received between January-September 2022, we applied single nucleotide variant-based cluster detection. We matched isolate information to case notifications to compare clusters regarding time and places of residence and hospitalisation, sex, age, sampled material, recent presence in Ukraine, and places before departure from Ukraine.

RESULTS
We identified 24 clusters (2-39 individuals/cluster), including 8 clusters with sufficient case information for back-tracing. Two clusters comprised 3 and 9 patients from one hospital, respectively, without prior presence in Ukraine. In the other clusters, prior hospitalisation in Ukraine predominated with diffuse covariate patterns. In the largest cluster, all 19/39 individuals with available information were from Ukraine or Russia, notified from 13 German districts, 1-83 years old, including 5 women and 10 (primarily wound) infections. Recent locations in Ukraine were documented for 6 but shared by at most 3 individuals. Only in one cluster, hospitalisation overlapped in time and location (Dnipro) for 2/6 individuals. In 2 clusters, a patient from Ukraine was screened positive on-admission and another patient was tested positive >3 days post-admission in the same German hospital.

CONCLUSIONS

Our analyses suggest three transmission scenarios: Local outbreaks in German hospitals unrelated to Ukraine, wide spread in Ukraine, and secondary transmission in Germany. Public health-measures should prioritise: Prevent transmission in Ukraine, prevent onward transmission within German hospitals, investigate and stop independent infection chains. We currently sequence retrospectively and prospectively collected isolates to enrich cluster information. Recommended on-admission CRE screening for patients with former hospitalisation in Ukraine remains important.

Keywords: Carbapenem-Resistant Enterobacteriaceae, Klebsiella pneumoniae, Beta-lactamase NDM-1, Ukraine, Whole Genome Sequencing, Population Surveillance

ABSTRACT ID: 193

PRESENTED BY: Mirco Sandfort, Germany / sandfortm@rki.de

POSTER TOUR 4

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Antimicrobial resistance

MODERATOR
Anna Machowska

Abstract

Consumption of antibiotics in response to invasive group A streptococcus outbreak and changed clinical guidelines in England, winter 2022

E. Budd [1]
S. Bou-Antoun [2], B. Muller-Pebody [3], A. Demirjian [4]

[1, 2, 3] UK Health Security Agency
[4] UK Health Security Agency | Evelina London Children's Hospital

BACKGROUND

Between November and December 2022 England experienced a surge of group A streptococcus (GAS) infections in children under 15 years. On December 9th (week 49) 2022 interim clinical guidance was introduced for diagnosis and treatment of children with suspected GAS infections. On December 15th a serious shortage protocol was introduced for phenoxymethylpenicillin (penV), allowing pharmacists to dispense alternative antibiotics. This study aims to describe trends in national community prescribing of respiratory antibiotics by age during this period.

METHODS

Antibiotic prescribing data in Defined Daily Doses (DDDs) for primary care in England 2017-2022 were provided by NHS Business Services Authority. Assessment of antibiotic trends were completed for antibiotics commonly prescribed for respiratory-tract infections (RTI): amoxicillin, azithromycin, cefalexin, clarithromycin, clindamycin, co-amoxiclav, erythromycin and penV.

RESULTS

Prescribing of all respiratory antibiotics increased in all age groups from week 46 2022; with peak prescribing in week 49 in ages 0-14 and week 51 in those aged 14-75+. Prescribing of penV for ages 0-14 peaked in week 49 and was 388% and 514% higher than the same week in 2019 and 2021 respectively. Prescribing of Amoxicillin for ages 0-14 peaked in week 50 and was 150% and 221% higher than week 50 in 2019 and 2021 respectively.

CONCLUSIONS

Prescribing of respiratory antibiotics for children, and penV specifically, was substantially higher during the winter 2022 in England compared to previous seasons; coinciding with a national GAS outbreak and changed clinical guidelines advising a lower threshold for antibiotic treatment of sore throat and recommending penV. Reported stock shortages led to subsequent increases in alternate RTI antibiotics.This study highlights the need for timely antibiotic surveillance data to inform medicines supplies and antibiotic stewardship initiatives.

Keywords: Anti-bacterial Agents, Public Health, Policy, Streptococcal Infections
ABSTRACT ID: 633
PRESENTED BY: Emma Budd, United Kingdom / emma.budd@ukhsa.gov.uk

POSTER TOUR 5

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

Household transmission of the omicron variant of SARS-CoV-2 – Results from the DigiHero study

B. Klee [1]
S. Diexer [2], C. Gottschick [3], A. Broda [4], O. Purschke [5], M. Binder [6], T. Frese [7], M. Girndt [8], J. Hoell [9], I. Moor [10], M. Gekle [11], R. Mikolajczyk [12]

[1] Institute for Medical Epidemiology, Biometry and Informatics (IMEBI), Interdisciplinary Centre for Health Sciences, Medical Faculty of the Martin Luther University Halle-Wittenberg, Germany
[2, 3, 4, 5, 12] Institute for Medical Epidemiology, Biometry and Informatics (IMEBI), Interdisciplinary Centre for Health Sciences, Medical Faculty of the Martin Luther University Halle-Wittenberg, Germany
[6] Department of Internal Medicine IV, Oncology/Haematology, Martin Luther University Halle-Wittenberg, Germany
[7] Institute of General Practice and Family Medicine, Interdisciplinary Centre for Health Sciences, Medical Faculty of the Martin Luther University Halle-Wittenberg, Germany
[8] Department of Internal Medicine II, Martin Luther University Halle-Wittenberg, Germany
[9] Paediatric Haematology and Oncology, Martin Luther University Halle-Wittenberg, Germany
[10] Institute for Medical Sociology, Martin Luther University Halle-Wittenberg, Germany
[11] Julius-Bernstein-Institute of Physiology, Medical Faculty of the Martin Luther University Halle-Wittenberg, Germany

BACKGROUND

The high transmissibility and the immune-evading ability of the omicron variant of SARS-CoV-2 caused a strong surge of infections in Germany in 2022. Households with documented exposure allow to assess transmission probability and secondary attack rates. Prospective data on the transmission of SARS-CoV-2 in households are still scarce.

METHODS

34,666 participants of the German online DigiHero cohort study with two or more household members were invited to a prospective household transmission study (July–December 2022). In case of a positive SARS-CoV-2 test in their household we provided them with individual symptom diaries, dry blood spot (DBS) cards, and a link to an online questionnaire. Symptom diaries were completed daily for at least 14 days, DBS were taken from all members at the beginning and six to eight weeks after the first infection. DBS were analysed using ELISA for SARS-CoV-2 antibodies (S- and N-protein).

RESULTS

We included 456 households with 1016 participants. Preliminary results of the complete data of the first 200 households showed that there was transmission of SARS-CoV-2 in 63.5% (95% CI 56.5%-69.9%) of households based on seroconversion (change from negative or undetermined to positive) or an 1.5 times or more increase of N-Protein or S-Protein titres (in case of a positive initial titre) amongst the household members. However, the applied serological criteria/reported positive tests (often confirmed by PCR) were not unambiguous as in 8% of index cases (i.e. cases with positive tests) no seroconversion or titre increase occurred. In these households also no transmissions were observed.

CONCLUSIONS

We found a high household transmission during the Omicron wave in Germany. Variable immune response and uncertainties regarding measurement precision make an unequivocal interpretation difficult.

Keywords: SARS-CoV-2, COVID-19, Antibodies, Pandemics
ABSTRACT ID: 503
PRESENTED BY: Bianca Klee, Germany / bianca.klee@uk-halle.de

POSTER TOUR 5

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

Importance of socioeconomic status for COVID-19 outcomes in urban Italy during the vaccine rollout, January - November 2021

E. Fotakis [1]
A. Mateo Urdiales [2], M. Fabiani [3], F. Riccardo [4], P. Pezzotti [5]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Istituto Superiore di Sanità, Department of Infectious Diseases, Italy
[2, 3, 4, 5] Istituto Superiore di Sanità, Department of Infectious Diseases, Italy

BACKGROUND

COVID-19 vaccination reduced global COVID-19 morbidity and mortality yet its effect on COVID-19 outcomes in populations with different socioeconomic status (SES) remains understudied. We aimed to investigate whether the association between SES and COVID-19 outcomes in urban Italy changed as vaccination coverage increased.

METHODS

We conducted a population-based retrospective cohort study between January-November 2021 on all Italians aged≥20 years, residing in urban municipalities. COVID-19 outcomes were retrieved from the Italian individual surveillance system. SES was measured with the Italian multidimensional socioeconomic index, calculated at census block level and categorized in tertiles. We estimated age-adjusted incidence rate ratios (IRR) and absolute rate (AR) differences, to evaluate the association between SES and COVID-19 infection, hospitalization and death, over three consecutive periods defined as low (0-10%), intermediate (11-60%), and high (61-80%) vaccination coverage, with at least 1 dose.

RESULTS

We included 16,014,631 persons living in 120,341 census blocks. Infection and hospitalisation risk increased with decreasing SES in all time periods. Hospitalization IRR between the lowest and highest (referent) SES groups were 1.37 (95%CI=1.05-1.79), 1.54 (95%CI=1.01-2.4) and 1.79 (95%CI=1.01-3.16) for the low, intermediate and high vaccination coverage periods respectively. Corresponding hospitalization AR differences were 7.72(95%CI=1.46-13.98), 4.25(95%CI=0.28-8.22), 2.44(95%CI= -0.16-5.04)/1.000.000 person-days. No clear pattern was observed for COVID-19 mortality.

CONCLUSIONS

Individuals in census blocks of the lowest SES faced the highest risk of COVID-19 infection and hospitalization throughout COVID-19 vaccination rollout in 2021. Increasing vaccination coverage reduced excess hospitalisation attributed to low SES but did not reduce relative hospitalization risk between the lowest and highest socioeconomic groups. These results highlight the need for enhanced social policies in urban settings to further capitalize on COVID-19 and potentially other respiratory disease vaccine rollouts amidst health crises.

Keywords: SARS-CoV-2, COVID-19 vaccination, Health inequalities, Socioeconomic deprivation
ABSTRACT ID: 318
PRESENTED BY: Emmanouil Alexandros Fotakis, Italy / emmanouil.fotakis@iss.it

POSTER TOUR 5

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

Timely detection of excess mortality attributable to COVID-19 in Europe compared to officially reported COVID-19 deaths: Estimates from 26 countries in the EuroMOMO network

L. Vestergaard [1]
S. Nørgaard [2], L. Nielsen [3], J. Nielsen [4], B. Søborg[5], T. Krause [6], (GROUP) The EuroMOMO Network
[1, 2, 3, 4, 5, 6] Statens Serum Institut | The EuroMOMO Network

BACKGROUND
Timely monitoring of mortality in society forms an essential part of epidemic early warning. However, to measure mortality caused by a new and unknown disease is challenging given the absence of established testing and reporting mechanisms. Estimating excess all-cause mortality is recognized as providing a more timely, complete and unbiased proxy measure of the full mortality impact of an epidemic, such as COVID-19 and influenza.

METHODS
Estimated weekly excess all-cause mortality (deaths per 100.000 person-years) in the 26 countries participating in the European Mortality Monitoring Network (see methodological details at www.euromomo.eu) were compared with estimates of the numbers of COVID-19 deaths officially notified by countries to the World Health Organization (WHO) during the first wave of COVID-19 in Europe, from week 8 to week 22, 2020.

RESULTS
EuroMOMO estimates showed an increasing all-cause mortality rate from week 8, 2020, while the number of official COVID-19 deaths only started to rise from week 10, 2020. During the first wave of COVID-19, EuroMOMO estimates showed a mortality rate (all ages) of 2468 per 100.000 person-years, while reported official COVID-19 deaths showed 1814 per 100.000 person-years, i.e. representing a 36% higher mortality detected by EuroMOMO. In week 14, at the peak of the first wave of COVID-19 in Europe, EuroMOMO detected 86% more deaths than officially reported COVID-19 deaths; however, in some countries, even a much larger excess mortality than the official COVID-19 deaths were observed, which will be presented.

CONCLUSIONS
The COVID-19 pandemic has again demonstrated that mortality monitoring forms an essential part of epidemic early warning, and confirms how continuous weekly monitoring of excess all-cause mortality serves as a simple, timely and yet powerful tool for public health action.

Keywords: COVID-19, Mortality, Early warning, Epidemics, EuroMOMO
ABSTRACT ID: 640
PRESENTED BY: Sarah Kristine Nørgaard, Denmark / sknd@ssi.dk

POSTER TOUR 5

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

COVID19 and influenza attributable mortality during the COVID19 pandemic in 31 European countries

J. Nielsen [1]
L. Vestergaard [2], M. Gram [3], S. Nørgaard [4], (GROUP) EuroMOMO Network
[1, 2, 4] Statens Serum Institut | EuroMOMO Network
[3] Statens Serum Institut

BACKGROUND
During the COVID-19 pandemic, varying levels of excess all-cause mortality were observed by the European Mortality Monitoring Network (EuroMOMO). To inform future pandemic preparedness, understanding the relative contribution of COVID-19, influenza and other infections to observed excess mortality is important.

METHODS
We estimated mortality (deaths per 100.000 person-years) attributable to COVID-19 and Influenza using the AttMOMO model, modified to account for variation in viral subtypes over time. All-cause deaths and populations were extracted from EuroSTAT and EuroMOMO. Data for the COVID-19 activity indicator (case incidence) were extracted from OurWoldInData, while data for the influenza indicator (case incidence x positive-percentage) were extracted from ECDC/TESSy. Temperature data were downloaded from NOAA. As COVID-19 variants changed throughout the pandemic period 2020-2023 and influenza changed by season, estimations were split in appropriate time periods. Complete data were available from 31 European countries. Pooled mortality estimates were stratified by country and the totals also by age.

RESULTS
Total COVID-19-attributable mortality varied from 64.1 to 134.8 deaths per 100.000 person-years, highest in the Alpha and Delta periods. Influenza-attributable mortality varied from 1.4 to 56.2 deaths per 100.000 person-years, lowest in the 2020/21 and 2021/22 seasons, highest in the 2022/23 season.

CONCLUSIONS
Excess mortality attributable to COVID-19 varied depending on the dominating SARS-CoV-2 variant. However, in the period dominated by SARS-CoV-2 Wuhan, COVID-19-attributable mortality was low compared to all-cause excess mortality. Preventive measures against COVID-19 reduced circulation of Influenza, resulting in low mortality attributable to Influenza in the 2020/21 and 2021/22 seasons, but with a high mortality in the first post-pandemic season, 2022/23. Estimating attributable mortality across countries can serve as an important tool for early epidemic warning.

Keywords: Excess mortality, Attributable mortality, COVID-19, Influenza, AttMOMO, EuroMOMO
ABSTRACT ID: 492
PRESENTED BY: Jens Nielsen, Denmark / nls@ssi.dk

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DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

Predictors of COVID-19 vaccination uptake among health care workers, in Albania, 2023

A. Xhaferi[1]

R. Daja[2], D. Toçi[3], A. Fico[4], E. Tomini[5], A. Ylli[6], M. Nika[7], A. Moci[8], N. Jani[9], S. Robinson[10], N. Mebonia[11], R. Pebody[12], M. Katz[13], S. Bino[14]

[1] Institute of Public Health, Tirana, Albania | Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET) Fellow, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3] Institute of Public Health, Tirana, Albania
[4] Univercity of Medicine, Tirana, Albania
[5, 6, 14] Institute of Public Health, Tirana, Albania | Univercity of Medicine, Tirana, Albania
[7] Mother Teresa University Hospital Tirana
[8] Regional Hospital of Fieri
[9] Regional Hospital of Durres
[10] Infectious Disease Epidemiology Program Director, Maine Department of Health and Human Services, USA
[11] European Center for Disease Prevention and Control, Stockholm, Sweden
[12, 13] World Health Organization, Regional Office for Europe, Copenhagen, Denmark

BACKGROUND
Healthcare workers (HCWs) are at high risk for SARS-CoV-2 infection due to their occupational exposures. We used data from a prospective COVID-19 vaccine effectiveness study to estimate factors associated with primary COVID-19 vaccine and booster uptake among HCWs in Albania.

METHODS
In 2021, we enrolled HCWs in Albania's three largest hospitals. For this analysis, we included data from 22 February 2022 – 27 February 2023. HCWs who received at least one single dose after primary vaccination series were considered to have received a booster dose. We used multivariable logistic regression to calculate adjusted Odds Ratio (aOR) and 95% Confidence Interval (95% CI) and examined associations with COVID-19 booster vaccine uptake.

RESULTS
We included 1456 HCWs in the analysis; the median age was 44.5 (range 22-71) years old; 65.3% were females. Overall, 93.6% (n=1363) HCWs received primary COVID-19 vaccines series, of whom 20% (n=272) received a booster. Booster uptake was higher among males (30% vs.17% females), HCWs >45 years old (24% vs.14% younger HCWs), and medical doctors (43% vs. 16% among nurses and midwives). Compared to unvaccinated, primary dose vaccination was associated with being >45 years (aOR: 3.9, 95% CI: 1.9-7.9). Compared to unvaccinated and primary vaccine, booster dose vaccination uptake was associated with being >45 years (3.0, 2.0-4.5), males (2.1, 1.5-2.8) being a medical doctor (9.0, 4.8-17.2), providing hands-on medical care to patients (1.6, 1.2-2.1) and believing that COVID-19 vaccines are safe (5.4, 0.7-43.7).

CONCLUSIONS

In Albania, COVID-19 booster uptake is low among HCWs, but higher among older HCWs, males, medical doctors and HCWs providing hands-on medical care to patients. Our results can inform interventions to promote booster dose acceptance among HCWs.

Keywords: COVID-19, Vaccination, Primary dose, Booster doses, Health Care Workers, Albania

ABSTRACT ID: 386

PRESENTED BY: Anisa Xhaferi, Albania / xhaferianisa@yahoo.com

POSTER TOUR 5

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: Burden of disease

MODERATOR
Charlotte Hammer

Abstract

COVID-19 knowledge and attitude towards COVID-19 among students and faculty of medical universities, Kazakhstan, February-March 2021

U. Kirpicheva [1]
D. Turegeldiyeva [2], R. Horth [3], T. Nurgozhin [4], E. Khaidar [5], A. Baimagembetova [6], D. Nabirova [7]

[1, 2] Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Scientific and Practical Center for Sanitary and Epidemiologica
Expertise and Monitoring, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[3, 7] U.S. Centers for Disease Control and Prevention, Central Asia Office, Almaty
Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[4] Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[5, 6] NJSC Astana Medical University, Astana, Kazakhstan

BACKGROUND

The COVID-19 pandemic had a significant impact on higher medical education. Medical university faculty and students were at increased risk of COVID-19 from work and education setting exposures. We aimed to assess the level of knowledge, attitude, and practice (KAP) towards COVID-19 and associated factors among medical universities.

METHODS

We conducted a cross-sectional study among students and faculty of two medical universities in Astana and Almaty in February-March 2021. A structured questionnaire was used to collect data on demographics, knowledge, attitude and practice. Cut-off for good KAP was ≥70% of correct answers. We used multivariable logistic regression to calculate adjusted odds ratio [aOR] and 95% confidence intervals [95%CI].

RESULTS

Of 1033 participants, 22% had good knowledge, 27% positive attitudes, and 45% good practices. Among them 76% were female, 73% were <30 years old, 71% were students and 35% worked at healthcare facilities. Positive attitude including avoiding public events (75%), wearing medical masks in public (72%), and physical distancing (76%). Nearly all (99%) maintained preventive measures. But, 60% used <4 masks/day and 19% reported having taken antibiotics without a prescription. Only 44% thought COVID-19 vaccination was necessary and 36% would get vaccinated. Good knowledge was associated with 25-29 age (aOR: 3.7, CI: 1.8–7.4), PhD studies (2.4, 1.2–5.0), and clinical practice (1.4, 1.1–1.8). Positive attitude was positively associated with good knowledge (1.8, 1.5–2.3). There was no significant association with practice.

CONCLUSIONS

Results confirm that adequate knowledge is associated with a positive attitude. Improvements are needed in medical education to reduce misinformation and improve attitude and prevention practices related to COVID-19 and other infectious. Efforts should focus on nonclinical students and faculty of medical universities in terms of increasing clinical practice.

Keywords: COVID-19, Knowledge, Attitude, Practice, Medical universality, Kazakhstan
ABSTRACT ID: 603
PRESENTED BY: Ulyana Kirpichev, Kazakhstan / ulyana.9355@gmail.com

POSTER TOUR 6

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Active tuberculosis screening among the displaced population fleeing Ukraine, France, February to October 2022

J. Guthmann [1]
P. Fraisse [2], I. Bonnet [3], J. Robert [4]

[1] Sante publique France
[2] Réseau National des Centres de lutte antituberculeuse (CLAT), Strasbourg
Groupe pour la recherche et l'enseignement en pneumo-infectiologie de la Société de pneumologie de langue française, Paris
[3, 4] Centre National de Référence des Mycobactéries, Laboratoire de Bactériologie-Hygiène, Site Pitié-Salpêtrière, Groupe hospitalo-universitaire APHP, Sorbonne Université, Paris | CIMI-Paris, Inserm U1135, Sorbonne Université, Paris

BACKGROUND
The French Ministry of health recommends screening of tuberculosis (TB) in immigrants arriving from a high incidence country. Following the Russian invasion in February 2022, a warning was issued regarding the need of systematic screening of displaced people arriving from Ukraine. We sought to evaluate the results of this strategy performed by an existing national network of 105 TB centres.

METHODS
A questionnaire was administered to assess the number of persons actively screened, i.e. those who received a chest X-ray, between February and October 2022 and among these, the number of TB cases. Clinical, demographic, and bacteriological characteristics were recorded for each TB case. Drug susceptibility tests were assessed by the National reference laboratory in case of MDR-TB. Outcomes were the TB prevalence (number of cases/number screened) and the number needed to screen (NNS), i.e. the inverse of the TB prevalence in the screened population.

RESULTS
All TB centres responded, and a total of ten bacteriologically confirmed TB cases were identified among 8,621 screened persons, resulting in a TB prevalence of 116 cases per 100,000 population. Consequently, the NNS was 862 persons screened to find one TB case. Nine cases were Ukrainians and one came from a high MDR TB burden country in the WHO European Region. Seven cases were non-symptomatic, three were smear positive and four were MDR.

CONCLUSIONS
The high TB prevalence shows that active screening was an effective intervention in France. Its relevance is further reinforced by the high proportion of asymptomatic (hence remaining undiagnosed), smear positive (hence highly contagious) and MDR (hence severe) cases. Our data may somewhat challenge the WHO/ECDC recommendation of not recommending universal screening of refugees arriving from Ukraine.

Keywords: Tuberculosis, Active screening, Displaced, France
ABSTRACT ID: 93
PRESENTED BY: Jean-Paul Guthman, France / jean-paul.guthmann@santepubliquefrance.fr

POSTER TOUR 6

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Trends in Tuberculosis in Cyprus: analysis of surveillance data from 2011 to 2021

A. Quattrocchi [1]
C. Constantinou [2], L. Hadjihannas [3], G. Siakallis [4], D. Alon-Ellenbogen [5], I. Mamais [6], V. Silvestros [7], A. Papandreou [8], C. Stavraki [9], C. Anaxagorou [10], C. Haralambous [11], G. Nikolopoulos [12], E. Constantinou [13]

[1] University of Nicosia Medical School, Nicosia, Cyprus
[2, 3] Nicosia General Hospital, Nicosia, Cyprus
[4] University of Nicosia Medical School, Nicosia, Cyprus | Larnaca General Hospital, Larnaca, Cyprus
[5] University of Nicosia Medical School, Nicosia, Cyprus
[6] School of Sciences, European University, Nicosia, Cyprus
[7, 8, 9, 10, 11, 13] Unit for Surveillance and Control of Communicable Diseases, Ministry of Health, Nicosia, Cyprus
[12] Medical School, University of Cyprus, Nicosia, Cyprus

BACKGROUND
The End-TB Strategy in Europe aims at reaching a notification rate of 2.4 per 100,000 population by 2030. We analysed TB notifications trends over time and by cases characteristics in Cyprus between 2011-2021.

METHODS
We analysed TB cases notified to the national surveillance system between the study period.Total, sex-specific and age-specific notification rates (NR) per 100,000 population were calculated using population census denominators. Similarly, NR were calculated by country of birth (Cyprus-born and born outside Cyprus).Annual percentage change (APC) in NRs were calculated using Joinpoint regression analysis.

RESULTS
Between 2011-2021 there were 586 TB cases notified (52% males), with peaks in NR (8 per 100,000) reached in 2012 and 2019.The APC for total and sex-specific NRs did not significantly decrease over time. By age group, NR significantly decreased by 39% for the age group 65+.By country of birth, 85% of all TB cases were notified among individuals born outside Cyprus (85% of all cases); in this group, NR ranged between 23.2 and 22.9 per 100,000 population during the 11 year-period with no significant change over time, while among Cyprus born cases the NR ranged between 0.2 and 0.04 per 100,000 population, showing a 12% decrease. Notably, multi-drug resistance infections and HIV-coinfection (each 2% of all cases) were reported only among individuals born outside Cyprus.

CONCLUSIONS
Despite TB rate among Cyprus-born is well below the 2030 END-TB target, a big challenge remains due to the high NR among migrants.Continuous efforts should be made to ensure screening, rapid diagnosis of TB and drug-resistant TB, and prompt and adequate treatment, especially among migrants and other vulnerable populations.

Keywords: Tuberculosis, Migrants, Annual Percentage change, Multi-drug resistance, Cyprus
ABSTRACT ID: 628
PRESENTED BY: Annalisa Quattrocchi, Cyprus / quattrocchi.a@unic.ac.cy

POSTER TOUR 6

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Effectiveness of preventive treatment for latent tuberculosis infection and its determinants in real-world settings: A retrospective cohort study in Korea, 2015-2018

K. Da Seul [1]
B. Chun [2]

[1] Korea Disease Control and Prevention Agency
[2] Korea University

BACKGROUND
The aim of this study is to assess the effectiveness of latent tuberculosis infection (LTBI) treatment to prevent active TB development and identify the determinants in real-world settings

METHODS
The study included 96,193 individuals who had contact with tuberculosis patients reported in Seoul and Gyeonggi Province, South Korea, from January 2015 to December 2018. The Korea Disease Control and Prevention Agency conducted testing and follow-up for LTBI among contacts of all identified patients. Tuberculin Skin Test and Interferon-Gamma Releasing Assay were used for testing, and free standard treatment was provided for LTBI. The observation period for tuberculosis among these contacts extended until December 2020. Cox regression model was used to analyze the preventive effect of latent tuberculosis treatment and its associated factors.

RESULTS
Among the contacts, 16,028 individuals (16.7%) were identified with latent tuberculosis infection (LTBI), and the average follow-up period for the entire study population was 3.97 (±1.17) years. Among LTBI patients, 5,548 individuals (34.6%) completed treatment, while the remaining either discontinued treatment (9.9%) or did not receive treatment. During the observation period, tuberculosis occurred in 240 individuals (0.25%) among the overall participants, with an incidence rate of 25.7 per 100,000 person-years for non-LTBI contacts, 45.5 for LTBI treatment completers, 387.2 for incomplete treatment/discontinuation, and 368.4 for non-treatment. In multivariate analysis, the tuberculosis preventive effect of LTBI treatment was 90.1%, and in addition to treatment and age, healthcare facilities as a contact setting (aHR=2.1, 95%CI 1.35-3.26) were significant factors associated with tuberculosis occurrence.

CONCLUSIONS
Testing and treatment for LTBI among contacts of tuberculosis patients are highly effective in TB control and should be recommended. Strategies are needed to ensure completion of treatment for individuals with LTBI.

Keywords: Tuberculosis, Latent tuberculosis, Effectiveness, Retrospective cohort study, Incidence, Korea
ABSTRACT ID: 597
PRESENTED BY: Kim Da Seul, South Korea / godkds09@gmail.com

POSTER TOUR 6

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Low sensitivity of the Tuberculosis surveillance system: a capture-recapture study, Tunis, Tunisia, 2022

I. Cherif [1]
R. Gharbi [2], M. Mlaouah [3], G. Kharroubi [4], H. Temmi [5], H. Rzigui [6], A. Mansouri [7], L. Maazaoui [8], A. Gzara [9], J. Bettaieb [10]

[1] Laboratory of medical epidemiology, Institut Pasteur de Tunis (IPT), Tunis, Tunisia
Mediterranean and Black Sea Programme in Intervention Epidemiology Training (MediPIET),
European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[2, 3, 4, 10] Laboratory of medical epidemiology, Institut Pasteur de Tunis (IPT), Tunis, Tunisia
[5] Anti-tuberculosis direction, Tunis, Tunisia
[6] Regional health directorate of Tunis, Tunis, Tunisia
[7, 8, 9] Primary Heallthcare Directorate, Tunis, Tunisia

BACKGROUND

Despite the rising trend of extra-pulmonary TB in Tunisia, no evaluation of the paper-based TB surveillance system has been conducted since its implementation in 1969. We aimed to estimate the sensitivity of the current system among pulmonary and extra-pulmonary cases diagnosed in 2022 in the Tunis region.

METHODS

We used a capture-recapture method with two-sources: mandatory notifications and TB treatment records from outpatient TB treatment facilities. Duplicates were identified based on name/surname, age, gender, and date of diagnosis. Total number of cases was estimated by using the Chapman modification of the Lincoln–Petersen estimator for the capture-recapture method and sensitivity by using the estimated total number of cases as the denominator. To assess independency of sources, we calculated the correlation coefficient (r) between data sources sensitivities by municipality.

RESULTS

In 2022, 59 TB cases were notified to the regional health directorate of Tunis (incidence:5.4/100,000 population) and 363 TB cases were registered in the TB treatment records (incidence:39/100,000). We identified 27 duplicates between the two data sources. The estimated total number of TB cases was 779(95%CI:[662-896]) (incidence:72/100,000 (95%CI:[62-83])). The estimated sensitivities were 8%(95%CI:[7-9]) for mandatory notifications and 47%(95%CI:[40-55]) for treatment records. The combined sensitivity of both systems was 61%(95%CI:[46-88]) for extra-pulmonary TB, 47%(95%CI:[37-66]) for pulmonary TB and 51%(95%CI:[44-60]) for all cases. Data sources sensitivities in each municipality were not significantly correlated (r=0.63, p=0.17) suggesting that the sources were independent.

CONCLUSIONS

We observed important underreporting of TB cases in Tunis which underestimates the disease burden and hampers the implementation of tailored control measures. Actions are urgently needed to increase the sensitivity of TB surveillance through the sensitization/training of healthcare workers and the development of an electronic system.

Keywords: Tuberculosis, Public Health Surveillance, Evaluation, Tunisia
ABSTRACT ID: 258
PRESENTED BY: Ines Cherif, Tunisia / ines.cherif1993@gmail.com

POSTER TOUR 6

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Evaluation of the implementation of the change to the BCG immunisation programme in England

K. Jones [1]
T. Crocker-Buque [2], G. Chisnall [3], S. Mounier-Jack [4], C. Campbell [5], V. Saliba [6], T. Chantler [7]

[1] UK Health Security Agency (UKHSA)
[2, 3, 4, 7] London School of Hygiene and Tropical Medicine (LSHTM)
[5, 6] UK Health Security Agency (UKHSA)

BACKGROUND
The introduction of a national pilot of newborn screening for Severe Combined Immunodeficiency (SCID) in England triggered a change to the selective Bacillus Calmette-Guerin (BCG) immunisation programme delivery pathway, as this live attenuated vaccine is contraindicated in infants with SCID. Since 1 September 2021 the BCG vaccine has been offered to infants at increased risk of tuberculosis after the SCID screening outcome is available (within 28 days of birth) instead of shortly after birth. We evaluated the implementation of this change to examine associated barriers and facilitators, and identify good practice.

METHODS
A mixed-methods evaluation was conducted between November 2022 and April 2023: i) a national online survey of BCG commissioners and providers and ii) qualitative semi-structured interviews with commissioners and providers in two geographical areas. Survey data was analysed using descriptive statistics and interview data was analysed thematically.

RESULTS
Survey responses were received from all England NHS Regions. Commissioner survey respondents (11), provider survey respondents (54) and qualitative interviewees (16) reported challenges in meeting the 28 day vaccination target due to inconsistent availability of SCID screening outcomes, delayed referral of eligible infants, high non-attendance rates, and increased workload. Reported benefits of the restructured pathway included improved information systems, which facilitated meaningful and consistent data capture for the first time. Examples of good practice included stakeholder collaboration, service training and additional engagement with parents.

CONCLUSIONS
The new BCG pathway has created an effective structure for monitoring and managing the BCG vaccination programme, but further work is required to support providers to deliver the 28 day vaccination target and improve uptake rates. When implementing national immunisation pathways, stakeholders should collaborate to address challenges, harness benefits and share learning.

Keywords: Evaluation, Tuberculosis, Bacillus Calmette-Guerin, Vaccine, England
ABSTRACT ID: 258
PRESENTED BY: Koren Jones, United Kingdom / koren.jones@ukhsa.gov.uk

POSTER TOUR 6
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

Tuberculosis

MODERATOR
Veronica Cristea

Abstract

Epidemiological investigations informed a TB screening event for the homeless population in Boston, England

M. Dave [1]
S. Thakrar [2], H. Bagnall [3], S. Ferris [4], A. Burkitt [5], K. Amin [6], J. Kumbang [7]

[1] UK Field Epidemiology Training Programme Fellow (UK-FETP) | Midlands Field Service, UK Health Security Agency
[2, 4, 7] East Midlands Health Protection Team, UK Health Security Agency
[3, 6] Midlands Field Service, UK Health Security Agency
[5] TB Cluster Investigator, Field Services, Regions Directorate, UK Health Security Agency

BACKGROUND
Boston is a town in England with low but increasing Tuberculosis (TB) incidence (9 per 100,000) and five whole genome sequencing (WGS) clusters of TB under investigation. In November 2022, the Health Protection Team (HPT) was alerted to a fifth case of TB linked to a factory setting in Boston. Epidemiological investigations were conducted to inform public health interventions and prevent further transmission.

METHODS
A confirmed case had culture confirmed TB with a WGS result within an existing Boston TB cluster and with an epidemiological link to another cluster case, notified since January 2010. A probable case had laboratory confirmed TB, with an epidemiological link to a confirmed case but no WGS result, notified since January 2010. Case data was extracted from the National Tuberculosis Surveillance System and the HPT case management system, supplemented with local TB service intelligence to produce descriptive epidemiology and a network diagram.

RESULTS
Twenty-nine individuals met the case definition (24 confirmed, 5 probable). Of recently notified cases (2020 to 2022; 3 confirmed, 4 probable), 100% were born outside of the United Kingdom and had experienced homelessness. The three recently confirmed cases belonged to three of the five Boston WGS clusters, indicating continued transmission in these clusters. In addition to local factories, the network diagram identified a homeless outreach centre.

CONCLUSIONS
The descriptive epidemiology and network diagram identified an additional population at risk for TB transmission – the homeless population of Boston. Following the identification of a homeless outreach centre in the network diagram, the setting was included in a multi-agency TB screening event and enabled good levels of uptake by a vulnerable population that have poorer TB outcomes.

Keywords: Tuberculosis, Homeless, Network diagram, Whole Genome Sequencing, Screening, Field Epidemiology
ABSTRACT ID: 261
PRESENTED BY: Mona Dave, United Kingdom / mona.dave@ukhsa.gov.uk

POSTER TOUR 7

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

HIV, STIs and viral hepatitis: Surveillance

MODERATOR
Esther Kukielka Zunzunegui

Abstract

A statistical method to estimate the number of duplicate entries in statutory infectious disease surveillance in the absence of personal identifiers: Example of hepatitis B in Germany, 2017-2022

A. Schoeps [1]
S. Bühler [2], R. Zimmermann [3], S. Dudareva [4], P. Zanger [5], M. an der Heiden [6]

[1] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), 17183 Stockholm, Sweden | Heidelberg Institute of Global Health (HIGH), Heidelberg University, Heidelberg, Germany | Landesuntersuchungsamt Rheinland-Pfalz (LUA), Koblenz, Germany Postgraduate Training for Applied Epidemiology (PAE), Department of Infectious Disease Epidemiology, Robert Koch Institute, 10113 Berlin, Germany
[2] Institut für Hygiene und Umwelt, Hamburg, Germany
[3, 4, 6] Department of Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany
[5] Landesuntersuchungsamt Rheinland-Pfalz (LUA), Koblenz, Germany
Heidelberg Institute of Global Health (HIGH), Heidelberg University, Heidelberg, Germany

BACKGROUND
In routine infectious disease surveillance, local health authorities (LHAs) may receive notifications of the same case multiple times, especially in chronic infections like hepatitis B. This project aimed to assess data quality by estimating the number of true hepatitis B duplicates between 2017 and 2022 in the absence of full personal identifiers on the federal state level in Rhineland-Palatinate and Hamburg, Germany.

METHODS
We used year and month of birth, sex, and place of residence for the identification of candidate duplicates. We determined the expected number of random duplicates in n cases by a simulation drawing 1000 times n independent samples from the marginal distribution of birthyear, -month, and sex. We predicted the number of true duplicates using the difference between the number of candidate duplicates and the expected number of random duplicates. To validate results, lists with all candidate duplicates between 01/2017-10/2022 were sent to the LHAs to identify the true duplicate cases using personal identifiers.

RESULTS
Within the 22 included LHAs from Rhineland-Palatinate and 5 LHAs from Hamburg, the search identified 130 and 85 candidate duplicates, respectively, of which 32 and 48 were true duplicates, corresponding to 1.7% and 6.1% of all reported cases during the study period. In 24 of the 27 included LHAs, the number of true duplicates was within the 95% prediction interval provided by the simulation.

CONCLUSIONS
We developed a method to swiftly assess surveillance data for duplicates by comparison of candidate duplicates with statistically expected duplicates. Although specific characteristics of single LHAs have to be considered before applying this method, results are valuable for data quality control and provide a tool for data correction in the absence of identifying information.

Keywords: Hepatitis B, Public health surveillance, Data management, Data accuracy, Chronic disease
ABSTRACT ID: 125
PRESENTED BY: Anja Schoeps, Germany / anja.schoeps@ntsx.de

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DAY 1 – WEDNESDAY 22 NOVEMBER 2023
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HIV, STIs and viral hepatitis: Surveillance

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Task Force for the rapid response to the outbreak of severe acute hepatitis of unknown aetiology in children in Portugal in 2022

B. Grau-Pujol [1]
J. Vieira Martins [2], I. Goncalves [3], F. Rodrigues [4], R. de Sousa [5], D. Oliveira [6], J. Bettencourt [7], D. Mendes [8], I. Mateus de Cunha [9], S. Pocinho [10], A. Firme [11], B. Estela dos Santos [12], A. Peralta Santos [13], M. Albuquerque [14], P. Pinto Leite [15], R. Tato Marinho [16], P. Vasconcelos 1[7]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Center for Public Health Emergencies, Directorate-General of Health, Lisbon, Portugal Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal
[2, 14, 15, 17] Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal
[3] Hospital Pediátrico, Centro Hospitalar e Universitário de Coimbra, Coimbra, Portugal
[4] Hospital Pediátrico, Centro Hospitalar e Universitário de Coimbra, Coimbra, Portugal
Faculdade de Medicina da Universidade de Coimbra, Coimbra, Portugal
[5] Infectious Diseases Department, National Institute of Health Doctor Ricardo Jorge, Lisboa, Portugal
[6] Division of Sexual, Reproductive, Child and Youth Health, Directorate-General of Health, Lisbon, Portugal
[7] National Program for Viral Hepatitis, Directorate-General of Health, Lisbon, Portugal
[8] Division of Communication and Public Relationships, Directorate-General of Health, Lisbon, Portugal
[9, 11] Center for Public Health Emergencies, Directorate-General of Health, Lisbon, Portugal
[10] Centro Hospitalar Lisboa Ocidental, Lisboa, Portugal
[12] Division of Disease Prevention and Health Promotion, Directorate-General of Health, Lisbon, Portugal
[13] Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal
Comprehensive Health Research Centre (CHRC), Escola Nacional de Saúde Pública, Universidade NOVA de Lisboa, Lisboa, Portugal
[16] Centro Hospitalar Universitário Lisboa Norte, Lisboa, Portugal
Faculdade de Medicina, Universidade de Lisboa, Portugal

BACKGROUND

On April 5th 2022, the United Kingdom reported an increase of severe acute hepatitis cases of unknown aetiology in children, some required liver transplant or died. Thereafter, 35 countries reported probable cases – nearly half in Europe. Portugal established a Task Force (TF) for detection of probable cases and response. Here, we synthesise the TF constitution and its outbreak management and response, while describing the outbreak in Portugal, to guide future outbreaks of this scale.

METHODS

We compiled and united all data available regarding the TF (e.g. standard operational procedures, meeting notes and guidelines) to describe the mechanism adopted in Portugal. Epidemiological data of the cases were collected through the digitalized National Epidemiological Surveillance System (SINAVE) applying the ECDC/WHO case definition. The outbreak was described in terms of time, person and place.

RESULTS

A multidisciplinary TF was created, composed by six sectors: clinical, laboratorial, epidemiological, public health and national and international communication. Adopting ECDC/WHO recommendations, the TF met regularly and provided tailored and timely evidence-based communications to all audiences: from guiding clinicians to informing the general population. Between April and December 2022, 28 probable cases in children (57% male) were reported across Portugal. Of all cases, 82% were hospitalized but none of them required liver transplant or died.

CONCLUSIONS

The establishment of the TF in Portugal may have played a crucial role in raising awareness amongst clinicians. This probably led to early detection and case management, leading to a null case fatality rate. We believe that sharing the mechanisms employed in Portugal could reinforce continued investment in the core public health systems, which is essential to guarantee adequate management and response to future national and cross-border outbreaks.

Keywords: Acute hepatitis unknown origin, Paediatrics, Outbreak response, Hospitalisation, Cross-border threat, Preparedness

ABSTRACT ID: 329

PRESENTED BY: Berta Grau-Pujol, Portugal / bertagrau@dgs.min-saude.pt

POSTER TOUR 7

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
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HIV, STIs and viral hepatitis: Surveillance

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Spatial epidemiology of genital herpes simplex in Korea: Clustering and Bayesian spatial regression analysis for its determinants

J. Jang [1]
T. Kisiju [2], S. Kim [3], B. Chun [4]
[1, 2, 3, 4] Korea University

BACKGROUND
The cases of sexually transmitted infections (STI) in Korea have rapidly increased over the past decade, including genital herpes simplex (HS). No study has explored possible contributors to genital HS infection within a spatial framework. This study was conducted to identify regional clusters of genital HS and their associated factors.

METHODS
The cases of genital HS for municipality-level (250 municipalities in Korea) in 2019 were extracted from the National Health Insurance data covering all Korean population. Global Moran's I statistics and Local Indicators of Spatial Association (LISA) clustering method were used to identify the spatial autocorrelation and regional clusters. Potential determinants were extracted from various sources. Bayesian spatial regression using the Integrated Nested Laplace Approximation were conducted to identify the determinants of the regional incidence of genital HS. After comparing the Deviance Information Criterion, the Intrinsic Conditional Auto-Regressive model was implemented as the final model.

RESULTS
A total of 182,289 genital HS patients were included in the study, with females accounting for 73.4% of the cases. Genital HS exhibited a significant positive spatial autocorrelation (Global Moran I = 0.503, p = 0.001). The LISA clustering analysis revealed high-risk clusters in the metropolitan and southeast areas of Korea. The percentage of single-person households (RR = 1.23, 95% credible interval (CrI) = 1.16–1.30) and regional sexual violence risk (RR = 1.05, 95% CrI = 1.00–1.09) were significant risk factors after adjusting socio-economic factors.

CONCLUSIONS
We identified significant spatial clustering of genital HS in specific regions and its associated factors in Korea using nationwide data. It is important to identify risk factors associated with high-risk areas for targeted intervention for STI prevention including genital HS.

Keywords: Sexually transmitted infections, Gental herpes simplex, Spatial epidemiology, Clustering, Bayesian analysis, Korea
ABSTRACT ID: 645
PRESENTED BY: Joonsu Jang, South Korea / c16329@korea.ac.kr

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HIV, STIs and viral hepatitis: Surveillance

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Mpox outbreak in France: the association between reported sexual activity and epidemiological characteristics of male cases aged 15 years or older, 2022

C. Krug [1]
A. Tarantola [2], E. Chazelle [3], E. Fougère [4], A. Velter [5], A. Guinard [6], Y. Souares [7], A. Mercier [8], C. Francois [9], K. Hamdad [10], L. Tan-Lhernould [11], A. Balestier 12, H. Lahbib [13], N. Etien [14], P. Bernillon [15], V. De Lauzun [16], J. Durand [17], M. Fayad [18], F. Beck [19], B. Coignard [20], F. Lot 2[1], A. Mailles [22]

[1] Santé publique France, The French Public Health Agency, Saint-Maurice, France
[2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22] Santé publique France, The French Public Health Agency, Saint-Maurice, France

BACKGROUND

The 2022 Mpox outbreak in France spread mainly among men-who-have-sex-with-men (MSM), suggesting sexual transmission. However, not all cases reported sexual activity. Our aim was to describe the associations between reported sexual activity and epidemiological characteristics, to generate hypotheses on additional transmission routes.

METHODS

We included 1,668 males aged ≥15 years diagnosed with Mpox May-August 2022 through the French surveillance system. Cases either tested PCR-positive or had clinical symptoms with an epidemiological link to a PCR-positive case. Cases were interviewed on demographics, lesion location, international travel, MSM venue attendance (e.g. backrooms, saunas) and number of sexual partners during the three weeks before symptom onset. We used Pearson's x2 to test associations between reported sexual activity and characteristics.

RESULTS

Individuals who reported no sexual partner (6% [103/1,668]) more often had facial (51% [44/86] vs 37% [500/1,364]) and palmar lesions (28% [24/86] vs 19% [260/1,364]), and less peri-anal lesions (29% [25/86] vs 40% [546/1,364]) than individuals who reported at least one partner. There were no differences in frequency of genital lesions (58% [50/86] vs 54% [734/1,364], p=0.435). Individuals who reported no sex also reported less international travel (14% [9/65] vs 25% [240/965], p=0.044), and less MSM venue attendance (20% [16/64] vs 49% [475/965], p<0.001).

CONCLUSIONS

We suggest based on lesion location, that a proportion of males who reported no sexual partners became infected through intimate contact (oral/anal sex, kissing, touching) with another Mpox case, not considered as sexual activity. However, our data is insufficient to test this hypothesis. Public health action should continue targeting sexually active MSM and recommendations should emphasize avoiding intimate contact for individuals with Mpox symptoms.

Keywords: France, Outbreak, Monkeypox, Mpox, Sexual and Gender Minorities, Sexual behaviour
ABSTRACT ID: 209
PRESENTED BY: Catarina Krug, Sweden / denoronhakrug@hotmail.com

POSTER TOUR 7

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

HIV, STIs and viral hepatitis: Surveillance

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Predictors of repeat testing and repeat infectious syphilis in men who have sex with men with a history of syphilis in the Netherlands

L. Kayaert [1]
L. Staritsky 2, H. Götz 3, B. van Benthem 4, F. van Aar 5
[1, 2, 4, 5] National Institute for Public Health and the Environment (RIVM), the Netherlands
[3] National Institute for Public Health and the Environment (RIVM), the Netherlands
Public Health Service Rotterdam Rijnmond, the Netherlands

BACKGROUND

Syphilis rates are increasing in men who have sex with men (MSM), with repeat infections possibly driving ongoing transmission. We aimed to assess frequency and predictors of repeat testing and reinfection in MSM after first syphilis diagnosis.

METHODS

This study included national surveillance data of STI consultations among MSM attending Dutch Sexual Health Centres between July 2014–December 2019. MSM with at least one infectious syphilis diagnosis (primary, secondary or early latent) and at least one year follow-up time were included. Proportions of MSM with repeat testing and reinfection were determined. We performed multinomial regression analysis to determine subjects' (demographic, behavioural and STI-history) characteristics at first diagnosis predicting reinfection relative to single testers and repeat testers.

RESULTS

We identified 4,037 MSM with a first syphilis diagnosis, of whom 22.2% were single testers, 62.1% tested repeatedly negative, and 15.7% had a reinfection (median days until reinfection: 485, IQR: 299-819). Relative to both single and repeat testers, being known HIV-positive (RRR: 1.79, 95%-CI: 1.34-2.40 and RRR: 1.94, 95%-CI: 1.52-2.46 respectively), having a history of STI (RRR: 2.29, 95%-CI: 1.71-3.08 and RRR: 1.33, 95%-CI: 1.05-1.69 respectively) and being aged 40+ (RRR: 2.18, 95%-CI: 1.34-3.55 and RRR: 1.63, 95%-CI: 1.04-2.54 respectively compared to age <25) were predictors of reinfection. Relative to single testing, age 25-39, having more than 9 partners and being asymptomatic were also positively associated.

CONCLUSIONS

The high proportion of reinfection after initial syphilis diagnosis indicates continued risk and ongoing transmission. This highlights the need for repeat testing in this group, which was already high. Additionally, syphilis prevention strategies specifically addressing reinfection are required, especially for HIV-positive MSM, MSM with a history of STI, and MSM of older age.

Keywords: Syphilis, Men who have sex with men, Reinfection, STI testing
ABSTRACT ID: 322
PRESENTED BY: Laura Kayaert, Netherlands / laura.kayaert@rivm.nl

POSTER TOUR 8

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

COVID-19 vaccine effectiveness by number of doses received in a multicentre test-negative design study at primary care level in Europe (VEBIS)

C. Lanièce Delaunay [1]
C. Trobajo-Sanmartín [2], C. Mazagatos [3], N. Sève [4], L. Domegan [5], L. Goerlitz [6], F. Dijkstra [7], A. Ivanciuc [8], A. Rodrigues [9], A. Carnahan [10], B. Oroszi [11], M. Ilic [12], M. Maurel [13], A. Melo [14], I. Martínez-Baz [15], G. Pérez-Gimeno [16], V. Enouf [17], J. O'Donnell [18], R. Dürrwald [19], A. Meijer [20], M. Lazar [21], L. Gomes [22], N. Latorre-Margalef [23], G. Túri [24], I. Mlinaric [25], S. Bacci [26], M. Kaczmarek [27], E. Kissling [28], (GROUP) European primary care vaccine effectiveness group

[1] Epiconcept, Paris, France
[2, 14, 15, 16, 18, 19, 20, 21, 23, 24, 25, 28] Instituto de Salud Pública de Navarra – IdiSNA – CIBERESP, Pamplona, Spain
[3] National Centre of Epidemiology, CIBERESP, Carlos III Health Institute, Madrid, Spain
[4] INSERM, Sorbonne Université, Institut Pierre Louis d'épidémiologie et de Santé Publique (IPLESP UMRS 1136), Paris, France
[5] Health Service Executive-Health Protection Surveillance Centre, Dublin, Ireland
[6] Robert Koch Institut, Berlin, Germany
[7] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[8] Cantacuzino National Military Medical Institute for Research and Development, Bucharest, Romania
[9] Epidemiology Department, National Institute of Health Doutor Ricardo Jorge, Lisbon, Portugal
[10] The Public Health Agency of Sweden, Stockholm, Sweden
[11] National Laboratory for Health Security, Epidemiology and Surveillance Centre, Semmelweis University, Budapest, Hungary
[12] Croatian Institute of Public Health CIPH , Zagreb, Croatia
[13] Epiconcept, Paris, France
[17] CNR des virus des infections respiratoires, WHO National Influenza Centre, Institut Pasteur, Paris, France
[22] Infectious Diseases Department, National Institute of Health Doutor Ricardo Jorge
[26, 27] European Centre for Disease Prevention and Control, Stockholm, Sweden

BACKGROUND
With multiple COVID-19 vaccination campaigns and different vaccines, collecting individual data on entire vaccination history has become challenging. We conducted a European multicentre test-negative design study at primary care level (VEBIS), to investigate whether the number of doses received was a key determinant of COVID-19 vaccine effectiveness (CVE).

METHODS
Physicians from 10 European countries swabbed patients presenting with acute respiratory infection and collected demographic, vaccination and clinical information. Cases and controls were RT-PCR positive and negative for SARS-CoV-2, respectively. We used logistic regression adjusting for site, age, sex, chronic conditions, and symptom onset date, to estimate CVE against symptomatic infection among adults aged ≥50 years, using unvaccinated patients as a reference group. We calculated the effectiveness of primary series (PS) and first booster vaccination with monovalent mRNA vaccines by time since vaccination in Omicron BA.1/BA.2 and BA.4/BA.5-dominant periods.

RESULTS

In the BA.1/BA.2 period, PS CVE was 82% (95% confidence interval [95%CI]: 68–89%) and 69% (95%CI: 52–80%) 0–3 and 3–6 months post-vaccination, respectively. First booster CVE was 78% (95%CI: 72–83%) and 53% (95%CI: 38–66%) 0–3 and 3–6 months post-vaccination, respectively. In the BA.4/BA.5 period, PS CVE was 72% (95%CI: 27–90%) 3–6 months after vaccination (low sample size 0–3-month post-vaccination). First booster CVE was 43% (95%CI: -48–79%) and 36% (95%CI: -17–66%) 0–3 and 3–6 months post-vaccination, respectively.

CONCLUSIONS

Confidence intervals of comparable PS and first booster CVE estimates overlapped, and point estimates differed from 4 to 36%. Depending on future strategy, e.g. integration of COVID-19 vaccination in seasonal vaccination campaigns for vulnerable groups, studies should consider the number of doses received when estimating CVE.

Keywords: COVID-19, SARS-CoV-2, Vaccines, Primary Health Care
ABSTRACT ID: 551
PRESENTED BY: Charlotte Lanièce Delaunay, France / c.laniece@epiconcept.fr

POSTER TOUR 8

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

Relative effectiveness of any COVID-19 vaccine booster doses against Omicron SARS-CoV-2 infections in an ECDC multi-centre healthcare worker cohort (VEBIS study), December 2021–March 2023

C. Savulescu [1]
(GROUP) VEBIS HCW VE study group

[1] Epiconcept, France

BACKGROUND
As healthcare workers (HCWs) are prioritised for COVID-19 vaccination, the number of unvaccinated HCWs diminishes over time. We measured the relative vaccine effectiveness (rVE) of any COVID-19 booster dose versus primary course vaccination in HCWs during Omicron predominant circulation period (December 2021–March 2023).

METHODS
We conducted a prospective cohort study among HCWs from 17 EU/EEA hospitals. HCWs were tested for SARS-CoV-2 in nasopharyngeal or saliva samples at enrolment and during weekly/biweekly follow-up. We measured the rVE against infection of any booster dose overall, by days since first booster dose (7–90/90+ days) and during Omicron BA.1/2 (December 2021–May 2022) and BA.4/5 (June 2022–March 2023) sublineage-dominated waves. Using Cox regression, we calculated the rVE as (1-hazard ratio)*100, adjusting for hospital, age, sex, underlying conditions, and pre-enrolment SARS-CoV-2 infection.

RESULTS
Among 2231 eligible HCW, 1882 (84%) were vaccinated with the first booster, including 416 (19%) with the second booster dose. Of the 776 SARS-CoV-2 infections detected in the study, 667 (87%) reported any booster dose. Adjusted rVE was 11% (95%CI: -12; 29) overall; 44% (95%CI: 24; 58) in 7–90 days and -15% (-49; 12) 90+ days following the first booster dose. The rVE was 17% (-13; 38) during Omicron BA.1/2 (total/events=1390/322) and 4% (95%CI: -35; 32) during Omicron BA.4/5 (total/events=1630/454) predominant circulation.

CONCLUSIONS
The COVID-19 vaccine offered additional protection against infection during the first 3 months following the first booster dose. Sample size in our study was insufficient to precisely identify differences in rVE between the periods of predominant circulation of different Omicron sublineages. The continuation of this study that includes regular testing for infection in HCW will help to better inform COVID-19 vaccination policies for this high-risk group.

Keywords: SARS-CoV-2 Infection, Healthcare Workers, Vaccine Effectiveness, COVID 19 Vaccine, Active surveillance
ABSTRACT ID: 411
PRESENTED BY: Camelia Savulescu, France / c.savulescu@epiconcept.fr

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COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

Estimating vaccine effectiveness against COVID-19 using related sick leaves as an indicator: A nationwide population-based cohort study, Norway, July 2021 – December 2022

H. Meijerink [1]
L. Veneti [2], A. Kristoffersen [3], A. Danielsen [4], M. Stecher [5], J. Starrfelt [6]
[1, 2, 3, 5, 6] Norwegian Institute of Public Health
[4] Norwegian Institute of Public Health | Department of Microbiology, Oslo University Hospital, Norway

BACKGROUND

SARS-CoV-2 infections are currently underreported due to changes in testing policy and increased use of rapid tests. We aimed to use certified medical leave due to COVID-19 (sick leave) instead of infections to estimate vaccine effectiveness (VE) against among employed individuals (25-64-years-old) in Norway.

METHODS

This nationwide cohort study used collated data from the Norwegian National Preparedness Register for COVID-19. Using Cox proportional hazard models, we estimated adjusted hazard ratios (aHRs) with 95% confidence intervals with vaccine status as a time-dependent covariate.

RESULTS

During the Delta period (July-December 2021), of the 2236419 individuals 73 776 (3.3%) reported infections and 54334 (2.4%) required sick leave. During the Omicron period (January-December 2022), 300140 (13.6%) of the 2206952 individuals required COVID-19 specific sick leave. Among individuals who had reported sick leave, 26 611 (55%) had a positive test during the Delta period and 96 445 (32%) during the Omicron period.During the Delta period, the VE against sick leave followed similar waning pattern to SARS-CoV-2 infections. Lowest aHRs against sick leave and infection were found for 2-7 weeks after the second (0.25; 0.24-0.26 / 0.16; 0.15-0.17) and third dose (0.26; 0.24-0.29 / 0.18; 0.16-0.19) respectively. During the Omicron period, aHRs against sick leave were higher than during the Delta period, but lowest aHRs were still found in the first period after receiving the second (0.61; 0.59-0.64) or third dose (0.63; 0.62-0.64).

CONCLUSIONS

Our results showed that sick leave could be used as a relevant indicator for surveillance of COVID-19, especially relevant in in periods of underreporting of infection and among groups with low risk of COVID-19 related severe outcomes.

Keywords: Public Health Surveillance, Comparative Effectiveness Research, COVID-19 Vaccines, Sick Leave, Population Registers
ABSTRACT ID: 257

PRESENTED BY: Hinta Meijerink, Norway / hinta.meijerink@fhi.no

POSTER TOUR 8

DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

Estimation of COVID-19 vaccine effectiveness against severe outcomes among adults hospitalized for severe acute respiratory infections in Albania, July 2022- March 2023

J. Sulo [1]
K. Mersini [2], I. Finci [3], I. Hasibra [4], N. Como [5], E. Meta [6], M. Qato [7], J. Howard [8], S. Cohuet [9], E. Kureta [10],
N. Mebonia [11], R. Pebody [12], M. Katz [13], S. Bino [14]

[1] Institute of Public Health, Tirana, Albania | Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET), European Centre for Disease Prevention and Control (ECDC),Stockholm, Sweden | Southeast European Center for Surveillance and Control of Infectious Disease, Tirana, Albania
[2] Institute of Public Health, Tirana, Albania | Faculty of Veterinary Medicine, Albania
[3, 12, 13] World Health Organization Regional Office for Europe, Copenhagen, Denmark
[4, 10] Institute of Public Health, Tirana, Albania
[5, 6, 7] University Medical Center of Tirana Mother Teresa
[8, 9] Epiconcept
[11] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[14] Institute of Public Health, Tirana, Albania
Southeast European Center for Surveillance and Control of Infectious Disease, Tirana, Albania

BACKGROUND
The COVID-19 pandemic caused high morbidity and mortality globally and highlighted the importance of effective surveillance systems. COVID-19 vaccine is an important tool to reduce morbidity and mortality. We aimed to estimate COVID-19 vaccine effectiveness (VE) against severe outcomes among adult patients hospitalized for severe acute respiratory infections (SARI) due to SARS-CoV-2 in Albania using data from the integrated electronic surveillance system of infectious diseases

METHODS
Between July 2022 and March 2023, we conducted a test-negative case-control study amongst SARI hospitalized patients >18 years, tested for SARS-CoV-2 by RT-PCR. We defined vaccinated persons those with primary series or booster dose, ≥14 days prior to symptom onset. Severe outcome was defined as admission to intensive care unit or need for supplemental oxygen or death. We compared the vaccination status of SARS-CoV-2-positive patients (cases) to negative patients (controls). We used logistic regression to estimate adjusted odds ratios (aOR) for demographics and calculated VE against SARS-CoV-2 hospitalization and severity outcomes as (1-aOR) x 100.

RESULTS
We included 423 cases and 1,221 test-negative controls. Median age was 66 (IQR: 54 – 75). Overall 286 (17%) had received primary vaccine series and 148 (9%) had received booster doses. VE against COVID-19 hospitalization was 68.2% (95%CI – 48.3: + 93.5) for those patients who received the last dose of vaccine within three months before symptoms onset, but dropped to -2% (95%CI –37.7:24.4) over six months. VE against severity outcome was 51.4% (95%CI -35.9:82.6).

CONCLUSIONS

COVID-19 vaccines effectively reduced risk of SARS-CoV-2 related to severe outcome in SARI patients in Albania during a period of mainly Omicron circulation. The timing of vaccination played a crucial role in determining waning of protection against SARI COVID-19 hospitalization.

Keywords: Severe Acute Respiratory Infection, COVID-19, Vaccine Effectiveness, Test-Negative Design
ABSTRACT ID: 808

PRESENTED BY: Jonilda Sulo, Albania / jonildasulo@gmail.com

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COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

Three reference groups for estimating the effectiveness of the most recent COVID-19 vaccination dose, Vaccine Effectiveness Burden and Impact Studies (VEBIS), December 2021–February 2023

R. Ri [1]

C. Mazagatos [2], I. Martínez-Baz [3], G. Petrovic [4], BELSARI-NEt[5], M. Borg [6], J. Donnell [7], A. Machado [8], L. Luong Nguyen [9], G. Gefenaite [10], C. Popescu 11, J. Horváth [12], K. Tolksdorf [13], P. Husa [14], S. Bacci 1[5], J. Howard [16], M. Álvarez [17], A. Echeverria [18], M. Ilic [19], A. Džiugyte [20], L. Domegan [21], V. Gomez [22], L. Lefrancois [23], L. Jancoriene [24], M. Lazar [25], B. Oroszi [26], R. Dürrwald [27,] L. Soucková [28], N. Nicolay [29], A. Rose [30], (GROUP) ECDC VEBIS Hospital Study Team

[1] Epiconcept, Paris, France
[2] National Centre of Epidemiology, CIBERESP, Carlos III Health Institute. Madrid, Spain
[3, 18] Instituto de Salud Pública de Navarra - IdiSNA - CIBERESP, Pamplona, Spain
[4, 19] Croatian Institue of Public Health, Zagreb, Croatia
[5] BELSARI-NET, Sciensano, Brussels
[6, 20] Infectious Disease Prevention and Control Unit (IDCU), Health Promotion and Disease Prevention, Msida, Malta
[7] Speisialtóir Sláinte Poiblí
Specialist in Public Health Medicine, Health Protection Surveillance Centre, Dublin, Ireland
[8, 22] Instituto Nacional De Saúde Doutor Ricardo Jorge / National Institute of Health Doutor Ricardo Jorge (INSA), Lisbon, Portugal
[9] CIC Cochin Pasteur, Assistance-Publique Hôpitaux de Paris, Paris, France
[10] Department of Health Sciences, Faculty of Medicine, Lund University, Lund, Sweden
[11] Dr. Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Bucharest, Romania
[12, 26] National Laboratory for Health Security, Epidemiology and Surveillance Centre, Semmelweis University, Budapest, Hungary
[13] Department for Infectious Disease Epidemiology, Respiratory Infections Unit, Robert Koch Institute, Berlin, Germany
[14, 28] University Hospital Brno, Faculty of Medicine, Masaryk University, Brno, Czechia
[15, 29] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[16, 30] Epiconcept, Paris, France
[17] National Centre of Epidemiology, Carlos III Health Institute. Madrid, Spain
[21] HSE-Health Protection Surveillance Centre (HPSC), Dublin, Ireland
[23] Innovative Clinical Research Network in Vaccinology (I-REIVAC), Inserm, Paris, France
[24] Clinic of Infectious Diseases and Dermatovenerology, Institute of Clinical Medicine, Medical Faculty, Vilnius University, Vilnius, Lithuania
[25] Cantacuzino National Military-Medical Institute for Research and Development, Bucharest, Romania
[27] National Reference Centre for Influenza, Robert Koch Institute, Berlin, Germany

BACKGROUND

Absolute COVID-19 vaccine effectiveness (VE) compares outcomes between vaccinated and never-vaccinated patients. Over time, never-vaccinated patients have become a disparate reference group. Influenza VE studies usually compare patients based on vaccination status within a given influenza season. We estimated COVID-19 VE using never-vaccinated and two other reference groups.

METHODS

In the “Vaccine Effectiveness, Burden and Impact Studies” ECDC-project, using the test-negative design, hospital teams from 41 hospitals in 12 European countries recruited severe acute respiratory infection (SARI) patients with onset from December 2021 to February 2023. Patients were swabbed ≤14 days after symptom onset and RT-PCR-tested for SARS-CoV-2. We estimated VE among hospitalised SARI patients aged ≥60 years adjusted for age, sex, chronic conditions, swab date, study site. Fully vaccinated patients (±any booster) with last dose ≤6 months before symptom onset (“recently vaccinated”) were compared with those (1) never vaccinated (“absolute VE”); (2) not recently vaccinated (“seasonal VE”: similar to influenza VE reference group); (3) fully vaccinated (±any booster) but not recently vaccinated (“relative VE”).

RESULTS

During the Omicron period (N=9451), there were 3326 (35%) recently-vaccinated, 1364 (14%) never-vaccinated, 6107 (65%) not recently-vaccinated, and 4694 (50%) fully- but not recently-vaccinated SARI patients. Never-vaccinated patients were younger, with fewer chronic conditions than recently-vaccinated. Absolute, seasonal, and relative VE were 59% (95% CI: 51–66%), 43% (35–49%), and 34% (24–43%), respectively.

CONCLUSIONS

As public health agencies recommend annual (or bi-annual) COVID-19 booster vaccination for high-risk populations for 2023 and beyond, reference groups for VE should be selected based on comparability between patients and appropriateness of public health messaging. For COVID-19 VE, the not recently-vaccinated reference group is more representative than never-vaccinated SARI patients and provides an understandable measure.

Keywords: COVID-19 Vaccines, Vaccine Effectiveness, Case-Control Studies, SARS-CoV-2, Hospital, Europe
ABSTRACT ID: 513

PRESENTED BY: Liliana Antunes, France / l.antunes@epiconcept.fr

POSTER TOUR 8
DAY 1 – WEDNESDAY 22 NOVEMBER 2023
15:45-16:30

COVID-19: vaccine effectiveness

MODERATOR
Nina Rodic

Abstract

Duration of COVID-19 vaccine effectiveness against Omicron and its sub-variants by dose: a systematic review

A. Baidya [1]
K. Walter [2], P. Babar [3], L. Hale [4], A. Schmidt [5], M. Patel [6], D. Feikin [7], M. Knoll [8], M. Higdon [9]

[1, 2, 8, 9] International Vaccine Access Center (IVAC) | Johns Hopkins Bloomberg School of Public Health
[3, 4, 5] Johns Hopkins Bloomberg School of Public Health
[6, 7] Department of Immunizations, Vaccines and Biologicals, World Health Organization (WHO)

BACKGROUND
Omicron has exhibited marked immune evasion, reducing COVID-19 vaccine effectiveness (VE). Monitoring the effect emerging variants have on VE and duration of protection is crucial for policymaking regarding booster doses.

METHODS
We systematically review this evidence in real time; summarized here are declines in VE since the last vaccination from published and preprint literature through March 2, 2023 (results will be updated at conference time). Eligible studies reported VE against Omicron comparing vaccinated to unvaccinated individuals at › 1-time point since the last dose (primary series, first, or second booster), among other eligibility criteria minimizing bias. Random effect meta-analysis was performed to estimate the average changes in VE over time, stratified by doses and subvariants.

RESULTS
Average VE against Omicron severe disease was 71.3% 1-month post-primary series vaccination and declined 10.5 percentage points (pp) (95% CI: 5.1–16.8) to 60.8% by six months; VE at one month was lower against symptomatic disease (57.1%) and infection (42.9%) and declines were greater: 46.5 pp (37.9–56.2) and 26.7 pp (19.5–34.7), respectively. A booster dose increased VE initially (89.7% for severe disease) but demonstrated similar waning (severe disease: 15.7 pp, 11.4–20.9; symptomatic disease: 32.6 pp, 23.7–42.9; infection: 46.8 pp, 23.1–79.6). Second booster VE estimated up to 4 months, showed a similar pattern. Average first booster VE against severe disease declined faster for BA.2 (20.0 pp, 6.6-42.2) and BA.4/BA.5 (30.2 pp, 13.8-56.2) than for BA.1 (8.9 pp, 5.0-13.7) but was not statistically significant (p=.11).

CONCLUSIONS
Boosters protect against severe Omicron disease but waned quickly for more recent subvariants. These findings help inform the need for and timing of future booster doses in the context of emerging variants.

Keywords: COVID-19 Vaccines, Vaccine Effectiveness, Systematic review, Immunity, Omicron, SARS-CoV-2 variants
ABSTRACT ID: 747
PRESENTED BY: Anurima Baidya, United States / abaidya1@jh.edu

POSTER TOUR 9

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Emerging diseases

MODERATOR
Justine Schaeffer

Abstract

Citizen science as an effective tool to detect the tiger mosquito (Aedes albopictus) in Belgium

J. Rebolledo [1]
M. Hermy [2], I. Deblauwe [3], M. Kont [4], V. Laisnez [5], A. Schneider [6], R. Müller [7], W. Van Bortel [8], T. Lernout [9]

[1, 2, 5, 9] Service of Epidemiology of Infectious Diseases, Sciensano, Brussels, Belgium
[3, 6, 7] Unit of Entomology, Institute of Tropical Medicine, Antwerp, Belgium
[4] Department of Infectious Disease Epidemiology, School of Public Health, Imperial College London, UK
[8] Unit of Entomology, Institute of Tropical Medicine, Antwerp, Belgium
Outbreak Research team, Institute of Tropical Medicine, Antwerp, Belgium

BACKGROUND

The tiger mosquito (Aedes albopictus) is an important vector of arboviruses. Over the past two decades, the species has invaded and expanded its range in Europe. In countries where it is established, it is responsible for local transmission of chikungunya, dengue and Zika. In Belgium, since 2012, its introduction is followed by active surveillance at points of entry such as parking lots along highways, used tire or lucky bamboo import companies, with tiger mosquitoes detected almost yearly. In order to expand the surveillance countrywide, passive surveillance through a citizen science platform was implemented in 2022.

METHODS

Citizens can notify a tiger mosquito by uploading a picture on the online platform. After passing three filtering questions, the notifier provides the sighting location and his/hers contact details. The species is confirmed by morphological identification. In case of a tiger mosquito, the notifier is contacted and a field inspection for confirmation is scheduled.

RESULTS

In 2022, 312 notifications were made in Belgium. Of these 143 showed a mosquito (Culicidae) including Aedes, Culex, and Culiseta species. Twelve tiger mosquitoes were notified from nine different locations, all except for one found inside houses and gardens in (semi-) urban areas. This led to six field inspections and the implementation of control measures at three locations.

CONCLUSIONS

Belgium is currently at the invasion front of the tiger mosquito. Citizen science as a tool for surveillance has proven to be very effective in discovering new locations with tiger mosquitoes which wouldn't have been detected through active surveillance. Promoting the citizen science platform in the coming years will increase our understanding about the presence, introduction and establishment of the tiger mosquito in Belgium.

Keywords: Citizen science, Surveillance, Arboviruses, Tiger mosquito, Aedes albopictus, Belgium
ABSTRACT ID: 615
PRESENTED BY: Javiera Rebolledo, Belgium / Javiera.RebolledoGonzalez@sciensano.be

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POSTER TOUR 9

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Emerging diseases

MODERATOR
Justine Schaeffer

Abstract

Elevated neuroinvasive Toscana Virus incidence in Italy during 2022: an emerging public health threat?

E. Fotakis [1]

E. Di Maggio [2], A. Mateo Urdiales [3], M. Del Manso [4], G. Perego [5], D. Petrone [6], A. Bella [7], F. Mellace [8], A. Oradini-Alacreu [9], M. Caporali [10], G. Bongiorno [11], I. Bernardini [12], M. Di Luca [13], G. Venturi [14], C. Fortuna [15], S. Giannitelli [16], F. Ferraro [17], F. Maraglino [18], P. Pezzotti [19], F. Riccardo [20]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Istituto Superiore di Sanità
[2, 9, 10, 11, 12, 13, 14, 15, 16, 19, 20] Scuola di Specializzazione in Igiene e Medicina preventiva, Università di Foggia, Italy
[3, 4, 6, 7] Istituto Superiore di Sanità, Department of Infectious Diseases, Italy
[5] Scuola di Specializzazione in Igiene e Medicina Preventiva, Università Vita-Salute San Raffaele, Italy
[8] Dipartimento di Area Medica, Università degli Studi di Udine, Italy
[17, 18] Ministry of Health, Directorate-General for Health Prevention

BACKGROUND
Toscana virus (TOSV) is a Phlebovirus transmitted to humans through bites of infected sand flies. Neuroinvasive TOSV infections are amongst the leading causes of meningitis and meningo-encephalitis in southern Europe and notifiable in Italy since 2016. In 2022, Italy experienced climate anomalies and a concomitant increase in mosquito and tick-borne disease transmission. We aimed to identify the spatiotemporal distribution and risk groups of neuroinvasive TOSV infections in Italy in 2022, comparative to 2016-2021.

METHODS
We describe notified cases of neuroinvasive TOSV in Italy, 2016-2022, using frequencies, incidences and incidence risk ratios (IRR) with 95% confidence intervals (CI), stratified by month-year, sex, age, region of diagnosis and exposure municipality by urbanization level.

RESULTS
In 2022, 153 locally acquired neuroinvasive TOSV infections were notified compared to an annual average of 55 cases (range:35-89) for the years 2016-21. The majority of cases reported illness in September (32.67%), extending the high transmission season compared to previous years. Cases were diagnosed in 9/20 regions, the majority of which in Emilia-Romagna (66%), as before, yet neuroinvasive infections were acquired for the first time in the north- and southmost regions of the country. Incidence was highest in rural municipalities (3.9 per 1,000,000 population) however increased more in peri-urban municipalities compared to 2016-21. During 2022 incidence was the highest ever recorded in all age groups, besides 2018 in adolescents. In concordance with previous years, male sex (IRR=2.5;95%CI=0.4-16) and being ≥20 (IRR=4.4;95%CI=0.3-61) were identified as possible risk factors.

CONCLUSIONS
In 2022, Italy experienced intense transmission of TOSV with an extended geographical distribution, possibly attributed to climate-driven vector dynamics. Raising public awareness across Italy on TOSV risk factors and personal protection measures may significantly enhance prevention efforts.

Keywords: Sand flies, TOSV, Surveillance, Epidemiology, Europe
ABSTRACT ID: 325
PRESENTED BY: Emmanouil Alexandros Fotaki, Italy / emmanouil.fotakis@iss.it

POSTER TOUR 9

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Emerging diseases

MODERATOR
Justine Schaeffer

Abstract

Acute hepatitis of unknown aetiology: examining the North-East England Cohort

E. Cullen [1]
J. Darke [2], N. Love [3], C. Molyneux [4], L. Sayeed [5], S. Troup [6], K. Watson [7], S. Waugh [8], A. Wort [9]

[1, 2, 3] UKHSA
[4] County Durham and Darlington NHS Foundation Trust
[5, 8] The Newcastle Upon Tyne Hospitals NHS Foundation Trust
[6, 9] Gateshead Health NHS Foundation Trust
[7] South Tyneside and Sunderland NHS Foundation Trust

BACKGROUND
The UK alerted international partners of a paediatric cluster of acute hepatitis of unknown aetiology on 05/04/2022. We aimed to describe the epidemiology of the North-East of England cohort (population 2,647,100), comparing it to regional historical data.

METHODS
Cases were defined as individuals with serum transaminase >500IU/L, of unknown cause, from 01/01/2022, resident in North-East England, aged ≤15 years. Epidemiological data were extracted from health protection, laboratory and hospital electronic records. Descriptive analysis was performed. Historic cases (age ≤15 years; serum transaminase >500IU/L) identified by one regional laboratory between 01/01/2017 and 31/12/2021 acted as a comparator.

RESULTS
18 cases were reported between 31/03/2022 and 24/06/2022 (39% female; median age 4, IQR 1.75), resident across 8/12 North-East local authorities. 16 cases reported jaundice (89%). All 18 cases presented to hospital (12 admitted >24h). Median time between symptom onset and hospital presentation was 7 days (IQR 8). One case required liver transplant. There were no deaths. Two cases were PCR positive for COVID-19 (11%) and 9/11 had Covid-19 antibodies. Adenovirus was detected in 12/15 cases tested, with seven typed, all Type F. Six historic cases with no clear diagnosis, meeting the case definition for this incident, were identified over the previous 5-year period by a single regional laboratory (one each in 2017,2019 and 2020, three in 2021; median age 7 years, IQR 4.68). This laboratory reported 8 cases in 2022.

CONCLUSIONS
The North-East cohort showed a similar pattern to the national incident. Adenovirus was the most common pathogen identified. 82% of those tested had evidence of prior COVID-19 infection. Cases of paediatric hepatitis of unknown aetiology have been identified prior to 2022 but fewer in number and in older children.

Keywords: Epidemiology, Hepatitis, Outbreak, Child
ABSTRACT ID: 238
PRESENTED BY: Emer Cullen, United Kingdom / emer.cullen@ukhsa.gov.uk

POSTER TOUR 9

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Emerging diseases

MODERATOR
Justine Schaeffer

Abstract

Hay exposure as a risk factor associated with the spread of Crimean-Congo Hemorrhagic fever (CCHF), Georgia, 2022

L. Liluashvili [1]
T. Khargaladze [2], N. Zhgenti [3], M. Mamardashvili [4], O. Tsagareishvili [5], N. Mamuchishvili [6], K. Zakhashvili [7], N. Chitadze [8], C. Ward [9], N. Malakmadze [10], T. Singh [11]

[1] National Center for Disease Control and Public Health, Tbilisi, Georgia (NCDC) | EESC FETP
[2] Ministry of Environmental Protection and Agriculture, LEPL National Food Agency | EESC FETP
[3, 4, 5] National Center for Disease Control and Public Health, Tbilisi, Georgia (NCDC) | EESC FETP
[6, 7, 8] National Center for Disease Control and Public Health, Tbilisi, Georgia (NCDC)
[9, 11] US CDC – Georgia Country Office
[10] EESC FETP | US CDC – Georgia Country Office

BACKGROUND
The largest reported outbreak of Crimean-Congo Hemorrhagic Fever (CCHF) in Georgia occurred in 2022 with 48 confirmed cases. During the initial investigation, exposure to hay was identified as a potential risk factor for transmission. To test the hypothesis on routes of transmission, we conducted a case-control study.

METHODS
Two controls were selected for each confirmed case, matched by age, sex, and village. We interviewed cases and controls using a standardized questionnaire. Blood samples from controls were tested by ELISA to exclude CCHF seropositive individuals. We calculated adjusted odds ratios (aOR) using multivariate logistic regression to adjust for marital status, education, and contact with cattle. To understand if there was unreported circulation of CCHF in neighboring villages without history of cases, we conducted a serosurvey among randomly selected workers at hay production sites and farms.

RESULTS
We interviewed 34 cases and 51 controls. Among cases, the mean age was 53.1 (SD=17.3) years and 41% were female. CCHF IgG antibodies were detected in 2 controls and excluded from analysis. Being a farmer (aOR=24.3; 95% CI=4.18-240.0), history of tick bite (aOR=11.4; 95% CI 1.99-111.0), and obtaining hay for animal feed from another village (aOR=17.9; 95% CI=2.03-366.0) were significantly associated with CCHF. We also identified 3/29 (10%) CCHF seropositive individuals in villages without known CCHF circulation.

CONCLUSIONS
The study revealed significant associations between farming, tick bites, and obtaining hay from villages outside their home area and CCHF. Further investigation is needed into hay storage to explain this finding and make public health recommendations. New cases in villages with unknown circulation suggest the possibility of unreported cases, warranting a seroprevalence study to assess their risk factors the actual extent of CCHF in Georgia.

Keywords: Crimean Congo Hemorrhagic Fever, Routes of transmission, Hay exposure, Case-Control study, Georgia Country
ABSTRACT ID: 641
PRESENTED BY: Levan Liluashvili, Georgia / levanliluashvili29@gmail.com

POSTER TOUR 9

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Emerging diseases

MODERATOR
Justine Schaeffer

Abstract

Aetiology of Acute Undifferentiated Febrile Illness (AUFI) at a tertiary care centre in Eastern Uttar Pradesh, India

V. Tiwari [1]
T. Rai [2], M. Gangwar [3], U. Rai [4], G. Nath [5], J. Chakravarty [6]
[1, 2, 4, 6] Department of General Medicine, Institute of Medical Sciences, Banaras Hindu University (BHU), Varanasi, India
[3, 5] Department of Microbiology, Institute of Medical Sciences, Banaras Hindu University (BHU), Varanasi

BACKGROUND
Acute undifferentiated febrile illness (AUFI) a common presenting complaint, can cause significant mortality and morbidity if left undiagnosed. There is a regional variation in the aetiology of AUFI. Moreover, similarity in the symptoms makes an accurate clinical diagnosis difficult without laboratory confirmation. Thus, this study was done to to identify the common aetiology of AUFI at a tertiary care centre in Eastern Uttar Pradesh, India.

METHODS
This cross-sectional study was conducted in SSL Hospital, Banaras Hindu University, Uttar Pradesh, India, between May 2021 and May 2022. All adult patients more than 18 year of age presenting with fever less than 14 days without any localizing sign were included in this study. ELISA tests were performed on all samples by Leptospira IgM ELISA (NovaTec), Chikjj IgM ELISA (InBios), ScrubTyphus IgM ELISA (InBios), DENV IgM Capture ELISA (InBios),as per the manufacturer protocol.

RESULTS
During the study period, 121 patients admitted with AUFI were included in the study. Mean duration of fever was found to be 5.81±3.97days. The most common aetiology found was Dengue comprising 41 (33.88%) of the total AUFI patients. Second most common aetiology were Leptospirosis and Scrub Typhus comprising 29 (23.96%) patients each.The patients found positive for Chikungunya were 9 (8.49%).There were 13 (10.74%) patients which were not found positive for any of the aetiology stated above.

CONCLUSIONS
The most common cause of AUFI was viral. Availability of cost-effective serological test for dengue, scrub typhus and leptospirosis at primary health care setting would lead to early diagnosis and effective management of AUFI in this region. The etiological profile will be of use in the development of rational guidelines for control and treatment of AUFI

Keywords: Dengue, Leptospirosis, Scrub Typhus, Chikungunya
ABSTRACT ID: 38
PRESENTED BY: Vishwa Deepak Tiwari, India / vishwadeepk@bhu.ac.in

POSTER TOUR 9
DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Late breakers I

MODERATOR
Justine Schaeffer

Abstract

Fatal Streptococcus pyogenes cases in Europe and Turkey, a case series including autopsy data

V. Saegeman [1]
N. Ziyade [2], R. Abad Moralejo [3], M. Cecilia Cohen [4], A. Fernandez-Rodriguez [5]

[1] Vitaz, Sint-Niklaas, Belgium | University Hospitals Leuven, Leuven, Belgium
ESGFOR - ESCMID Study Group of Forensic and Postmortem Microbiology
[2] Ministry of Justice, Council of Forensic Medicine, Istanbul, Turkey
ESGFOR - ESCMID Study Group of Forensic and Postmortem Microbiology
[3] Microbiology Laboratory, Biology Department, Instituto Nacional de Toxicología y Ciencias Forenses, Las Rozas de Madrid, Madrid, Spain
[4] Histopathology Department. Sheffield Children's NHS FT, UK
ESGFOR - ESCMID Study Group of Forensic and Postmortem Microbiology
[5] Microbiology Laboratory, Biology Department, Instituto Nacional de Toxicología y Ciencias Forenses, Las Rozas de Madrid, Madrid, Spain | ESGFOR - ESCMID Study Group of Forensic and Postmortem Microbiology

BACKGROUND
Invasive Streptococcus pyogenes infections have been reported worldwide in the end of the COVID pandemic. The aim of our study was to define common characteristics among fatal cases from both community and hospital deaths.

METHODS
We selected positive culture results for S. pyogenes in four cooperating laboratories' databases from UK, Spain, Turkey and Belgium, checking predefined variables of patients, clinical and histopathological findings and strains.

RESULTS
Forty cases were retrieved in 4 different centres (17 males/22 females/1 unknown gender), (median age 16.67/3 months-66 years). The average time between symptom onset and death was 5.56 (0-60) days. Interestingly, S. pyogenes Emm-types 1.0 and 12.0 were the most frequent (11 and 10 respectively) in the 25 cases investigated. The most frequent combination of toxins' expression was streptococcal A, G, J and Z (7/20 strains analysed), always associated to Emm-type 1.0. Diagnosis was made at forensic post-mortem investigation in 38 cases. Only 2 cases were diagnosed by hemocultures shortly antemortem. Hemocultures were positive in 24 postmortem cases, while the lung was positive in 12 cases in which hemocultures were negative. Histopathology showed tissue inflammation in 23/25 cases. Septic shock was the predominant form of presentation (17/40 cases), associated to soft-tissue infection (2 cases). Respiratory infection was detected in 18 cases and peritonitis in one case. Streptococcus pneumoniae was also associated to respiratory infection in 2 cases.

CONCLUSIONS
S. pyogenes Emm-types 1.0 and 12.0 are the main responsible of fatal European cases, consistently to De Gier et al's recent results. This study highlights the importance and contribution of autopsy data to identify the characteristics of invasive fatal S. pyogenes cases, which otherwise wouldn't be diagnosed antemortem.

Keywords: Autopsy data, S. pyogenes, Virulence factors, Fatality, Postmortem microbiology, Autopsy, Forensic microbiology
ABSTRACT ID: 834
PRESENTED BY: Veroniek Saegeman, Spain / Veroniek.saegeman@vitaz.be

POSTER TOUR 10

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Foodborne disease outbreak investigations

MODERATOR
Margaret Fitzgerald

Abstract

Foodborne outbreak investigation in a Public High School in Cinfães, Northern Region of Portugal, February 2023

D. Fernandes [1]
R. Cardoso [2], A. Vieira [3], A. Afonso [4], C. Roseira [5], D. Almeida [6], A. Natividade [7], G. Saldanha [8], A. Figueiredo [9]

[1] Porto International Vaccination Center | Public Health Unit, Primary Health Care Grouping Baixo Tâmega
[2, 3, 4, 5, 6, 7] Public Health Unit, Primary Health Care Grouping Baixo Tâmega
[8] Porto International Vaccination Center | Public Health Unit, Primary Health Care Grouping Baixo Tâmega
[9] Public Health Unit, Primary Health Care Grouping Baixo Tâmega | Portuguese Directorate General of Health

BACKGROUND
On February 2nd, 2023, an acute gastroenteritis outbreak was reported at Cinfães Public High School, affecting 52 students who had consumed lunch at the school canteen A prompt investigation was carried out by the Public Health Unit (PHU) of Baixo Tâmega to identify the cause and implement necessary control measures.

METHODS
On February 3rd, the Health Authority and the Regional Authority for Economic and Food Safety inspected the school and conducted an investigation through a cohort study, defining a case as a school student or staff experiencing vomiting and/or diarrhea starting from February 1st. Samples for testing were collected from food, swabs from food handlers hands and surfaces, as well as vomit and feces specimens.

RESULTS
The investigation revealed that 123 individuals met the case definition, accounting for 53,9% of the 228 people exposed. Onset of symptoms occurred between 14:00 and 20:00 on February 2nd. Vomiting was reported in 76.4% of cases and 53.7% experienced diarrhoea. Leftovers of February 2nd lunch, namely, poultry rice, mushroom rice and carrot cream, tested positive for Staphylococcus and Staphylococcal Enterotoxin. One food handler hands tested positive for Staphylococcal Enterotoxin, while surface swabs tested negative. Six vomit specimens were positive for Staphylococcal Enterotoxin.

CONCLUSIONS
The investigation concluded that the acute gastroenteritis outbreak was caused by Staphylococcus, originating from the contaminated hands of a food handler, with the February 2nd lunch meals serving as the vehicles of the outbreak. Immediate control measures were implemented to mitigate the spread of infection.The Food and Health authorities need to reinforce compliance with established recommendations (Hazard Analysis and Critical Control Point), enhance education and provide specific training for food handlers in the areas of hygiene and food safety.

Keywords: Foodborne outbreak, Gastroenteritis, Public high school, Staphylococcal enterotoxin
ABSTRACT ID: 122
PRESENTED BY: Davy Fernandes, Portugal / davy.b.fernandes@gmail.com

POSTER TOUR 10

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Foodborne disease outbreak investigations

MODERATOR
Margaret Fitzgerald

Abstract

Outbreak of Salmonella Typhimurium linked to Swedish rocket salad, Sweden, September-November 2022

K. Fischerström [1]
R. Dryselius [2], M. Lindblad [3], S. Kühlmann-Berenzon [4], N. Karamehmedovic [5], S. Börjesson [6], N. Hashemi [7], I. Gunn [8], A. Gustavsson [9], N. Lindroos [10], J. Nederby-Öhd [11], M. Widerström [12], R. Rimhanen-Finne [13], A. Vainio [14], M. Rehn [15]

[1] Public Health Agency of Sweden (PHAS), Solna, Sweden |
ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 4, 5, 7, 15] Public Health Agency of Sweden (PHAS), Solna, Sweden
[3] Swedish Food Agency (SFA), Uppsala, Sweden
[6] School of Health Science, Örebro University, Örebro, Sweden
[8] Department of Communicable Diseases and Disease Control, Region Kalmar County, Sweden
[9] Department of Infection Prevention and Control, Region Värmland, Sweden
[10] Department of Infectious Disease Prevention and Control, Region Halland
[11] Department of Infectious Disease Prevention and Control, Stockholm Region, Sweden
[12] Department of Clinical Microbiology, Umeå University, Umeå, Sweden
[13, 14] Department of Health Security, Finnish Institute for Health and Welfare, Helsinki, Finland

BACKGROUND

In September 2022, the Public Health Agency of Sweden detected a national outbreak of Salmonella Typhimurium through routine surveillance, including whole genome sequencing (WGS). National and regional authorities investigated the outbreak to identify a common source and stop the outbreak.

METHODS

WGS-confirmed cases were identified through the national notification system. We compared exposures, collected in a web-based questionnaire, between cases and controls matched on sex and age selected from a national random pool of controls. In an unmatched analysis, we calculated age and sex adjusted odds ratios (aOR) and 95% confidence intervals (95% CI) using logistic regression. We collected supermarket receipts from cases and conducted a trace-back investigation, supported by findings from simultaneous investigations of cases within the same WGS-cluster in Finland, identified through EpiPulse.

RESULTS

109 cases were reported by 20/21 Swedish regions, with symptom onset 17 September-24 November 2022. The median age was 52 years (range 4-87) and 62% were female. Cases were more likely than controls to report consumption of rocket salad (aOR: 4.9, 95% CI: 2.4-10), mixed salad bags (aOR: 4.0, 95% CI: 1.9-8.1) and shopping at retail chain A (aOR: 3.1, 95% CI: 1.0-9.5). 19/21 cases' retail chain A receipts included bagged rocket and/or mixed salad. Trace-back identified two Swedish growers of rocket salad and one company, responsible for pre-washing and packing rocket salad, solely and in mixed salad bags for retail chain A. No food samples were obtained for laboratory analysis.

CONCLUSIONS

Swedish-produced rocket salad was the likely source of this outbreak and should be regarded a potential risk product. Our findings emphasise the importance of producers of leafy greens to identify potential sources of enteropathogens and to prevent contamination of products.

Keywords: Salmonella, Case-Control Studies, Disease Outbreaks, Epidemiology
ABSTRACT ID: 356

PRESENTED BY: Karolina Fischerström, Sweden / karolina.fischerstrom@folkhalsomyndigheten.se

POSTER TOUR 10

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Foodborne disease outbreak investigations

MODERATOR
Margaret Fitzgerald

Abstract

Shigella flexneri outbreak linked to a takeaway in South Wales, February 2023: a case-control study

A. Plimmer [1]
L. Fina [2], O. Orife [3], A. Lench [4], B. Griggs [5], M. Saavedra-Campos [6], D. Thomas [7]

[1] Public Health Wales , Communicable Disease Surveillance Centre, Cardiff, UK
Field Epidemiology Training Programme, UK Health Security Agency, UK
[2, 3, 4, 7] Public Health Wales, Communicable Disease Surveillance Centre, Cardiff, UK
[5] Public Health Wales, Health Protection Team, Cardiff, UK
[6] Field Epidemiology Training Programme, UK Health Security Agency, UK

BACKGROUND
51 cases of gastrointestinal illness in customers of takeaway A, South Wales, were reported to Public Health Wales in February 2023. Shigella flexneri was identified in 29 cases. Sequenced samples were clustered within 5 single nucleotide polymorphisms. An outbreak investigation was conducted to determine the extent and vehicle of the outbreak.

METHODS
Following initial descriptive summary, a case-control study was completed. Cases were individuals who ate from takeaway A on 10th/11th February 2023, who were PCR positive for Shigella sp on faecal sample. Controls were identified by cases and from a customer list, as people who had eaten from takeaway A on the same dates who did not report illness. Participants completed a telephone questionnaire on food, travel and environmental exposures. A multivariable logistic regression model was built including exposures with p-values 0.2 and interactions identified on stratified analysis. Staff faecal samples were screened for Shigella sp.

RESULTS
31 cases, of which 9 required hospitalisation, and 29 controls were included in the study. Cases were older (43 vs. 33 years, p=0.024) and proportionally more female (68% vs 38%, p=0.021). 87% cases and 76% controls ate from takeaway A on 10th February 2023. Eating coleslaw and cabbage were the main associated factors, with odds ratios of 18 (95%CI:4-87) and 4 (95%CI:1-15) respectively, and 57 (95%CI:6-541) after accounting for an interaction. Shigella sp were not detected in any staff samples.

CONCLUSIONS
Coleslaw was the most likely vehicle. Though contamination route is unknown, a food-handler is the most likely source. This large outbreak differs from recent European outbreaks, which primarily have been associated with sexual transmission. Although uncommon in the UK, Shigella flexneri should be considered a cause of foodborne outbreaks.

Keywords: Epidemiology, Outbreak, Shigellosis, Case-control studies
ABSTRACT ID: 251
PRESENTED BY: Amy Plimmer, United Kingdom / amy.plimmer@wales.nhs.uk

POSTER TOUR 10

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Foodborne disease outbreak investigations

MODERATOR
Margaret Fitzgerald

Abstract

A Foodborne Outbreak of B. cereus associated with Consumption of Bonito Fish, in a Factory, Gebze, Kocaeli, Türkiye, January 2023

N. Gürbüz-Adem [1]
K. Kalip [2], M. Toptas [3], E. Caliskan [4], D. Furkan-Sevindi [5], B. Levent [6], Y. Demirbilek [7], F. Temel [8], S. Kaygusuz [9]
[1, 2, 3, 4, 5, 6, 7, 8, 9] Republic of Türkiye, MoH

BACKGROUND
On 27.01.2023, after dinner at a factory with 165 evening shift workers, 38 cases with nausea, vomiting, abdominal pain, facial flushing admitted to the hospital. We conducted epidemiological and microbiological investigations to identify the outbreak source and implement control measures.

METHODS
We conducted a retrospective cohort study, collected information from 162 workers, on food (soup, pasta, salad, fish, halva) consumption and symptoms. We interviewed factory production manager, workplace physician and kitchen chef, and examined fish sales place that supplies fish to the factory. Suspected cases (n=86) were those who ate dinner and had at least one of following symptoms: abdominal pain, nausea, vomiting, diarrhoea, rash, headache, dizziness, fever, and itching. We calculated attack rates (AR) and Risk Ratios (RRs) with 95% Confidence Intervals (CIs). Eight stool, and five food samples were tested for enteric pathogens using Polymerase Chain Reaction.

RESULTS
Most common symptoms were abdominal pain (58%), diarrhoea (57%), headache (51%) and nausea (47%). The epidemic curve revealed a single-source outbreak. The mean incubation-period was 2.6±3.1 hours. Bonito fish consumption (AR:63%) was significantly associated with illness (RR:18, 95%CI:2.6-122, p0.001). Environmental investigation revealed that fish were left outside for approximately two or three hours while cleaning and slaughtering process. B. cereus was isolated from cooked fish samples. Histamine release that occurs after eating bacterially contaminated fish might have caused facial flushing and itching. B. cereus was not isolated from stool samples.

CONCLUSIONS
This foodborne outbreak was due to consumption of bonito fish contaminated with B. cereus. We recommended hygiene measures to be implemented, and we trained kitchen workers and fishmonger on hygiene.

Keywords: Bacillus cereus, Histamine, Foodborne diseases, Cohort studies
ABSTRACT ID: 540
PRESENTED BY: Nurhayat Gürbüz-Adem, Turkey / nurhayatgurbuz@hotmail.com

POSTER TOUR 10
DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Foodborne disease outbreak investigations

MODERATOR
Margaret Fitzgerald

Abstract

Gastroenteritis outbreak at a delivery restaurant, Talgar, Kazakhstan, 2023

F. Ablimitova [1]
D. Nabirova [2], A. Balmagambetov [3], R. Horth [4]

[1] Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
Scientific and Practical Center for Sanitary and Epidemiological Expertise and Monitoring
[2] U.S. Centers for Disease Control and Prevention, Central Asia Office, Almaty, Kazakhstan
Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[3] Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan
[4] U.S. Centers for Disease Control and Prevention, Central Asia Office, Almaty, Kazakhstan
Central Asia Field Epidemiology Training Program, Almaty, Kazakhstan
Asfendiyarov Kazakh National Medical University, Almaty, Kazakhstan

BACKGROUND
On February 3, 2023, 71 hospitalized cases of gastroenteritis were notified among people who had ordered food from a delivery restaurant in Talgar. We aimed to identify risk factors for this outbreak.

METHODS
We conducted a retrospective cohort study among people who consumed food from the restaurant from January 31 to February 1, 2023. We interviewed customers by telephone and face-to-face. We performed multivariate Poisson regression to determine factors associated with illness. Patients' gastric and food samples were tested. We conducted an environmental assessment.

RESULTS
Of 381 people identified, 364 were interviewed, of which 59% were ill. Patients had abdominal pain (98%), diarrhea (94%), nausea (94%), headache (91%), chills (82%), fever (81%), and vomiting (55%). Mean illness duration was four days (range=1-8). Mean onset time was 34 hours (range=6-91 hours) and 33% were hospitalized. Risk of illness was higher among people who ate Caesar sushi (Adjusted risk ratio [ARR]=1.6, 95% confidence interval [CI]=1.2-2.0), Chicken pizza (ARR=1.7, CI=1.2-2.5), and American pizza (ARR=1.6, CI=1.2-2.1). We did not identify common ingredients in the foods. E.coli at concentration 10 and Enterococcus spp. were detected in sushi. Of 22 gastric samples tested, we detected B. cereus (45%), Enterococcus (50%), E.coli (23%). Environmental assessment found several food safety violations including improper storage conditions, prepared foods being stored with raw materials, and missing or expired workers' health and food certifications.

CONCLUSIONS
Because multiple pathogens were detected in food and patient samples and disease was associated with multiple foods, we suspect that food contaminated at different points in the preparation process was likely the source of the outbreak. The restaurant was closed and sanitized. We made recommendations to improve food handling and safety practices.

Keywords: Disease outbreak, Gastrointestinal diseases, Foodborne illness, Epidemiology, Cohort studies, Kazakhstan
ABSTRACT ID: 378
PRESENTED BY: Feruza Ablimitova, Kazakhstan / ablimitova.2608@gmail.com

POSTER TOUR 11

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

A pseudo-outbreak of Bordetella parapertussis centred on a hospital in France, revealing contamination of nasopharyngeal swabs, July 2023

D. Kelly [1]
L. Pascal [2], P. Chaud [3], S. Beretta [4], F. Ait El Belghiti [5], S. Aboukais [6], D. Segond [7], A. Ramdani [8], M. de Barbentane [9], F. Pospisil [10], J. Delaroziere 1[1], V. Bouchez [12], J. Toubiana [13], C. Rodrigues [14], S. Brisse [15]

[1] Santé publique France, French National Public Health Agency, Marseille, France | ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4] Santé publique France, French National Public Health Agency, Marseille, France
[5] Santé publique France, French National Public Health Agency, Saint Maurice, France
[6, 7, 8] Département de veille et sécurité sanitaire, Agence Régionale de Santé Provence-Alpes Côte d'Azur, France
[9, 10] Centre Hospitalier d'Avignon, Avignon, France
[11] Centre d'appui et de Prévention des Infections Associées aux Soins en Paca, France
[12, 13, 14, 15] Institut Pasteur, National Reference Centre for Whooping Cough and Other Bordetella infections, Paris, France

BACKGROUND
On 6 July 2023, a hospital in Vaucluse, France, reported nine nosocomial cases of Bordetella parapertussis to the regional health authority. Santé Publique France investigated this alert, given the unexpected rise in cases.

METHODS
We defined a case as laboratory-confirmed qPCR detection of B. parapertussis (IS1001 target) in a person residing in Vaucluse area, tested from 1st June 2023. Patients and staff in services with cases were tested locally using nasopharyngeal swabs and qPCR (B. parapertussis R-GENE® and Rotor-Gene Q platform). A random sample of positive specimens underwent confirmatory qPCR testing (B. parapertussis R-GENE® and LC480-II platform) at the National Reference Centre (NRC). We interviewed case-patients and checked for positive specimens elsewhere in Vaucluse.

RESULTS
136 specimens tested qPCR-positive for B. parapertussis from 24th June to 15th July 2023. Only 15 cases (11%) were children. Among 26 case-patients interviewed, few had pertussis-like symptoms: only nine reported at least one respiratory symptom. No other laboratories in Vaucluse reported positive B. parapertussis specimens since 1st April 2023. Local cycle threshold (Ct)-values for 131 positive specimens ranged from 31.3–36.5 (mean 33.7, standard deviation 1.1). The NRC retested four positive specimens, and all had Ct-values ›39. Testing of sterile swabs from the same hospital batch detected B. parapertussis with IS1001 Ct-values ›39.

CONCLUSIONS
The elevated and homogeneous Ct-values, atypical clinical presentation, absence of positive specimens from other laboratories and detection of B. parapertussis in sterile swabbing materials, strongly indicated false positives. Regional and national health authorities, advised by microbiologists, concluded a pseudo-outbreak due to contamination of swabs used, and opened a materiovigilance inquiry. This investigation calls for cautious interpretation of Ct-values, considering epidemiological and clinical contexts, to validate epidemic alerts.

Keywords: Whooping cough, Vaccine-preventable disease, Clinical laboratory techniques, Disease outbreaks, Bordetella parapertussis
ABSTRACT ID: 846
PRESENTED BY: David Kelly, France / david.kelly@santepubliquefrance.fr

POSTER TOUR 11

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

Attitude towards antibiotic prophylaxis among household contacts of patients with invasive Group A Streptococcal (iGAS) disease and its impact on the incidence of iGAS among contacts in the Netherland

Suhreta Mujakovic [1]
H. ter Waarbeek [2], J. van den Boogaard [3]

[1] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg PublicHealth Service, Heerlen, Netherlands | Centre for Infectious Diseases Control, National Institute for Public Health and the Environment, Bilthoven, the Netherlands
[2] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg PublicHealth Service, Heerlen, Netherlands | Centre for Infectious Diseases Control, National Institute for Public Health and the Environment, Bilthoven, the Netherlands
[3] Centre for Infectious Diseases Control, National Institute for Public Health and the Environment, Bilthoven, the Netherlands

BACKGROUND
In 2022, European countries reported a rise in invasive group A streptococcal infections (iGAS). Because of a more than twofold increase in the Netherlands, authorities broadened notification requirements from three to all iGAS-infection types to enable providing prophylactic antibiotics to a larger group of household contacts to prevent iGAS-infections. This study aimed to determine antibiotic prophylaxis acceptance and development of GAS-like symptoms in household-contacts, as well occurrence of secondary iGAS-infections.

METHODS
Of all 25 regional public health services (PHS), 20 PHS conducted a standardized 30-day follow-up phone survey to collect contacts' data from February till June 2023. Among others, iGAS-infection type of index case, number of household-contacts, antibiotic prophylaxis compliance, contacts' symptoms and course of infection were assessed on t=0, t=15 and t=30, starting at the notification date of the index case to PHS. Descriptive analysis was performed using MS Excel.

RESULTS
Of 273 notifications and 634 identified household contacts, 163 cases (60%) and 346 contacts (55%) met new notification criteria. At t=0, 84 contacts (13%) reported GAS-like symptoms for which they received treatment. Relating index cases' type of iGAS-infection was STSS in 18%, sepsis in 21%, and pneumonia-(pleura)empyema in 24%. Contacts with no symptoms (n=550) were eligible for chemoprophylaxis, taken by 524 (95%) between t=0 and t=15. After chemoprophylaxis 23 contacts (4.4%) developed symptoms like sore throat, fever and rash, but no secondary iGAS-cases were seen.

CONCLUSIONS
The adjusted notification criteria increased the number of identified contacts eligible for chemoprophylaxis by 55%. Their acceptance of prophylactic antibiotics was high and only a small number developed mild GAS-symptoms. No secondary iGAS-infections were observed. More research is needed on personal risk factors, spread of GAS-infections and chemoprophylactic effectiveness.

Keywords: Houshold, Group A streptococcus, Chemoprophylaxis, Intervention, Prevention
ABSTRACT ID: 951
PRESENTED BY: Henriëtte ter Waarbeek, Netherlands / Henriette.terWaarbeek@ggdzl.nl

POSTER TOUR 11

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

Measuring the impact of sequential guest bedroom bookings and the effectiveness of interventions in a large, prolonged norovirus outbreak at an allinclusive resort in England, May-June 2023

R. Hams [1]
E. Blakey [2], E. Heinsbroek [3]

[1] Field Service East of England, UK Health Security Agency (UKHSA), Cambridge, United Kingdom
East of England Health Protection Team, UK Health Security Agency (UKHSA), Cambridge, United Kingdom
[2, 3] Field Service East of England, UK Health Security Agency (UKHSA), Cambridge, United Kingdom

BACKGROUND

A suspected norovirus outbreak occurred 22nd May-19th June 2023 at an all-inclusive resort in England. We measured the impact of sequential guest bedroom bookings and the effectiveness of interventions in this outbreak.

METHODS

Cases of diarrhoea and vomiting among guests and staff were identified through resort notifications and a retrospective cohort study using an online questionnaire sent out to all guests and staff. Guest attack rates (AR) were calculated using resort booking information as the denominator for pre-peak, peak and post peak outbreak stages. Interventions implemented were mapped to the stage of the outbreak to assess their combined effectiveness. To further assess cleaning interventions, we calculated a risk ratio (RR) to compare the attack rate for guests staying in a bedroom previously occupied by a case with guests staying in a bedroom not previously occupied by a case.

RESULTS

In total, 261 guest cases were identified (overall AR 10%) and 15 staff cases (overall AR 7%). During the peak outbreak stage, guest AR was 25%; this reduced to 4% after implementation of interventions including removal of self-serve food, reduced leisure activities and enhanced cleaning practices. Staying in a bedroom previously occupied by a case was associated with becoming unwell before enhanced cleaning measures were in place (RR 1.45, 95%CI 1.01-2.09) but not afterwards (RR 0.88, 95%CI 0.32-2.44). The resort closed for deep cleaning on 19-23 June 2023: no guest or staff cases were reported thereafter.

CONCLUSIONS

This large, prolonged outbreak demonstrated the importance and effectiveness of a suite of measures implemented. Early interventions such as not booking to capacity and closing a bedroom following a case, combined with enhanced cleaning practices should be taken to assist outbreak management.

Keywords: Outbreak, Norovirus, Gastroenteritis, Hotel, Holidays, Interventions
ABSTRACT ID: 895
PRESENTED BY: Rebecca Hams, United Kingdom / rebecca.hams@ukhsa.gov.uk

POSTER TOUR 11

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

National wastewater-based surveillance in Belgium of SARS-CoV-2 variants in summer 2023

J. Raphael [1]
H. Sven [2], M. Hadrien [3], L. Marie [4], M. Jonathan [5], D. Peter [6], V. Laura [7], R. Nancy [8], V. Bavo [9], V. Koenraad [10], H. Veronik [11]
[1, 2, 3, 4, 7, 8, 9, 10, 11] Sciensano, Belgium
[5] E-biom, Belgium
[6] UAntwerpen, Belgium

BACKGROUND

Background : In Belgium, a national wastewater-based surveillance program has been established to monitor the continuous emergence of SARS-COV-2 variants, as well as the evolution of viral concentrations. In this work, two SARS-CoV-2 outbreaks observed in Belgium in 2023 are presented.

METHODS

Over 5 million inhabitants representing 40% of the Belgian population are monitored throughout 42 wastewater treatment plants since September 2020. Quantification of SARS-CoV-2 viral concentration is performed by qPCR. Samples of interest are sequenced by Illumina MiSeq. for detecting ermerging variants. The weekly epidemiological assessments are conducted using three wastewater-based indicators: High Circulation, Fast Increase, and Increasing Trend. These indicators are computed on normalized concentrations per individual treatment plant to allow for a comparison with a reference period as well as between analyses performed by distinct laboratories. Weekly assessments are published by the Belgian Public Health Institute, Sciensano.

RESULTS

In January 2023, a rise of the “Increasing trend” indicator indicated the emergence of a COVID-19 outbreak. On March 13th, the peak of this outbreak was observed in wastewater when the “High Circulation” indicator reached a maximal level. Sequencing analysis showed that the XBB.1.5 variant was responsible for that outbreak. More recently, another outbreak starting on July 26th was highlighted by the wastewater-based surveillance. Since this date, viral loads have increased at a national level. Results of molecular analysis showed that the XBB.1.5+F456L variant of interest, including the EG.5 lineage, was present at 25% in samples dated of August the 16th, 2023.

CONCLUSIONS

In a post pandemic context of low clinical testing, the national wastewater-based surveillance proves to be of added value in providing important information for monitoring the SARS-CoV-2 circulation and genetic mutations in the Belgian population.

Keywords: Wastewater-based epidemiology, SARS-CoV-2, Genomic, Surveillance, Alerting indicator
ABSTRACT ID: 853
PRESENTED BY: Raphael Janssens, Belgium / raphael.janssens@sciensano.be

POSTER TOUR 11
DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

A nosocomial outbreak of invasive Group A Streptococcus infection during a national upsurge in incidence in Ireland

C. Ni Bhuachalla [1]
C. D'arcy Walsh [2], A. Ronayne [3], M. Creedon [4], M. Meehan [5], P. Barrett [6]

[1, 2, 6] Department of Public Health - HSE South West, St. Finbarr's Hospital, Douglas, Cork T12XH60, Ireland
[3, 4] Mercy University Hospital, Grenville Place, Cork T12WE28, Ireland
[5] Irish Meningitis and Sepsis Reference Laboratory, Children's Health Ireland at Temple Street, Temple Street, Dublin D01YC67, Ireland

BACKGROUND
The epidemiology of invasive Group A Streptococcal (iGAS) infection has changed since 2022, and while overall incidence has increased significantly in Ireland, nosocomial outbreaks remain very uncommon. We describe the Public Health (PH) management of a complex nosocomial outbreak of iGAS in a vulnerable population on an oto-rhino-laryngology ward in an acute hospital.

METHODS
Following notification of two epidemiologically linked inpatient cases of iGAS, a multidisciplinary outbreak control team (OCT) was convened. There is no current national guideline for management of nosocomial iGAS outbreaks in Ireland. Standardised case definitions from the national Health Protection Surveillance Centre (HPSC) were used. Initial control measures included; prompt case isolation, risk assessment and cohorting of close-contacts, and an environmental deep-clean including curtain change. Environmental screening and hospital staff screening were conducted. Outbreak isolates were sent to the Irish Meningitis and Sepsis Reference Laboratory (IMSRL) for emm-typing and whole genome sequencing (WGS).

RESULTS
Five linked patient cases of iGAS infection (3 confirmed, 2 probable) were identified across two separate hospital wards, with overlap of staff across both wards. These cases generated 64 patient close-contacts. Communication alerts were issued to all close-contacts, of whom 13 received chemoprophylaxis; 20 close-contacts were followed-up by PH. Of 138 staff members screened, 3/138 (2.2%) returned positive GAS results but only 2/138 were linked by emm-typing (both asymptomatic). Six outbreak isolates tested by IMSRL revealed emm-type 28 sequence type 458, WGS revealed high relatedness.

CONCLUSIONS
Management of this outbreak was challenging due to; an evolving iGAS picture; paucity of current nosocomial guidance; absence of a national outbreak and case management system for outbreak investigation. Prompt multidisciplinary engagement and public health actions, including communication alerts, controlled the outbreak.

Keywords: iGAS outbreak, Healthcare-associated infection, Nosocomial
ABSTRACT ID: 956
PRESENTED BY: Cliodhna Ni Bhuachalla, Ireland / c_ni_bhuachalla@hotmail.com

POSTER TOUR 11

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Late breakers I

MODERATOR
Ettore Amato

Abstract

High prevalence of toxigenic Corynebacterium diphtheriae in wounds of refugees arriving in the Netherlands in June and July 2023

D. Van Meijeren [1]
H. Ruijs [2], R. Mariman [3], P. Tolsma [4], I. Goverse [5], M. de Graaf [6], G. Padilha Matias [7], S. Hahné [8], H. de Melker [9], M. Lanzl [10], M. van den Beld [11], D. Notermans [12]

[1, 2, 3, 7, 8, 9, 10, 11, 12] Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Antonie van Leeuwenhoeklaan 9, 3721 MA Bilthoven, The Netherlands
[4] Municipal health service Brabant Zuid-Oost, Clausplein 10, 5611 XP Eindhoven, The Netherlands
[5] Municipal health service Groningen, Hanzeplein 120, 9713 GW Groningen, The Netherlands
[6] Unilabs-Saltro Diagnostic Centre, Department of Medical Microbiology, Utrecht

BACKGROUND

An increase of diphtheria in refugees caused by Corynebacterium diphtheriae was reported from several EU/EEA countries in 2022-2023. We studied the prevalence of toxigenic C. diphtheriae among refugees arriving in the Netherlands and presenting with wound(s).

METHODS

Refugees aged ≥ 16 years, arriving at one of the two national first-registration centers and consulting a GP for wound(s) between June 5 and July 30, 2023, were asked to participate. A swab was collected from the most suspicious wound and the throat. Primary diagnostics was performed using culturing combined with PCR on first-day culture and on C. diphtheriae isolates. Positive isolates were sequenced. Prevalence of toxin gene-bearing C. diphtheriae was estimated with 95% confidence interval by Fisher's exact test.

RESULTS

Of 61 participants, nearly all were male (95%) and mainly from Syria (68%). Ages ranged between 16-54 years (median 23 years). From 45 participants both a wound and throat swab, from 15 participants only a wound swab and from 1 participant only a throat swab was examined. In 6/60 (10%, 95% CI: 3.8%-20.5%) wounds, toxin gene-bearing C. diphtheriae was detected. Throat carriage was only present in 3 of these cases. Sequence type (ST)377, a frequently found ST among refugees in Europe, was found in cases from Syria (n=4). Cases from Eritrea (n=2) were genetically identical to each other and from a non-defined ST.

CONCLUSIONS

The prevalence of toxin gene-bearing C. diphtheriae in wounds and throats of refugees arriving in the Netherlands might be of concern, with Syrian and Eritrean refugees most at risk. Continuation of the study to obtain more precise prevalence estimates is recommended, to support policy making for early detection and control of diphtheria.

Keywords: Diphtheria, Corynebacterium diphtheriae, Refugees, Wounds, Throat carriage
ABSTRACT ID: 953
PRESENTED BY: Dimphey Van Meijeren, Netherlands / dimphey.van.meijeren@rivm.nl

POSTER TOUR 12

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

One Health, global health and climate change

MODERATOR
Anna Machowska

Abstract

Effect of seawater temperature on incidence of severe Vibrio spp infections in Norway, 2014-2018

B. Valcarcel Salamanca [1]
S. Hyllestad [2], A. King [3], A. Deininger [4], E. Macdonald [5], M. Naseer [6], E. Amato [7]

[1] Norwegian Institute of Public Health (NIPH), EPIET
[2, 5, 6, 7] Norwegian Institute of Public Health (NIPH)
[3] Norwegian Institute for Water Research (NIVA)
[4] Norwegian Institute for Water Research (NIVA) | Norwegian Geotechnical Institute (NGI)

BACKGROUND
Vibrio bacteria are ubiquitous in brackish and marine water. In the last decade, the incidence of vibriosis increased worldwide, particularly in Northern Europe. This increase has been linked to climate change. Clinical manifestations range from mild gastroenteritis to severe illness with potentially fatal outcome. Predicting changes in the occurrence of vibriosis can facilitate early public health responses. We aimed to explore environmental factors as potential predictors for vibriosis to propose recommendations for preventive measures in Norway.

METHODS
We conducted a retrospective observational study analysing geographical distribution, seasonality, and hospitalization of vibriosis cases. We included all domestic vibriosis cases reported by the Norwegian laboratory-based surveillance for the period 2014-2018. Data on seawater temperature and salinity were collected in four geographical locations through sensors installed aboard ferries travelling along the Norwegian coastline. Time series Poisson regression analyses were performed using monthly data on mean seawater temperature and salinity, and monthly reported vibriosis cases. Logistic regression analyses were used to explore factors associated with hospitalization.

RESULTS
We observed an increase both in total number and hospitalized vibriosis cases during the study period. The occurrence of vibriosis showed a distinct geographical pattern, with larger number of cases reported in the Norwegian Eastern region (57%). Mean seawater temperature, at a lag of one month, was positively associated with the number of vibriosis cases in the Eastern region. Logistic regression analysis showed that seawater temperature above 20°C was associated with hospitalization (OR:4.5; 95%CI:1.06-19; p=0.04).

CONCLUSIONS
Warmer seawater temperature may play an important role in the occurrence of vibriosis in Norway and can potentially be used as a predictor for early warning purposes. We recommend raising awareness among clinicians and risk population considering environmental conditions.

Keywords: Surveillance, Vibriosis, Time-series, Heatwaves, Early warning signals, Norway
ABSTRACT ID: 496
PRESENTED BY: Beatriz Valcarcel, Norway / beatriz.valcarcelsalamanca@fhi.no

POSTER TOUR 12

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

One Health, global health and climate change

MODERATOR
Anna Machowska

Abstract

SARS-CoV-2 in lions, gorilla's and zookeepers in the Rotterdam zoo: a one health investigation

A. Tjon-A-Tsien [1]
F. Dusseldorp [2], M. Buskermolen [3], H. Niphuis [4], M. Dirven [5], J. Whelan [6], B. Oude Munnik [7], M. Koopmans [8],
E. Fanoy [9], R. Sikkema [10], L. Bruins-van Sonsbeek [11]

[1, 2, 3, 5, 6, 9] infectious disease department, Public Health Service Rotterdam Rijnmond, Rotterdam
[4] Biomedical Primate Research Centre, Rijswijk
[7, 8, 10] Department of Viroscience, Erasmus MC, WHO Collaborating Centre for Arbovirus and Viral Hemrrhagic Fever reference and Research, Rotterdam
[11] Rotterdam Zoo

BACKGROUND

SARS-CoV-2 is a coronavirus of zoonotic origin and infections in animals can occur. In November 2021, seven Western lowland gorillas and four Asiatic lions at Rotterdam Zoo were diagnosed with COVID-19 at Rotterdam zoo. A collaborative outbreak investigation was undertaken to determine the source and extent of the outbreak, to identify transmission routes and help prevent future outbreaks.

METHODS

Interviews were conducted with staff to identify human and animal contacts and cases, compliance with personal protective equipment (PPE) and potential transmission routes. Sanitation and ventilation of animal enclosures were assessed. Contacts of sick animals were direct (›15 minutes face-to-face at ‹1.5 metre distance) and indirect (sharing the animal enclosure, in food preparation, or having contact with faeces). Cases were confirmed using SARS-CoV-2-specific real-time polymerase chain reaction (RT-PCR) tests and positive samples were subjected to whole genome sequencing.

RESULTS

In total 19 species were RT-PCR tested. All gorillas of the gorilla group (3 out of 7) and lions (2 out of 4) which could be tested were RT-PCR positive between 12 November and 10 December, 2021. No other animal species were SARS-CoV-2 RNA positive. Of 185 staff, 40 direct and indirect human contacts were identified, of whom two tested RT-PCR positive, 10 days after the first COVID-19 symptoms in animals. The zookeeper's viral genome sequence clustered with the those of gorillas (100% genome coverage) and lions (50% coverage). PPE compliance was suboptimal. No significant environmental risks were identified.

CONCLUSIONS

Findings support transmission of SARS-CoV-2 between humans and animals, although the source and directionality could not be established. Sick animals should promptly be tested and isolated/quarantined. Zookeepers were the most likely source and should have periodic PPE training.

Keywords: Zoonosis, One health, SARS-CoV-2, Zoo, Outbreak investigation, Lions, Gorillas
ABSTRACT ID: 785
PRESENTED BY: Aimée Tjon-A-Tsien, Netherlands / aml.tjonatsien@rotterdam.nl

POSTER TOUR 12

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

One Health, global health and climate change

MODERATOR
Anna Machowska

Abstract

Climate change and public health – stepping up to the challenge of the Asian tiger mosquito in Baden-Wuerttemberg, Germany

M. Meincke [1]
T. Orgassa [2], C. Wagner-Wiening [3]

[1] Ministry of Social Affairs, Health and Integration Baden-Wuerttemberg, State Health Office, Stuttgart, Germany
[2] Local health office Rems-Murr-District, Waiblingen, Germany
[3] Ministry of Social Affairs, Health and Integration Baden-Wuerttemberg, State Health Office, Stuttgart, Germany

BACKGROUND

Aedes albopictus – the Asian tiger mosquito – was first identified in the state of Baden-Wuerttemberg in 2013. In 2022, 21 of 44 districts were affected. Ae. albopictus' establishment constitutes a public health risk, as autochthonous sporadic chikungunya, Zika and dengue outbreaks might occur due to climate change. Currently, no policy framework or public health structures for integrated vector management (IVM) exist in Germany. By assessing the response mechanisms at local and state level, we provide recommendations for policy makers to adequately respond to this new public health threat.

METHODS

We conducted theme-guided interviews with 27 purposeful-sampled vector control experts and key actors from municipalities/districts with and without Ae. albopictus detection from July 2019 until September 2020. Data, investigator and methodological triangulation was applied. A selection of themes and topics guided data collection and analysis, flanked by an additional inductive analysis.

RESULTS

In absence of IVM policies, roles and responsibilities, implementing Ae. albopictus control measures in affected municipalities highly depends on individual risk perceptions of local decision makers. Further barriers are a lack of relevant knowledge at local level, limited access to vector control specialists and high costs of control measures. Enabling factors were early public involvement.

CONCLUSIONS

Political leadership and public health regulatory support are needed to ensure multi-level intersectoral control of Ae. albopictus to reduce the climate-change-induced risk of autochthonous tropical arboviral infections. Based on our study, we recommend joining entomological and infectious disease surveillance data at local and state health office level, strengthening entomological and vector control skills of pest control operators, ensuring affordable access to vector control in affected municipalities, and conducting widespread public information campaigns to strengthen passive citizen-based Ae. albopictus monitoring.

Keywords: Vector-borne diseases, Climate Change, Mosquito Vectors, Environment and Public Health
ABSTRACT ID: 690
PRESENTED BY: Maylin Meincke, Germany / maylin.meincke@sm.bwl.de

POSTER TOUR 12

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

One Health, global health and climate change

MODERATOR
Anna Machowska

Abstract

Mosquito-borne virus preparedness and response: a stakeholder network analysis for the Netherlands

P. de Best [1]
H. Broekhuizen [2], R. Sikkema 3, M. Koopmans [4], A. Timen [5]

[1] Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[2] Department of Social Sciences, Health and Society, Wageningen University & Research, Wageningen, the Netherlands
[3] Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
Centre for Avian Migration, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, the Netherlands.
[4] Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
[5] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
Department of Primary and Community Care, Radboud University Medical Center, Nijmegen, the Netherlands
Athena Institute, VU University Amsterdam, Amsterdam, the Netherlands

BACKGROUND

Emerging mosquito-borne virus (MBV) preparedness and response require knowledge integration and collaboration across the human, animal, vector, and environmental health domains, aligning with the One Health concept. In practice, however, not all domains are involved. Therefore, this study aims to map knowledge sharing and collaborations between stakeholders and their respective domains involved (in)directly in preparedness and response for MBVs in the Netherlands.

METHODS

This study used combined stakeholder and social network analyses. Stakeholders were identified through document analysis and snowballing. Semi-structured interviews were conducted with representatives from 26 stakeholder organisations between June 2021 and May 2022. Five additional interviews were conducted between January 2023 and April 2023. Stakeholders' collaborations, dependencies, and their roles in MBV preparedness and response were discussed. Interview transripts were coded to identify collaborations and knowledge flows between stakeholder organisations. Identified connections were mapped using Cytoscape.

RESULTS

58 stakeholders were identified and grouped into five domains (animal, vector, human, environment, and other) and four policy levels (international, national, regional, and local). Network mapping showed stakeholder organisations in the human, animal, and vector domain are connected but connections with the environmental domain. Bidirectional collaborations and knowledge flows between national stakeholders were identified. Knowledge dissemination from national to regional and local stakeholders was limited and mostly unidirectional.

CONCLUSIONS

Although the benefits of a One Health approach for MBV preparedness and response are well-recognized, this study shows the connection with the environmental domain is limited. Additionally, knowledge dissemination from national to regional and local levels, responsible for policy implementation, can be enhanced. Dutch MBV preparedness and response could be strengthened by increasing collaborations with the environmental domain and knowledge dissemination to local stakeholders.

Keywords: Vector Borne Diseases, One health, Intersectoral Collaboration, Communicable Disease Control, Qualitative research
ABSTRACT ID: 598
PRESENTED BY: Pauline Amber de Best, Netherlands / p.debest@erasmusmc.nl

POSTER TOUR 13
DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

Whole genome sequencing versus PCR ribotyping for investigation of Clostridioides difficile – infection, prevention and control impacts

V. Daniel [1]
M. Cronin [2], C. Mahoney [3], Y. Hyde [4], G. Forbes [5], R. Dhillon [6], T. Morris [7], M. Perry [8]

[1] Microbiology, Public Health Wales, Cardiff, UK
[2] Communicable Disease Surveillance Centre, Public Health Wales, Cardiff, UK
[3, 4] Infection, Prevention & Control, Cardiff and Vale University Health Board, Cardiff, UK
[5, 6] Microbiology, Public Health Wales, Cardiff, UK
[7, 8] UK Anaerobe Reference Unit, Cardiff, UK

BACKGROUND

The UK Anaerobe Reference Unit (UKARU) provides a prospective Whole Genome Sequencing (WGS) typing service for all polymerase chain reaction (PCR) and glutamate dehydrogenase (GDH) positive Clostridioides difficile (C. difficile) cases within Wales. In early 2022, we received notification of two patients within the same ward with indistinguishable isolates, strongly indicating transmission. Despite re-enforcement of infection, prevention and control (IPC) measures, further symptomatic patients instigated a formal investigation in mid-2022.

METHODS

UKARU alert IPC teams to patients with isolates that cluster at two single nucleotide polymorphisms (SNPs) or less. An outbreak control team was convened and, in addition to other control measures, epidemiological analysis of each patient was undertaken. Post outbreak, repeat analysis was performed using PCR ribotyping (PCR RT) as a comparator to the WGS results.

RESULTS

We investigated 12 C. difficile positive patients over an 8-month period. WGS identified four indistinguishable cases, including one patient that became symptomatic several weeks post exposure following transfer to a different ward. Despite epidemiological links, we excluded the remaining eight patients through WGS typing results (>2 SNPs). Retrospective analysis using PCR RT identified types 020 (n=5) and 014 (n=3). The reduced discriminatory power of PCR RT, combined with complex patient movements, would have doubled confirmed case numbers (including a second cluster) and lengthened the course of the investigation.

CONCLUSIONS

WGS is now the standard typing method for investigating C. difficile epidemiology across Wales. Prospective WGS provides prompt identification of potentially linked cases and, equally as important, exclusion of cases investigated as part of a suspected cluster. Efficient exclusion of cases provided reassurance that IPC measures were effective, permitting the outbreak team to focus on other interventions.

Keywords: Clostridioides difficile, Transmission, Infection Control, Outbreak
ABSTRACT ID: 650
PRESENTED BY: Victoria Daniel, United Kingdom / victoria.daniel@wales.nhs.uk

POSTER TOUR 13

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

Increase of Group A Streptococcus (GAS) infections in Austria in 2023 - a genome-based characterization of invasive and non-invasive Streptococcus pyogenes isolates

M. Cardoso [1]
A. Cabal Rosel [2], A. Stoeger [3], L. Richter [4], P. Hasenberger [5], S. Stadlbauer [6], H. Kerschner [7], A. Indra [8], M. Hell [9], W. Ruppitsch [10]

[1] Institute of Medical Microbiology and Hygiene, Austrian Agency for Health and Food Safety, Vienna, Austria
ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5, 6, 8, 10] Institute of Medical Microbiology and Hygiene, Austrian Agency for Health and Food Safety, Vienna, Austria
[7] National Reference Center for Antimicrobial Resistance, Institute for Hygiene, Microbiology and Tropical Medicine, Ordensklinikum Linz Elisabethinen, Linz, Austria
[9] Medizinisch-chemisches Labor Medilab, Clinical Microbiology and Hygiene Department, Teaching Lab of the Paracelsus Medical University, Salzburg, Austria

BACKGROUND

An increased number of Group A Streptococcus mild (GAS) and invasive (iGAS) infections has been observed in Austrian hospitals since beginning of 2023. This laboratory-based surveillance study characterizes Streptococcus pyogenes isolates in Austria from January to April 2023.

METHODS

Fifty-one S. pyogenes isolates from clinics' outpatients and eight hospitals (12 iGAS; 39 GAS), were characterized by whole genome sequencing. Genetic relatedness was assessed with multilocus sequence typing (MLST) and core genome (cg)MLST. Comparison with S. pyogenes complete genomes available at Genbank (n=58) and one isolate's genome from Statens Serum Institut was performed. We searched for the presence of mobile genetic elements, virulence and antimicrobial resistance genes. Diagnosis per each isolate was communicated by sender laboratories/hospitals, according to invasiveness and severity of infection (iGAS) or localization in normal nonsterile body sites (GAS).

RESULTS

Patients' median age was 12 years (1 –89) and one 11 year-old died. Otitis represented 33% of GAS infections, and sepsis 33% of iGAS. Eight sequence types (STs) were identified. The most prevalent clones were for iGAS: ST28/emm1-58% and GAS: ST36/emm12-38%. Seven cgMLST clusters were observed, the largest one comprised 6 iGAS (ST28/emm1) and 8 GAS (7 ST28/emm1, 1 ST28/emm12), with maximum two allelic differences. Twenty-six virulence profiles were observed. Two GAS isolates presented a new ST, another two carried hmrM and arsR genes and another one carried transposon Tn6009, with ermA and tet(M) genes. Erythromycin, clindamycin and tetracycline resistances were phenotypically confirmed.

CONCLUSIONS

In Austria, similarly to other countries, ST28/emm1 caused most invasive disease. However, we couldn't highlight iGAS isolates characteristics vs those of GAS. The increasing number of iGAS in Europe after the pandemic and the development of antimicrobial resistances calls for further genomic surveillance.

Keywords: Invasiveness, Virulence profile, M1 GAS, Antimicrobial resistance, Surveillance
ABSTRACT ID: 783
PRESENTED BY: Maria João Cardoso, Austria / maria.cardoso@ages.at

POSTER TOUR 13

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

A multi-serotype Salmonella public house outbreak (2020-2023) identified through Whole Genome Sequencing (WGS) in the Midlands, UK

D. Blackman [1]
M. Harrison [2], H. Bagnall [3], P. Hallam [4], R. Johnston [5], K. Choudhury [6]
[1, 2, 3] Field Service Midlands, UK Health Security Agency
[4, 6] East Midlands Health Protection Team, UK Health Security Agency
[5] Food, Water and Environmental Microbiology Laboratories, UK Health Security Agency

BACKGROUND
In February 2023, a five-single nucleotide polymorphism (5 SNP) WGS cluster of six Salmonella Panama cases was identified in England. Routine Salmonella case questionnaires identified a public house with primary or secondary links to four cases. We investigated to determine the source of the outbreak and implement control measures to prevent further cases.

METHODS
Cases were defined as Salmonella Panama infection within a 5 SNP cluster between September 2020 to January 2023. Cases were described by time, place and person. The venue was visited multiple times to carry out environmental investigations and environmental sampling.

RESULTS
Four of the Salmonella Panama cases were male, and age range was 0 to 58 years. In December 2021, environmental sampling in the kitchen identified Salmonella Panama within the same 5 SNP cluster as the cases, in the drain to one of four ovens. Control measures were implemented and resampling in January 2022 was satisfactory. Three subsequent Salmonella Panama cases were identified, two of which had known exposure to the pub. Environmental sampling in February 2023 found 7/16 (43%) of isolates from the kitchen, including the ovens, tested positive for Salmonella Panama within the 5 SNP cluster, or Salmonella Derby. Two cases of Salmonella Derby identified in 2019 and 2022 were within 5 SNPs of the environmental samples. Oven replacement was recommended and carried out in April 2023.

CONCLUSIONS
Combining epidemiological and microbiological information identified an oven as a potential source of a prolonged multi-serotype Salmonella outbreak. Salmonella had persisted in the environment despite control measures being taken. Oven replacement is an expensive control measure and while it appears to have been successful thus far, these Salmonella clusters will continue to be monitored.

Keywords: Salmonella Panama, Whole Genome Sequencing, Outbreak investigation, Public house
ABSTRACT ID: 618
PRESENTED BY: Daniel Blackman, United Kingdom / dan.blackman@ukhsa.gov.uk

POSTER TOUR 13
DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

Multi-country outbreak of Salmonella Senftenberg linked to cherry tomatoes, 2022 to 2023

L. Giese [1]
M. Pietsch [2], S. Simon [3], J. Walter [4], N. Jourdan-da Silva [5], M. Pardos de la Gandara [6], C. Kornschober [7], S. Maritschnik [8], E. Mertens [9], K. Usipbekova [10], A. Meinen [11], (GROUP) the Outbreak Team

[1, 2, 3, 4, 11] Robert Koch Institute (RKI)
[5] Santé publique France
[6] Institut Pasteur
[7, 8] Österreichische Agentur für Gesundheit und Ernährungssicherheit (AGES)
[9, 10] Niedersächsisches Landesgesundheitsamt (NLGA)

BACKGROUND
In January 2023, an unusually high number of isolates of the rare serovar Salmonella (S.) Senftenberg was reported by the national reference laboratory for Salmonella in Germany and subsequently by other countries. To identify the vehicle of infection, Public Health institutes initiated outbreak investigations.

METHODS
Cases were defined as persons with laboratory-confirmed S. Senftenberg infection (possible) or with NGS-analysed isolates belonging to the outbreak cluster (confirmed). Germany, Austria and France conducted explorative interviews on food consumption. An online survey in healthy controls is ongoing in Germany.

RESULTS
Between August 2022 and April 2023, 71 confirmed and 16 possible cases have been reported from 12 European countries and the US, with most confirmed cases in Germany (20), France (16) and Finland (11). Cases occurred among all age groups primarily affecting women. A 32-year-old German man with underlying comorbidities died due to the salmonellosis. Explorative interviews in Germany, Austria and France revealed that 15 out of 16 cases had eaten cherry tomatoes prior to infection. The majority of German and Austrian cases purchased tomatoes of certain packaging types from two supermarket chains. No other common food item was identified. In addition, cherry tomatoes were served in two hospitals and two nursing homes where cases occurred marking possible starting points for trace-back investigations. In April 2023, France reported a genetic match between the human outbreak strain and a food isolate detected in mixed salad containing cherry tomatoes from August 2022.

CONCLUSIONS
Cherry tomatoes are the likely vehicle of infection. Even without a food match, results from explorative interviews should be considered to guide trace-back investigations to identify the origin of contamination in order to implement effective public health interventions.

Keywords: Disease outbreaks, Salmonellosis, Foodborne diseases, Tomatoes, DNA sequencing
ABSTRACT ID: 335
PRESENTED BY: Laura Giese, Germany / giesel@rki.de

POSTER TOUR 13

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

Consumer purchase data facilitated identification of fish patties as the source of an invasive Listeria monocytogenes outbreak, Denmark 2022

P. Kold Munch [1]

L. Espenhain [2] , M. Søby [3] , A. Ribert Larsen [4] , L. Müller [5] , S. Schjørring [6]

[1, 2, 5, 6] Statens Serum Institut

[3, 4] The Danish Veterinary and Food Administration (DVFA)

BACKGROUND

In Denmark, invasive infections with Listeria monocytogenes are under surveillance. Early October 2022, the national reference laboratory reported a genetic cluster of Listeria monocytogenes sequence type 7. We describe the outbreak investigation carried out by national health and food authorities and demonstrate how comparing consumer purchase data facilitated rapid identification of the source.

METHODS

We contacted cases or relatives for hypothesis-generating interviews, obtained consumer purchase data from the incubation period, performed traceback-investigations, and visited relevant production sites.

RESULTS

In total, 11 cases were identified as being part of the outbreak. Cases were living all over Denmark. No other countries reported cases belonging to this cluster. Three patients died within 30 days of testing positive. Interviews or consumer purchase data from seven patients indicated that all had eaten or bought fish patties. Product traceback-investigations led to suspicion of one fish patty manufacturer. At control visits, samples were taken from the production environment and the fish patties, in which Listeria monocytogenes was found. Whole genome sequencing showed that Listeria monocytogenes sequences from the control visits were identical to those identified in the patients. In early November, the company recalled all fish patties produced and the outbreak stopped.

CONCLUSIONS

Epidemiological investigations quickly pointed towards fish patties or a fish product. Consumer purchase data allowed for valuable targeted traceback and control visits, where samples could be taken for comparison. The best-before date of the recalled fish patties was mid-December 2022 (refrigerated) and early May 2023 (frozen), why the intervention is likely to have prevented further cases. Prospectively, collecting consumer purchase data could complement regular tools for listeria outbreak investigation.

Keywords: Listeria monocytogenes, WGS, Infectious disease outbreaks, Epidemiology
ABSTRACT ID: 481
PRESENTED BY: Pernille Kold Munch, Denmark/ pkmu@ssi.dk

POSTER TOUR 13

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Genome sequencing in surveillance and outbreak investigations

MODERATOR
Andreas Hoefer

Abstract

Molecular epidemiology of TB in Ireland over 10 years reveals a heterogeneous population and over-estimation of transmission events using traditional genotyping methods

E. Roycroft [1]
S. Jackson [2], P. Flanagan [3], S. Mok [4], P. Downes [5], B. Boyle [6], J. Wagener [7], T. Rogers [8], M. Fitzgibbon [9]

[1] Dept. of Clinical Microbiology, Trinity College, Dublin | Irish Mycobacteria Reference Laboratory, Dublin, Ireland
[2] Health Protection Surveillance Centre, Dublin, Ireland
[3, 4, 6, 7, 9] Dept. of Clinical Microbiology, Trinity College, Dublin | Irish Mycobacteria Reference Laboratory, Dublin, Ireland
[5] Health Service Executive (HSE), Department of Public Health, HSE-East, Dublin
[8] Dept. of Clinical Microbiology, Trinity College, Dublin

BACKGROUND
Although Ireland is a low tuberculosis (TB) burden country with declining incidence, interruption of TB transmission is still needed to meet WHO End TB Strategy goals. Mycobacterial interspersed repetitive unit – variable number tandem repeats (MIRU-VNTR) genotyping has been replaced by whole genome sequencing (WGS) as the gold standard method for Mycobacterium tuberculosis Complex (MTBC). We performed a comprehensive analysis of MTBC over 10 years using MIRU-VNTR data and compared results of MIRU-VNTR with WGS to investigate if MIRU-VNTR genotyping over-estimated TB transmission.

METHODS
We used MIRU-VNTR data to characterise the molecular epidemiology of MTBC isolates collected nationally (Jan 2010 - Dec 2019) and received in the Irish Mycobacteria Reference Laboratory (IMRL). We selected 23 clusters with identical MIRU-VNTR genotype, representing a range of lineages and cluster sizes, for investigation with WGS using an Illumina platform, core-genome multi-locus sequence typing (cgMLST) and whole-genome single-nucleotide-polymorphism (wgSNP) analysis (MTBseq).

RESULTS
Six global lineages were found, including West-African I and II (n=2275). Euro-American lineage 4 predominated (66%). 43% of isolates clustered using MIRU-VNTR genotyping (n=972 isolates, n=231 clusters). Median cluster size was 2 (range 2-52). The largest clusters mainly involved Irish-born cases.MIRU-VNTR and WGS matched for 52.2% of 23 clusters investigated. WGS genotyping gave a more highly-resolved view of relatedness in 47.8% of clusters (n=11). 13% were completely refuted, 17.4% had some isolates ruled out, but others confirmed, within the cluster, and 17.4% had more than one sub-cluster found with WGS.

CONCLUSIONS
Ireland has a heterogeneous MTBC population, dominated by Lineage 4. MIRU-VNTR genotyping has over-estimated TB transmission in Ireland, confirmed by WGS genotyping now in place. Public health outbreak investigation can be better targeted with WGS genotyping.

Keywords: Epidemiology, TB, WGS, Clusters, cgMLST, MTBseq, MIRU-VNTR
ABSTRACT ID: 129
PRESENTED BY: Emma Roycroft, Ireland / eroycroft@stjames.ie

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Vaccine effectiveness using the 23-valent pneumococcal polysaccharide vaccine against invasive pneumococcal disease in those ≥65 years old: Estimating effectiveness over time and stratified by age

K. Finderup Nielsen [1]
L. Birk Nielsen [2], F. Kristensen Lomholt [3], T. Dalby [4], P. Valentiner-Branth [5]
[1, 2, 3, 4, 5] Statens Serum Institut (Denmark)

BACKGROUND

To protect individuals ≥ 65 years old, a vaccination programme against invasive pneumococcal disease (IPD) was put in place in Denmark, using the pneumococcal polysaccharide vaccine PPV23.This study aimed to estimate vaccine effectiveness (VE) against all-type IPD, PPV23-vaccine type IPD (VT-IPD) and VT-IPD excluding serotype 3 (VT-IPD-3) stratified by age and over time.

METHODS

Using nationwide Danish registries, we identified all residents in Denmark who were older than or turned 65 years old between 22 April 2020 and 15 January 2023, with follow up until 15 March 2023, date of IPD (event), emigration or death – whichever came first.Exposure to PPV23 was considered a time varying variable. VE estimates were calculated by Cox regression model to estimate hazard ratios (HR) with calendar time as the underlying timescale, and adjusted for age and sex, and as VE = (1-HR)*100% with 95% confidence intervals (95% CI).VE was calculated by time since vaccination (0-1, 1-2, ≥ 2 years) or stratified by age groups 65-74 and 75+ years.

RESULTS

VE against all-serotype IPD was 38% (CI: 19%-53%) 0-1 years after vaccination, VE against VT-IPD was 51% 0-1 years after vaccination, while VT-IPD-3 was 65%. All estimates declined moderately over time.VE in 65-74 year olds were 24% (CI: 0%-42%) against all-serotype IPD, 37% (CI: 12%-55%) against VT-IPD and 61% (CI: 39%-74%) against VT-IPD-3, while the estimates for 75+ year olds were 37% (CI: 17%-51%), 41% (CI: 18%-57%) and 53% (CI: 31%-68%).

CONCLUSIONS

Our study shows protection against VT-IPD, which stays moderate ›2 years after vaccination, and that the protection remains despite higher age. Our results support the use of PPV23 in a vaccination programme to protect the elderly from severe disease.

Keywords: Pneumococcal Polysaccharide Vaccine, Vaccine effectiveness, Invasive pneumococcal disease, Epidemiology, Public health programmes
ABSTRACT ID: 491
PRESENTED BY: Katrine Finderup Nielsen, Denmark / kafn@ssi.dk

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Knowledge, attitudes and practices (KAP) towards pneumococcal infection and vaccination among primary health care physicians, Ukraine, 2021

O. Artemchuk [1]
I. Evlampidou [2], R. Rodyna [3]

[1] Public Health Centre of Ministry of Health of Ukraine, Kyiv, Ukraine
Mediterranean and Black Sea Field Epidemiology Training programme (MediPIET), Madrid, Spain
[2] Mediterranean and Black Sea Field Epidemiology Training programme (MediPIET), Madrid, Spain
[3] Public Health Centre of Ministry of Health of Ukraine, Kyiv, Ukraine

BACKGROUND
In 2022, the Ukraine Ministry of Health planned to introduce pneumococcal vaccine (PCV) targeting children <5 years old for the first time in Ukraine. We assessed doctors' knowledge, attitudes and practices towards pneumococcal disease (PD) and PCV to address gaps and support PCV implementation.

METHODS
In March 2021, primary care doctors, selected using simple random sampling, completed a self-administered online questionnaire. We considered PD knowledge as high if ≥80% were correct answers, PCV knowledge as moderate/high if ≥50% were correct answers and attitudes (high importance, effectiveness and safety of PCV) and practices (recommendation of PCV to children and/or the elderly) as positive if mean scores were 3.5-5.0 on 5-point Likert-scale. We calculated prevalence ratios (PRs) using Poisson regression.

RESULTS
Overall, 46% (286/628) responded. Females represented 85% (243/285); median age was 47 (interquartile range: 33-59) years. Those aged <47 years (PR=1.93, 95%CI:1.12-3.34) and those aware of childhood vaccination recommendations (PR=1.78, 95%CI:1.04-3.08) were more likely to have high PD knowledge. Those with positive attitudes towards PCV (PR=2.08, 95%CI:1.20-3.59) were more likely to have moderate/high PCV knowledge. Those with positive attitudes (PR=3.40, 95%CI:1.23-9.39), female doctors (PR=2.11, 95%CI: 1.09-4.09), and those considering vaccine unavailability as important barrier (PR=1.66, 95%CI: 1.02-2.72) were more likely to recommend PCV.

CONCLUSIONS
Younger age of doctors and awareness of vaccination recommendations was associated with PD knowledge. Female doctors, those who perceived limited vaccine supply as barrier to vaccination and those with positive attitudes were more likely to recommend PCV. For successful PCV implementation, we recommended proper planning and educational activities among primary care doctors, especially targeting older males, to improve knowledge, and address concerns while ensuring uninterrupted vaccine supply.

Keywords: Health knowledge, Attitudes, Practice, Pneumococcal vaccines, Physicians, Ukraine
ABSTRACT ID: 161
PRESENTED BY: Oksana Artemchuk, Ukraine / ko.artemchuk@gmail.com

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Effectiveness of the 23-valent pneumococcal polysaccharide vaccine against invasive pneumococcal disease and serotype specific disease aimed at those ≥65 years of age

L. Birk Nielsen [1]
K. Finderup Nielsen [2], F. Kristensen Lomholt [3], T. Dalby [4], P. Valentiner-Brandt [5]
[1, 2, 3, 4, 5] Statens Serum Institut (Denmark)

BACKGROUND
Invasive Streptococcus pneumoniae infections can cause severe and life-threatening conditions like meningitis and bacteraemia. To protect individuals ≥ 65 years old, a vaccination programme against invasive pneumococcal disease (IPD) was put in place in Denmark, using the pneumococcal polysaccharide vaccine PPV23.This study aimed to estimate vaccine effectiveness (VE) against all-type IPD, PPV23-vaccine type IPD (VT-IPD) as well as against the most common serotypes causing IPD in Denmark (serotype 3, 8 and 22F).

METHODS
Using nationwide Danish registries and linking them via a unique personal identifier, we identified all residents in Denmark who were older than or turned 65 years old between 22 April 2020 and 15 January 2023. Individuals were followed until 15 March 2023, date of IPD (event), emigration or death – whichever came first. Exposure to PPV23 was considered a time varying variable. VE estimates were calculated using a Cox regression model to estimate hazard ratios (HR) with calendar time as the underlying timescale, and adjusted for age and sex. VE estimates were given as (1-HR)*100% with 95% confidence intervals (95% CI).

RESULTS
The estimated VE against all-serotype IPD was 33% (95% CI: 19% - 44%). VE against VT-IPD was 41% (95% CI: 25% - 53%). VE against VT-IPD excluding serotype 3 was 58% (95% CI: 44% - 68%). VE estimates against serotypes 8 and 22F was 60% (95% CI: 33% - 76%) and 88% (CI: 75% - 94%) respectively.

CONCLUSIONS
Our study shows that vaccinating those ≥ 65 years old with PPV23 gives moderate protection against all-type IPD and vaccine-type IPD, while the protection against serotypes 8 and 22F was high. This supports the effect of a vaccination programme in protecting the elderly against severe disease.

Keywords: Pneumococcal Polysaccharide Vaccine, Vaccine effectiveness, Invasive pneumococcal disease, Epidemiology, Public health programmes
ABSTRACT ID: 482
PRESENTED BY: Lise Birk Nielsen, Denmark / libn@ssi.dk

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Maternal and infant immunity against pertussis in Norway

M. Greve-Isdahl [1]
T. Møller [2], M. Baranowska-Hustad [3], T. Bekkevold [4], C. Julin [5], A. Berg [6], P. Aavitsland [7], P. Knudsen [8], A. Aase [9], K. Størdal [10]

[1, 2, 3, 4, 5, 6, 9] Norwegian Institute of Public Health (NIPH)
[7] Norwegian Institute of Public Health | Pandemic Centre, University of Bergen
[8] Division of Pediatric and Adolescent Medicine, Oslo University Hospital, Oslo
[10] Division of Pediatric and Adolescent Medicine, Oslo University Hospital, Oslo
Department of Pediatric Research, Faculty of Medicine, University of Oslo, Oslo

BACKGROUND
Maternal vaccination against pertussis can protect the infant against severe disease until postnatal vaccination is initiated, due to prenatal transfer of maternally derived antibodies. In Norway, infants are immunized with an acellular pertussis vaccine (aP) at 3, 5, and 12 months of age, while maternal vaccination against pertussis has not yet been introduced. The aim of the current study is to investigate vulnerability for pertussis among Norwegian infants.

METHODS
We collected blood samples from 398 mother-infant pairs: from the mothers in late pregnancy, from cord blood at delivery, and from the infants before their first aP vaccine and after their booster dose at 12 months. We quantified IgG antibodies in serum against pertussis toxin (PT), filamentous haemagglutinin (FHA), and pertactin (PRN) in the first 62 pairs.

RESULTS
The geometric mean IgG levels for anti-PT, anti-FHA, and anti-PRN in mothers were 5.3 IU/ml, 33.1 IU/ml and 61.6 IU/ml. Notably, 33.8% (21/62) had anti-PT levels below the estimated level of protection at 5 IU/ml. The antibody levels in cord blood against PT were 1.6-fold higher than maternal levels, while those against FHA and PRN were 1.5-fold higher. Still, in 29.0% (18/62) the anti-PT levels were below 5 IU/ml in cord blood, and in 67.7% (43/62) of samples at 3 months of age. After the booster dose, all infants achieved levels above 5 IU/ml, with a geometric mean IgG of 64.4 IU/ml for anti-PT.

CONCLUSIONS
A high proportion of pregnant women and their infants younger than 3 months in this study had low levels of anti-PT and thus considered highly susceptible to pertussis infection. Preliminary results from this ongoing study support introduction of maternal vaccination against pertussis in Norway.

Keywords: Pertussis Vaccine, Vaccination, Pregnancy, Infant, Immunity Maternally-Acquired, Whooping cough
ABSTRACT ID: 31
PRESENTED BY: Margrethe Greve-Isdahl, Norway / margrethe.greve-isdahl@fhi.no

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Measles and Rubella immune status from serological cross-sectional surveys in 1995-1996, 2006-2007 and 2016-2017 in The Netherlands

T. Woudenberg [1]
T. Woudenberg [2], G. Smits [3], H. Ten Hulscher [4], F. van der Klis [5], H. de Melker [6], R. van Binnendijk [7]
[1, 2, 3, 4, 5, 6, 7] Centre for Infectious Disease Control, National Institute for Public Health and the Environment

BACKGROUND
Routine vaccination with combined measles-mumps-rubella vaccine (MMR) was introduced in The Netherlands in 1987, replacing single girls-only vaccination for rubella since 1974 and measles since 1976. To evaluate the long-term effectiveness of rubella and measles vaccination and progress towards elimination of these diseases, we measured the population-wide immunity.

METHODS
As part of a national sero-survey in 2016-7, participants (n=7604, age: 0-88 years) filled out a questionnaire and provided a serum sample. Besides a national sample (n=5146), an additional sample was taken in low-vaccination coverage areas (n=1355). Immunity to measles and rubella was assessed using a multiplex-based immunoassay detecting specific serum IgG antibody levels, complemented with the levels of measles neutralizing antibodies for a subset of the samples (n=385).

RESULTS
Sero-prevalence weighted by age and sex was 95.5% (95%CI:88.2-98.0) for measles. For rubella, sero-positivity (>10IU/ml) amounted to 97.5% among 16-40 years old women. In low vaccination coverage areas, sero-positivity for measles (>0.12IU/ml) was low among unvaccinated children born before the last large outbreak of 2013 (7.7%, 95%CI:1.6%-20.9%), and low for rubella among unvaccinated individuals born since the last rubella outbreak in 2004 (5%, 95%CI:1.4-12.3%). Among individuals who adhered to the vaccination programme, eldest vaccinated cohorts had lowest IgG antibody levels, yet sufficiently neutralizing to confer immune protection (preliminary data).

CONCLUSIONS
Vaccination programmes implemented since the 70s provide long-lasting immunity for measles and rubella. Preliminary data suggest eldest vaccinated cohorts have functional immunity to measles, and immunity to rubella is present beyond childbearing age. The gap of immunity among socio-geographically clustered orthodox reformed unvaccinated women (born since last rubella outbreak) in low vaccination coverage areas gives a potential risk of congenital rubella syndrome in case of a rubella outbreak.

Keywords: Measles, Rubella, Sero-epidemiology, Humoral immunity, Vaccine-preventable diseases
ABSTRACT ID: 479
PRESENTED BY: Tom Woudenberg, Netherlands / tom.woudenberg@rivm.nl

POSTER TOUR 14

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Implementation science and vaccine preventable diseases

MODERATOR
Jane Whelan

Abstract

Low seroprotection against diphtheria and tetanus in Lao adolescents

L. Hefele [1]
S. Vantava [2], S. Virachith [3], S. Vannachone [4], V. Khounvisith [5], P. Nouanthong [6], J. Hübschen [7], S. Sayasone [8], A. Black [9]

[1] Department of Infection and Immunity, Luxembourg Institute of Health, Esch-sur-Alzette, Grand-Duchy of Luxembourg
[2, 4, 8] Lao Tropical and Public Health Institute, Vientiane, Lao People's Democratic Republic
[3, 5, 6, 9] Lao-Lux Laboratory, Institut Pasteur du Laos, Vientiane, Lao People's Democratic Republic
[7] Department of Infection and Immunity, Luxembourg Institute of Health, Esch-sur-Alzette, Grand-Duchy of Luxembourg

BACKGROUND
Diphtheria and tetanus are serious vaccine-preventable diseases with high morbidity and mortality. There is currently no diphtheria or tetanus booster vaccine for Lao children before the age of 15, despite international recommendations. In this study, we aimed to determine the seroprotection against diphtheria and tetanus among Lao adolescents in Vientiane capital and Bolikhamxay province.

METHODS
Highschool students between 11 and 18 years were randomly selected and invited to take part in the study. Serum samples from 779 students were tested for antibodies against diphtheria and tetanus by commercial enzyme-linked immunosorbent assays. Data analyses were conducted in R, the code is available on GitHub (https://github.com/lhefele/lao-h-078_analysis_public). Logistic regression was used to calculate odds ratio (OR), 95% confidence intervals (CI) and p-values.

RESULTS
Approximately half (49%) of the participants were male and the median age was 15 years. Overall, only 25.8% and 30.9% of the adolescents had antibody titers corresponding to protection against diphtheria and to sufficient immunity against tetanus, respectively. Female participants older than 16 years were more likely to be protected against diphtheria (OR=3.6, CI=2.0-6.6; p=0.0004) and tetanus (OR=2.4, CI=1.5-4.1; p<0.03).

CONCLUSIONS
The overall low seroprotection against diphtheria and tetanus might be due to low vaccination coverage or anti-body waning. The higher protection levels in older, female students may reflect the policy to vaccinate women of reproductive ages with tetanus-containing vaccines. We recommend to assess the disease burden in adolescents and to consider the benefits of a booster vaccination against tetanus and diphtheria before adolescence.

Keywords: Vaccination coverage, Diphtheria, Tetanus, Antibodies, Laos, Adolescent
ABSTRACT ID: 88
PRESENTED BY: Lisa Hefele, Luxembourg / lisa.hefele@lih.lu

POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

Global epidemiology of the multicounty monkeypox outbreak, 2022-23

A. Hoxha [1]

H. Laurenson-Schafer [2], S. Kerr [3], B. Mirembe [4], P. Ndumbi [5], B. Ajong [6], R. Lewis [7], O. le Polain de Waroux [8], B. Pavlin [9], (GROUP) WHO mpox Surveillance and Analytics team

[1, 2, 4, 5, 6, 7, 8, 9] World Health Organization

[3] CPC Analytics

BACKGROUND

The 2022-2023 multi-country mpox outbreak represents the diseases' largest recorded epidemic. A rapid global surveillance system was put in place in 2022 by WHO and key partners to collect aggregated and case-based information on cases in order to support the outbreak response.

METHODS

We analysed surveillance data from January 2022 to April 2023, to describe demographic, clinical and transmission features of the outbreak. We used binary logistic regression to estimate risk factors for hospitalisation and death due to mpox.

RESULTS

In total 87,377 mpox cases and 140 related deaths were reported from 111 countries. Median age was 34 (IQR 29-41) years and 96.2% (77,869/80,925) were male, the majority of whom (84.1% (25,880/30,770) self-identified as men who have sex with men. The main transmission route was sexual contact (82.0%, 16,413/20,011). Where HIV status was recorded, 52.3% (21,178/40,498) were HIV positive, and of these 54.3% (4,055/7,474) were reported as being immunosuppressed. The main reported symptoms were any rash (57.1 %, 27,595/48,327), fever (41.9%, 20,254/48,327), genital rash (31.1%, 15,049/48,327), headache (21.9%, 10,581/48,327) and lymphadenopathy (20.6%, 9,969/48,327). 3,589 cases were hospitalised, with increased odds for those aged <5 years (aOR [95% CI] = 2.23 [1.36-3.64]) and ≥65 years (aOR= 1.48 [1.02-2.14]) compared to 15-44 years old, females (aOR= 1.49 [1.15-1.93]), HIV positive (aOR=1.73 [1.48-2.03], immunosuppressed (aOR= 3.19 [2.23-4.45]), and both (aOR= 2.20 [1.89-2.55]). Increased odds of death were observed for those HIV positive (OR= 10.6 [2.73-69.6]), immunosuppressed (OR= 16.2 [0.75-170]), or both (OR= 20.8 [6.15-130]).

CONCLUSIONS

Our analysis represents the largest and most geographically diverse sample of mpox cases. Its insights about case description and risk factors for hospitalization and death supported risk communication, clinical advice and overall global outbreak response.

Keywords: Mpox, Monkeypox, Epidemiology, Surveillance, MPXV
ABSTRACT ID: 527
PRESENTED BY: Ana Hoxha, Switzerland / hoxhaa@who.int

POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

Monkeypox outbreak surveillance based on emergency department visits

V. Bernadette [1]
C. Forgeot [2], G. Viudes [3], G. Pedrono [4], A. Fouillet [5], C. Caserio-Schönemann [6]
[1, 2, 4, 5, 6] Santé publique France, French national public health agency
[3] Hyères hospital, 83400 Hyères

BACKGROUND
In May 2022, cases of monkeypox were detected in Europe. In addition to strengthening surveillance for orthopoxvirus infections through mandatory reporting of confirmed cases, the French health authority conducted epidemic surveillance based on visits to OSCOUR® network emergency departments (EDs) with a medical diagnosis of mpox (confirmed or suspected). The aim of this study was to evaluate the relevance of using ED data to monitor this epidemic.

METHODS
The OSCOUR® network collects and transmits daily data on ED visits (95% of national visits), including medical diagnoses. We described ED visits with a diagnosis of mpox (ICD10 codes: B03 "smallpox" or B04 "monkeypox") by day, sex, age and region, between 21/05/2022 and 31/12/2022.

RESULTS
957 ED visits with mpox diagnosis were recorded. Of these visits, 68% were in the Paris area, 88% were male, the mean age was 31 years [min=1; max=81], and 5% of visits resulted in hospitalisation. Mpox was coded as the primary diagnosis in 97% of cases. The temporal dynamics and geographical distribution of ED visits and confirmed cases were highly correlated.

CONCLUSIONS
Data from the OSCOUR network's allow early reactive monitoring of epidemic dynamics without additional data entry by clinicians. Although the existing ICD-10 codes do not allow us to distinguish between a biologically confirmed case of monkeypox from a suspected case, the results of our study show good concordance between epidemic surveillance based on ED data (suspected or confirmed cases) and data from mandatory reporting of confirmed cases. To validate the indicator based on mpox ED visits, an evaluation of the positive predictive value of the coding using the biological results available in patients' files is ongoing.

Keywords: Monkeypox, Syndromic surveillance, Epidemiology, Infectious diseases, Emergency care
ABSTRACT ID: 679
PRESENTED BY: Bernadette Verrat, France / bernadette.verrat@santepubliquefrance.fr

POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

In-action evaluation of surveillance processes of mpox in EU/EEA, 2022

X. Andrianou [1]

J. Reyes-Urueña [2], L. Alves de Sousa [3], J. Haussig [4], G. Spiteri [5]

[1, 2, 3, 4, 5] European Centre for Disease Prevention and Control

BACKGROUND

Following the detection of autochthonous mpox cases in EU/EEA, ECDC implemented a surveillance system that used publicly available aggregated data collected from official sources and, later, indicator-based surveillance through the European Surveillance System (TESSy). We performed an in-action evaluation of the two systems while they ran in parallel, during June-September 2022, to assess their performance in monitoring trends/epidemiological indicators and to identify strengths and limitations to inform future ECDC surveillance strategies.

METHODS

We compared data collected from open sources with data reported in TESSy for the following indicators: number of cases, by week and overall; date the first case was reported by country (considering the date of TESSy implementation); concordance of trends and of epidemiological features.

RESULTS

Until the week starting 19 September 2022, 29 EU/EEA countries had reported 19584 and 19827 mpox cases in public sources and TESSy, respectively. The first case in a country was always reported in the public domain first with the delay for reporting in TESSy ranging from 1 day to >1 week. Public data were particularly informative in the early stages of the outbreak while TESSy reporting was being established (concordance: 14% in mid-June). Overall concordance reached 100% during the week starting 29 August. ECDC used publicly available data for monitoring trends until September 2022 and then switched exclusively to TESSy when concordance remained high. Public sources had very limited epidemiological information on cases and therefore TESSy data were used for epidemiological bulletins.

CONCLUSIONS

In-action evaluation of mpox surveillance, allowed timely data quality assessment and switching between sources when relevant depending on the reporting objectives. Future surveillance strategies should incorporate in-action evaluation especially when integrating different data sources for monitoring epidemiological trends.

Keywords: Surveillance, Mpox, Emergency, Evaluation
ABSTRACT ID: 670
PRESENTED BY: Xanthi Andrianou, Sweden / xanthi.andrianou@ecdc.europa.eu

POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

Household mpox transmission: estimating the secondary attack rate and factors associated with transmission within households in the UK mpox outbreak between May and November 2022

C. Anderson [1]
P. Patrzylas [2], L. Findlater [3], R. Merrrick [4], C. Sawyer [5], W. Crowe [6], A. McAuley [7], C. Turner [8], S. Packer [9]
[1, 2, 3, 8, 9] UK Health Security Agency
[4, 5] Public Health Wales
[6] Public Health Agency (Northern Ireland)
[7] Public Health Scotland

BACKGROUND
In May 2022, a large outbreak of mpox emerged in the UK and worldwide. By 24 November 2022, there were 3713 confirmed/highly probable cases in the UK, predominantly amongst men who identified as gay, bisexual, or other men who have sex with men. We aimed to estimate secondary attack rates of mpox among household contacts, and assess factors associated with transmission to inform management of contacts.

METHODS
We carried out a UK cohort study of household contacts named by cases. Information was reported via public health and sexual health services, and included age, sex assigned at birth, place of residence, setting and type of contact. Aggregate information was summarised for the UK. Record level data was combined for England, Wales and Northern Ireland, and multivariable logistic regression used to determine factors associated with transmission.

RESULTS
The secondary attack rate for UK household mpox contacts was 4% (60/1,511). Sexual contact with the index case was associated with an 18x increase in odds of becoming a case (95% CI 7.73-52.4, $p<0.001$). Household contacts outside of London had increased odds of becoming a secondary case (adjusted OR 3.5, 95%CI 1.9-6.6, $p<0.001$), while persons assigned female at birth had reduced odds of becoming a secondary case (adjusted OR: 0.23, 95% CI: 0.07-0.60).

CONCLUSIONS
We found a low overall secondary attack rate to household mpox contacts. There was strong evidence of a risk associated with sexual contact. This evidence supports risk assessment of contacts, with prioritisation of those with close intimate contact for follow up. Limitations include lack of information on vaccination, exposures outside the household, and onset dates to validate transmission links.

Keywords: Monkeypox, Contact tracing, Epidemiology, Transmission, Secondary attack rate
ABSTRACT ID: 605
PRESENTED BY: Charlotte Charlotte, United Kingdom / charlotte.anderson@ukhsa.gov.uk

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POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

Effectiveness of historical childhood smallpox vaccination against mpox: estimation using the screening method on surveillance data from countries in Europe, 2022-2023

S. Colombe [1]
L. Alves de Sousa [2], A. Vaughan [3], A. Koch [4], H. Emborg [5], S. von Schreeb [6], M. Haverkate [7], S. Hahné [8], C. van Ewijk [9], A. Díaz [10], C. Olmedo [11], S. Monge [12], S. Funke [13], J. Hagan [14], N. Nicolay [15], R. Pebody [16]

[1] World Health Organization Regional Office for Europe, Copenhagen, Denmark
Institute of Tropical Medicine, Antwerp, Belgium
[2, 13 ,15, 16] European Centre for Disease Prevention and Control !ECDC), Stockholm, Sweden
[3, 14] World Health Organization Regional Office for Europe, Copenhagen, Denmark
[4, 5] Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark
[6] Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark
Department of Infectious Diseases, Copenhagen University Hospital - Amager and Hvidovre Hospital, Denmark
[7, 8] National Institute for Public Health and the Environment RIVM), Bilthoven, the Netherlands
[9] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
European Programme for Intervention Epidemiology Training (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[10 ,12] National Centre of Epidemiology, Carlos III Institute of Health, CIBERINFEC, Madrid, Spain
[11] Vaccination Programme, Ministry of Health, Madrid, Spain

BACKGROUND

The surge of mpox cases in Europe since May 2022 raises the question of duration and level of cross-protection against mpox of smallpox vaccination (SV) administered in Europe prior to 1980. We aimed to measure the vaccine effectiveness (VE) of past SV against recent laboratory-confirmed mpox in Denmark, the Netherlands and Spain using the screening method.

METHODS

Childhood SV status of male mpox cases, native-born before the end of countries' SV programs, was collected through routine surveillance. SV coverage for separate time periods during countries' SV programs was obtained through publicly available sources and/or country's archives. Age-adjusted, country-specific VE and 95% confidence intervals (CI) were calculated using logistic regression. Pooled VE was estimated using a fixed-effect model.

RESULTS

Between 13 May 2022 and 8 May 2023, Denmark, the Netherlands and Spain had reported 196, 1,264 and 7,551 mpox cases, respectively. Out of these, 39 (20%), 165 (13%), and 562 (7%) were eligible; and 23 (59%), 115 (70%), and 190 (34%) had been vaccinated during childhood. Population coverage during the peak of the SV program was 80-89% before dropping sharply. Age-adjusted VE of prior SV against mpox was -62% [95% CI: -304 to 34] in Denmark, 6% [-44 to 38] in the Netherlands, and 61% [52 to 68] in Spain. The pooled age-adjusted VE was 52% [43 to 60] (I2= 90%).

CONCLUSIONS

Our study suggests that one in two persons historically vaccinated against smallpox may be protected against mpox, indicating likely residual moderate cross-protection, although there is significant heterogeneity in VE between countries. Low number of cases and mis-ascertainment of SV might impact the VE. Better understanding of residual cross-immunity is needed to optimize vaccination strategies with third-generation vaccines.

Keywords: Europe, Mpox, Vaccine effectiveness, Monkeypox, Childhood smallpox vaccination, Screening method
ABSTRACT ID: 327

PRESENTED BY: Soledad Colomb, Belgium / colombes@who.int

POSTER TOUR 15

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

Mpox: surveillance and outbreak investigations

MODERATOR
Silvia Funke

Abstract

Investigation of a suspected case of monkey pox, Iboke, health district of Tabou, Côte d'Ivoire, July 2022

C. Kalifa [1]
W. Pierre [2], J. Otshudiandjeka [3], S. Moussa Pegnontaye [4], I. Tiembre [5], V. Beni Bi [6]

[1] AFENET | FETP
[2, 3] AFENET
[4, 5, 6] MOH / FETP

BACKGROUND

Monkeypox is a global public health problem. In West Africa more than 35 cases have been reported to WHO. On July 30, 2022, health district of Tabou was informed by the detection of monkepox suspected case in Iboké, a health area bordering Liberia, a country to which a confirmed case of monkeypox was reported. An investigation was carried out to describe the case, search other cases and proposing prevention and control measures

METHODS

A cross-sectional descriptive study was conducted. Case was any person presenting with an acute rash & one or more of the following symptoms: headache, fever, lymphadenopathy, myalgia, body aches, asthenia. Data were taken from consultation registers, interviews with identified contacts. Sociodemographic and clinical characteristics were collected. Data were analyzed and frequencies measures were calculated

RESULTS

35 years old, man with disseminated rashes on face & the rest of the body accompanied by fever, with no notion of travel outside Iboké but having been in contact with a confirmed case. The result of his sample was negative. Ten (10) contacts were identified without signs & symptoms, of which 8 (80%) linked to the suspected case and 2(20%) linked to the confirmed case in Liberia. 80% of the contacts of the suspected case live in Iboké versus 50% (1/2) for the confirmed case. Median age of contacts is 28.5 (range: 5 – 43). Sex ratio is 1.7 male to 1 female

CONCLUSIONS

Young man had contact with the confirmed case from Liberia. Majority of contacts lives in Cote d'Ivoire. No case of monkeypox has been detected in Cote d'Ivoire so far. Case management has been recalled and measures have been taken to strengthen cross-border surveillance between both countries.

Keywords: Investigation, Monkeypox, Iboke, Côte d'Ivoire
ABSTRACT ID: 838
PRESENTED BY: Coulibaly Kalifa, Côte d'Ivoire/ stkalif73@gmail.com

POSTER TOUR 16

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

COVID-19 and other respiratory diseases

MODERATOR
Maximilian Riess

Abstract

Real-world evaluation of daily self-administered lateral flow tests for SARS-CoV2 for contacts of COVID-19 cases

N. Love [1]
D. Ready [2], J. Aveyard [3], C. Caiado [4], P. Hughes [5], N. Silva [6], R. Kulasegaran [7], J. Rubin [8], L. Yardley [9], S. Hopkins [10], I. Oliver [11]

[1] UK Health Security Agency | University of Liverpool
[2, 7, 10, 11] UK Health Security Agency
[3] NHS Digital
[4] Durham University
[5, 6] UnifAI Technology
[8] King's college London
[9] University of Bristol | University of Southampton

BACKGROUND
Decentralised diagnostics including lateral flow tests (LFTs) widen testing access and provide rapid results in the community. During the COVID-19 pandemic, these attributes led to the consideration of strategies, such as daily contact testing (DCT), to target self-isolation more effectively.

METHODS
We conducted a >50,000 participant non-inferiority randomised controlled trial of adult contacts of COVID-19 cases in England to evaluate DCT as an alternative to self-isolation. Participants were randomised to self-isolation (single PCR, 10 days self-isolation) or DCT arms (7 Innova LFTs, 2 PCRs, no isolation if negative) and prospectively followed-up. LFT images were sent to the study team and digitally read and compared with self-reported results.

RESULTS
20,795 DCT participants (20,795/26,123;79.6%) submitted 124,010 unique LFT results, of which 21,787 had a paired (same day) PCR result. LFT specificity was 99.9% (19,078/19,095) and sensitivity was 49.9% (1,342/2,692) when compared with same day PCR swabs. Sensitivity increased to 91.6% for symptomatic individuals (vs. 30% for asymptomatic), and with lower ct values (sensitivity with ct <18: 89.3% vs. 6.7% >30). 32,341 images were digitally read and compared with self-reported results, 99.3% of negative (31,014/31,242) and 91.6% (620/677) positive results were correctly self-reported. Incorrect reporting occurred where test band intensity was lowest (7.3 (IQR: 12.4) vs. 45.6 (IQR: 35.3) for concordant results).

CONCLUSIONS
Self-administered daily LFTs could be performed and interpreted by members of the public. There are opportunities from the application of rapid home and other point of care tests to control infection including during pandemic response. Digital reading and reporting can help improve accuracy.

Keywords: SARS-CoV-2 Testing, COVID-19, Self-Testing, Contact Screening
ABSTRACT ID: 187
PRESENTED BY: Nicola Love, United Kingdom / nicola.love@ukhsa.gov.uk

POSTER TOUR 16

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

COVID-19 and other respiratory diseases

MODERATOR
Maximilian Riess

Abstract

How the COVID pandemic and physical distancing measures implemented impacted on the social contacts and mixing patterns in Norway? Insights from a panel study, April to September 2020

L. Veneti [1]
B. Robberstad [2], A. Steens [3], F. Forland [4], B. Winje [5], D. Vestrheim [6], C. Jarvis [7], A. Gimma [8], J. Edmunds [9], K. Van Zandvoort [10], B. Freiesleben de Blasio [11]

[1] Department of Infection Control and Preparedness, Norwegian Institute of Public Health, Oslo, Norway
[2] Division for Health Services, Norwegian Institute of Public Health, Oslo, Norway
Department of Global Public Health and Primary Care, University of Bergen, Bergen, Norway
[3, 5, 6] Department of Infection Control and Vaccine, Norwegian Institute of Public Health, Oslo, Norway
[4] Department of Infection Control and Preparedness, Norwegian Institute of Public Health, Oslo, Norway
[7, 8, 9, 10] Centre for Mathematical Modelling of Infectious Diseases, Department of Infectious Disease Epidemiology, London School of Hygiene & Tropical Medicine, London, United Kingdom
[11] Department of Method Development and Analytics, Norwegian Institute of Public Health, Oslo, Norway
Oslo Center for Biostatistics and Epidemiology, Department of Biostatistics, Institute of Basic Medical Sciences, University of Oslo, Oslo, Norway

BACKGROUND
During the COVID-19 pandemic, many countries implemented physical distancing measures in order to contain the transmission and limit the burden of the disease. Social contact patterns are essential in driving the spread of respiratory infections, and country-specific measurements are needed. This study aimed to gain insights into changes in social contacts and behaviour during the early pandemic in Norway.

METHODS
We conducted a panel study among a representative sample of the Norwegian adult population (by age and gender) including six data collections (waves) between April and September 2020, and used survey data from 2017 as baseline. Participants provided socio-economic, demographic information and details regarding their social contacts. The questionnaires defined a social contact as either an in-person conversation or physical contact (involving touch). We calculated mean daily contacts, and estimated age-stratified contact matrices that were used to estimate reproduction numbers during the study period.

RESULTS
Across the six waves, the mean number of contacts of adults varied between 3.2 (95%CI 3.0-3.4) to 3.9 (95%CI 3.6-4.2) representing a decline of 67-73% compared prepandemic levels. Fewer contacts in the community setting largely drove the reduction; the drop in social contacts was most prominent among younger adults. Despite the easement of measures during the survey, population contact matrices remained relatively stable and displayed more inter-age group mixing than in the baseline. Contacts in the household and community contacts outside schools and workplaces contributed the most to social encounters.

CONCLUSIONS
Social contacts were markedly reduced in the months following the 2020 lockdown in Norway, coinciding with strict physical distancing measures. Our findings can be used to improve parameterisation of policy-relevant models when a future crisis such as COVID-19 emerges.

Keywords: Physical distancing measure, Contact pattern, Social mixing, Modelling, Control measures
ABSTRACT ID: 813
PRESENTED BY: Lamprini Veneti, Norway / lamprini.veneti@fhi.no

POSTER TOUR 16

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

COVID-19 and other respiratory diseases

MODERATOR
Maximilian Riess

Abstract

Characterisation of serological correlates of protection against SARS-CoV-2 throughout the pandemic within the UK-based SIREN study

A. Atti [1]
F. Insalata [2], E. Carr [3], A. Otter [4], S. Foulkes [5], M. Wu [6], M. Cole [7], E. Linley [8], A. Semper [9], T. Brooks [10], S. Hopkins [11], A. Charlett [12], R. Beale [13], V. Hall [14], (GROUP) The SIREN Study Group
[1, 2, 4, 5, 7, 8, 9, 10, 11, 12, 14] UK Health Security Agency
[3, 6, 13] Francis Crick Institute

BACKGROUND
Since the emergence of SARS-CoV-2, it has become critical to identify an immune marker that could be used to infer protection against reinfection and, furthermore, against infection after vaccination. We aimed to characterise serological correlates of protection against SARS-CoV-2 infection across different phases of the COVID-19 pandemic within the SIREN study.

METHODS
Within the SIREN study, a frequently PCR and antibody tested cohort, we performed (1) descriptive case series of early reinfections, (2) case-control study of reinfections pre-vaccination and (3) case-control study of Delta infections post-vaccination. We tested sequential serum samples for anti-SARS-CoV-2 spike (anti-S), anti-SARS-CoV-2 nucleocapsid (anti-N) and neutralising antibodies. Controls were matched according to age, region, gender and, in (3), time since vaccination. We described and modelled antibody levels and neutralising antibody titres (nAbT) before infection/reinfection and, in (2) and (3), compared with serological levels from controls.

RESULTS
In the case series of our first two confirmed reinfection cases (1) in October 2020, nAbT were low or absent before reinfection, indicating a potential correlate of protection against SARS-CoV-2 infection. We tested this hypothesis in (2), comparing 23 cases of reinfection pre-vaccination identified until February 2021 with matched controls, finding that detectable nAbT (>40) were associated with a significant reduction in odds of reinfection (>90%). In (3), including 130 Delta infection cases post-vaccination (April-October 2021), we found that Delta nAbT >40 were also associated with a substantial reduction in odds of infection (89%) when compared to controls.

CONCLUSIONS
Throughout different pandemic stages, we have demonstrated that nAbT correlate with protection against SARS-CoV-2 infection and identified potential thresholds that could be applied to assess population immunity, to plan future vaccine deployment and, therefore, reduce COVID-19 pandemic burden.

Keywords: SARS-CoV-2, Neutralising Antibodies, SARS-CoV-2 serology, Immunity, Reinfection, Vaccination
ABSTRACT ID: 408
PRESENTED BY: Ana Atti, United Kingdom / ana.atti@ukhsa.gov.uk

POSTER TOUR 16

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30 - 16:15

COVID-19 and other respiratory diseases

MODERATOR
Maximilian Riess

Abstract

Severity assessment of Acute Respiratory infections during the pandemic seasons 2019/2020- 2022/23 in Germany

T. Jung-Sendzik [1]
K. Tolksdorf [2], S. Buda [3]

[1] Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
Unit for Respiratory Infections, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[2, 3] Unit for Respiratory Infections, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND
The 2009 influenza pandemic revealed a lack of standardized methods for national severity assessments, and COVID-19 highlighted the need to extend their scope to other acute respiratory diseases. We aimed to assess the pandemic seasons 2020-2023 in Germany using data from our national sentinel systems for Acute Respiratory Infections (ARI), and to make recommendations for further improvement.

METHODS
We analysed three severity indicators, based on seven parameters: Transmissibility: population level weekly ARI rates (1), medically attended ARI incidences (2); Seriousness: proportion of patients in ICU among SARI (Severe ARI) (3), proportion of deceased SARI (4); Impact (ongoing): weekly SARI hospitalisations (5) and ICU admissions (6), weekly fatal outcomes of SARI (7). We stratified by age groups (0-4, 5-14, 15-34, 35-59 and 60+y).Based on the WHO Pandemic Influenza Severity Assessment Tool, we established and applied thresholds (baseline, low, moderate, high, and extraordinary), and looked at virological sentinel data to identify circulating pathogens.

RESULTS
In Season 2020/2021, transmissibility was low across all age groups. Seriousness was high overall, affecting mainly 60+y, with SARS-COV-2 as the main virus circulating in this age group. Season 2021/2022-transmissibility was high, seriousness moderate overall. Season 2022/2023 showed extraordinary transmissibility due to influenza and RSV. Seriousness was low in all age groups, except in those 0-4, with an extraordinary proportion of ICU patients amongst SARI, mainly caused by RSV.

CONCLUSIONS
The pandemic seasons 2020-2023 could be assessed for severity using ARI and SARI data; we recommend to include this assessment in national routine reporting to support decisions on resource allocations and interventions during an epidemic or pandemic. Inclusion of virological data is crucial to differentiate effects of COVID-19, Influenza and RSV on different age groups.

Keywords: Acute respiratory infections, Pandemic, Epidemic, Severity assessment, COVID-19
ABSTRACT ID: 347
PRESENTED BY: Tanja Jung-Sendzik, Germany / jung-sendzikt@rki.de

POSTER TOUR 16

DAY 2 – THURSDAY 23 NOVEMBER 2023
15:30-16:15

COVID-19 and other respiratory diseases

MODERATOR
Maximilian Riess

Abstract

Annual Burden of Hospitalized Influenza in Albania, 2009/2010 - 2021/2022

A. Simaku [1]
S. Bino [2], I. Hasibra [3], E. Kureta [4], A. Vasili [5], J. Sulo [6], E. Tomini [7]

[1] Institute of Public Health

[2] Institute of Public Health, Tirana, Southeast European Center for Surveillance and Control of Infectious Disease, Tirana

[3, 4, 5, 7] Institute of Public Health, Tirana

[6] Institute of Public Health, Tirana, Mediterranean and Black Sea Programme for interventional Epidemiology Training (MediPiet), European Centre for Disease prevention and Control (ECDC) Stockholm, Sweden

BACKGROUND
In 2009, Albania began surveillance for influenza at sentinel clinics and hospitals to describe seasonality and circulating viruses and estimate burden data to guide vaccine policy decisions.

METHODS
All hospitalized patients with severe acute respiratory infections (SARI) at 11 hospitals in 9 regions were sampled and tested year-round. SARI was defined as admission to hospital with fever and cough within 10 days of onset. Specimens were tested for influenza viruses rRT-PCR at the national influenza center. We collected total SARI cases and were using ICD-10 codes J9-J22 to estimate the hospital burden for influenza and population census data by age group to estimate rates and 95% CI per 100 000 persons.

RESULTS
Between 2009 and 2022, 2713/14506 SARI cases were influenza positive. Each year 8890-17438 cases were hospitalized with SARI. Annual estimated rates were highest in young children <5 years. In <5 years, rates ranged from 90 (10-170) in 2010/2011 to 469 (272-665) in 2017/2018 which were both A(H1N1)pdm09 seasons. In 5-14 years, rates ranged from 27 (4-50) in 2010/2011 to 216 (177-255) in 2011/2012 which were A (H1N1)pdm09 and A(H3N2) seasons, respectively. In >65 it ranged from 4 (1-9) in 2010/2011 to 55 (46-65) in 2011/2012 which were A (H1N1)pdm09 and A(H3N2) seasons, respectively. During the first COVID-19 pandemic season 2021/2021 there was no influenza activity while the rates of influenza were lower in the subsequent 2021/2022 season as compared to before pandemic.

CONCLUSIONS
Annual burden of influenza in Albania was substantial, particularly in young and school age children. The SARI surveillance data are robust and can be used to estimate burden of disease and guide vaccine decisions.

Keywords: Influenza, Surveillance, Burden, Young children
ABSTRACT ID: 549
PRESENTED BY: Artan Simaku, Albania / artan.simaku@gmail.com

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POSTER TOUR 17

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

Malaria spatial genomics to infer connectivity, importation and transmission flow of Plasmodium falciparum in Mozambique

A. Pujol [1]
A. Chidimatembue [2], C. da Silva [3], S. Boene [4], H. Mbeve [5], D. Tembisse [6], J. Inacio [7], K. Bapú [8], K. Comiche [9], P. Cisteró [10], C. Garcia-Fernandez [11], N. Brokhattingen [12], A. Aranda-Diaz [13], N. Hathaway [14], B. Rafael [15], F. Luis [16], N. Canana [17], E. Rovira-Vallbona [18], C. Guinovart [19], B. Greenhouse [20], S. Enosse [21], F. Saúte [22], P. Aide [23], B. Candrinho [24], A. Mayor [25]

[1] Barcelona Institute for Global Health (ISGlobal)
[2, 3, 4, 5, 6, 7, 8, 9, 12, 15, 16, 18, 19, 22, 23, 25] Manhiça Health Research Center (CISM)
[10, 11] Barcelona Institute for Global Health (ISGlobal)
[13, 20] University of California San Francisco (UCSF)
[14] University of Massachusetts Medical School
[17, 21] Malaria Consortium
[24] National Malaria Control Program

BACKGROUND

Malaria genomics represents a promising tool to improve current surveillance systems and tailor control and elimination interventions. However, available data is usually limited in sample size and spatially sparsity. Modelling spatial genomics allows for inferring genetic populations in areas with no data and identifying imported cases and transmission sources in low-transmission settings.

METHODS

An amplicon sequencing panel was used to generate 272 genetic microhaplotypes targeting ~250bp regions of the P. falciparum genome that are highly informative of diversity, gene deletions (hrp2/3) associated with rapid diagnostic test failure, and antimalarial drug resistance mutations. Genetic relatedness was analysed as identity-by-descent (IBD) between sample pairs, and isolation-by-distance was studied using Mandel tests. Imported cases in two low-transmission (Magude and Matutuine) districts in Maputo Province (southern Mozambique) were assessed from IBD statistics with samples from 9 provinces in the country, and correlated with travel history data. Geospatial models were applied to estimate allele frequencies and prevalence of diagnostic and antimalarial resistance mutations in the country to identify key target areas for interventions.

RESULTS

We found strong spatial genetic structure across the country, with higher fractions of IBD-related pairs within regions (north-north or south-south) than between regions (north-south). We observed a stronger isolation-by-distance at large scales (between provinces), than at small scales (within province). No correlation was found between travel history data and spatial relatedness of samples. Geospatial models observed spatial patterns in the prevalence of some alleles and genetic markers.

CONCLUSIONS

We found a strong spatial differentiation of genetic P. falciparum populations, but no significant contribution of imported cases in the low-transmission areas studied, indicating that transmission in these areas is mainly local and interventions should be locally targeted.

Keywords: Modelling, Boinformatics, Genomics, Malaria, Epidemiology
ABSTRACT ID: 233
PRESENTED BY: Arnau Pujol, Spain / arnau.pujol@isglobal.org

POSTER TOUR 17

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

Modelling COVID-19 outbreaks and response options in the 30 EU/EEA countries: Insights from continuous model development and reflections for winter 2023-2024

F. Sandmann [1]
B. Prasse [2], R. Grah [3], R. Niehus [4]
[1, 2, 3, 4] ECDC

BACKGROUND
Throughout the COVID-19 pandemic, the European Centre for Disease Prevention and Control (ECDC) used mathematical modelling for addressing public health questions in Europe. Modelling COVID-19 for the 30 EU/EEA countries proved challenging due to their great diversity with respect to vaccination policies, nonpharmaceutical interventions, socio-economic indicators, and human behaviour. We present the general experiences of modelling at ECDC based on the application of evaluating vaccination campaigns for autumn 2023.

METHODS
We used a deterministic metapopulation model that was age-structured into ten groups and the vaccine status of individuals, with country-specific parameters. The model had a Susceptible-Exposed-Infectious-Recovered (SEIR)-type structure with reinfections and considered the waning of natural, vaccine-induced, and hybrid immunity against infection and severe outcomes. Stochasticity was captured by describing model parameters as random variables. The European Surveillance System (TESSy) informed the model calibration, supplemented with information about demography, disease progression, and social contact data.

RESULTS
Our main results are threefold. First, we expect an autumn vaccination campaign for individuals above 60 years to prevent up to 21-32% of the COVID-19-related hospitalisations in winter 2023-2024. The range captures parameter uncertainties, variations across countries, the possible emergence of new Omicron sublineages, and temporal changes in human behaviour (including seasonality). Second, achieving a higher vaccine uptake is more important than expanding the target age group. Third, a similar reduction of hospitalisation burden is achieved by targeting people above 50 years as for people above 60 years.

CONCLUSIONS
ECDC's mathematical model, and variations thereof, have informed European policy advice since 2020. COVID-19 vaccination will continue being important in winter 2023-2024. Our results demonstrate the high value of COVID-19 modelling for supporting public-health decisions in the diverse EU/EEA countries.

Keywords: COVID-19, Modelling, Vaccination
ABSTRACT ID: 535
PRESENTED BY: Rene Niehus, Sweden/ rene.niehus@ecdc.europa.eu

POSTER TOUR 17

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

Causal relationships between human mobility and the spread of Covid19 in Spain

C. Pontes [1]
M. Ponce de León [2], A. Arenas [3], A. Valencia [4]

[1, 2, 4] Barcelona Supercomputing Center
[3] Universitat Rovira i Virgili

BACKGROUND

Human mobility plays a crucial role in the dissemination of infectious diseases. The rapid transmission of the SARS-CoV-2 virus during the Covid-19 pandemic lead to overwhelmed healthcare systems and significant mortality rates in many countries. To prevent similar outcomes in the future, it is imperative to comprehend the relationship between commuting patterns and disease spread.

METHODS

We employed transfer entropy (TE), an information-theoretic measure denoted as TE(X→Y), to evaluate the directed influence of mobility-associated risk from a specific geographic patch, X, on the Covid-19 incidence in another patch, Y, over time. Initially, we validated our approach using simulated data generated by the EpiCommute SIR epidemiological model. We then analyzed time-series data obtained from the Spanish cross-referenced Covid-19 Flow-Maps geographic information system to compute TE between all provinces in Spain.

RESULTS

Our results demonstrated the effectiveness of TE in capturing epidemic's spreading patterns and the underlying mobility network topology when considering associations between mobility-associated risk and incidence. Conversely, TE analysis between incidences in different patches proved less effective, emphasizing the pivotal role of mobility in epidemic studies. Furthermore, this investigation enabled us to identify the key drivers of the pandemic at different temporal intervals, both on a global and local scale. Notably, our findings unveiled significant epidemiological events, such as the outbreak in Lleida during the Summer of 2020, attributed to an influx of temporary workers. Additionally, we discerned the primary sources of infection for individual provinces.

CONCLUSIONS

Overall, our research provides valuable insights into the dynamic spread of infectious diseases by elucidating the substantial contribution of human mobility. These findings can serve as a foundation for developing future non-pharmaceutical interventions and strategies aimed at curtailing disease transmission.

Keywords: Epidemiological Models, Causality, Decision Support Techniques, Spatial Interaction
ABSTRACT ID: 494
PRESENTED BY: Camila Pontes, Spain / camila.pontes@bsc.es

POSTER TOUR 17

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15:30-16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

A spatio-temporal predictive model inferring the year-to-year probability of occurrence of TBE human cases in Europe

F. Dagostin [1]
D. Erazo [2], G. Marini [3], D. Da Re [4], V. Tagliapietra [5], A. Corradini [6], W. Wint [7], N. Alexander [8], R. Olyazadeh [9], H. Mäkelä [10], T. Dub [11], S. Dellicour [12], A. Rizzoli [13]

[1] Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige (TN), Italy
[2, 13] Spatial Epidemiology Lab, Université Libre de Bruxelles, Bruxelles, Belgium
[3, 5, 6, 12] Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige (TN), Italy
[4] Center for Agriculture Food Environment, University of Trento, Trento, Italy
[7, 8, 9] Environmental Research Group Oxford Ltd, c/o Dept Zoology, Oxford, United Kingdom
[10, 11] Department of Health Security, Finnish Institute for Health and Welfare, Helsinki, Finland
[12] Spatial Epidemiology Lab (SpELL), Université Libre de Bruxelles, Bruxelles, Belgium

BACKGROUND
The number of tick-borne encephalitis (TBE) human cases reported in Europe has increased in recent years, peaking during the Covid-19 pandemic phase. To improve the capability to identify high-risk areas, we developed a spatio-temporal predictive model inferring the year-to-year probability of occurrence of TBE human cases in Europe.

METHODS
We used data provided by the European Surveillance System (TESSy, ECDC) to infer the distribution of TBE human cases at the regional (NUTS3) level during the period 2017-2021. We included variables related to temperature, precipitation, land cover and ticks' hosts presence to account for the natural hazard of viral circulation. We also used indexes based on recorded intensities of human outdoor activity in forests as proxies of human exposure to tick bites. We identified the yearly probability of TBE occurrence using a boosted regression tree modeling framework.

RESULTS
Areas with higher probability for transmission were identified in Central-Eastern Europe and along the coastline of Nordic countries up to the Bothnian Bay. Our results highlighted a westbound and northbound spread of TBE-positive regions throughout the years. Areas at higher risks are characterized by the occurrence of key rodent reservoir and cervid species, intense human recreational activities in forests, steep drops in late summer temperatures and high annual precipitation amounts. The predictive accuracy of the model was assessed through internal and external validation (AUC = 0.81; CBI =0.98).

CONCLUSIONS
Our study provides an assessment of the European regions at risk of TBE human infections on a yearly basis. Our results can therefore be used for year-to-year disease risk mapping in support of surveillance and prevention campaigns within endemic and potential new risk areas.

Keywords: Encephalitis, Tick-Borne, Europe, Decision Making, Models, Statistical
ABSTRACT ID: 199
PRESENTED BY: Francesca Dagostin, Italy / francesca.dagostin@fmach.it

POSTER TOUR 17

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

Studying time-evolution of age-specific differences in susceptibility to SARS-CoV-2 infection based on social contact data

N. Franco [1]
P. Coletti [2], L. Willem [3], L. Angeli [4], A. Lajot [5], S. Abrams [6], P. Beutels [7], C. Faes [8], N. Hens [9]

[1] University of Namur
[2, 4, 8] University of Hasselt
[3, 7] University of Antwerp
[5] Sciensano
[6, 9] University of Hasselt | University of Antwerp

BACKGROUND
After the start of the COVID-19 pandemic, it became apparent that some of the disease characteristics are strongly age-dependent. In particular the susceptibility to SARS-CoV-2 infection was lower for children than for adults. Timely knowledge of such a difference could have had an important impact on public health strategies in terms of prioritisation of vaccination or the choice of targeted non-pharmaceutical interventions. However, susceptibility may also vary in time due to vaccine or infection induced protection or due to immune escape for variants of concern.

METHODS
We extend a published method based on computer analysis of social contact data combined with daily incidence data. The method uses the next generation principle – a projection of the age repartition of newly infected from previous incidence – to evaluate the presence of relative differences in susceptibility by age. We analyse the long-term evolution based on Belgian social contact data collected between December 2020 and July 2022.

RESULTS
While in December 2020 the estimated susceptibility in children was around half of the susceptibility in adults, this situation is inverted several times due to continuous changes in susceptibility for some age classes. Decreasing susceptibility periods correspond to initial vaccination and boosters campaigns for the considered age classes, but these are interspersed by periods of increased susceptibility.

CONCLUSIONS
The increasing susceptibility periods show a continuous waning of the previous protections, especially during the emergence of the omicron variant. The repetitive exchange of relative susceptibility indicates that some specific age categories constitute more vulnerable groups with regard to infection in certain periods, which is an argument for age-specific targeted non-pharmaceutical interventions.

Keywords: Mathematical Model, Disease Susceptibility, COVID-19, Immune Evasion, Age Factors, Computer Simulation
ABSTRACT ID: 165
PRESENTED BY: Nicolas Franco, Belgium / nicolas.franco@unamur.be

POSTER TOUR 17

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Modelling, biostatistics, and health informatics

MODERATOR
Gaetano Marrone

Abstract

A novel approach to analyzing seasonal patterns in epidemics using a higher-dimensional state space

L. Pribylova [1]
V. Eclerova [2], D. Sen [3]

[1, 2, 3] Dept. of Mathematics and Statistics, Faculty of Science, Masaryk University, Brno, Czech Republic

BACKGROUND
Compared to the analysis of endemic equilibrium, analyzing the dependence of the endemic cycle on the epidemiological parameters is a complex and relatively unexplored problem. Even the question of cycle continuation with respect to parameters presents a significant challenge. However, this perspective provides valuable insights into the emergence and disappearance of endemic seasonal epidemics, as well as the possibility of biennial or multi-year cyclic outbreaks. Our approach offers a new tool for addressing these challenging questions and sheds light on the complex dynamics of infectious diseases over time.

METHODS
We present a novel method for analyzing seasonality in compartmental epidemiological models. Our method involves embedding a dynamical system, such as the SEIRS type model, into a higher-dimensional state space with a seasonal attracting cycle. To achieve this, we use a parameterized normal form of the Hopf bifurcation to introduce an artificial variable that impacts the parameters with variable amplitude seasonal fluctuations. Despite the additional complexity, our approach affords the ability to analyze the system using standard continuation methods and programs, such as MatCont.

RESULTS
We demonstrate the advantages of this approach and its potential applications in both theoretical biology and practical problems related to respiratory epidemics, including the Covid-19 pandemic.

CONCLUSIONS
We demonstrate how to address important epidemiological questions using our approach. These questions can include determining the feasibility of eradicating an endemic disease, assessing the possibility of a transition from massive COVID-19 outbreaks in a naive population to a seasonally synchronized respiratory disease, and exploring other important issues related to the control and prevention of infectious diseases.

Keywords: Mathematical Computing, Epidemiology, Endemic Diseases, Epidemiologic Methods
ABSTRACT ID: 111
PRESENTED BY: Lenka Pribylova, Czechia / pribylova@math.muni.cz

POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Implementing a subnational family-doctor-based respiratory disease surveillance system in Baden-Wuerttemberg, Germany, 2022

J. Klein [1]

L. Dangel [2], M. Meincke [3], E. Aichinger [4], I. Piechotowski [5], S. Brockmann [6], C. Wagner-Wiening [7]

[1] Postgraduate Training for Applied Epidemiology, Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany | ECDC Fellowship Programme, Field Epidemiology path (EPIET, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Ministry of Social Affairs, Health and Integration Baden-Wuerttemberg, State Health Office, Stuttgart, Germany

[2] ECDC Fellowship Programme, Public health microbiology path (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden Ministry of Social Affairs, Health and Integration Baden-Wuerttemberg, State Health Office, Stuttgart, Germany

[3, 4, 5, 6, 7] Ministry of Social Affairs, Health and Integration Baden-Wuerttemberg, State Health Office, Stuttgart, Germany

BACKGROUND

The COVID-19 pandemic underscored the necessity of subnational-level epidemiological data as a basis for decision-making on targeted measures accepted by the public. Therefore, additionally to the nationwide German sentinel surveillance system for acute respiratory diseases (ARD), a family-doctor-based voluntary surveillance system was implemented in Baden-Wuerttemberg (BW). The surveillance covers not only SARS-CoV-2 and influenza, but also a broad spectrum of pathogens, allowing to assess which ARD are currently circulating.

METHODS

Since November 2022, the frequency of respiratory pathogens is monitored with samples from outpatients consulting family doctors and pediatricians with ARD symptoms (e.g. fever, cough, sore throat). State laboratory conducts comprehensive testing of the respiratory samples including SARS-CoV-2, influenza, RSV, human metapneumoviruses and several bacterial pathogens. Additional patient questionnaires gather supplementary data like symptoms and vaccination status. The descriptive analysis of the surveillance data is published weekly online in a surveillance report.

RESULTS

Between November 2022 and April 2023, our surveillance system included 3,314 samples and complementing questionnaires collected from 78 family doctors and pediatricians, with a weekly sample count ranging from 79 to 307. In comparison, the national ARD surveillance included 3,415 samples (54-363 per week) in the same time period. Concurrent to the national surveillance data, the respiratory season 2022/23 in BW was characterized by an unusually early Influenza-A-peak in week 50 (positivity rate (PR): 54%) and a simultaneous RSV-peak in week 52 (PR:17%). In contrast, SARS-CoV-2 diagnoses peaked in week 08 (PR:19%).

CONCLUSIONS

Alongside the nationwide surveillance system our subnational system allows a broad regional overview of circulating respiratory pathogens and the corresponding epidemiological patient data. Therefore, policymakers in BW can use regional surveillance data to initiate targeted and timely measures.

Keywords: Influenza viruses, Respiratory syncytial virus, Acute respiratory infections, Surveillance
ABSTRACT ID: 515

PRESENTED BY: Juliana Klein, Germany / juliana.klein@sm.bwl.de

POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
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Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Improving Compliance of Village Health Centers to the Mandatory Reporting of Notifiable Diseases in the Municipality of Itogon, Province of Benguet, Philippines, 2022

R. Balisto [1]
M. Blanco [2], K. Lonogan [3], R. Magpantay [4]

[1, 2] Field Epidemiology Training Program - Intermediate Course, Northern Luzon, Philippines
[3, 4] Department of Health - Cordillera Center for Health Development, Philippines

BACKGROUND
In 2019, the Mandatory Reporting of Notifiable Disease was enacted in the country mandating to reporting of notifiable diseases and events of public health concerns from all levels of health care. However, from January 1 to June 25, 2022, all Village Health Centers (VHCs) in Itogon, Benguet have a 12.5% compliance rate. Hence, this study was conducted to identify gaps in reporting surveillance data and provide recommendations to improve reporting outputs.

METHODS
Implementation study was conducted. We reviewed records and interviewed health workers assigned at the VHCs. We utilized the Ishikawa diagram to show potential causes of low reports from January 1 to June 25, 2022. Process improvement activities and interventions were to improve reporting process and output. Compliance with weekly reporting was monitored from September 3 to January 31, 2023.

RESULTS
The insufficient workforce, non-trained/oriented personnel on disease surveillance, and the absence of local policy to support surveillance activities were the reasons for the low reporting rate. After the implementation of improvement measures such as the conduct of training and series of orientations among VHWs, regularly scheduled surveillance updates, the creation of an Executive Order institutionalizing surveillance activities, and a unified schedule in the submission of disease surveillance reports, an average of 41% reporting rate was noted for from September 3 to January 31, 2023.

CONCLUSIONS
Reporting rate for the 22 VHCs in Itogon had increased from 12.5% to 41%. However, there is a need to revisit the current health worker structure in a village to address the fast turnover of personnel. This study can be a basis for the development of a disease surveillance reporting framework and other health policies for the VHCs in the country.

Keywords: Notifiable disease, Surveillance systems, Disease surveillance
ABSTRACT ID: 436
PRESENTED BY: Rossan Balisto, Philippines / rossbuds.2604@gmail.com

POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Nationwide system for early warning and monitoring of nosocomial outbreaks of (highly resistant) microorganisms in the Netherlands: characteristics of outbreaks in 2012-2021

S. Woudt [1]
F. Frakking [2], E. Reuland [3], J. Severin [4], M. den Drijver [5], S. Feenstra-Gols [6], A. Haenen [7], M. Nonneman [8], D. Notermans [9], D. aan de Stegge [10], S. de Stoppelaar [11], M. Wooning [12], C. Vandenbroucke-Grauls [13], S. de Greeff [14], A. Schoffelen [15]

[1] Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
[2] Department of Medical Microbiology, University Medical Center Utrecht, Utrecht, The Netherlands
Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
[3] Department of Medical Microbiology, University Medical Center Utrecht, Utrecht, The Netherlands
Saltro Diagnostic Center for Primary Care, Utrecht, The Netherlands
Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
[4] Department of Medical Microbiology and Infectious Diseases, Erasmus MC University Medical Center, Rotterdam, The Netherlands
[5] Department of Infection Control, Maasstad Hospital, Rotterdam, The Netherlands
[6, 7, 14, 15] Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
[8] TanteLouise, Bergen op Zoom, The Netherlands
[9] Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands | Department of Medical Microbiology and Infection Prevention, Amsterdam University Medical Centers, Amsterdam, The Netherlands
[10] Beweging 3.0 (long-term care facility), Amersfoort, The Netherlands, and representing Verenso, the Dutch Association of Elderly Care Physicians
[11] Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands |Infectious diseases department, Amsterdam Academic Medical Center, Amsterdam, the Netherlands
[12] Department of Infection Control, Langeland Ziekenhuis, Zoetermeer, The Netherlands
[13] Department of Medical Microbiology and Infection Prevention, Amsterdam University Medical Centers, Amsterdam, The Netherlands Department of Clinical Medicine, Department of Clinical Epidemiology, Aarhus Universitet, Aarhus, Denmark

BACKGROUND

The Dutch Healthcare-associated Infections and AntiMicrobial Resistance Monitoring Group (SO-ZI/AMR) was initiated in 2012 for timely national nosocomial outbreak monitoring and risk assessment. We analysed the characteristics of outbreaks reported from 2012 to 2021.

METHODS

Hospitals and, since 2015, long-term care facilities (LTCF) were requested to report outbreaks when 1) continuity of care was threatened, or 2) transmission continued despite control measures. A multi-disciplinary expert panel (re-)assessed the public health risk of outbreaks during monthly SO-ZI/AMR meetings, using 5 severity phases. We studied the severity, distribution of microorganism and resistance profile, duration and size of outbreaks between 2012 and 2021.

RESULTS

In total, 353 hospital outbreaks and 110 LTCF outbreaks were reported. Most outbreaks (n=412, 89%) did not progress beyond phase 1 (no public health implications), one hospital outbreak reached phase 4 (possible public health threat: support offered). Highly resistant microorganisms (HRMO) were involved in 372/463 outbreaks (80%). Most outbreaks were caused by methicillin-resistant Staphylococcus aureus (n=93 (26%) in hospitals, n=80 (72%) in LTCF), vancomycin-resistant Enterococcus faecium (VRE; n=116 (33%) in hospitals, n=2 (2%) in LTCF) and highly resistant Enterobacterales (n=41 (12%) in hospitals, n=20 (18%) in LTCF). Overall, 37/463 outbreaks (8.0%) were caused by carbapenemase-producing gram-negative bacteria. Hospital VRE outbreaks had the longest duration (median 2.3; range 0.0-22.8 months) and broadest range of affected patients (median 9; range 2-483).

CONCLUSIONS

The SO-ZI/AMR provided national insight into the characteristics, including severity based on expert consensus, of nosocomial outbreaks over the past decade. HRMO outbreaks occurred regularly, but most of them were controlled quickly and did not develop into a public health threat. The SO-ZI/AMR has become a solid monitoring body, essential to raise awareness of potential HRMO threats.

Keywords: Nosocomial Infections, Outbreaks, Multidrug Resistance, Early warning system
ABSTRACT ID: 550
PRESENTED BY: Sjoukje Woudt, Netherlands / sjoukje.woudt@rivm.nl

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POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
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Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Enhancing Respiratory Infection Monitoring in Albania: The Role of Integrated Surveillance Information System

K. Mersini [1]
S. Bino [2], J. Sulo [3], A. Vasili [4], E. Kureta [5], E. Tomini [6], A. Simaku [7], V. Zefi [8], J. Nanaj [9], L. Agolli [10], L. Alla [11], M. Dervishi [12], D. Bardhi [13], A. Bashllari [14], A. Moci [15], F. Konomi [16], A. Crawley [17], J. Mantero [18], N. Divi [19], M. Smolinski [20]

[1] Southeast European Center for Surveillance and Control of Infectious Disease, Tirana, Albania
Faculty of Veterinary Medicine, Tirana, Albania
[2, 3, 8, 9, 10] Southeast European Center for Surveillance and Control of Infectious Disease, Tirana, Albania
Institute of Public Health, Tirana, Albania
[4, 5, 6, 7 11, 12, 13] Institute of Public Health, Tirana, Albania
[14] Vlora Regional Epidemiology Service, Vlore, Albania
[15] Fieri Regional Epidemiological Service, Fier, Albania
[16] Tirana Regional Epidemiological Service, Tirana, Albania
[17, 18, 19, 20] Ending Pandemic, San Francisco, US

BACKGROUND
The World Health Organization has recently published the Mosaic Respiratory Surveillance Framework advocating the development and use of multiple well-coordinated surveillance approaches for viruses of epidemic and pandemic potential. The open-source Integrated Surveillance Information System (SISI) was developed in 2018 and adopted in Albania in 2020. This study aims to demonstrate how the deployment of a digitalized multi-surveillance system can serve as a model to showcase the operational viability of the Mosaic Framework.

METHODS
We evaluated how SISI collates and provides data interoperability from various surveillance systems into a cohesive web-based platform. Included are case-based notification for COVID-19 and Influenza; syndromic surveillance for Influenza-Like Illness, Acute Respiratory Infections, and Severe Acute Respiratory Infection (SARI); participatory one health event-based surveillance; media horizon scanning; and, veterinary information cross-platform data exchange. These surveillance systems are complemented with investigation modules including clinical and epidemiological data, contact-tracing, and mitigation measures such as vaccinations, isolation, quarantine, etc. Additionally, laboratory findings and vaccination history are dynamically retrieved from the respective information systems.

RESULTS
Drawing on the Mosaic Framework domains, SISI has been instrumental in the early detection and assessment of the emerging SARS-COV-2 virus, supporting the first one hundred cases and contact investigations. The system has enabled real-time monitoring of epidemiological, clinical and laboratory characteristics of various respiratory infections. It informed public health interventions and is currently employed for epidemiological studies, such as COVID-19 breakthrough infections and vaccine effectiveness estimation in SARI patients.

CONCLUSIONS

SISI is an effective tool for respiratory surveillance harmonization, offering efficient multi-source mechanisms for detection, monitoring, and generating actionable data to guide strategic public health interventions. The development of multi-surveillance indicators represents a significant future enhancement within this integrative approach.

Keywords: Integrated Surveillance Information System, Mosaic Framework, Respiratory diseases, Surveillance
ABSTRACT ID: 818
PRESENTED BY: Kujtim Mersini, Albania / mersini2003@yahoo.com

POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

The StopptCOVID Study: Analysing the Effectiveness of Non-Pharmaceutical Interventions in Germany Across Three Waves

A. Hicketier [1]
V. Bremer [2], M. an der Heiden [3]
[1, 2,3] Dept. Infectious Disease Epidemiology, Robert Koch Institute (RKI)

BACKGROUND
The StopptCOVID study explored the effectiveness of non-pharmaceutical interventions (NPIs) in Germany, covering the time frame from the first wave to the early stages of the fourth wave between March 2020 and August 2021.

METHODS
We employed linear regression on the logarithm of the R-value, utilising daily data on NPI regulations for counties and federal states. Adjustments were made for variants, vaccination rates, seasonality, and holidays. Sensitivity analyses were conducted to identify optimal lags, compare different pandemic waves, age groups, weighting schemes, seasonalities, and model types, including generalised linear models.

RESULTS
Our findings demonstrate that NPIs were effective, but restrictions in a single area were not sufficient to control the spread of SARS-CoV 2. Combining NPIs in many areas like private and public spaces, culture, education and businesses led in the most stringent adaption to a reduction of the R-value by 66% (95%-CI: 64% - 67%). Reducing the stringency step by step resulted in reductions of 60% (58% - 61%), 52% (50% - 54%) and 41% (37% - 45%). In comparison, we estimate a reduction of the R-value by 34% with 50% of the population vaccinated, 57% reduction with 75% vaccinated and 72% reduction with 87.5% vaccinated. The models also reveal the difficulty in quantifying the effect of individual measures, highlighting the limitations of such analytical methods.

CONCLUSIONS
Our findings underscore the importance of a systematic approach to controlling the spread of a respiratory pathogen, since transmissions occur in many settings. Potential pitfalls are in modelling and the inherent uncertainty resulting from data issues, e.g. data on regulations not on actual human behaviour, and the observational nature of the study.

Keywords: COVID-19, Public Health Surveillance, Germany, Statistical Models, Prevention and Control, Public Policy
ABSTRACT ID: 118
PRESENTED BY: Andreas Hicketier, Germany / hicketiera@rki.de

POSTER TOUR 18

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Surveillance in action: strategies, challenges, and innovations

MODERATOR
Esther Kukielka Zunzunegui

Abstract

Using passive samplers in sewage to monitor a hepatitis A outbreak at an Amsterdam school

M. de Jong [1]
R. Schilperoort [2], H. Vennema [3], C. van der Weijden [4], J. Langeveld [5], M. Welkers [6], M. Schim van der Loeff [7], M. Prins [8], A. de Roda Husman [9], E. Fanoy [10], G. Medema [11]

[1, 4, 6] Department of Infectious Diseases, Public Health Service Amsterdam (GGD Amsterdam), Amsterdam, the Netherlands
[2, 5, 9, 10] Partners4UrbanWater, Nijmegen, the Netherlands
[3] Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[7, 8] Department of Infectious Diseases, Public Health Service Amsterdam (GGD Amsterdam), Amsterdam, the Netherlands | Amsterdam UMC, University of Amsterdam, Internal Medicine, Amsterdam Infection & Immunity Institute, Amsterdam, the Netherlands
[11] KWR Water Research Institute, Nieuwegein, the Netherlands

BACKGROUND
Hepatitis A virus (HAV) infections during childhood are frequently asymptomatic. Sewage monitoring using passive samplers could be useful for detecting ongoing circulation of HAV. We report the applicability of sewage monitoring during an HAV outbreak at a primary school.

METHODS
In a primary school five HAV cases were reported between 19 October 2022 and 27 December 2022. Passive samplers (small tools holding an absorbent to collect specimens) were deployed from 10 November 2022 until 24 March 2023 in two manholes and two sewage pumping stations in the surroundings of the school. Twice per week the passive samplers were replaced and sent for viral RNA extraction and HAV testing using digital droplet PCR. Passive samplers positive for RNA of HAV were also sequenced. PCR and sequencing was also performed on blood and feces of the HAV cases.

RESULTS
Sewage monitoring indicated ongoing presence of HAV during and after case reports. All HAV-RNA-positive sewage specimens until 8 February 2023 shared an identical HAV strain with suspected origin in Somalia (type 1.B), which matched the strain detected in cases. Another strain of HAV with suspected origin in Morocco (type 1.A) was detected in sewage from 15 February 2023 onwards, but no associated cases were reported. Parents and teachers were informed about hygiene and vaccination. Sewage monitoring was stopped three months after the last reported case.

CONCLUSIONS
Passive sampler-based sewage monitoring is a low-cost method to rapidly detect HAV shedding which can be linked to diagnosed cases. It detects unnoticed viral shedding and it allows monitoring of outbreak courses and intervention impact. This makes it a valuable tool for public health authorities to adapt their response during HAV and other pathogen outbreaks.

Keywords: Sewage sampling, Passive samplers, Hepatitis A Virus, Outbreak detection, Sewage monitoring, Sewage diagnostics
ABSTRACT ID: 35
PRESENTED BY: Maarten de Jong, Netherlands / maadjong@ggd.amsterdam.nl

POSTER TOUR 19

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Evaluating the hepatitis B vaccination impact in the Republic of Moldova – a nationwide representative serosurvey of children born in 2013

M. Brandl [1]
A. Ceban [2], O. Sajin [3], V. Bucov [4], A. Cataraga [5], S. Stratulat [6], N. Furtuna [7], V. Gutu [8], S. Gheorghita [9], M. Gassowski [10], L. Mosina [11], A. Mozalevskis [12], S. Dudareva [13], S. Datta [14]

[1] Robert Koch Institute, Berlin, Germany | Charité – Universitätsmedizin Berlin, corporate member of Freie Universität Berlin and Humboldt-Universität zu Berlin, Germany
[2, 9] WHO Country Office, Chisinau, Republic of Moldova
[3, 4, 5, 6, 7, 8] National Agency for Public Health, Chisinau, Republic of Moldova
[10, 13] Robert Koch Institute, Berlin, Germany
[11, 14] WHO Regional Office for Europe, Copenhagen, Denmark
[12] WHO Headquarters, Geneva, Switzerland

BACKGROUND
The Action plan for the health sector response to viral hepatitis in the WHO European Region set regional targets for the control of hepatitis B (HepB) through immunization, including a prevalence of HepB antigen (HBsAg) of maximum 0.5% in vaccinated cohorts. The Republic of Moldova (MDA) has implemented universal HepB vaccination of new-borns since 1995. We conducted a nationwide representative serosurvey to estimate HBsAg prevalence in children born in MDA in 2013 to validate achievement of HepB control targets.

METHODS
We used probability-based sampling and a two-stage cluster design yielding a sample stratified by region (Chisinau/North/Central/South) and degree of urbanization (urban/rural), reflecting the population distribution. All children born in 2013 and registered in primary healthcare facilities were eligible for participation. We collected blood samples from all participants and tested for HepB core antibodies (anti-HBc), using Enzyme-Linked Immunosorbent Assay (ELISA). Anti-HBc-positive samples were tested for HBsAg and HBsAg-positive samples confirmed, using ELISA. We obtained information on HepB vaccination from vaccination cards.

RESULTS
Out of a target population of 42,372 children, 3,352 were sampled. Of the sampled children, 3,064 (91%) participated. Most participating children were 7 years old (n=3,030, 99%), 1,604 (52%) were boys. We found a weighted, national seroprevalence estimate of 3.1% (95%CI=2.1–4.5) for anti-HBc and of 0.21% (95%CI=0.08–0.53) for HBsAg. Of participants, 93% had received HepB birth dose vaccination and 92% at least three doses in total of HepB vaccine.

CONCLUSIONS
Our study demonstrated the impact of HepB vaccination and allowed MDA to validate the achievement of regional HepB control targets. Other countries with high vaccination coverage could use HepB serosurveys and apply for validation. Sustained efforts in MDA will be crucial on the path to HepB elimination.

Keywords: Hepatitis B, Moldova, Europe, Seroepidemiologic studies, Prevalence, Vaccination
ABSTRACT ID: 676
PRESENTED BY: Michael Brandl, Germany / brandlm@rki.de

POSTER TOUR 19

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Outcomes of post-exposure vaccination prophylaxis for Mpox in paediatric contacts during 2022 outbreak in Catalonia

B. Borras-Bermejo [1]
L. Pinós-Tella [2], O. Parés-Padell [3], G. Tejada [4], A. Peñalver-Piñol [5], M. Martínez-Marcos [6], I. Martínez [7], J. Mendioroz [8], X. Martínez-Gómez [9]

[1, 2, 3, 4, 5, 9] Preventive Medicine and Epidemiology Department, Hospital Univeristari Vall d'Hebron, Barcelona, Spain
[6] Preventive Medicine Service, Sub-directorate General for Health Promotion, Secretariat of Public Health, Department of Health, Generalitat de Catalunya, Barcelona, Spain
[7, 8] Subdirecció General de Vigilància i Resposta a Emergències de Salut Pública. Agència de Salut Pública de Catalunya. Secretariat of Public Health, Department of Health, Generalitat de Catalunya, Barcelona, Spain

BACKGROUND
Since June 2022, the Spanish Health Authorities recommended post-exposure prophylaxis for contacts of Mpox cases with a high risk of severe disease (children, pregnant women and immunosuppressed patients). One dose of MVA-BN vaccine (live, non-replicating) was offered up to 14 days after exposure to prevent infection (off-label use for ‹18 years old). The aim of this study is to describe the characteristics of vaccinated paediatric contacts and their clinical outcomes in Catalonia.

METHODS
A cohort study of all paediatric Mpox contacts identified by Epidemiology Surveillance Units in Catalonia and referred to Vall d'Hebron Hospital for prophylaxis. Age, sex, and characteristics of the exposure to index case were collected, and MVA-BN vaccine was administered after obtaining informed consent. Patients were followed up weekly up to 28 days for active surveillance of Mpox symptoms onset and appearance of any adverse event related to vaccination.

RESULTS
32 children were vaccinated (53% males, mean age of 7.2 years, Standard Deviation (SD) 5.3). Most parents agreed to vaccinate their children (84%), only 4 refused. The mean days from the last day of exposure to vaccination were 3.9 (SD 3). 3 children were exposed to multiple household Mpox cases. No contact developed the disease. Due to compatible symptoms, 2 children seek medical consultation, but laboratory tests ruled out the suspicion. No severe adverse events were registered.

CONCLUSIONS
Postexposure prophylaxis seemed effective in preventing disease in children and it was well tolerated and accepted. We add information to the little that exists regarding MVA-BN vaccine safety and effectiveness in vulnerable populations. Vaccination was a key strategy in the control of Mpox outbreak and it should continue to be recommended among those most at risk.

Keywords: Vaccine, Mpox, Post-exposure prophylaxis, Paediatric
ABSTRACT ID: 611
PRESENTED BY: Blanca Borras-Bermejo, Spain / blanca.borras@vallhebron.cat

POSTER TOUR 19

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Taking stock of vaccine hesitancy, associated characteristics and moral values among Dutch parents

D. Bussink-Voorend [1]
J. Hautvast [2], R. Akkermans [3], A. Krom [4], M. Hulscher[5]

[1, 2] Radboud University Medical Center, Radboud Institute for Health Sciences, Primary and Community Care, Nijmegen, the Netherlands
[3, 5] Radboud University Medical Center, Radboud Institute for Health Sciences, IQ Healthcare, Nijmegen, the Netherlands
[4] Leiden University Medical Center, Medical Ethics and Health Law, Leiden, the Netherlands

BACKGROUND
The acceptance of routine childhood vaccinations is relatively high in the Netherlands. However, coverage rates have gradually declined in the past decade. We aimed to assess the prevalence of vaccine hesitancy (VH), associated socio-demographic and vaccination related characteristics and moral values among parents of newborn children.

METHODS
Through a cross-sectional study eligible parents of newborn children were asked to fill out a questionnaire. Associations of characteristics with the outcome measure VH were analyzed univariate and multivariate. Adjusted odds ratio's (aOR) with 95% confidence intervals (CI) were calculated.

RESULTS
We included 533 parents and found that 27% of parents had some level of VH. In the multivariate analysis a parent's low or middle education level (AOR 2.00, CI 1.19-3.35) and having a religious or anthroposophical life philosophy (AOR 1.77, CI 1.65-2.92) were positively associated with VH. Having a positive intention to vaccinate (AOR 0.321, CI 0.14-0.74) and higher age (AOR 0.918, CI 0.87-0.97) were negatively associated with VH. Additionally, parents with VH considered the value vaccine risks more important ($p = 0.003$) and the values universalism/ benevolence ($p < 0.001$) and disease prevention ($p < 0.001$) less important compared to parents without VH.

CONCLUSIONS
Parents with VH more often had a lower education level or a religious or anthroposophical life philosophy compared to parents without VH. Less often, parents with VH were older or had the intention to vaccinate their child. These findings give cause to further explore VH among parents with a low or middle education level, or a religious or anthroposophical life philosophy. Furthermore, these finding provide valuable information to support parents in their decision making about vaccination, taking characteristics and moral values into account.

Keywords: Vaccine hesitancy, Childhood vaccination, Parents, Moral values
ABSTRACT ID: 99
PRESENTED BY: Daphne Bussink-Voorend, Netherlands/ daphne.bussink-voorend@radboudumc.nl

POSTER TOUR 19

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Impact of under-reporting on vaccine effectiveness estimates derived from retrospective cohort studies: a simulation study

C. Sacco [1]
M. Manica [2], V. Marziano [3], M. Fabiani [4], A. Mateo Urdiales [5], G. Guzzetta [6], S. Merler [7], P. Pezzotti [8]

[1] Istituto Superiore di Sanità
ECDC Fellowship Programme, Field Epidemiology path (EPIET)
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 6, 7] Fondazione Bruno Kessler
[4, 5, 8] Istituto Superiore di Sanità

BACKGROUND
During the COVID-19 pandemic observational studies of vaccine effectiveness (VE) became key for public health decision-making. In this context, studies using surveillance data linked with vaccination registries are used but may be biased due to underreporting of cases (i.e. under-ascertainment and under-notification). We aimed to explore the magnitude and the direction of this source of bias on VE estimates over time.

METHODS
We developed a stochastic individual-based model (IBM) to simulate the transmission dynamics of a respiratory virus, assuming a timeframe of one year, under different scenarios varying the following parameters: reporting rate, attack rate (AR), magnitude and duration of protection provided by natural infection and vaccination. We used the produced synthetic data to estimate the expected bias of VE against notified infection at different time intervals after vaccination and at different calendar periods, using the unvaccinated and 0-14 days post-vaccination, separately, as reference groups.

RESULTS
Non-differential underreporting of cases between vaccinated and unvaccinated biased VE estimates towards underestimation, particularly at longer time intervals since vaccination, and the magnitude of the bias increased with high AR (ie. ≥50%). With low AR, underreporting of up to 70% of cases did not affect VE estimates. In presence of differential underreporting, the use of 0-14 days post-vaccination as reference group provided more robust estimates as oppose of the non-vaccinated.

CONCLUSIONS
This study highlights that underreporting of cases is an important issue in the estimation of the VE, especially in epidemics characterized by high AR. Public health bodies should be aware that in such context the estimated VE against infection may appear to wane more quickly over time than in reality.

Keywords: Vaccine effectiveness, Selection bias, Respiratory viruses, Under-reporting, Simulation studies
ABSTRACT ID: 717
PRESENTED BY: Chiara Sacco, Italy / chiara.sacco@iss.it

POSTER TOUR 19
DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Effectiveness of control interventions during a large meningococcal C outbreak in Tuscany, Italy

G. Guzzetta [1]
M. Ajelli [2], A. Miglietta [3], C. Fazio [4], A. Neri [5], S. Merler [6], G. Rezza [7], P. Stefanelli [8]

[1] Fondazione Bruno Kessler
[2] Indiana University School of Public Health
[3] Central Tuscany Health Authority | Regional Health Agency of Tuscany | Istituto Superiore di Sanità
[4, 5, 8] Istituto Superiore di Sanità
[6] Fondazione Bruno Kessler
[7] Ministry of Health

BACKGROUND
Neisseria meningitidis is a bacterium that causes invasive meningococcal disease (IMD), a major cause of meningitis and sepsis. We evaluated the impact of interventions during the response to a large outbreak caused by serogroup C meningococci (MenC) belonging to the hyperinvasive strain ST-11 cc-11 in Tuscany, Italy, during 2015–16, and compared results with alternative intervention scenarios. The outbreak disproportionately affected the gay and bisexual community and transmission was amplified by overcrowded attendance to discos and clubs.

METHODS
We applied an individual-based model of MenC transmission calibrated to data from the 2015–16 outbreak, derived from genomic and epidemiological investigations. The model accounts for transmission in households, schools, discos/clubs and the general community.

RESULTS
We estimated an outbreak reproduction number of 1.35 (95% prediction interval: 1.13–1.47), and a probability of developing IMD of 4.6 for every 1,000 new MenC carriage episodes (95% confidence interval: 1.8–12.2). The implemented interventions (chemoprophylaxis, vaccination of close contacts of IMD cases and an age-targeted vaccination campaign), were effective in ending the outbreak. Case-based interventions (including ring vaccination) alone would have not been sufficient to control the outbreak in absence of widespread reactive vaccination. The definition of which age groups should be prioritized for immunization critically impacted the effectiveness and efficiency of control measures.

CONCLUSIONS
We suggest that widespread reactive vaccination prioritized on age groups at highest risk should be the preferred response during outbreaks of highly transmissible MenC strains. These results can support effective guidelines for the control of outbreaks caused by hypervirulent and hyperinvasive meningococcal strains.

Keywords: Serogroup C Neisseria meningitidis, Contact tracing, Vaccination, Statistical data interpretation, Stochastic processes
ABSTRACT ID: 167
PRESENTED BY: Giorgio Guzzetta, Italy / guzzetta@fbk.eu

POSTER TOUR 19

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Insights on vaccination

MODERATOR
Nina Rodic

Abstract

Knowledge, attitudes and practices of influenza vaccination among healthcare workers in Bitola, Republic of North Macedonia

S. Popovska Kljuseva [1]
D. Kochinski [2]

[1] Center for Public Health Bitola
[2] Institut for Public Health Skopje

BACKGROUND

Influenza vaccination is generally recommended for all healthcare workers (HCWs). However, the vaccination rates among this group is still low. This study aimed to assess HCWs' knowledge, attitude, and practice (KAP) about the influenza vaccine, among HCWs' in Bitola, Republic of North Macedonia.

METHODS

From June 2019 to July 2019 we conducted a descriptive cross-sectional study in the Clininic hospital in Bitola, Republic of North Macedonia. A total of 67 HCWs' were randomly selected. The questionnaire was completed in the Department of epidemiology in the Center for Public Health Bitola. Questions included demographic and social data and KAP regarding influenza and influenza vaccination.

RESULTS

Of the 67 HCWs invited in this study, 64 (95,5%) responded and completed the questionnaire in full. Only 5 (7,8%) HCWs had ever received influenza vaccine; 41 (64,1%) HCWs reported that vaccine manufacturer and country of origin influenced their vaccination decision. Main reasons cited by the participants for refuse/ would refuse vaccination against influenza included: fear of side effects (26; 40,6%), and a perception of good personal health, without the need for vaccination (23; 35,9%). Only 30 (46,9%) HCWs recommend vaccination as protection against influenza on their patients.

CONCLUSIONS

Influenza vaccination coverage among healthcare workers is very low in Bitola. Fear of adverse effects and vaccine safety are important barriers. Measures to increase coverage are urgently needed.

Keywords: Knowledge, Attitudes, Practices, Influenza vaccination, Health care workers
ABSTRACT ID: 450
PRESENTED BY: Svetlana Popovska Kljuseva, North Macedonia, Republic of / svetlanapopovska@yahoo.com

POSTER TOUR 20

FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Waterborne outbreaks and related intervention

MODERATOR
Margaret Fitzgerald

Abstract

A community waterborne outbreak due to Salmonella Bovismorbificans, Greece, August 2022

L. Politi [1]
T. Sideroglou [2], A. Chrysostomou [3], G. Mandilara [4], I. Spiliopoulou [5], A. Theofilou [6], A. Bordhoka [7], S. Poufta [8], K. Mellou [9], T. Zaoutis [10], D. Paraskevis [11]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden | Department of Microbial Resistance and Infections in Health Care Settings, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization
[2, 8] Department of Foodborne and Waterborne Diseases, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organisation, Athens, Greece
[3] Department of Foodborne and Waterborne Diseases, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[4] National Reference Centre for Salmonella and Shigella, School of Public Health, University of West Attica, Athens, Greece
[5] ECDC Fellowship Programme, Public Health Microbiology (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden Water Microbiology Laboratory, Central Public Health Laboratory, National Public Health Organization, Athens, Greece
[6] Central Public Health Laboratory, National Public Health Organization, Vari, Greece
[7] Public Health Directorate, Peloponnese Region, Tripoli, Greece
[9] Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[10, 11] National Public Health Organization, Athens, Greece

BACKGROUND
In August 2022, the Greek National Public Health Organisation was notified about increased gastroenteritis cases in a small town (A) in Southern Greece. We conducted an outbreak investigation to identify the source and implement control measures.

METHODS
In an unmatched 1:3 case-control study, cases and controls were defined as individuals residing or visiting town A between 10-24 August 2022, with and without diarrhea, vomiting, and fever, respectively. They were interviewed about food and drink exposures. Cases' stool samples were cultured on agar plates and further characterised by serotyping, antimicrobial susceptibility testing (Disc Diffusion Method) and Pulse Field Gel Electrophoresis (PFGE). Environmental investigations included tap water sampling for microbiological and chemical analysis in town A, and inspection of the water supply system.

RESULTS
We identified 33 cases (55% female) with median age of 9 years (range: 0-79 years). Tap water consumption was the only significant risk factor (OR=5.46, 95%CI= 1.02-53.95). Salmonella (S.) Bovismorbificans isolated from stool (n = 8) and a tap water sample (n = 1) had identical PFGE profiles. No resistant isolates were identified. Salmonella spp. was detected in the water supply system, and chlorination levels were found to be below acceptable limits in samples prior and during the outbreak. Despite investigations, no conclusion was drawn on how bacterial contamination occurred. We released public advice to consume bottled water and adhere to strict hand hygiene rules until tap water was declared suitable for drinking.

CONCLUSIONS

Epidemiological, laboratory and environmental investigation revealed a short-lived waterborne S. Bovismorbificans outbreak in town A in August 2022. We recommend regional and municipal water safety authorities to monitor more efficiently the water supply systems, towards water safety planning, to mitigate risks.

Keywords: Salmonella enterica serovar Bovismorbificans, Waterborne outbreak, Acute gastroenteritis, Sase-control study, Water safety monitoring

ABSTRACT ID: 75

PRESENTED BY: Lida Politi, Greece / l.politi@eody.gov.gr

POSTER TOUR 20

FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Waterborne outbreaks and related interventions

MODERATOR
Margaret Fitzgerald

Abstract

Cholera: back to the basics of community sanitation - an outbreak in the Municipality of Manay, Philippines, 2021

I. Gonzales [1]
K. Gecosala [2], R. Martinez [3], A. Segarra [4]

[1] Department of Health | Epidemiology Bureau | Philippine Field Epidemiology Training Program
[2, 3, 4] Department of Health

BACKGROUND
On 10 October 2021, the event-based surveillance unit captured a media report on a clustering of diarrheal diseases in Manay. Upon verification, a total of 101 cases with seven deaths were reported. An investigation was initiated to determine the existence of an outbreak, identify the source and mode of transmission, determine risk and protective factors, and recommend control measures.

METHODS
A case was a previously well individual who is a resident of Manay with onset of acute diarrhea (≥3 episodes/24 hours) between 26 September to 16 November 2021. Active case finding was done. Baseline incidence was established through records review. Water sources were sampled. Rectal swabs were obtained for bacteriologic testing. An unmatched case-control study was conducted to identify risk and protective factors.

RESULTS
Previous data showed only 26 acute watery diarrhea cases in the same period. A total of 171 cases with 15 deaths were identified. Cases initially peaked on 29 September, followed by two other peaks in October and November after rainy days. The median age was 23 years (IQR: 9 to 38 years). Untreated wells were the primary water source. All sources were positive for E. coli on rapid testing. Eight cases were positive for Vibrio cholerae Ogawa Biotype El Tor. Cases were more likely to have a toilet (OR: 4.78, CI: 1.51-19.87) or find garbage (OR: 4.58, CI: 1.23-25.36) around their water source, or have a household member with diarrhea (OR 3.89, CI: 1.89-8.99).

CONCLUSIONS
There was a Cholera outbreak in Manay. Poor sanitation practices were identified factors. We recommended proper toilet placement and garbage disposal, improving water systems with water treatment at the source, and infection prevention practices when caring for the ill.

Keywords: Cholera, Sanitation, Disease, Outbreak, Case-control study
ABSTRACT ID: 394
PRESENTED BY: Ian Christian Gonzales, Philippines / icagonzales@doh.gov.ph

POSTER TOUR 20
FRIDAY 24 NOVEMBER 2023
15:30-16:15

Waterborne outbreaks and related intervention

MODERATOR
Margaret Fitzgerald

Abstract

A Waterborne Outbreak of Hemolytic Uremic Syndrome (HUS) caused by Verotoxigenic E. Coli O104:H4 after Feast of Sacrifice in Turkiye

B. Kurt [1]
O. Koyu [2], M. Beslen [3], S. Topal [4], F. Temel [5], G. Barlas [6], M. Ozdemir [7], S. Aydemir [8], B. Levent [9], S. Senses-Ergul [10]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10] Republic of Turkiye Ministry of Health

BACKGROUND
In July 2022, after the feast of sacrifice 17 cases from Yuva Village in Bolu were admitted to hospital with symptoms of fever, abdominal pain, vomiting, and diarrhoea including 6 children admitted for dialysis and intensive care. During the follow-up, 103 additional cases, including 67 acute gastroenteritis and 36 haemolytic uremic syndromes (HUS), with one death were reported from the same village. We investigated the outbreak to identify risk factors and recommend control measures.

METHODS
We conducted a retrospective cohort study and enrolled 472 residents. A suspected case was defined as a person residing in Yuva village with abdominal pain or nausea or vomiting or diarrhoea during July 2022. A confirmed HUS case was defined as a suspected case with clinically/microbiologically confirmed. We collected 87 stool samples, 18 food samples and 4 water samples from the community. We calculated RR(95%CI) for water sources with significance level of 5%.

RESULTS
Among 103 suspected cases 35% developed HUS with a mean age of 27±24. Majority of cases were female (69%), and half of the cases were under 16 years of age. Most common symptoms were abdominal pain (100%), diarrhoea (92%), and nausea (81%). Consumption of tap water was significantly associated with illness (RR:3.3, 95%CI:1.4-7.6). Verotoxigenic E. Coli O104:H4 were detected in the neighbourhood water tank (1/1), tap water (2/3) and clinical samples (11/30). Environmental investigation revealed an additional water supply contaminated with sacrificial animal waste was connected to water tank.

CONCLUSIONS
Our investigation confirmed the single source outbreak associated with consumption of contaminated tap water. Water tanks were cleaned and chlorinated. Uncontrolled additional water source was disconnected, and the local community were educated on water sanitation.

Keywords: Verotoxigenic E. Coli, Haemolytic Uremic Syndrome, Outbreak Investigation, Feast of Sacrifice
ABSTRACT ID: 180
PRESENTED BY: Burak Kurt, Turkey / kurtburak@msn.com

POSTER TOUR 20
FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Waterborne outbreaks and related intervention

MODERATOR
Margaret Fitzgerald

Abstract

Waterborne outbreak in Bilecik, Türkiye, February 2022

T. Baltaci [1]
G. Dogan-Türkçelik [2], R. Arslan [3], N. Gürsoy [4], Y. Demirbilek [5], F. Temel [6], D. Furkan-Sevindi [7], S. Senses-Ergül [8]
[1, 2, 3, 4, 5, 6, 7, 8] Republic of Türkiye MoH

BACKGROUND
In Türkiye, acute gastroenteritis cases are monitored through syndromic surveillance. In February 2022, an outbreak of acute gastroenteritis was reported in Bilecik Province, Türkiye. We investigated the outbreak to identify risk factors and recommend control measures.

METHODS
We defined a probable case who is admitted to the provincial hospital with symptoms of nausea or vomiting or diarrhoea between February 1-8, 2023. We conducted 1:1 unmatched case control study to identify modifiable risk factor. We analysed 217 probable cases and their asymptomatic neighbourhood controls and calculated the adjusted OR (ORadj) by controlling age. We evaluated stool and water samples microbiologically and chemically and measured free chlorine in water.

RESULTS
Of 4069 acute gastroenteritis cases, 57% were female. The crude attack rate was 17.8‰, with no hospitalizations. Forty-six percent of probable cases were between 5-24 age. Most common symptoms were nausea (81%), vomiting (81%), diarrhoea (69%). When age was controlled for, illness was significantly associated (twice in cases compared) with consumption of tap water (95% CI:1.1-4.1, p=0.025). Entamoeba Histolytica Adhesin Antigen was detected in two, and Norovirus GI/II was detected in all (5) stool samples. Rotavirus, Escherichia coli, coliform bacteria, Norovirus GII, and enterococcus/faecal streptococci were found in the water samples. Environmental investigation showed that an additional water source from an uncontrolled water tank was connected to the water network.

CONCLUSIONS
Our investigation confirmed the single source acute gastroenteritis outbreak associated with consumption of tap water. Pathogens isolated from stool samples indicated that drinking water was contaminated by sewage water. We educated the community to avoid the use of contaminated water source. The water source, which was added to the network later, was disconnected from the water network system.

Keywords: Norovirus, Gastroenteritis, Waterborne diseases, Outbreak, Case-control studies
ABSTRACT ID: 185
PRESENTED BY: Tugba Baltaci, Turkey / tubism.tubism@hotmail.com

POSTER TOUR 20

FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Waterborne outbreaks and related intervention

MODERATOR
Margaret Fitzgerald

Abstract

A large outbreak of Hepatitis A Outbreak in a northern community in Canada 2021-2022: Public Health Interventions and Immunisation in a Remote Context

Y. Tcholakov [1]
[1] McGill University | Nunavik Regional Board of Health and Social Services

BACKGROUND
In October 2021, four cases of hepatitis A were reported in a non-endemic remote Indigenous community in northern Canada. We conducted an outbreak investigation to identify the source, understand transmission dynamics and contain spread.

METHODS
We defined cases by specific anti-HAV IgM serology or detection of genotype 1a Hepatitis A nucleic acids. We explored common food exposure for the initial cases, attempted to identify source cases among high-risk populations and settings, namely food handlers and daycares, and performed an environmental investigation exploring drinking water contamination.

RESULTS
We identified 39 cases across two communities; sixty-seven percent (26/39) were 10 years of age or younger and fifty-one percent (20/39) required hospitalization. Whole-genome sequencing linked this outbreak to four prior cases elsewhere in Canada. No food item or epidemiological link with cases outside the region was identified as the source of the outbreak; drinking water investigations did not reveal contamination. We identified two under-immunized groups in the region: children under 9 due to a change in the provincial schedule, and adults born between 1970 and 1981 who were never targeted in mass vaccination campaigns. Investigations brought to light disparities in determinants of health such as unreliable water and sanitation services, overcrowded homes, and a strained fragile health system. We controlled the outbreak by rapid case investigations, post-exposure prophylaxis, the expansion of the regular immunization program to younger ages, catch-up vaccination for non-immune adults, and population-wide communications.

CONCLUSIONS
This study describes the interventions deployed to control one of the largest recent Hepatitis A outbreaks in Canada. Addressing these core determinants of health is a critical public health priority to prevent future outbreaks and enhance community resilience.

Keywords: Hepatitis A, Disease Outbreak, Epidemiology, Public Health
ABSTRACT ID: 25
PRESENTED BY: Yassen Tcholakov, Canada / yassentch@gmail.com

POSTER TOUR 20
FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Waterborne outbreaks and related intervention

MODERATOR
Margaret Fitzgerald

Abstract

Investigation and characterisation of a cholera outbreak in Lebanon after three decades cholera-free, 2022

A. Jouny [1]
E. White Johansson [2], M. Baaklini [3], A. Abou Fayad [4], N. Ghosn [5]

[1] Ministry of Public Health (MOPH) | Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET), European Centre
[2] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[3, 5] Ministry of Public Health (MOPH)
[4] American University of Beirut Medical Center

BACKGROUND
On 5 October 2022, Lebanon confirmed its first case of cholera in a Syrian refugee in the context of cholera outbreak in Syria. This was the first cholera case recorded in Lebanon since 1993. An outbreak investigation was conducted to characterize cases, identify the source, and recommend containment measures.

METHODS
Suspected cases were defined by acute watery diarrhoea symptoms in cholera-confirmed settlements or having suspected case symptoms with complications (dehydration or death) in non-cholera settlements. Confirmed cases were defined by a positive stool culture for toxigenic Vibrio cholera (O1 or O139). Upon notification, we interviewed cases to obtain demographic information, clinical symptoms, and risk factors. Environmental samples from water infrastructure were collected in new cholera-confirmed settlements.

RESULTS
In October-December 2022, 5,715 cholera cases were identified, of which 18% were hospitalised (n=1049/5715) and <1% died (23/5715). Among cases, 14% (848/5715) had stool specimen collected for culture and 8% (484/5715) were positive showing Vibrio Cholerae O1 subtype Ogawa Sequencing Type 69. The attack rate was 1/1000. The median age was 16 years (range: <1-89 years); 53% were female; and 63% were Lebanese versus 30% Syrian nationality. 77% resided in the Great North. V. cholerae was detected in 32% of drinking water (24/74), 19% of domestic water (23/121) and 50% of irrigation water (5/10) samples.

CONCLUSIONS
Epidemiological and microbiological findings confirmed cholera presence in the population and water infrastructure. The recommendations for the environmental response include proper maintenance of water plants, assessment of sanitation infrastructure, promotion of chlorine use in households, and community engagement in water testing. The recommendations for the public health response include hygiene education, enhanced surveillance, proper case management, and use of oral cholera vaccine in high-risk areas.

Keywords: Cholera, Lebanon, Outbreak, Acute diarrheal diseases, Drinking water, Sanitation
ABSTRACT ID: 368
PRESENTED BY: Abass Jouny, Lebanon / jounyabass@gmail.com

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POSTER TOUR 21

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

Measurement of Population-Level Measles Immunity in Ontario, Canada Using Serology Data Linked to Health Administrative Data

A. Ariyarajah [1]
N. Crowcroft [2], K. Brown [3], J. Kwong [4], S. Bolotin [5]

[1] University of Toront | Centre for Vaccine Preventable Diseases | ICES
[2] World Health Organization | University of Toronto
[3] University of Toronto | Public Health Ontario | ICES
[4] University of Toronto | ICES | Public Health Ontario|Centre for Vaccine Preventable Diseases
[5] University of Toronto | Centre for Vaccine Preventable Diseases | Public Health Ontario

BACKGROUND
Although Canada eliminated measles in 1998, the risk of importation remains. It is thought that population measles immunity at 95% is needed to prevent sustained endemic transmission. However, measles vaccine coverage data in Ontario is available only in schoolchildren. Our study aims to measure population measles immunity in Ontario by sociodemographic factors.

METHODS
Measles seroprevalence was measured among 349,705 individuals who had diagnostic testing performed at Public Health Ontario laboratories in 2014-2016. We counted individuals with IgG antibody concentration ≥275mIU/mL as seropositive. We obtained sociodemographic and health information from health administrative databases at ICES. We conducted sensitivity analyses and post-stratification estimation to reduce bias.

RESULTS
We found that measles seroprevalence was 83.4% (95% CI, 83.2-83.5%), falling below the 95% target immunity. Seroprevalence varied significantly by age, with children aged 1-5 years at 83.4% (95% CI, 81.6-84.9%), adolescents and young adults aged 12-29 years having the lowest at 75.6% (95% CI, 75.4-75.9%), and adults aged ≥50 years having the highest at 96.9% (95% CI, 96.7-97.0%) (p<0.001). Immigrant data were available only as of 1985 and therefore, among individuals aged 28 years, immigrants had a significantly lower seroprevalence of 69.3% (95%CI, 68.8-69.8%) compared to individuals born in Canada, who had a seroprevalence of 77.5% (95%CI, 77.2-77.8%) (p<0.001).

CONCLUSIONS
Measles seroprevalence is below 95%, which may pose a risk for the potential re-establishment of endemic transmission. Older individuals had higher seroprevalence, possibly due to robust immunity from previous infection. Adolescents, young adults, and young immigrants had lower seroprevalence, potentially due to lower vaccine coverage or waning immunity. Further work is needed to understand the implications of this, including vaccine coverage estimates among adults in Ontario and cellular immunity in vaccinated individuals.

Keywords: Measles, Serology, Routinely Collected Health Data, Humoral Immunity
ABSTRACT ID: 425
PRESENTED BY: Archchun Ariyarajah, Canada/ archchun.ariyarajah@mail.utoronto.ca

POSTER TOUR 21
DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

20 years of MERIN (Meningitis and Encephalitis Registry in Lower Saxony and Bremen) – design and main results of a syndromic surveillance system

M. Wollenweber [1]
K. Beyrer [2], A. Baillot [3], M. Monazahian [4], I. Holle [5], E. Mertens [6], S. Rettenbacher-Riefler [7]

[1] Public Health Agency of Lower Saxony (NLGA), Department of Infectious Disease Epidemiology, Hannover, Germany, PAE | Postgraduate Training for Applied Epidemiology, Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany | ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5, 6, 7] Public Health Agency of Lower Saxony, (NLGA), Department of Infectious Disease Epidemiology, Hannover, Germany

BACKGROUND
In 2003, the MERIN surveillance system was implemented to monitor circulating pathogens that cause aseptic neurological complications in Lower Saxony and Bremen, Germany.MERIN offers free laboratory diagnostics for hospitalized patients with suspected aseptic meningitis/encephalitis or polio-like symptoms, thereby detecting various neurotropic pathogens such as enteroviruses.We present the main findings of 20 years of MERIN surveillance, focussing on its ability to detect non-polio-enteroviruses (NPEV), the most common cause of viral meningitis.

METHODS
We analysed MERIN surveillance data collected from 2003–2022 to describe patient demographics, absolute and relative frequencies of sample material, pathogens, including NPEV and their most frequent serotypes detected with direct and serological laboratory methods, and seasonal patterns.

RESULTS
A total of 33,000 samples (38% cerebrospinal fluid, 34% serum, 25% stool) from 13,200 patients, 55% male, 56% <10 years old (median=7, min=0, max=91, IQR=12) were analysed, with 30% testing positive for NPEV. The most frequently detected serotypes were Echovirus 30 (11%), Echovirus 06 (5%), and Coxsackie B-virus (3%). Polioviruses were not identified.Consistent seasonality was detected with higher sample submissions and positive rates during summer (May to September).Additional to NPEV, MERIN revealed at least 17 other pathogens (e.g. Borrelia 7%, Adenovirus 2%, Varicella 1%).

CONCLUSIONS
MERIN is a surveillance system based on clinical signs. It elucidates the spectrum and circulation of pathogens, mostly NPEV, that may cause aseptic infections of the central nervous system, hence enabling targeted individualized therapy, improving patient management and forming the basis for public health actions.By detecting and identifying enteroviruses, MERIN also provides information required to document the polio-free status of Lower-Saxony and Bremen, thus contributing to the national enterovirus surveillance.

Keywords: Syndromic surveillance, Enterovirus, Meningitis, Encephalitis, Poliovirus surveillance
ABSTRACT ID: 300
PRESENTED BY: Mareike Wollenweber, Germany / mareike.wollenweber@nlga.niedersachsen.de

POSTER TOUR 21

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

Local increase of serogroup B invasive meningococcal disease caused by an emerging strain, Auvergne-Rhône-Alpes region, France, 2021-2022

A. Thabuis [1]
G. Terpant [2], M. Taha [3], A. Ronnaux-Baron [4], A. Deghmane [5], C. Saura [6], L. Zanetti [7], A. Barret [8]

[1, 2, 6] Santé publique France, the national public health agency, regional office, Auvergne-Rhône-Alpes, Lyon
[3, 5] National Reference Centre for Meningococci, Institut Pasteur, Paris
[4] Regional health agency, Auvergne-Rhône-Alpes, Lyon
[7, 8] Santé publique France, the national public health agency, Department of Infectious Diseases, Saint-Maurice

BACKGROUND
During the Covid-19 pandemic, while the incidence of invasive meningococcal disease (IMD) in France was lower than usual, a new serogroup B meningococcal strain emerged locally in the Auvergne-Rhône-Alpes region.

METHODS
Investigations combined bacteriological characterisation and epidemiological analysis. Whole genome sequencing was performed on isolates in order to characterise genomic relatedness. Coverage of isolates by meningococcal B vaccines was also assessed through genomic prediction and serological analysis. Characteristics of cases and their epidemiological links, and risk analysis by calculating local incidence rates and standardised incidence ratios (SIR) were used to guide control measures.

RESULTS
Twelve cases were reported over a twelve months period (August 2021 – July 2022). Isolates from all cases belonged to a new sequence type ST-3753 of the clonal complex cc41/44, covered by vaccines against serogroup B meningococci. Most cases (11/12) were aged between 16 and 21 years and 7 of them reported partying. One case died. Two areas were considered as hyperendemic, with incidence rates above the threshold defined in French guidelines for serogroup B IMD (3 per 100,000 inhabitants) and a number of cases significantly higher than expected in the 16-24 year-old population (respective SIR: 35 and 56). Health authorities decided to recommend meningococcal B vaccination to 16-24 years-old individuals in both areas from July 2022. In January 2023, vaccination coverages were estimated at 18% for one dose and 11% for two doses.

CONCLUSIONS
In one hyperendemic area, without new case, the vaccination campaign ended in January 2023. In the other area, two new cases occurred between November 2022 and March 2023 in young adults, suggesting an ongoing risk of IMD, so the vaccination campaign was reinforced in this population.

Keywords: Meningococcal Infections, Neisseria meningitidis, Serogroup B, Disease Outbreak, Public Health Surveillance, Immunization Programs
ABSTRACT ID: 286

PRESENTED BY: Alexandra Thabuis, France / alexandra.thabuis@santepubliquefrance.fr

POSTER TOUR 21

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

Varicella burden in Portugal from 2013 to 2022: implications of the COVID-19 pandemic in a context of a missing varicella vaccine recommendation

B. Grau-Pujol [1]

M. Perez Duque [2], M. Valente Pinto [3], T. Fernandes [4], P. Vasconcelos [5], P. Pinto Leite [6], A. Peralta Santos [7]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Center for Public Health Emergencies, Directorate-General of Health, Lisbon, Portugal | Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal

[2] Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal | Pathogen Dynamics Group, Department of Genetics, University of Cambridge, Cambridge, United Kingdom

[3] Primary Immunodeficiencies Unit, Hospital Dona Estefânia, Pediatric University Hospital, Lisbon, Portugal
Centro de investigação Interdisciplinar Egas Moniz (CiiEM), Instituto Universitário Egas Moniz, Caparica, Portugal

[4] National Vaccination Program, Directorate of Disease Prevention and Health Promotion, Directorate-General of Health, Lisbon, Portugal

[5] Center for Public Health Emergencies, Directorate-General of Health, Lisbon, Portugal

[6] Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal

[7] Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal | Comprehensive Health Research Centre (CHRC), Escola Nacional de Saúde Pública, Universidade NOVA de Lisboa, Lisboa, Portugal

BACKGROUND

Varicella spreads through direct contact or respiratory droplets. Several European countries recommend varicella vaccination, particularly in view of vulnerable populations prone to complications. Notably, Portugal lacks a varicella vaccine recommendation. Within the National Immunization Technical Advisory Group framework, this study aims to investigate varicella patterns in hospitalized cases in Portugal, considering the impact of non-pharmaceutical interventions such as lockdowns during the COVID-19 pandemic.

METHODS

We utilized electronic health records from public hospitals to gather information on varicella hospitalizations (coded as ICD-9 052 and ICD-10 B01). This data included patient age group, sex, residency region, duration of hospital admission, and complications in Portugal from 2013 to 2022. We calculated the annual hospitalization incidence and the proportion of complications. We segmented the timeline into pre-lockdowns (January 2013 to February 2020), during-lockdowns (March 2020 to May 2021), and post-lockdowns periods (June 2021 to December 2022). Subsequently, we employed an interrupted time-series analysis to compare hospitalization incidence trends across these periods. We fitted a negative binomial regression model adjusted for seasonality and calculated the relative rates (RR).

RESULTS

During 2013-2022, Portugal had 3,423 varicella hospitalizations: 2,635 (77%) patients were < 15-year-old, 1,369 (40%) patients had at least one complication, and 43 (1%) patients died. Pre-lockdowns, annual hospitalisation incidence was 26/100,000 in 2019, and it was stable during the period (RR=0.99, 95%CI 0.99-1.00). Hospitalisations declined 78% during-lockdowns (RR=0.22, 95%CI 0.14-0.35) and increased 11% monthly post-lockdowns (RR=1.11, 95%CI 1.08-1.14), though still below pre-lockdown levels.

CONCLUSIONS

Our study shows stable pre-lockdowns varicella-related hospitalizations, but decreasing during the pandemic in Portugal. The possible accumulation of susceptible individuals could trigger varicella outbreaks, where varicella vaccine recommendations could be needed. Further research should explore the accumulation of varicella-susceptibles.

Keywords: Vaccine, Chickenpox, Portugal, COVID-19, Time-series analysis, Lockdown
ABSTRACT ID: 332
PRESENTED BY: Berta Grau-Pujol, Portugal / bertagrau6@gmail.com

POSTER TOUR 21

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

Genomic characterization, antimicrobial susceptibility and vaccine reactivity to 4CMenB of Neisseria meningitidis producing invasive meningococcal disease in Spain

J. Roca [1]
A. Mir-Cros [2], C. Ardanuy [3], A. Bellés [4], J. Calvo [5], J. Càmara [6], E. Cendejas-Bueno [7], E. Cercenado [8], P. Egea [9], F. Gómez-Bertomeu [10], P. López-Roa [11], L. Martínez-Martínez [12], C. Muñoz-Almagro [13], D. Navarro De La Cruz [14], M. Orellana [15], A. Pérez [16], M. Quesada [17], C. Rodrigo [18], A. Rodríguez-Fernández [19], E. Ruiz De Gopegui [20], C. Sarvisé [21], J. González-López [22]

[1, 2, 22] Hospital Universitari Vall d´Hebron, Barcelona, Spain|Centro de Investigación Biomédica en Red de Enfermedades Infecciosas (CIBERINFEC), Madrid, Spain
[3, 6] Hospital Universitari de Bellvitge, L'Hospitalet De Llobregat, Spain
[4] Hospital Universitari Arnau de Vilanova, Lleida, Spain
[5, 19] Hospital Universitario Marqués de Valdecilla, Santander, Spain
[7] Hospital Universitario La Paz, Madrid, Spain
[8] Hospital Universitario Gregorio Marañón, Madrid, Spain
[9, 12] Hospital Universitario Reina Sofía, Córdoba, Spain
[10, 21] Hospital Universitario Joan XXIII, Tarragona, Spain
[11, 15] Hospital Universitario 12 de Octubre, Madrid, Spain
[13, 16] Hospital Sant Joan de Déu, Esplugues De Llobregat, Spain
[14] Hospital Clínico Universitario de Santiago, Santiago De Compostela, Spain
[17, 18] Hospital Universitari Germans Trias i Pujol, Badalona, Spain
[20] Hospital Universitari Son Espases, Palma, Spain

BACKGROUND

The 4CMenB (Bexsero®) effectively prevents meningococcal disease (IMD) caused by serogrup B Neisseria meningitidis (Nm). However, it does not protect against all NmB variants.This study aims to describe the genomic epidemiology, antimicrobial susceptibility and expected reactivity to 4CMenB of IMD-causing Nm in Spain.

METHODS

A total of 284 Nm producing IMD were collected from various clinical microbiology laboratories in Spain between 2011-2022. Molecular characterization was performed by WGS. Antigenic reactivity prediction (ARP) to 4CMenB was studied through MenDeVAR index and antimicrobial susceptibility testing was performed by gradient diffusion test.

RESULTS

An increase in IMD cases was observed from 2011 to 2019. Serogroup B was the most prevalent (57.4%), followed by W (23.0%), C (10.3%) and Y (7.1%). The most prevalent lineages among NmB were CC-ST213 (35.8%), CC-ST461 (13%), CC-ST269 (12.3%), and CC-ST32 (11.7%). For NmW and NmC, the predominant lineage was CC-ST11 (89.2% and 82.8%, respectively). ARP showed that 17.3% of NmB would be covered by 4CMenB, 22.2% not covered and for the remaining 60.5% the reactivity was unknown.No isolates showed resistance to cephalosporins or carbapenems. Fourteen isolates (7%) were resistant to azithromycin and nineteen (10%) to penicillin. Only one isolate was resistant to ciprofloxacin and another one to rifampicin.

CONCLUSIONS

NmB and NmW are the leading causes of IMD in Spain, with pandemic lineages being the predominant circulating strains. While the reactivity of most NmB isolates to 4CMenB is unknown, a significant proportion (22.2%) may evade 4CMenB protection, especially those linked to CC-ST213. Nm isolates remain susceptible to current antimicrobial treatments and prophylaxis. Surveillance of Nm's molecular epidemiology, antimicrobial susceptibility and vaccine reactivity is crucial for adjusting vaccination schedules and optimizing antimicrobial therapies.

Keywords: Neisseria meningitidis, Whole genome sequencing, 4CMenB vaccine, Vaccine reactivity, Invasive meningococcal disease

ABSTRACT ID: 601

PRESENTED BY: Josep Roca, Spain / josep.roca@vhir.org

POSTER TOUR 21

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Vaccine preventable diseases: surveillance, outbreaks and burden of disease

MODERATOR
Silvia Funke

Abstract

Insufficient access to diagnosis hampers surveillance of invasive meningococcal disease in the Republic of Moldova

V. Gutu [1]

[1] National Agency for Public Health, Chisinau, Moldova, MediPIET

BACKGROUND

The burden of invasive meningococcal disease (IMD) is currently not well established. Vaccines are available in the private sector, but not included in the vaccination program. Because IMD symptoms resemble other invasive bacterial infections, microbiological investigation is necessary to confirm the diagnosis. We reviewed the diagnostic accuracy of IMD cases notified in Moldova from 2009-2021.

METHODS

We reviewed the medical records of cases notified to the National Agency for Public Health. We listed the laboratory methods used to diagnose IMD cases. According to the official case classification, confirmed cases are clinically-compatible cases, in which the etiology has been confirmed by microbiological methods. Probable cases are ascertained by a medical panel based on symptoms if the laboratory and epidemiological information is missing.

RESULTS

During 2009-2021, physicians notified 342 cases of IMD. Of these, 112 (32%) did not have any biological specimen collected, 169 (49%) had a negative result of their microbiological investigation, and 61 (18%) were confirmed following a microbiological investigation. The following tests gave positive results: nasopharyngeal smear (17), culture from blood specimen (17), thick drop (7), cerebrospinal fluid (CSF) microscopy (9), culture from CSF (2), rash bacteriology (1), PCR from CSF (8). Only 3 cases of infants had the Neisseria meningitides serogroup determined, 2 of which serotype C and 1 is serotype B.

CONCLUSIONS

Most IMD cases in Moldova are not laboratory confirmed. Confirmation of meningococcal etiology is important to guide antimicrobial therapy, chemoprophylaxis, and vaccination of close contacts. Identification of circulating serogroups, in turn, can inform strategies for future vaccination programs. We recommend implementing standardized diagnostic protocols in healthcare institutions of Moldova, and serogroup determination for all diagnosed cases.

Keywords: Invasive meningococcal disease, Neisseria meningitidis, Laboratory diagnosis
ABSTRACT ID: 713
PRESENTED BY: Veaceslav Gutu, Moldova / veaceslav.gutu@gmail.com

POSTER TOUR 22

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

Socioeconomical inequalities in the incidence of bacteraemias in England: a national surveillance and data linkage study

A. Mazzella [1]
A. Charlett [2], R. Hope [3], C. Brown [4], D. Chudasama [5]
[1, 2, 3, 4, 5] UK Health Security Agency

BACKGROUND
Health inequities across deprivation and ethnic groups are known to exist in England; however, the extent of this in bacteraemia has not been investigated. Identifying high-incidence groups could facilitate risk mitigation.

METHODS
We used data from England's bacteraemia surveillance system (MRSA, MSSA, E. coli, Klebsiella spp., P. aeruginosa), NHS data on mortality and ethnicity, Index of Multiple Deprivation, and Office of National Statistics population denominators by geographical area and ethnic group.All patients with bacteraemia between 2018 and 2022 were included; age-standardised annual incidence rates were determined.

RESULTS
Incidence of bacteraemia increased with deprivation, from 91.7 (95% CI 91.0 – 92.5) to 176.7 (95% CI 175.5 – 178.0) bacteraemias per 100,000 in the 20% least and most deprived areas, respectively. These inequalities were most pronounced with MRSA (0.9 vs 2.2 per 100,000 in the least and most deprived areas, respectively); less with P. aeruginosa (6.4 vs 9.4, respectively).Incidence was higher among the Asian (139.5 bacteraemias per 100,000 population, 95% CI 137.2 – 141.7) and Black (131.6, 95% CI 128.4 – 134.8) ethnic groups compared to White (110.7, 95% CI 110.3 – 111.2), whilst it was lowest among the Mixed (89.2, 95% CI 84.2 – 94.3) and Other (44.9, 95% CI 42.3 – 47.7) ethnic groups. This pattern was observed for all pathogens except MSSA: incidence for MRSA (2.0, 1.7, 1.2), E. coli (85.3, 71.1, 64.8), Klebsiella spp. (27.9, 30.4, 19.4), and P. aeruginosa (7.6, 11.5, 6.9 bacteraemias per 100,000 population) were determined in the Asian, Black, and White ethnic groups respectively.

CONCLUSIONS
Between 2018 and 2022, people living in deprived areas of England and the Asian and Black ethnic minorities were disproportionately affected by bacteraemia.

Keywords: Bacteremia, Ethnicity, Socioeconomic factors, Health inequities, Public health surveillance
ABSTRACT ID: 334
PRESENTED BY: Andrea Mazzella, United Kingdom / andrea.mazzella@ukhsa.gov.uk

POSTER TOUR 22

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

Group B Streptococcus maternal colonization and neonatal sepsis in Belgium between 2012 and 2021: a description of the epidemiological situation

Z. Bognar [1]
C. Leroy [2], V. Van Leeuw [3], R. Goemaes [4], P. Melin [5], C. Meex [6], R. Sacheli [7], L. Cornelissen [8]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Department of Epidemiology and Public Health, Sciensano, Brussels, Belgium
[2, 3] Centre d'Épidémiologie Périnatale (CEpiP)
[4] Studiecentrum voor Perinatale Epidemiologie (SPE)
[5, 6, 7] Centre National de Référence (CNR-NRC) Streptococcus agalactiae (GBS), CHULiège
[8] Department of Epidemiology and Public Health, Sciensano, Brussels, Belgium

BACKGROUND
Maternal Group B Streptococcus (GBS) vaccines are under development and supported by WHO. Genital maternal GBS colonization can lead to early onset neonatal sepsis. In Belgium, GBS screening between 35-37 gestational weeks and, if positive, intrapartum antibiotic prophylaxis is recommended since 2003. However, limited information on GBS colonization in pregnant women and neonatal sepsis is available. Therefore, we aimed to provide the first comprehensive overview to inform future prevention campaigns.

METHODS
We calculated the proportion of pregnancies in which women were GBS-screened, -colonized and treated between 2012-2020 in Belgium, using birth certificates. We estimated the yearly nation-wide incidence of neonatal (GBS) sepsis (age <1 year) between 2016-2021 using ICD-coded hospital data.

RESULTS
In Belgium, overall 90% (1040666/1156565) of pregnant women was GBS-screened of which 18% (192317/1040666) tested positive. Proportions remained stable over the years. Of positives, 85% (163189/192317) received intrapartum antibiotic prophylaxis. Additionally, 4% (33797/848349) of GBS-negative and 28% (32032/114798) of untested pregnant women received prophylaxis.From 2016 to 2021, the incidence of bacterial neonatal sepsis declined from 8.8/1000 to 6.5/1000 live births, and neonatal GBS sepsis from 1.3/1000 to 0.3/1000 live births. Male:female ratio of GBS neonatal sepsis was 1.4:1 and early-onset disease (age <7 days) accounted for 86% of cases. Every year, 1-4 deaths due to neonatal GBS sepsis were reported.

CONCLUSIONS
The proportion of maternal colonization and the incidence of neonatal GBS sepsis in Belgium are comparable with other European countries. The screening proportion could be improved and still considerable number of neonatal GBS cases could be prevented. Our study provides baseline data that can contribute to the assessment of additional preventive strategies, such as maternal GBS immunization, further reducing cases and antibiotic usage.

Keywords: Group B Streptococcus (GBS), Neonatal sepsis, Maternal colonisation, Pregnancy, Belgium
ABSTRACT ID: 189
PRESENTED BY: Zsofia Bogna, Belgium / dr.bognar.zsofia@gmail.com

POSTER TOUR 22

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

An outbreak of invasive Group A Streptoccocus in a residential care facility in the North-East of Ireland

C. Carroll [1]
J. Prendergast [2], C. Magnone [3], A. Meehan [4], C. Carpenter [5], C. Migone [6], K. Quintyne [7], H. Byrne [8], S. Owens [9], R. Cunney [10], M. Meehan [11], R. Connolly [12], P. Mullane [13]

[1] HSE Public Health, Area A, Dr Steevens Hospital, Dublin 8
[2, 3, 4, 5, 8] HSE Public Health, Area A, Kells Business Park, Kells, Co. Meath
[6, 7, 13] HSE Public Health, Area A, Dr Steevens Hospital, Dublin 8
[9] Clermont Health, Haggardstown, Co. Louth
[10, 11] Irish Meningitis and Sepsis Reference Laboratory, Children's Health Ireland at Temple Street, Dublin 1
[12] MIcrobiology Department, Our Lady of Lourdes Hospital, Drogheda, Co. Louth

BACKGROUND
There has been an unseasonal increase in invasive Group A Streptococcus (iGAS) notifications in Ireland since October 2022. We describe an iGAS outbreak involving three residents in a residential care facility (RCF) in North-East Ireland in early 2023.

METHODS
HSE Public Health Area A were notified of an iGAS infection in a resident of a 69-bedded RCF on 31/01/2023. An outbreak was declared and an outbreak control team (OCT) convened on 07/02/2023 when two further iGAS cases in the RCF were notified. Risk assessment of staff and resident contacts was undertaken. Surveillance commenced for symptoms and signs of GAS/iGAS infection in residents and staff. The Public Health team performed a site visit to provide infection prevention and control (IPC) support. Isolates were sent for emm sequence typing.

RESULTS
The OCT considered screening of contacts, but prophylaxis was deemed preferable to reduce delays in instituting control measures. Prophylaxis was provided to 38 residents and 34 staff. Probable localised GAS infection was identified in a staff member; suspected localised GAS infection in a resident was ruled out by microbiological investigation. No further cases of iGAS were identified. Recommendations from the site visit included advice on terminal cleaning and cleaning of shared equipment, and ongoing education on hand hygiene and masking. All isolates possessed an identical emm sequence type (emm18.12), an emm subtype not previously detected in Ireland.

CONCLUSIONS
Rapid delivery of IPC support and prophylaxis were key outbreak control measures. Emm18 is infrequently associated with GAS infections in Ireland and elsewhere; there is limited evidence on its pathogenicity. Irish national iGAS guidance should be expanded to include management of cases and outbreaks in RCFs.

Keywords: Streptococcus pyogenes, Nursing Homes, Infection Control, Surveillance, Prophylaxis
ABSTRACT ID: 582
PRESENTED BY: Ciara Carroll, Ireland / ciara.carroll2@hse.ie

POSTER TOUR 22

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

STEC clearance times in children and risk of transmission in childcare setting remain unchanged despite increase in detected non-O157 cases in England

A. Vusirikala [1]
S. Rowell[2], G. Fox[3], J. Bell[4], R. Manuel[5], D. Sumilo[6], G. Dabke[7], N. Love[8], C. Jenkins[9], N. McCarthy[10], S. Balasegaram[11]

[1] UK FETP Fellow UK Health Security Agency
[2, 3, 4, 5, 7] UK Health Security Agency Health Protection Operations
[6, 10] NIHR HPRU in Gastrointestinal Infections
[8] UK Health Security Agency Health Protection Operations | NIHR HPRU in Gastrointestinal Infections
[9, 11] NIHR HPRU in Gastrointestinal Infections | UK Health Security Agency Health Protection Operations

BACKGROUND
Shiga toxin producing Escherichia coli (STEC) causes severe symptoms, including haemolytic uraemic syndrome (HUS). In England, children aged ≤ 5 years with STEC are excluded from childcare until they have two negative faecal specimens. Prolonged carriage extends exclusion, disrupting family life, education and earnings. Detection of non-O157 STEC serotypes has increased in England since PCR introduction (18 cases in 2011, 655 in 2020). We aimed to review clearance time by serotype and transmission risk to guide exclusion advice from changing STEC epidemiology.

METHODS
We extracted laboratory confirmed STEC cases aged ≤5 years, residing in England and attending childcare facilities, with diarrhoea onset or sample date from 01/04/2018-31/03/2022. Time to clearance was the interval between date of onset or first positive specimen and first negative specimen. We identified transmission risk by assessing whether secondary cases were linked to settings attended by infectious cases.

RESULTS
124/367 cases were non-O157. The median time to clearance was 32 days (IQR 20-44) with no significant difference between O157 and non-O157 serotypes. Six cases (2%) shed for ≥ 90 days, of which four were female aged 1-2 years old and three were non-O157. Cases who reported bloody diarrhoea had a 17% (95% CI 4-29) decrease in time to clearance. Sixteen settings were screened (13 O157, 3 non-O157); four settings (2 O157, 2 O26) had secondary cases, with a 13% attack rate in close contacts.

CONCLUSIONS
The clearance estimates were consistent with previous findings (median 31 days, IQR 17-41) and the transmission risk identified was low. These do not provide evidence indicating a need to change guidance regarding exclusion and supervised return of prolonged shedders, due to changes in identified serotypes.

Keywords: Shiga-Toxigenic Escherichia coli, Clearance, Transmission, Childcare settings
ABSTRACT ID: 270
PRESENTED BY: Amoolya Vusirikala, United Kingdom / amoolyav@gmail.com

POSTER TOUR 22

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

Impact of COVID-19 on thirty-day all-cause mortality associated with Gram-negative Bacteraemia in England

T. Hasan [1]
N. Zhu [2], R. Hope [3]

[1] Healthcare Associated Infection and Antimicrobial Resistance Division, UK Health Security Agency (UKHSA) Health Protection Research Unit (HPRU) in Healthcare Associated Infections and Antimicrobial Resistance, Imperial College London, UK
[2] Health Protection Research Unit (HPRU) in Healthcare Associated Infections and Antimicrobial Resistance, Imperial College London, UK
[3] Healthcare Associated Infection and Antimicrobial Resistance Division, UK Health Security Agency (UKHSA)

BACKGROUND
Hospital-onset Gram-negative bloodstream infection (GNBSI) rates during the COVID-19 pandemic were the highest we had seen in England and coincided with an increase in associated thirty-day all-cause mortality. We investigate how COVID-19 impacted this rise in GNBSI associated mortality.

METHODS
Data on Escherichia coli, Pseudomonas aeruginosa and Klebsiella spp. cases in England from 1st January 2015 to 31st December 2021, was extracted. A GNBSI was considered COVID-19 associated if the COVID-19 onset was within 28 days before or after the date of first positive blood culture. The impact of COVID-19 on thirty-day all-cause mortality was estimated using seasonally adjusted logistic regression models.

RESULTS
Total E. coli, P. aeruginosa and Klebsiella spp. infections were 220,421, 22,834 and 57,913, respectively. During the pandemic,7.1% E. coli (3,984/56, 142),10.9% P. aeruginosa (711/6,504) and 11.2% Klebsiella spp. (1,921/17,130) cases had an associated COVID-19 infection.Mortality during the pandemic was significantly higher compared to prepandemic period in all organisms (E. coli aOR 1.23, 95% CI: 1.18-1.29; P. aeruginosa aOR 1.25, 95% CI: 1.12-1.39; Klebsiella spp. aOR 1.35, 95% CI: 1.25-1.45). These odds were mostly mitigated when only non-COVID-19 associated infections were modelled (E. coli aOR 1.13, 95% CI: 1.08-1.18; P. aeruginosa aOR 1.07, 95% CI: 0.95-1.20; Klebsiella spp. aOR 1.16, 95% CI: 1.08-1.26).During the pandemic, cases with an associated COVID-19 infection were more likely to die (E. coli aOR: 2.30, 95% CI: 2.13-2.48; P. aeruginosa aOR 3.14, 95% CI: 2.64-3.73; Klebsiella spp. aOR 2.43, 95% CI: 2.18-2.71).

CONCLUSIONS
Higher GNBSI associated mortality during the COVID-19 pandemic was largely driven by cases that had an associated COVID-19 infection, however, a smaller increase in mortality was still observed for non-COVID-19 associated cases.

Keywords: Gram-Negative Bacterial Infections, Bloodstream Infection, COVID-19, Healthcare Associated Infections, Mortality, Public Health Surveillance
ABSTRACT ID: 295
PRESENTED BY: Taimoor Hasan, United Kingdom/ taimoor.hasan@ukhsa.gov.uk

POSTER TOUR 22
DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Infectious diseases and at risk populations

MODERATOR
Charlotte Hammer

Abstract

Preparing long-term care facilities for future pandemics – a systematic review on the effectiveness of non-pharmacological interventions against viral, respiratory pathogens with pandemic potential

S. Jan M [1]
S. Bimczok [2], S. Lisak-Wahl [3], H. Schütt [4], L. Arnold [5]

[1] European Programme for Intervention Epidemiology Training, European Centre for Disease Prevention and Control, Solna, Sweden | Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[2, 3, 4, 5] Academy of Public Health Services, Duesseldorf, Germany

BACKGROUND
In pandemics due to air-borne pathogens, long-term care facilities (LTCF) constitute high-risk settings. LTCF residents accounted for 30–60% of all deaths attributed to COVID-19 in Europe during the early phase of the pandemic. We assessed the effectiveness of non-pharmacological interventions (NPIs; e.g., visiting restrictions, masks usage, screening) in preventing and mitigating outbreaks of viral, respiratory pathogens with pandemic potential, including SARS-CoV-2 and influenza.

METHODS
We performed a systematic review following Cochrane guidance. We conducted database searches for the period 1970–2022 without geographic restrictions in MEDLINE, Embase, CINAHL and the specialized registries on COVID 19-literature by Cochrane and WHO. We included experimental and quasi-experimental studies assessing the effects of NPIs on infection-related outcomes among LTCF residents and staff, compared to no intervention. We assessed risk of bias using RoB2 and ROBINS-I and certainty of evidence (CoE) using GRADE.

RESULTS
We included 18 studies, 15 of which focused on SARS-CoV-2. Risk of bias was high in all but 3 studies.We found evidence of effectiveness for: mask and PPE use by staff (3/3 studies; CoE: very low), outbreak control measures (2/2 studies CoE: very low), cohorting of staff (1/1 study; CoE: low) regular testing of staff (3/3 studies, CoE: moderate), hand hygiene interventions (3/3 studies, CoE: moderate), and a combination of multiple NPIs (3/3 studies; CoE: moderate). No eligible study assessed visiting restrictions, air filtration, or prolonged solitary confinement.

CONCLUSIONS
Empirical studies to close the identified research gaps on NPIs in LCTFs are needed; especially on NPIs with severe adverse consequences such as visiting restrictions. In the context of high disease burden in LTCFs in past pandemics, preparedness strategies ought to consider the assessed NPIs as mitigating measures despite remaining uncertainties.

Keywords: SARS-CoV-2, Nursing Homes, Pandemics, Communicable Disease Control, Infection Control, Non-pharmacological interventions
ABSTRACT ID: 499
PRESENTED BY: Jan M Stratil, Germany / stratilj@rki.de

POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

Ongoing mumps genotype G outbreak among primary school children, June September 2023, The Hague, The Netherlands

K. Wassing [1]
T. Garcia Vilaplana [2], K. te Paske [3], L. de Vos Klootwijk [4], M. Petrigani [5]

[1] Department of Infectious Diseases, Public Health Service Haaglanden, Den Haag, the Netherlands
[2] Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[3, 4, 5] Department of Infectious Diseases, Public Health Service Haaglanden, Den Haag, the Netherlands

BACKGROUND

Outbreaks of mumps among primary school-aged children in the Netherlands were infrequent, with the last reported in 2007-2009. Since the 1987 introduction of the MMR vaccine into the Dutch immunization program, mumps outbreaks had been rare, primarily affecting a specific orthodox community known for vaccine refusal and, more recently, vaccinated students due to waning immunity. However, in June 2023, a mumps outbreak emerged in The Hague, affecting both vaccinated and unvaccinated children.

METHODS

We collected probable and confirmed mumps cases in the Haaglanden area since June 2023. Probable cases exhibited clinical symptoms and epidemiological links with confirmed cases, which were laboratory-diagnosed and, if sequenced, matched the outbreak strain. Contact tracing provided demographic and epidemiological data, used in the outbreak analysis.

RESULTS

Cases included children under 12 (16/24, median age 6, range 1-10, 50% female) and adults (8/24, range 30-44, 100% female). Of the cases, 12/24 were vaccinated (7/16 children, 5/8 adults), with 3/8 having an unknown vaccination status. Eight cases attended one primary school, and ten had household-type contact. We identified six household clusters (range 2-3 cases each), with one having no known link to the school or related cases except residing in the same neighborhood, and one unlinked adult case.

CONCLUSIONS

This outbreak suggests mumps may re-emerge as a childhood infection in the Netherlands due to declining vaccine coverage. Despite the small case numbers, the proportion of vaccinated cases among young children is unexpectedly high. Waning immunity has been a suggested cause for outbreaks in vaccinated adolescents, it appears less likely in younger children, warranting further investigation. Alongside efforts to improve vaccine uptake, assessing the risk of future mumps outbreaks in the vaccinated younger population remains essential.

Keywords: Mumps, Outbreak, Vaccine Coverage, Public Health, Chilhood immunisation, Vaccination
ABSTRACT ID: 963

PRESENTED BY: Kevin Wassing, Netherlands / kevin.wassing@ggdhaaglanden.nl

POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

Triangulated phylodynamic-spatio-temporal analysis of A/H5N1 outbreak in cats in Poland during spring/summer 2023

A. Jarynowski [1]
V. Belik [2]

[1] Institute of Veterinary Epidemiology and Biostatistics, FUB | Polish Society of Hygiene, Wroc?aw
[2] Institute of Veterinary Epidemiology and Biostatistics, FUB

BACKGROUND

We performed phylodynamic-spatio-temporal analysis of A/H5N1 epizootic in cats in Poland in Spring-Summer 2023.

METHODS

Data and methods triangulation were applied based on: 1) 30 (positive) and 27 (negative) cases from WOAH reference lab, 2) suspected 87 cases submitted by animal owners (participatory epidemiology), 3) daily time series of i) Google queries for Avian Influenza (AI), cats disease and cats deaths, as well as ii) mentions of cat/cats and AI in social and traditional media. 4) 19 RNA sentences of viruses.Wildbirds abundance and distance to water reservoirs and trajectories of birds migratory paths were used as covariates. We compared chain and hierarchical structure of clusters of various types of data in multidimensional space.

RESULTS

Positive cases form chains structure both on bird migration paths and close to high abundance of nesting sites of waterbird (verified by comparison of Average Nearest Neighbour distance and betweenness clustering of positive case vs both controls); the A/H5N1 was already probably circulating in cats in the second half of May in regions bordering with Ukraine (a moth before first confirmed case); there are at least 2 (eastern and western Poland) separate introductions of viruses (according to k-mean and DBScan).

CONCLUSIONS

We recommend to perform active monitoring (serology) of water birds (these overwintering for some reasons), rodents and cats in Pomerania and selected sites in Western Poland (as maybe some low viral pressure were still there the latest in July). Common outbreak investigation of veterinary and sanitary inspection revealed multiple gaps in emerging new zoonotic threats. Thus, use of unconventional data and infodemic management should be incorporated into surveillance/risk assessment schema, becase we might handle with similar probles in next years in Europe.

Keywords: Phylodynamic-spatio-temporal analysis, Avian influenza, Zoonotic disease of poultry, Spillovers, Companion animals

ABSTRACT ID: 926
PRESENTED BY: Andrzej Jarynowski, Poland / ajarynowski@gmail.com

POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

Ongoing multidrug-resistant tuberculosis outbreak among the African immigrant population from 2019 to 2023 in Bilbao, Spain

C. Jacqueline [1]
X. Beraza Ortiz [2], C. Castells Carrillo [3], F. Garros Garay [4], J. Unzaga Barañano [5], S. Quiros Fernandez [6], M. Bilbao Calvo [7], L. Herrera-Leon [8]

[1] Instituto de Salud Carlos III, Centro Nacional de Microbiologia, Majadahonda, Spain|ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 6, 7] Unidad de Epidemiologia, Delegación Territorial de Salud de Bizkaia, Bilbao, Spain
[4] Departamento de Neumologia, Hospital de Santa Marina, Bilbao, Spain
[5] Servicio de Microbiologia, Hospital de Basurto, Bilbao, Spain
[8] Instituto de Salud Carlos III, Centro Nacional de Microbiologia, Majadahonda, Spain

BACKGROUND
In June 2023, a case of multidrug-resistant tuberculosis (TB) was reported in Bilbao, Spain, and showed a similar resistance profile as the one described in a local 2019-2022 outbreak within primarily African immigrant population. The first case in 2019 was a child with negative sputum and no active TB cases were identified among contacts. Later, nine additional cases were reported as part of the same cluster based on single nucleotide polymorphism (SNP, cut-off <5 SNPs). The outbreak investigation was reactivated to confirm if the case belonged to the outbreak.

METHODS
Contact-tracing was realized based on the principle of concentric circles of exposure and TB testing was performed using the Mantoux method. Active case finding was done by alerting the regional laboratories and European countries. The cultivated sample from the suspected case was analyzed with whole genome sequencing followed by SNP analyses.

RESULTS
Contact-tracing established an epidemiological link between the original outbreak and the new case. In total five other contacts were identified, two tested positive for latent TB. No other country or Spanish region reported related cases. The 2023 case-sample belonged to the same SNP cluster as the 10 original outbreak cases. Further, the case showed an identical sequence to the first case and three other cases of the outbreak.

CONCLUSIONS
Epidemiological and microbiological methods were key to confirm that the outbreak is still ongoing but also to identify this outbreak initially as no epidemiological link was observed between the first cases of 2019. The outbreak control is challenging, and relies on a multidisciplinary approach including communication, to increase awareness in city hospitals and in the community, and social sciences to consider culture differences and language barrier.

Keywords: Multi-drug resistance, SNP analyses, Contact tracing, Immigrants
ABSTRACT ID: 889
PRESENTED BY: Camille Jacqueline, Spain / camjacqueline.pro@gmail.com

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POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
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Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

Epidemiologically independent and genetically distinct dengue local transmission events in Italy, summer 2023

F. Riccardo [1]
F. Ferraro [2], D. Cereda [3], M. Viscardi [4], M. Faccini [5], F. Vairo [6], G. De Carli [7], E. Di Rosa [8], F. Baldanti [9], F. Maggi [10], M. Del Manso [11], A. Bella [12], E. Di Maggio [13], A. Mateo Urdiales [14], G. Venturi [15], C. Argentini [16], M. Di Luca [17], F. Monaco [18], M. Perrotta [19], F. Defilippo [20], M. Sciсluna [21], I. Pati [22], S. Pupella [23], M. Cardillo [24], L. Lombardini [25], P. Poletti [26], S. Merler [27], P. Pezzotti [28], F. Maraglino [29], A. Palamara [30]

[1] Istituto Superiore di Sanità, Rome
[2, 4, 7, 15, 16, 17, 19, 22, 23, 24, 25, 28, 29, 30] Italian Ministry of Health, Rome
[3] General Directorate of Welfare, Regione Lombardia, Milan
[5] Health Protection Agency, Metropolitan Area of Milan, Milan
[6] SERESMI, INMI L. Spallanzani Rome Italy
[8] Service of Hygiene and Public Health (SISP), Rome
[9] Reference Laboratory for arboviruses, Lombardy Region, Pavia
[10] Reference laboratory for arboviruses, Lazio Region, INMI L. Spallanzani, Rome
[11, 12, 13, 14] Istituto Superiore di Sanità, Rome
[18] Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise G. Caporale, Teramo
[20] Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Brescia
[21] Istituto Zooprofilattico Sperimentale del Lazio e della Toscana, Rome
[26, 27] Fondazione Bruno Kessler, Trento

BACKGROUND

In 2020, the first limited local transmission event of dengue virus was detected in Italy driven by Aedes albopictus, a widespread competent mosquito vector. Following this event, no further local transmission was identified until August 2023, when several locally acquired cases were notified. We aim to describe the ongoing investigation.

METHODS

We describe local transmission events of confirmed human dengue infection in 2023 under investigation and reported to the national surveillance system. We report the number of cases, their demographic characteristics, spatial distribution and period of symptoms onset.

RESULTS

As of September 7 2023, 132 cases of PCR-confirmed human dengue infection were reported: 15 were locally acquired (72% males, median age 57, age range 3-88 years) with symptoms onset between August 2 and September 2. Local transmission events were epidemiologically and genetically distinct. The largest cluster is being actively investigated in a village in Lombardy, where DENV1 infections were confirmed. In the Lazio region, four confirmed cases were notified. Two DENV1 infections were probably exposed in the city of Rome and two DENV3 infections in a holiday resort in the province of Latina. All cases presented mild disease. Analyzed human sequences in Lombardy and Lazio did not show clustering, also within serotype 1. Dengue virus infections were confirmed in mosquito pools in both Regions.

CONCLUSIONS

Given prevailing favourable climatic conditions, a widespread competent vector and numerous imported cases each year, local dengue transmission in Italy is an expected event. Alerts to epidemiological, microbiological and SoHO reference authorities are immediate upon notification, however delayed notification delays response. There is a need to increase awareness among clinical professionals and the community to improve detection timeliness.

Keywords: Italy, Dengue virus, Autochthonous Transmission, Mosquito Vectors
ABSTRACT ID: 919
PRESENTED BY: Flavia Riccardo, Italy / flavia.riccardo@iss.it

POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

Application of MALDI-MS and Machine Learning for detection of SARS-CoV-2 and non-COVID acute respiratory infections

I. Kadyrova [1]
S. Yegorov [2], D. Babenko [3], I. Korshukov [4]

[1] Karaganda Medical University | Research Centre, Karaganda Medical University, Karaganda, Kazakhstan
[2] Michael G. DeGroote Institute for Infectious Disease Research; McMaster Immunology Research Centre; Department of Biochemistry and Biomedical Sciences, McMaster University, Hamilton, ON, Canada
[3, 4] Research Centre, Karaganda Medical University, Karaganda, Kazakhstan

BACKGROUND
Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) offers a cost-effective method for diagnosing respiratory conditions like SARS-CoV-2. Given its utility on standard respiratory samples without specialized preparation, MALDI-MS is ideal for resource-limited settings. This study assessed its efficacy in differentiating SARS-CoV-2 from other acute respiratory infections (NCARI) in Kazakhstan lab settings.

METHODS
Nasopharyngeal swabs were collected from in- and outpatients with respiratory symptoms and from asymptomatic controls (AC) in 2020-2022. PCR was used to differentiate SARS-CoV-2+ and NCARI cases. MALDI-MS mass spectra were obtained for 252 samples (115 SARS-CoV-2+, 98 NCARI, and 39 AC). In our first sub-analysis, we followed a previously established protocol for peak preprocessing and Machine Learning (ML), which was trained on publicly available spectra from South American SARS-CoV-2+ and NCARI samples. Our analysis trained ML models on a peak intensity matrix representative of both South American (SA) and Kazakhstan (Kaz) samples.

RESULTS
Applying the pre-existing MALDI-MS procedure "as is" resulted in a significant detection rate (91.0%) for SARS-CoV-2+ samples. However, the accuracy was lower for NCARI (48.0%) and AC (67.0%) using the best-performing Random Forest model. After retraining the ML algorithms with the combined SA-Kaz peak intensity matrix, the top-performing Decision Tree model achieved detection accuracies of 91.0%, 95.0%, and 70% for the SARS-CoV-2+, NCARI, and AC subjects from Kazakhstan. The ROC AUC for differentiating SARS-CoV-2 vs. other samples was 0.97, maintaining a high differentiation accuracy for South America's SARS-CoV-2 and NCARI samples.

CONCLUSIONS
MALDI-MS/ML offers an effective method to differentiate respiratory infections, particularly during the early stages of outbreaks when pathogen information is scarce. However, its application in clinical laboratories requires ongoing ML training to adapt to the dynamic nature of respiratory diseases.

Keywords: COVID-19, SARS-CoV-2, MALDI-MS, Machine Learning, Respiratory infection
ABSTRACT ID: 855
PRESENTED BY: Irina Kadyrova, Kazakhstan / irina.adilevna@gmail.com

POSTER TOUR 23

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Late breakers II

MODERATOR
Pawel Stefanoff

Abstract

The evolving relationship between SARS-CoV-2 cases and wastewater concentrations in Luxembourg from lockdown in 2020 until autumn in 2023

J. Mossong [1]
D. Bejko [2], C. Ernst [3], V. Amina [4], C. Walczak [5], L. Ogorzaly [6], H. Cauchie [7], A. Vergison [8]
[1, 2, 4, 8] Health Directorate
[3] Health Directorate | EPIET fellow
[5, 6, 7] Luxembourg Institute of Science and Technology

BACKGROUND
Luxembourg initiated monitoring of SARS-CoV-2 concentrations in wastewater from the onset of the pandemic in 2020, alongside an extensive testing and mandatory isolation with paid sick leave strategy that remained in place until March 2023. In this study, we compared viral concentrations in wastewater and laboratory-confirmed cases of SARS-CoV-2 throughout the pandemic.

METHODS
We compared the weekly count of laboratory-confirmed cases of SARS-CoV-2 with the corresponding weekly viral flux concentrations in wastewater, spanning from April 2020 to September 2023, across a minimum of three wastewater treatment plants. Utilizing linear regression, we developed predictive models to estimate the number of reported cases based on RNA concentrations in wastewater at various time intervals during the pandemic.

RESULTS
Our analysis revealed a high concordance between wastewater data and reported case data for identifying the various waves of SARS-CoV-2 variants. The ratio of reported SARS-CoV-2 cases to wastewater concentrations exhibited substantial variability throughout the pandemic and varied seasonally. The ratio of cases to wastewater peaked in the first quarter of 2022, coinciding with the emergence of the BA.1 variant. A sharp decrease in the ratio was observed when the testing and isolation regimen ended in April 2023, suggesting a significant reduction in test-seeking behaviour. While reported case number was low over the summer of 2023, our analysis indicates a substantial reduction in case ascertainment by 87% (95% confidence interval: 82-89%) relative to the period 2020-2022.

CONCLUSIONS
Our findings demonstrate that the relationship between wastewater concentrations and reported cases changed substantially over the course of the pandemic. Wastewater-based assessment of SARS-CoV-2 RNA concentrations offers a valuable measure of the prevalence of population-level infection, which is independent of testing capacity, strategy, or public acceptance.

Keywords: SARS-CoV-2, Wastewater, Case reporting, Predictive modelling
ABSTRACT ID: 902
PRESENTED BY: Joël Mossong, Luxembourg / joel.mossong@ms.etat.lu

POSTER TOUR 24

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Implementation of primary health care surveillance in Malta: a data completion evaluation

A. Wijermans [1]
A. Dziugyte [2], S. Buttigieg [3], R. Pace Asciak [4], M. Borg [5]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Infectious Disease Prevention and Control Unit (IDCU) – Health Promotion and Disease Prevention Directorate, Malta
[2, 5] Infectious Disease Prevention and Control Unit (IDCU) – Health Promotion and Disease Prevention Directorate, Malta
[3] Information Management Unit, Ministry for Health, Pieta', Malta
[4] Primary HealthCare, Ministry for Health, Malta

BACKGROUND
In 2020, the Electronic Patient Records for Primary Healthcare system was deployed across Malta. Since 2023, the Infectious Disease Prevention and Control Unit is piloting the implementation of syndromic surveillance for early warning using primary healthcare data. In this study we evaluate completeness of the surveillance data of this system focussing on respiratory and diarrhoeal symptoms.

METHODS
For visits in Malta during 2022, we calculated proportions of completeness for key variables of interest. Subsequently, variables from 1,000 random visits were evaluated for presence of symptoms (fever, cough, shortness of breath (SOB), diarrhoea and vomiting/nausea) using manual and automatic analysis. We used automatic free-text analysis using R-scripts with positive/negative keyword extraction of symptoms (yes/no/NA). We calculated accuracy and Positive/Negative Predictive Value (PPV/NPV) per symptom.

RESULTS
In 2022, 435,980 completed visits were registered. Overall, completion of variables for date, age, and locality were 97-100%, while diagnosis, symptoms and physician notes were 16%, 4%, and 56%, respectively. From the random sample (n=1,000), 634 visits had notes with 409 containing information on symptoms, specifically for fever (n=126), cough (n=125), SOB (n=90), vomit/nausea (n=90) and diarrhoea (n=69). Automatic extraction of symptoms from notes had an accuracy of 81-96% compared to manual extraction, with symptom specific PPV between 81-96% and NPV 86-95%.

CONCLUSIONS
Although, primary care syndromic surveillance can be a useful tool for public health, data completion in Malta needs to be enhanced to allow for effective surveillance. Although automated free-text analysis can increase data completion with high accuracy, completion rates would still be below 80%. We therefore recommend mandatory reporting for crucial surveillance symptoms, increasing awareness for general practitioners on proper data entry and enhancing training in this regard.

Keywords: Primary Health Care, Syndromic Surveillance, Evaluation, Electronic Health Record Data, Automatic Data Processing
ABSTRACT ID: 423
PRESENTED BY: Ariana Wijerman, Malta / ariana.wijermans@gov.mt

POSTER TOUR 24

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Using artificial intelligence to improve epidemic intelligence processes: development and impact measurement of R templates for validating and summarising public health threats

L. Espinosa [1]
K. Crawford [2], L. Antunes [3], R. Croci [4], L. Merdrignac [5]

[1, 2, 4] European Centre for Disease Prevention and Control
[3, 5] Epiconcept

BACKGROUND
Global threat detection and assessment is a core activity of ECDC. However, routine epidemic intelligence operations, including organizing and disseminating information daily, are complex and resource-intense. The aim of this study was to evaluate whether the production of routine epidemic intelligence reports can be automated and with what benefits.

METHODS
R scripts were developed for and tested on case-based and aggregated databases for COVID-19, dengue and MERS-CoV using standardized functions and scripts that could be easily adapted to all diseases. An R product was implemented for the monthly reports on cholera data worldwide and measured its impact in comparison with the manually produced reports.

RESULTS
The development of the final R product required 31 days from two biostatisticians and one epidemiologist part-time over four months and six additional days for adapting it to the cholera database by two EI experts in one month. The report which summarises cholera data per continent and country is created in less than 5 minutes which also includes a systematic data quality check. In comparison, the previous manual approach required 8-10 hours to produce a report with less information and without a quality check. On an annual basis, for monthly reports, this automation has reduced the workload from 18 to 7 days.

CONCLUSIONS
In conclusion, this project has shown that R templates for routine EI activities require fewer resources and lead to increased quality of monthly reports on public health threats. Despite the initial efforts, this new approach has increased the efficacy of the production of EI reports allowing for repeated and fast iterations of reports' production. Sharing these templates in open-source repositories could help other public health experts in their routine activities.

Keywords: Artificial intelligence, Cholera, Surveillance, Reports, Automation
ABSTRACT ID: 213
PRESENTED BY: Laura Espinosa, Sweden / laura.espinosa@ecdc.europa.eu

POSTER TOUR 24

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30-16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Extracting Contextual Information about Infectious Diseases from Electronic Case Notes for Situational Awareness

M. Drakesmith [1]
A. Yung [2], R. Merrick [3], C. Sawyer [4], D. Ishola [5], J. Song [6]
[1] Public Health Wales | Cardiff University
[2, 3, 4, 6] Public Health Wales
[5] Public Health Wales | Liverpool School of Tropical Medicine

BACKGROUND
Situational awareness is a key function to understand what contextual factors drive transmission of infectious diseases. Electronic case management systems provide a means of submitting contextual information in free text fields. However, this data is unstructured, and usually requires manually reading case notes, which is time-consuming and laborious. Natural language processing (NLP) methods can potentially alleviate some of this burden.

METHODS
A method to extract locations and events from digital case notes on an in-house case management system using named entity recognition (NER) was developed. The method was applied to 45 Monkeypox cases in Wales, UK. Using existing manual labelling as a ground truth, the performance of the method to identify UK cities, international travel and social events associated with cases was assessed. Further grammatic dependency parsing was applied to identify subject-verb-object constructs in which named entities were mentioned.

RESULTS
Identification of UK cities and international travel have very high sensitivity (>90%) and moderate specificity (>75%). However, sensitivity to events was low (41%), mostly due to these not being routinely mentioned in the notes, but in supplemental forms not accessible through digital notes. Most false positives were due to locations being mentioned with respect to a contact instead of the case. When subject of a subject-verb-object construct involving a named entity was identified, specificity increased (>85%).

CONCLUSIONS
NER can effectively extract contextual information from digital case notes and can supplement existing structural data where such data is incomplete or missing. NER can be improved if accompanied by extraction of context of entity mentions. While not completely automated, the extraction and tabulation of this information can significantly reduce the burden of manually reading large volumes of text.

Keywords: Data Science, Medical Informatics Computing, Public Health Informatics, Natural Language Processing, Communicable Diseases Sentinel Surveillance
ABSTRACT ID: 157
PRESENTED BY: Mark Drakesmith, United Kingdom / mark.drakesmith@wales.nhs.uk

POSTER TOUR 24

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Evalution of a newly implemented electronic reporting system for notifiable diseases in Denmark

S. Agger [1]
S. Kjær Lefèvre [2], S. Voss [3]

[1] Data Integration and Analysis, Statens Serum Institut, Artillerivej 5, 2300 Copenhagen S, Denmark
[2, 3] Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Artillerivej 5, 2300 Copenhagen S, Denmark

BACKGROUND
Disease surveillance is essential to rapidly identify and respond to outbreaks in order to implement precautionary measures. In 2021/2022, Denmark implemented electronic reporting for more than 40 notifiable diseases, replacing paper forms. The aim of this study was to compare timeliness and completeness of a web-based electronic reporting system with the previous paper-based reporting system.

METHODS
Paper and electronic reports were reviewed for completeness and timeliness. Reports received between 1 January 2015 and 4 May 2023 were included. To avoid any bias due to covid-19, all reports from 2020 were excluded. Timeliness was evaluated based on the time between date of sampling and receipt of the report.The completeness of data was evaluated on selected epidemiological variables.The difference in timeliness between the paper and electronic reports was evaluated by a Welch's t-test and the completeness by a Fisher's exact test.

RESULTS
A total of 36,365 unique reports were identified of which 29,594 were submitted using paper forms and 6,771 were submitted electronically. Electronic reports had on average a higher data completion rate (90.2%) compared to paper forms (67.6%). Of 14 data fields common to electronic and paper formats, electronic reports were more likely to be complete for any field (OR 4.26; 95% CI 4.08-4.44). The paper forms had a higher completion rate for only two of the 14 common fields. On average, electronic reports arrived on an average of 15 (95% CI 14.6-16.01) days earlier than paper forms.

CONCLUSIONS
Tailored electronic reporting was more complete and timelier, suggesting that electronic reporting facilitates a more rapid and comprehensive disease surveillance. Additionally, the evaluation has identified areas where there is room for improvement in the electronic notification forms.

Keywords: Infectious disease reporting, Digitalization, Electronic, Evaluation study, Surveillance
ABSTRACT ID: 617
PRESENTED BY: Sidsel Skou Voss, Denmark / SISV@ssi.dk

POSTER TOUR 24

DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Development and validation of syndromic surveillance for gastrointestinal infections in emergency departments: a novel tool that complements existing surveillance, Germany, January 2019 – August 2022

J. Baum [1]
A. Dörre [2], S. Boender [3], K. Heldt [4], H. Wilking [5], M. Schranz [6]

[1] Robert Koch Institute (RKI), Department for Infectious Disease Epidemiology, Berlin, Germany
European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden | Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
[2, 4, 5, 6] Robert Koch Institute (RKI), Department for Infectious Disease Epidemiology, Berlin, Germany
[3] Robert Koch Institute, Risk Communication Unit, Berlin, Germany

BACKGROUND

Gastrointestinal infections (GI) account for 24.5 million outpatient visits annually in Germany. Surveillance of GI in emergency departments (EDs) is therefore important for timely monitoring of disease trends and outbreak detection. We developed a syndrome definition for automated GI surveillance in EDs and validated it against existing indicator-based surveillance.

METHODS

We used case-based anonymised routine attendance data from the German emergency department registry (AKTIN) and included EDs that continuously transferred data from 01/2019–08/2022 (request ID2019_003; www.aktin.org). Our syndrome definition combined ICD-10 coded diagnosis (A01–A09, R11) and chief complaints (diarrhoea, vomiting, nausea) according to the Canadian Emergency Department Information System. We described cases over time by sex and age groups. We validated the syndrome definition through time series and cross-correlation analysis, comparing trends between syndromic and indicator-based surveillance. Hereto, we combined notified norovirus, rotavirus, campylobacter and Salmonella cases.

RESULTS

Among 7 EDs, 3.1% (50,439; weekly range: 2.4%–5.9%) of visits (1,643,476) were GI cases. 57% of GI cases were female (28,622); 28% were 65–79 years old (14,036) and 10% were 0–19 years old (5,007). We observed seasonal variation with winter/summer peaks and a decrease of GI cases in both surveillance systems during the COVID-19-pandemic. Cross-correlation was 0.7 ($p<0.001$) at lag=1, consistent with 1-week relative reporting delay of indicator-based-surveillance.

CONCLUSIONS

The significant cross-correlation, observed trends and seasonality validated our syndrome definition. Thus, it accurately captures GI cases in EDs and is ready for implementation in routine surveillance. Children may be underrepresented, as specialised children's EDs were not included in the dataset. Our novel automated surveillance offers advantages regarding timeliness and reduced workload and complements existing indicator-based surveillance. We recommend implementation also for other syndrome definitions and settings.

Keywords: Hospital Emergency Service, Public Health Surveillance, Sentinel Surveillance, Gastrointestinal Diseases, Gastroenteritis, Foodborne Diseases
ABSTRACT ID: 741
PRESENTED BY: Jonathan Hans Josef Baum, Germany / BaumJ@rki.de

POSTER TOUR 24
DAY 3 – FRIDAY 24 NOVEMBER 2023
15:30 - 16:15

Surveillance methods and tools

MODERATOR
Andreas Hoefer

Abstract

Development of Acute Respiratory Illness (ARI) surveillance through sentinel pharmacies: a Welsh pilot

F. Rowley [1]
S. Cottrell [2], J. Zitha [3], P. Kalapotharakou [4], S. Morgans [5], C. Moore [6], C. Johnson [7], C. Williams [8]

[1] UKFETP | Public Health Wales | UK Health Security Agency
[2, 3, 4, 5, 7, 8] Public Health Wales
[6] Wales Specialist Virology Centre | Public Health Wales

BACKGROUND
The COVID-19 pandemic resulted in changes to healthcare seeking behaviour, with increasing attendance at pharmacies for acute respiratory illness (ARI). Public Health Wales (PHW) developed a pilot scheme in community pharmacies to complement the existing sentinel network of general practitioners (GPs). Here we present the results of the pilot implementation of the Wales ARI pharmacies network.

METHODS
We recruited pharmacies via advertisement in the national pharmacy network monthly newsletter. Enrolled pharmacies were provided with surveillance kits containing a swab, surveillance form and prepaid postage. Pharmacists swabbed consenting patients presenting with ARI, and asked questions regarding symptoms and demographics. Completed kits were posted to the national centre of virology and tested against a respiratory panel for common respiratory viruses (including influenza A&B and SARS-CoV-2). Results were linked to completed forms and included in routine surveillance activity.To inform the implementation of the network, pharmacies participating in the pilot were asked for feedback.

RESULTS
Six pilot pharmacies were enrolled via initial advertisement, and four through snowball recruitment. Between 07/11/2022 and 16/04/2023, 275 samples have been tested. We observed a range of 0-180 samples per pharmacy in this period (median 9, IQR 7-19). Sample positivity was 47%, compared to 51% in GPs.Four of six pilot pharmacies provided feedback. Of the responding sites that have commenced swabbing (3/4), all were satisfied with the process. Suggestions for improvement included a mechanism to feedback swab results.

CONCLUSIONS
This pilot scheme demonstrates the feasibility of sentinel surveillance in a pharmacy setting for collecting ARI information in the community. Implementation of a result reporting mechanism is being explored. Further advertisement for recruitment and a formal evaluation is planned.

Keywords: Sentinel Surveillance, Pharmacies, Feasibility Studies, Respiratory Tract Infections, Wales
ABSTRACT ID: 210
PRESENTED BY: Frances Rowley, United Kingdom / frances.rowley@wales.nhs.uk

Online-only posters

ANTIMICROBIAL RESISTANCE

Surveillance

Abstract

Antimicrobial use in acute care hospitals in Greece remains high; results of the third Point Prevalence Survey, April – December 2022

D. Krystallaki [1]
K. Palaiopanos 2, K. Mellou 3, A. Maragkos 4, L. Politi 5, T. Zaoutis 6, D. Paraskevis 7
[1, 2] National Public Health Organization, Athens, Greece
[3] Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[4] Department of Microbial Resistance and Infections in Health Care Settings, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[5] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
Department of Microbial Resistance and Infections in Health Care Settings, Directorate of Surveillance and Prevention of Infectious Diseases, National Public Health Organization, Athens, Greece
[6, 7] National Public Health Organization, Athens, Greece

BACKGROUND

Point prevalence surveys (PPS) of healthcare-associated infections (HAIs) and antimicrobial use (AU) in acute care hospitals in Europe provide insight to the extent of AU. In two previous ECDC-coordinated PPS in 2012 and 2016, Greece ranked highest with more than 55% of inpatients receiving at least one antimicrobial. The 2022 PPS aimed to estimate AU again, especially amid COVID-19 pandemic.

METHODS

A cross-sectional study was performed in a representative sample of 50 Greek hospitals during April-December 2022 based on ECDC PPS protocol version 6.1. We included all inpatients on the study day after excluding those admitted after 8.00am. Infection control teams recorded data on hospitals and wards (beds, physician specialties, infection control indicators) and antimicrobial use (agent, indication).

RESULTS

Overall, 5,376 of 9,707 (55.4%) inpatients were receiving at least one antimicrobial; 48.1% received two or more (range 2-9). AU prevalence was highest in intensive care units (71.3%), surgical (59.4%) and medical wards (58.2%) and lowest in psychiatric wards (1.4%). Overall, 9,003 antimicrobials were recorded. Antimicrobials were commonly prescribed for treatment of community-acquired infections (34.6%) and HAIs (28%, including 5.1% for long-term care facility acquired infections), and for prophylaxis (29.3%, including 18.4% for surgical prophylaxis). Most surgical prophylaxis courses (75.7%, 1,253/1,656) lasted more than one day. The most frequently prescribed agents were piperacillin-tazobactam (11.6%), meropenem (7.7%), metronidazole (6.6%), vancomycin (6.2%), cefoxitin (5.4%) and ceftriaxone (5.4%). For surgical prophylaxis, cefoxitin was most commonly used (20.2%).

CONCLUSIONS

The 2022 PPS study showed repeatedly high AU in inpatients of Greek hospitals, especially with broad spectrum antimicrobials. Subsequent studies will provide further understanding of prescription attitudes and other potentially modifiable practices. Support of antimicrobial stewardship programs are needed in these settings.

Keywords: Antimicrobials, Hospital, Inpatients, Prevalence, COVID-19, Prescription, Stewardship, Greece
ABSTRACT ID: 77
PRESENTED BY: Lida Politi, Greece / l.politi@eody.gov.gr

ANTIMICROBIAL RESISTANCE

Surveillance

Abstract

Assessing Antimicrobial Consumption in Belgian Nursing Homes (2016-2022): A First-Time National Surveillance Study

M. Kelly [1]
B. Catry [2], L. Catteau [3]
[1, 2, 3] Sciensano

BACKGROUND
Inappropriate antimicrobial consumption (AMC) drives the uncontrolled emergence of antimicrobial resistance. Across Europe, AMC surveillance, with national targets, exists for the ambulatory and hospital sectors, without consideration of nursing homes (NHs); variably including NHs within the ambulatory or hospital sector, both or neither. Here, we characterise AMC in comparable populations residing inside or outside NHs in Belgium to assess the impact and requirement for targeted AMC surveillance and stewardship.

METHODS
The National Institute for Health and Disability Insurance supplied reimbursement AMC data for the ambulatory sector from 2016 to 2022. Data were classified by the Anatomical Therapeutic Chemical system, expressed as Defined Daily Doses (DDD) and aggregated by prescription month, province, patient age, gender and location inside/outside a NH. The number of insured beneficiaries, aggregated by the same geographic and demographic variables, were collected from the Intermutualistic Agency. AMC metrics for national and international targets were compared for analogous populations inside and outside NHs.

RESULTS
Total AMC (J01) in DDD/1000 beneficiaries/day significantly decreased in NHs from 2016-2021 (Spearman's rho=-0.943, p=0.0167), but exceeds by double that of the general (outside) population (t = 19.478, p = 6.6e-06). NH residents received proportionally lower volumes of tetracyclines, macrolides and beta-lactams, but higher proportions of urinary tract infection treatments, such as nitrofuran derivatives and fosfomycin. Considering prescription quality metrics, ratios of second:first line treatments and amoxicillin:amoxicillin-clavulanic acid were consistently assessed as "worse" within NHs, with values further diverging during the COVID-19 era.

CONCLUSIONS
NH populations show distinct infection risks and higher AMC. In Belgium, including NHs in the AMC data of the ambulatory sector does not compromise national interpretation. However, antimicrobial stewardship goals should be targeted for this vulnerable population.

Keywords: Nursing Homes, Antimicrobial Stewardship, Antimicrobial Drug Resistance, Public Health Surveillance
ABSTRACT ID: 206
PRESENTED BY: Moira Kelly, Belgium / moira.kelly@sciensano.be

ANTIMICROBIAL RESISTANCE

Surveillance

Abstract

Increase of multidrug resistance in Shigella spp. among travel-acquired cases in Norway, 2012-2021

M. Stecher [1]
J. Pires [2], L. Brandal [3], U. Naseer [4]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
Department of Infection Control and Vaccines, Norwegian Institute of Public Health, EPIET
[2] ECDC fellowship Programme, Public Health Microbiology path (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
Department of Infection Control and Preparedness, Norwegian Institute of Public Health, EUPHEM
[3, 4] Department of Infection Control and Preparedness, Norwegian Institute of Public Health

BACKGROUND
Shigella spp. are a major cause of dysentery worldwide and can lead to severe illness. The increasing trend of multidrug resistant (MDR) Shigella spp. is a global public health concern. In Norway, Shigellosis is mainly travel associated, and global trends impact local spread and infection control. Thus, we aim to describe antimicrobial resistance (AMR) developments over time in Shigella spp. isolates in Norway and to identify potential risk groups associated with international travel.

METHODS
We included all Shigella spp. isolates submitted to the National Reference Laboratory (NRL) between 01/2012 and 12/2021. Antibiotic susceptibility testing results were retrieved from the NRL for a panel of antibiotics. We conducted descriptive analysis by species, antibiotic class, year of isolation, and recent travel outside of Norway. Associations were analysed using logistic regression models.

RESULTS
Of 717 isolates tested for antimicrobial susceptibility, the three most prevalent species were S. sonnei (62%, 446), S. flexneri (30%, 215), and S. boydii (6%, 41). Among these, we observed an increase in resistance to third-generation cephalosporins by a factor 1.20 (odds ratio (OR)=1.20, 95% confidence interval (CI)=1.09-1.33) and MDR strains by a factor 1.23 (OR=1.23, 95%CI=1.14-1.32) per year. Of the150 MDR isolates, the majority (77%, 116/150) were identified in international travellers, particularly those returning from Southeast Asia (20%; 24/116) and Africa (9%; 11/116).

CONCLUSIONS
Increasing MDR in Shigella spp. and resistance to clinically important antibiotics indicate serious limitations in current treatment options. We recommend improved targeted risk communication to primary care and international travellers to prevent infection and local spread of AMR. In addition, increased reporting to a global database to determine the impact of international travel on the spread of AMR in Shigella.

Keywords: S. sonnei, S. flexneri, Antimicrobial resistance, Enteric bacteria, International travel, Travel medicine
ABSTRACT ID: 207
PRESENTED BY: Melanie Stecher, Norway / melanie.stecher@gmx.net

ANTIMICROBIAL RESISTANCE

Surveillance

Abstract

Automatizing contact tracing of antimicrobial multi-resistant infections: R Shiny-based web application

J. Gualda Gea [1]
L. Barón Miras [2], A. Vilella i Morató [3], I. Torá Rocamora [4], B. Torralbo [5], I. Fortes [6], S. Valls [7], L. Rodriguez [8], R. Parejo [9], G. Santana [10], J. Martínez Martínez [11], M. Bertran Luengo [12]

[1, 2, 5, 6, 7, 8, 9, 12] Department of Preventive Medicine and Epidemiology, Hospital Clinic de Barcelona (HCB), Barcelona, Spain | Barcelona Institute for Global Health (ISGlobal), Barcelona, Spain
[3, 4, 10] Department of Preventive Medicine and Epidemiology, Hospital Clinic de Barcelona (HCB), Barcelona, Spain
Barcelona Institute for Global Health (ISGlobal), Barcelona, Spain
Medicine Department, Faculty of Medicine and Health Sciences, University of Barcelona, Barcelona, Spain
[11] Department of Infectious Diseases, Hospital Clinic de Barcelona (HCB), Barcelona, Spain
Medicine Department, Faculty of Medicine and Health Sciences, University of Barcelona, Barcelona, Spain

BACKGROUND

Antimicrobial multidrug-resistant (AMR) infections' concern is accelerating as their prevalence and the lack of antibiotic alternatives increase. Healthcare facilities are the most vulnerable settings. Traditional contact tracing relying on manual record-keeping and analysis are time-consuming and obstruct a much-needed early detection. Consequently, automated tools can potentially aid to contain nosocomial infections spread. This study presents the development of an R Shiny application automatizing contact identification of AMR infections.

METHODS

Our web-based application was developed with R Shiny, using the Hospital Information Systems (HIS) as data source. Inputs include patient records and movements within the hospital (e.g., dates, times, and rooms) and laboratory results. Its user-friendly interface allows quick and easy detection of contacts and clusters. To validate the application performance, we conducted a retrospective analysis including all laboratory-confirmed AMR cases and the contacts who shared room from admission to isolation of a tertiary hospital between October and November 2022. We excluded Methicillin-Resistant Staphylococcus aureus cases. We calculated sensitivity, specificity and total time saved.

RESULTS

Out of 6313 inpatients during the study period, the application successfully identified 175 contacts from 68 infections, achieving a sensitivity of 100% and a specificity of 95%. The estimated time to track the contacts of these 68 patients manually is 650 minutes, while the application spends approximately 12 minutes (98% reduction).

CONCLUSIONS

Our application represents a significant step forward in contact tracing automation, as a time-saving and reliable solution. As it is based on systematically recorded data by HIS, its extrapolation potential for other infection surveillance purposes is high. Its web interface allows its use without technical knowledge requirements. Furthermore, as it uses free code, customization is easy.

Keywords: Drug Resistance, Healthcare Associated Infections, Infection Control, Contact Tracing, Automation
ABSTRACT ID: 632
PRESENTED BY: Juan Jose Gualda Gea, Spain / jjgualda@clinic.cat

ANTIMICROBIAL RESISTANCE

Surveillance

Abstract

Carbapenemase-producing Enterobacterales in intensive care units: England 2022 point prevalence survey

H. Higgins [1]

R. L Guy [2], H. Emmett [3], A. Charlett [4], J. Elmes [5], A. Demirjian [6], K. L Henderson [7], C. S Brown [8], S. Gerver [9]

[1, 2, 3, 4, 5, 7, 8, 9] UK Health Security Agency

[6] UK Health Security Agency | Department of Paediatric Infectious Diseases & Immunology, Evelina London Children's Hospital, London, UK | Faculty of Life Sciences & Medicine, King's College London, London, UK

BACKGROUND

Hospital outbreaks associated with carbapenemase-producing Enterobacterales (CPE) have been identified increasingly in England. In site-specific studies, hospitals have assessed CPE prevalence at 0-11%. No national intensive care unit (ICU) CPE prevalence study has been conducted. We therefore aimed to generate CPE prevalence estimates among patients in England ICUs.

METHODS

A prospective, randomly selected cross-sectional cluster survey was used to estimate CPE prevalence. From randomly selected acute-care providers in England, ≤20 eligible patients were randomly selected per ICU, with trust-level, ICU-level and patient-level data collected on a single date (between 18/04/2022 to 02/05/2022) by ICU staff using existing medical notes. Estimates were determined by adult, paediatric and neonatal ICU prevalence.

RESULTS

Seventy-four hospital Trusts participated (66 invited; 8 voluntary), with data from 94 adult ICUs, 13 paediatric ICUs (PICUs) and 49 neonatal ICUs (NICUs). Non-participation from invited Trusts was 25/62 (40%) for adults, 10/19 (53%) for paediatrics, and 54/92 (59%) for neonates. 56.3% (n=424/753) of adults, 74.7% (n=68/91) of paediatrics, and 36.1% (n=145/402) of neonates were tested for CPE. Screening accounted for 95.3% of adult CPE tests (versus 4.7% clinical investigation); this was higher for paediatrics (100% (n=68/68)) and lower for neonates (93.7% (n=136/145)). CPE prevalence in tested adults was 1.2% (n=5/424), and 2.8% in tested neonates (n=4/145). No CPE were detected in paediatric patients tested. More than 80% of trusts had CPE screening policies, varying by age range (adults:95.6% n=43/45; paediatrics:100% n=10/10; neonates:82.1% n=32/39).

CONCLUSIONS

The first national CPE point-prevalence survey identified low prevalence (<3%) in ICUs in England, although low numbers makes risk factor elucidation challenging. While a high proportion of trusts operate a CPE screening policy, improvements can be made, particularly in NICUs.

Keywords: Carbapenemase, Prevalence, Drug Resistance, Screening, Antimicrobial resistance, Intensive care
ABSTRACT ID: 682
PRESENTED BY: Hannah Higgins, United Kingdom / hannah.higgins@ukhsa.gov.uk

COVID-19

Surveillance

Abstract

Analysis of severity indicators for hospitalised Covid-19 cases in France, 2020-2023

A. Maisa [1]
F. Chereau [2], S. Bernard-Stoecklin [3], N. Méthy [4], L. Fonteneau [5], D. Viriot [6], J. Schaeffer [7], A. Duvaux [8], I. Parent du Châtelet [9], C. Sommen [10]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10] Santé publique France

BACKGROUND
The SIVIC database in France initially created as an information system of victims of attacks and exceptional health emergencies, has been rapidly adapted in March 2020 to monitor COVID-19 hospitalisations, intensive care admissions and in-hospital deaths. The database includes limited information in order to minimise the workload for healthcare professionals, as manual entry is required. The aim of this retrospective study was to analyse indicators to determine the risk for severe outcome for Covid-19.

METHODS
Data linkage of three databases was performed, including data on testing (SIDEP), vaccination (VACSI) and hospitalisations (SIVIC) between December 2020 and March 2023. We used multivariate quasi Poisson regression to model the effect of variants (based on mutation screening PCR results) on a severe outcome (admission to intensive care/or in-hospital death) among hospitalised Covid-19 cases, adjusted for age, sex, co-morbidities and vaccination status.

RESULTS
Compared to infection with wild type variant, an infection with Delta increased the severe outcome rate (aRR=1.45, p‹0.001), while an infection with any Omicron sub-lineage decreased the severe outcome rate (aRR=0.78, p‹0.001). The risk of severe outcome was decreased by vaccination with at least two doses (aRR=0.64, p‹0.001).

CONCLUSIONS
Although the SIVIC system allowed timely monitoring of epidemic dynamics at all territorial levels, this database alone has not been designed for an accurate assessment of severity of a pathogen. Data linkage with other databases was necessary to make meaningful conclusions, especially concerning the impact of SARS-CoV-2 variants and vaccination. Insights from this retrospective analysis include the feasibility of undertaking a severity analysis with limited but linked data, and the need for a sustainable hospital surveillance system in the future, ideally using electronic health records.

Keywords: COVID-19, SARS-CoV-2, Surveillance, Hospitalisation, Risk factors
ABSTRACT ID: 53
PRESENTED BY: Anna Maisa, France / anna.maisa@santepubliquefrance.fr

COVID-19

Surveillance

Abstract

Temporary Disability register as a complementary system of epidemiological monitoring of the COVID-19 pandemic in Spain

D. Culqui Lévan [1]
S. Escalona López [2], A. Gherasim [3], J. Oliva Dominguez [4], M. Disdier Rico [5], M. García Gomez [6]
[1, 2, 3, 4, 5, 6] Ministry of health Spain

BACKGROUND
During the COVID-19 pandemic, the Spanish authorities implemented a range of social measures for the preservation of business activity and the protection of workers. One of these measures was issuing the Temporary Disability (TD) for COVID-19 cases, close contacts, and especially vulnerable workers. The objective of this study was analyse whether the TD registry could be used as a complementary source to traditional epidemiological surveillance.

METHODS
We carried out a time series with a cross-correlation analysis of TD and COVID-19 cases between 16 and 65 years old reported to the National Epidemiological Surveillance Network (RENAVE). The analysis included six pandemic waves between 10/03/2020 and 31/12/2021 in Spain. Cross-correlation coefficients (r) were calculated using a time lag of -14 days.

RESULTS
We considered for the analysis 2,253,573 TD due to COVID-19 infection 4,894,802 COVID-19 cases notified to the RENAVE. Significant positive correlations were observed at time lags -7, -10 and -14, indicating that TD notification preceded RENAVE notification. In the first and sixth pandemic waves, TD notification preceded RENAVE by 12 and 7 days, respectively. Negative correlations between the two series were observed in the second and fourth waves, coinciding with a lower minimum number of notified cases. In the third and fifth waves, TD notification also preceded RENAVE (lags of -1, -5 and -14, -7, respectively)

CONCLUSIONS
Our results confirmed the Temporary Disability Register as a useful tool for complementing traditional epidemiological monitoring. We observed a better positive correlation in waves with increased pandemic intensity. Based on these results, we are currently working on integrating the TD on the Spanish surveillance network.

Keywords: Surveillance, Warm alert system, COVID-19, Sick leave
ABSTRACT ID: 61
PRESENTED BY: Dante Roger Culqui Lévano, Spain / danteroger@hotmail.com

COVID-19

Surveillance

Abstract

Health-related quality of life among long-covid patients in Tunisia, 2020–2021

S. Dhaouadi [1]
M. Safer [2], H. Letaief [3], A. Hechaichi [4], H. Bouguerra [5], A. Zouayti [6], C. Aichouch [7], A. Neffati [8], M. Bougatef [9], R. Mhadhbi [10], N. ELMili [11], K. Talmoudi [12], N. Bouafif ép Ben Alaya [13]

[1] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Mediterranean and Black Sea Programme in Intervention Epidemiology Training (MediPIET),
European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
Faculty of Medicine of Tunis, University Tunis El Manar, Tunis, Tunisia
[2] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Faculty of Medicine of Tunis, University Tunis El Manar, Tunis, Tunisia
[3, 4, 5, 13] National Observatory of New and Emerging Diseases, Tunis, Tunisia
Mediterranean and Black Sea Programme in Intervention Epidemiology Training (MediPIET),
European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
Faculty of Medicine of Tunis, University Tunis El Manar, Tunis, Tunisia
[6, 7, 8, 9, 10, 11, 12] National Observatory of New and Emerging Diseases, Tunis, Tunisia

BACKGROUND
Long-covid affect patients' well-being and quality of life. We aimed to assess the impact of long-covid on the patients' health-related quality of life in Tunisia.

METHODS
We surveyed a representative sample of COVID-19 survivors registered in the national SARS-Cov-2 surveillance database in Tunisia from September 2020–September 2021(n=479,743). We defined long-covid as self-reported one or more symptoms lasting for at least four weeks after the first SARS-Cov-2 infection and not explained by alternative diagnosis. Trained health care workers interviewed consenting respondents by phone using the EQ-5D-3L questionnaire to examine five dimensions of their quality of life: mobility, self-care, usual activities, pain-discomfort and anxiety-depression. Each dimension was scored on: none; some or extreme problems. Interviewers recorded respondents' perceived quality of life the day of the survey on the numerical visual analog scale VAS (0–100). We measured the internal consistency of the survey items using Cronbach's Alpha. We compared quality of life measures between respondents reporting long-covid symptoms and those without long-covid.

RESULTS
Of 1094 persons contacted, 416 responded(38%). Among respondents, long-covid prevalence was 64% (95%CI 59%-69%). 31%(95%CI 26%-35%) of participants reported problem in all dimensions: 41% among long-covid respondent vs 13% among non long-covid ($p<0.001$). Compared to responders without long-covid, long-covid respondents reported more problem on all dimensions: mobility: 14.8% vs 4.1% ($p=0.001$), usual activity: 12.6% vs 4.8%($p=0.010$), pain-discomfort:22.4% vs 3.4% ($p<0.001$) and anxiety-depression: 19.8% vs 8.1%($p=0.002$). The VAS score was significantly lower among long-covid responders compared to non-long covid: 73 vs 84 ($p<10^{-3}$). Cronbach Alpha's was 0.7.

CONCLUSIONS
Long-covid impacted quality of life, affected mobility and caused disability. We recommend psychological healthcare services during and after acute COVID-19 episode to preserve the well-being of affected patients.

Keywords: Long-covid, Quality of life, Tunisia, Well-being
ABSTRACT ID: 152
PRESENTED BY: Sonia Dhaouadi, Tunisia / sonidhaouadi88@gmail.com

COVID-19

Surveillance

Abstract

The early warning potential of wastewater surveillance of SARS-CoV-2: experiences from Norway

P. Langlete [1]
E. Madslien [2], E. Amato [3], S. Hyllestad [4], P. Aavitsland [5]
[1, 2, 3, 4, 5] Norwegian Institute of Public Health

BACKGROUND
During the COVID-19 pandemic, several countries initiated monitoring of SARS-CoV-2 in wastewater. In Norway, such monitoring started in June 2022, in order to strengthen COVID-19 surveillance after a change of testing strategy. We aimed to evaluate the early warning potential of wastewater surveillance in Norway during periods of low individual SARS-CoV-2 testing activity.

METHODS
Wastewater samples were collected from treatment plants in the largest Norwegian municipalities between June 2022 and April 2023. SARS-CoV-2 RNA concentrations, quantified by RT-qPCR, were normalised by a faecal indicator (PMMoV) and weighted by the population in the catchment area. The wastewater data were compared to clinical indicators such as the number of notified positive and hospitalised cases. Cross-correlation and regression analyses were performed using time series data during periods of increasing and decreasing trends to quantify the early warning timeframes.

RESULTS
We observed an earlier warning for a new wave of infection from wastewater surveillance compared to registered positive cases and hospitalisations. During increasing trends, we found a significant positive correlation between peak rise in wastewater data and clinical indicators with a lead time of 1-2 weeks. During the decreasing trends, the correlation was highest with no leading time.

CONCLUSIONS
Wastewater surveillance could function as an early warning system for increasing trends of SARS-CoV-2 by 1-2 weeks. However, no early signal was detected during decreasing trends. Wastewater surveillance could complement clinical-based surveillance systems, providing valuable information to monitor disease trends when individual testing activity is low.

Keywords: Wastewater-Based Epidemiological Monitoring, SARS-CoV-2, Correlation of Data, COVID-19, COVID-19 Nucleic Acid Testing, Norway
ABSTRACT ID: 228
PRESENTED BY: Petter Langlete, Norway / petzlang@gmail.com

COVID-19

Burden of disease

Abstract

The impact of the COVID-19 pandemic on surgery: A systematic review of the literature

C. Tsagkaris [1]
A. Toska [2], D. Latsou [3], V. Marchenko [4], D. Boiko [5], M. Saridi [6]

[1] Neapolis University, Pafos, Cyprus
European Student Think Tank, Public Health and Policy Working Group, Amsterdam, Netherlands
[2] School of Finance, Administration and Informatics, Neapolis University Pafos, 8042 Paphos, Cyprus
Department of Social and Education Policy, School of Social Sciences, University of Peloponnese, Tripoli, Greece.
[3, 6] School of Finance, Administration and Informatics, Neapolis University Pafos, 8042 Paphos, Cyprus
[4] Bukovinian State Medical University (BSMU), Chernivtsi, Ukraine
[5] Poltava State Medical University, Poltava, Ukraine

BACKGROUND
The COVID-19 pandemic has affected various domains of healthcare including surgery. Sanitary restrictions have directed the prioritization of emergency operations and operations related to life – threatening conditions such as cancer and heart failure. Although the impact of COVID-19 on the medical management of non – communicable diseases has been widely assessed, there is limited knowledge about its implications on surgical care. The aim of this systematic review is to examine the impact of the COVID-19 pandemic on surgery, namely the delivery of surgical care and training, and the progress of surgical research.

METHODS
Studies were accessed through an electronic web-based search strategy from PubMed, Scopus and Cochrane Library by using a combination of search terms. This review was reported according to the Preferred Reporting Items for Systematic Review and Meta-analysis (PRISMA) guidelines. A narrative synthesis approach was used in the interpretation of the findings.

RESULTS
Of 149 records screened, 23 studies fulfilled the inclusion criteria. Evidence suggests that surgery was considerably restricted due to measures directing the postponement of elective operations, use of operating theaters as intensive care stations, deployment of surgical healthcare workers in COVID-19 wards, infection spread among patients and healthcare workers in surgical departments and delayed presentation of patients to surgical emergencies. This has resulted in longer waiting times, progression of surgical pathologies, worse pre- and postoperative outcomes and lower quality surgical education. Telemedicine and remote surgical education have shown potential to reduce the shortcomings of the pandemic on surgery.

CONCLUSIONS
In light of upcoming infectious threats potentially hindering access to and availability of surgical services, it is pivotal to analyze the disrupting impact of COVID-19 on surgery and enhance surgical capacity accordingly.

Keywords: COVID-19, SARS-CoV-2, Surgery, Healthcare services, Complications
ABSTRACT ID: 404
PRESENTED BY: Christos Tsagkaris, Greece / chriss20x@gmail.com

COVID-19

Surveillance

Abstract

Mitigating the burden on public health during a pandemic – A pilot study on random sampling of notified COVID-19 cases for eliciting epidemiological information in Berlin

D. Werber [1]
S. McFarland [2], C. Ruscher [3], B. Hoffmann [4], F. Steitz [5], J. Bitzegeio [6], A. Bartel [7], (GROUP) Local Health Department study group

[1] State Office for Health|State Office for Health and Social Affairs
[2, 3, 6, 7] State Office for Health and Social Affairs
[4] Local Healtth Department Friedrichshain-Kreuzberg
[5] Local Health Department Mitte

BACKGROUND
Situation reports during the COVID-19 pandemic often relied on surveillance data of notified COVID-19 cases. During peak phases, case numbers drastically exceeded the capacity of local public health departments responsible for case interviews, which raises the issue of the validity of reported epidemiological parameters, e.g. vaccination status. To address this, we piloted random sampling of COVID-19 cases in Berlin to evaluate acceptability, representativeness and simplicity.

METHODS
The analysed study period was from October 2022 to February 2023, when the SARS-CoV-2 variant Omicron was dominant. We took a LPHD-stratified random sample of electronically transmitted cases, so that each LPHD received an equal amount of cases (25 per day). Excel lists for each district were generated and sent twice weekly. Sampling and sending of lists was fully automated using the software R. LPHD were involved in the design and afterwards asked to provide feedback, including on simplicity and acceptability.

RESULTS
Of 158,965 cases notified during the study period (median weekly incidence:192/100,000 population), 25,984 (16%) were sampled, from which 20,335 (78%) were interviewed. Interviewed and non-interviewed cases were similar with respect to age and gender. LPHD supported the rationale of sampling and reported personnel resources were freed up for other relevant health tasks - in addition to being a motivating factor. Interviews could be conducted only after LPHD received lists of sampled cases, which were already notified and transmitted to the state of Berlin.

CONCLUSIONS
Acceptance was high among Berlin's LPHD and interviewed cases were representative of sampled cases. Sampling should be integrated into the surveillance system software to facilitate immediate processing of sampled cases. It could also be implemented routinely for other conditions with high case numbers, e.g., for influenza.

Keywords: Public health surveillance, Epidemiological monitoring, COVID-19, Sampling study, Disease notification
ABSTRACT ID: 473
PRESENTED BY: Dirk Werber, Germany / dirk.werber@lageso.berlin.de

COVID-19

Burden of disease

Abstract

Risk factors of COVID-19 breakthrough infections in a tertiary hospital: a case-control study

G. Tejada [1]
L. Pinós Tella [2], S. Otero-Romero [3], Í. Carbonés Fargas [4], B. Borrás-Bermejo [5], C. Andrés [6], A. Antón [7],
O. Parés-Badell [8]

[1] Preventive Medicine and Epidemiology Department, Hospital Universitari Vall d'Hebron, Barcelona, Spain
[2, 3, 5, 8] Preventive Medicine and Epidemiology Department, Hospital Universitari Vall d'Hebron, Barcelona, Spain Vall d'Hebron Institut of Research (VHIR), Barcelona, Spain | Grup de recerca de Epidemiologia i Salut Pública, Vall d'Hebron Institut de Recerca (VHIR), Vall d'Hebron Hospital Universitari, Vall d'Hebron Barcelona Hospital Campus, Barcelona, Spain
[4] Vall d'Hebron Institut of Research (VHIR), Barcelona, Spain | Grup de recerca de Epidemiologia i Salut Pública, Vall d'Hebron Institut de Recerca (VHIR), Vall d'Hebron Hospital Universitari, Vall d'Hebron Barcelona Hospital Campus, Barcelona, Spain
[6, 7] Respiratory Viruses Unit, Microbiology Department, Vall d'Hebron Hospital Universitari, Vall d'Hebron Institut of Research (VHIR), Vall d'Hebron Barcelona Hospital Campus, Passeig Vall d'Hebron 119-129, 08035 Barcelona, Spain | Centro de Investigación Biomédica en red de Enfermedades Infecciosas CIBERINFEC, Instituto Carlos III, Madrid, Spain

BACKGROUND
Defining potential risk factors for breakthrough SARS-CoV-2 infection is key to define public health policies and vaccination campaigns, but evidence is conflicting. We aimed to identify risk factors for breakthrough SARS-CoV-2 infection.

METHODS
Case-control test-negative design study in hospitalized adult patients with a PCR-test performed between 1 November 2021 to 28 June 2022 and at least one dose of any COVID-19 vaccine prior to infection. Cases (positive SARS-CoV-2 PCR-test) and controls (negative PCR-test) were matched by age and date of test (1:3 ratio). We analysed sociodemographic characteristics (socioeconomic status), vaccine-related variables and comorbidities (lung disease, hypertension, renal disease, immunosuppression, among others). A logistic regression model was performed to obtain crude and adjusted odds ratios and 95% confidence intervals.

RESULTS
We analysed 1,340 breakthrough SARS-CoV-2 infections matched to 4,016 controls. 66% of the controls received at least 3 doses of any vaccine, as compared to 57% of the cases. The probability of breakthrough infection was 19% lower in patients with the highest socioeconomic status compared to the lowest (crude OR 0,81 CI 95%, 0.68-0.97). When adjusting by comorbidities and time since last vaccine dose, we lost association with socioeconomic status. Nevertheless, immunosuppression (ORa 1.99; CI 95%, 1.55-2.57) and time since last vaccine dose (ORa, 1.01; CI 95%, 1.01-1.02) remained significantly associated with breakthrough infection.

CONCLUSIONS
The risk of COVID-19 breakthrough infection is two-fold higher in patients with immunosupression and increases 1% per day since last vaccine dose. They are both independent risk factors that should be taken into account when designing prevention stategies against COVID-19. Even though association between the socioeconomic status and breakthrough infection was lost after adjustment, it remains an important factor for public health policies.

Keywords: Risk factors, COVID-19, Breakthrough infection, Vaccines
ABSTRACT ID: 595
PRESENTED BY: Gabriela Tejada, Spain / gabriela.tejada.p@gmail.com

COVID-19

Communication and health promotion

Abstract

Infodemiology: untangling the relationship between mental distress, trust in the pandemic response, and COVID-19 health literacy during the COVID-19 'infodemic' in Ireland

J. Arnott [1]
M. Troya Bermeo [2], M. Joyce [3], Z. Kabir [4], P. Corcoran [5], A. Khashan [6], M. Connolly[7], I. Perry [8]

[1] School of Public Health, University College Cork
[2, 8] National Suicide Research Foundation | School of Public Health, University College Cork
[3] National Suicide Research Foundation
[4, 6] School of Public Health, University College Cork
[5] School of Public Health, University College Cork | National Suicide Research Foundation
[7] University of Galway

BACKGROUND

The World Health Organisation (WHO) declared an ‘infodemic’ in 2020. The impact of excessive COVID-19 information promoted confusion, worry, and fear, but also created distrust in health authorities and impacted public mental health.

METHODS

A nationally-representative cross-sectional telephone survey conducted data collection during three study periods: May, July, September 2020. Mental health was assessed by the Patient Health Questionnaire Anxiety Depression Scale (PHQ-ADS), score of 10+ indicated mental distress. Exposures of interest were analysed including COVID-19 Health Literacy (HL), Trust in the pandemic response(Trust), and health-seeking behaviour (HSB). Descriptive analysis and univariate logistic regression were conducted in STATA17.

RESULTS

Of the 2,914 participants, 27.6% experienced mental distress(n=804), 10.85% had low/moderate HL, and 42.2% had low/moderate Trust(n=1,136); increasing over time from 34% in May 2020 to 47% in Sept 2020. Mental distress was associated with Trust; mental distress was highest in participants with lowest Trust, 36% compared to 24% (OR:1.8;95%CI:1.44-2.26). Trust was associated with HL, highest Trust in participants with highest HL (OR:2.68;95%CI:1.50-4.79). Significant indicators of both HL and Trust are education level and employment status. Significant indicators of both mental distress and HL include income and age. Sex-differences were only observed in mental distress; women were almost twice as likely to experience mental distress than men; 34% compared to 21% (OR:1.91;95%CI:1.62-2.26). Age was associated with mental distress and HL; both were highest in the youngest age groups, with significant decreasing trends. During May2020, HSB was affected, those experiencing mental distress were more likely to avoid accessing necessary healthcare,41% compared to 21 (OR:2.59;95%CI:1.94-3.46).

CONCLUSIONS

The WHO recommends promoting the understanding of risk to mitigate harm to the public’s mental and physical health. Health literacy may be a modifiable risk factor for future emergencies to increase public trust and reduce unnecessary harm like mental distress and healthcare avoidance.

Keywords: COVID-19, Infodemic, Infodemiology, Mental Health, Trust, Health literacy
ABSTRACT ID: 627
PRESENTED BY: Julie Arnott, Ireland / jarnott@ucc.ie

COVID-19

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

Combined protection of SARS-CoV-2 infection and booster vaccination during the Omicron variant wave in an ECDC multi-centre healthcare worker cohort (VEBIS study), December 2021–March 2023

C. Savulescu [1]
(GROUP) ECDC VEBIS HCW VE study group

[1] Epiconcept, France

BACKGROUND

Protection from naturally acquired SARS-CoV-2 infection needs to be considered when evaluating COVID-19 vaccine performance. We measured the combined effect of any COVID-19 booster vaccination and natural infection against the SARS-CoV-2 infection in healthcare workers (HCWs) during the Omicron variant-dominated wave (December 2021–March 2023).

METHODS

We conducted a prospective cohort study among HCWs from 17 EU/EEA hospitals. We defined natural infection as any reported SARS-CoV-2 episode before study enrolment. Among HCW with primary vaccination, we defined four levels of exposure: booster vaccination plus natural infection (booster+infection), primary vaccination series plus natural infection (primary+infection), booster without natural infection (booster only) and primary vaccination without natural infection (primary only). We measured the relative vaccine effectiveness (rVE) of these exposure levels with primary vaccination only as reference. Using Cox regression, we calculated rVE as (1-hazard ratio)*100, adjusted for hospital, age, sex and underlying conditions.

RESULTS

Of 2231 HCW followed during the study period, 862 (39%) had a pre-enrolment SARS-CoV-2 infection, including 645 (75%) HCWs vaccinated with any booster dose. We detected by testing during follow-up, 773 new SARS-CoV-2 infections: 197 (23%) in HCWs with and 576 (43%) in those without a pre-enrolment infection. Adjusted rVE was 52% (95%CI: 32–66) for booster+infection, 50% (24–67) for primary+infection and 17% (-13 to 38) for booster only.

CONCLUSIONS

The results suggest a higher additional protection of any booster vaccination in HCWs that went through a natural SARS-CoV-2 infection, than in those that were never infected before enrolment in the study, supporting the recommendations of vaccination (including boosters) for individuals with a history of COVID-19. Using a prospective cohort study with repeated testing provides valuable information on the effect of hybrid immunity against repeated SARS-CoV-2 infections.

Keywords: SARS-CoV-2 Infection, Healthcare Workers, Vaccine Effectiveness, COVID 19 Vaccine, Active surveillance
ABSTRACT ID: 638
PRESENTED BY: Camelia Savulescu, France / c.savulescu@epiconcept.fr

COVID-19

Burden of disease

Abstract

Prevalence of SARS-CoV-2 infection among several populations of primary healthcare workers in comparison to the general population and associated factors, France, May-August 2021

M. Pouquet [1]
D. Decarreaux [2], L. Di Domenico [3], C. Sabbatini [4], P. Prévot-Monsacre [5], T. Fourié [6], P. Saba Villarroel [7], S. Priet [8], H. Blanché [9], J. Sebaoun [10], J. Deleuze [11], C. Turbelin [12], L. Rossignol [13], A. Werner [14], F. Kochert [15], B. Grosgogeat [16], P. Rabiega [17], J. Laupie [18], N. Abraham [19], H. Noël [20], S. van der Werf [21], V. Colizza [22], F. Carrat [23], R. Charrel [24], X. de Lamballerie [25], T. Blanchon [26], A. Falchi [27]

[1] Sorbonne Université, INSERM, Institut Pierre Louis d’Epidémiologie et de Santé Publique, (IPLESP), F-75012 Paris, France
[2] Laboratoire de Virologie, Université de Corse Pascal Paoli, UR7310 Bioscope, 20250 Corte, France
Sorbonne Université, INSERM, Institut Pierre Louis d’Epidémiologie et de Santé Publique, (IPLESP), F-75012 Paris, France
Unité des Virus Emergents, Aix Marseille University, IRD 190, INSERM U1207, 13005 Marseille, France
[3, 4, 5, 12, 13, 22, 26] Sorbonne Université, INSERM, Institut Pierre Louis d’Epidémiologie et de Santé Publique, (IPLESP), F-75012 Paris, France
[6, 7, 8, 24, 25] Unité des Virus Emergents, Aix Marseille University, IRD 190, INSERM U1207, 13005 Marseille, France
[9, 10, 11] Fondation Jean Dausset-CEPH, 75000, Paris, France
[14, 15] Association Française de Pédiatrie Ambulatoire (AFPA), 44150, Ancenis Saint-Gereon, France
[16] Faculté d'Odontologie, Université Claude Bernard Lyon 1, Université de Lyon, 69000, Lyon, France
Laboratoire des Multimatériaux et Interfaces, UMR CNRS 5615, Université Claude Bernard Lyon 1, Université de Lyon, 69000, Lyon, France | Réseau ReCOL, Association Dentaire Française, 75000, Paris, France
Service d’Odontologie, Hospices Civils de Lyon, 69007 Lyon, France
[17, 19] IQVIA, Réseau de pharmaciens, 75000, Paris, France
[18] Réseau ReCOL, Association Dentaire Française, 75000, Paris, France
[20] Infectious Diseases Division, Santé publique France, 94410, Saint Maurice, France
[21] Institut Pasteur, Université Paris Cité, National Reference Center for Respiratory Viruses, F-75015 Paris, France
Institut Pasteur, Université Paris Cité, CNRS UMR3569, Molecular Genetics of RNA Viruses Unit, F-75015, Paris, France
[23] Département de Santé Publique, Hôpital Saint-Antoine, APHP, 75012 Paris
Sorbonne Université, INSERM, Institut Pierre Louis d’Epidémiologie et de Santé Publique, (IPLESP), F-75012 Paris, France
[27] Laboratoire de Virologie, Université de Corse Pascal Paoli, UR7310 Bioscope, 20250 Corte, France
Unité des Virus Emergents, Aix Marseille University, IRD 190, INSERM U1207, 13005 Marseille, France

BACKGROUND

Data to understand the SARS-CoV-2 infection among primary healthcare workers (PHCWs) are scarce but essential to reflect on policy regarding prevention and control measures. We aimed to assess the prevalence of PHCWs infected by SARS-CoV-2 since the beginning of the pandemic in comparison with modelling from the general population in metropolitan France, and to identify associated factors.

METHODS

We conducted a cross-sectional study among general practitioners (GPs), pediatricians, dental and pharmacy workers in primary care in May-August 2021. Volunteers took a dried-blood spot for assessment of antibodies against SARS-CoV-2 and completed a questionnaire. The primary outcome was defined as the detection of infection-induced antibodies or previous self-reported diagnoses. Estimates were adjusted using weights on age and region for representativeness and compared with prediction from the general population. Poisson regressions were used to quantify associated factors.

RESULTS

The analysis included 1612 PHCWs. Weighted prevalences were: 31.7% (95%CI: 27.5-36.0) for GPs, 28.7% (95%CI: 24.4-33.0) for pediatricians, 25.2% (95%CI: 20.6-31.0) for dentists, and 25.5% (95%CI: 18.2-34.0) for pharmacists. There were no differences with the prediction from the general population. PHCWs more likely to be infected were: GPs compared to pharmacist assistants (adjusted prevalence ratio [aPR] = 2.26; CI95% 1.01-5.07), those living in Île-de-France (aPR= 1.53; CI95% 1.14-2.05), South-East (aPR = 1.57; CI95% 1.19-2.08), North-East (aPR= 1.81; CI95% 1.38-2.37), and those having an unprotected contact with a COVID-19 case within the household (aPR = 1.48; CI95% 1.22-1.80). Occupational exposure factors were not associated with infection.

CONCLUSIONS

Results suggest that prevention practices implemented in primary care in France were effective, but should be strengthened around a case at home detected, in line with previously published data from HCWs of other specialties and countries.

Keywords: SARS-CoV-2, Healthcare workers, Primary healthcare, Prevalence, Risk factors
ABSTRACT ID: 700
PRESENTED BY: Marie Pouquet, France / marie.pouquet@iplesp.upmc.fr

COVID-19

Field epidemiology (e.g. outbreak investigations)

Abstract

The burden of COVID-19 was not the same for all long-term care facilities: results from the 3-years COVID-19 surveillance experience in Ile de France region

L. Barón Miras [1]
G. Modenesi [2], L. Mercuriali [3], L. Reques [4]

[1] Hospital Clínic of Barcelona | ISGlobal | Agence Régionale de Santé d'Ile-de-France, Saint-Denis, France
[2] Cellule Régionale de Santé Publique France en Ile-de-France, Saint-Denis, France
[3, 4] Agence Régionale de Santé d'Ile-de-France, Saint-Denis, France

BACKGROUND
Although COVID-19 continued to disproportionally affect long-term care facilities (LTCF) after the first wave of contagion, its impact was not uniform within centres. Identifying factors linked to these differences can inform outbreak response measures. Objective: to describe and compare transmission and morbimortality of COVID-19 in LTCF.

METHODS
Observational analytic study of COVID-19 episodes in LTCF between July 2020 and December 2022. Data came from the Île-de-France Regional Health Agency, receptor of LTCFs episodes (1 suspected or laboratory-confirmed case or more among residents or staff). Number of episodes, case incidence, hospitalisations and mortality rates (in-hospital or in-LCTF) were compared by crude relative risks (RRc) between housing for people with disabilities (HPD) and care facilities for elderly people (dependent, D-CFEP and non-dependent, ND-CFEP).

RESULTS
Out of 5,973 episodes, 3,546 (59%), 1,780 (30%) and 647 (11%) occurred among D-CFEP, ND-CFEP and HPD respectively. Episodes seasonally peaked in winter, with an unadjusted attributable fraction of 59% (50%-66%). CFEPs for dependent (D-CFEP) had 44,607 cases (76%), followed by HPD with 11738 (20%). D-CFEP had the highest weekly incidence along all periods, peaking during winter 2021-22 (1,335 cases/10.000 individuals). ND-CFEP had higher hospitalisation rates than D-CFEP (RRc 2.1 CI95% 1.8-2.3), but in-LTCF incidence and global mortality were much greater in D-CFEP (RRc 12.2 CI95% 5.5-27.2 and RRc 1.8 CI95% 1.4-2.3).

CONCLUSIONS
LTCFs with elderly and dependent residents were the most impacted even after the first pandemic wave. Incidence of episodes peaked every winter, aggravating the burden of other winter infections. This should be considered for healthcare planning. Extended multivariate analysis is ongoing.

Keywords: COVID-19, Long-term care, Outbreaks, Personal Autonomy, Aged
ABSTRACT ID: 716
PRESENTED BY: Lourdes Estefanía Barón Miras, Spain / lebaron@clinic.cat

COVID-19

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

MODERATOR
Nom

Abstract

Protection conferred by prior SARS-CoV-2 infection with or without bivalent mRNA booster vaccination against symptomatic Omicron SARS-CoV-2 infection in a Dutch prospective cohort study (VASCO)

G. Matias [1]
A. Huiberts [2], B. de Gier [3], H. de Melker [4], S. van den Hof [5], S. Hahne [6], M. Knol [7]

[1] Centre for Infectious Disease Control, National Institute for Public Health and Environment (RIVM), Bilthoven, the Netherlands | ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5, 6, 7] Centre for Infectious Disease Control, National Institute for Public Health and Environment (RIVM), Bilthoven, the Netherlands

BACKGROUND
Since September 2022, bivalent mRNA vaccines targeting the Omicron BA.1 and original SARS-CoV-2 strain have been administered as boosters in the Netherlands. We assessed the effect of bivalent vaccination and/or prior infection against symptomatic SARS-CoV-2 infections.

METHODS
We analyzed data from an ongoing prospective cohort study (VASCO) in community-dwelling adults (18-85 years), collecting 6-monthly serum samples. The last prior infection was identified via serology or self-reported positive tests. The primary endpoint was symptomatic infection (excluding infections with only local respiratory symptoms) confirmed by SARS-CoV-2 testing. Among subjects who received primary vaccination and one or two monovalent boosters, we used Cox regression to estimate age-stratified (18-59, 60-85) relative reduction of infection (RR) in those with prior pre-Omicron, Omicron-BA.1/BA.2 or post-Omicron-BA.2 infection with/without bivalent vaccination compared to no bivalent vaccination and no prior infection.

RESULTS
From September 2022 to April 2023, we analyzed data from 33,877 participants (mean age 58.9 years). The dominant circulating sub-variants were Omicron BA.5, BQ.1 and XBB. In 60-85-year-olds without prior infection, RR of bivalent vaccination was 20% (95%CI 8-30).RR from prior infection was 47% (33-57), 81% (77-85), and 94% (92-96) for pre-Omicron, Omicron-BA.1/BA.2, and post-Omicron-BA.2 infection, respectively. RR from prior infection and bivalent booster increased to 64% (54-72), 83% (79-86), and 95% (93-97) for pre-Omicron, Omicron-BA.1/BA.2, and post-Omicron-BA.2 infection, respectively. For 18-59-year-olds, RRs were similar, except for a higher RR of bivalent vaccination without prior infection (36% (24-47)).

CONCLUSIONS
Bivalent vaccination added limited protection against symptomatic infection for those already having primary vaccination and one or two monovalent boosters. Prior infections significantly enhanced protection, highlighting the role of hybrid immunity. Vaccination remains important, particularly for high risk individuals.

Keywords: COVID-19, Vaccine effectiveness, SARS-CoV-2, Cohort studies
ABSTRACT ID: 730
PRESENTED BY: Goncalo Matias, Netherlands / goncalo.padilha.matias@rivm.nl

EMERGING AND VECTOR-BORNE DISEASES

Modelling, biostatistics, and health informatics

Abstract

European projections of West Nile virus transmission under climate change scenarios

Z. Farooq [1]
H. Sjödin [2], J. Semenza [3], Y. Tozan [4], M. Sewe [5], J. Wallin [6], J. Rocklöv [7]

[1] Umeå University
[2, 5, 7] Department of public health and clinical medicine, Section of sustainable health, Umea, University, Sweden
[3] Heidelberg institute of global health and Interdisciplinary center for scientific computing, University of Heidelberg, Im Neuenheimer Feld 205, Heidelberg 69120, Germany
Department of public health and clinical medicine, Section of sustainable health, Umea, University, Sweden
[4] New York University, New York, USA
[6] Department of statistics, Lund university, Sweden

BACKGROUND
West Nile virus (WNV), a mosquito-borne zoonosis, has emerged as a disease of public health concern in Europe. Recent outbreaks have been attributed to suitable climatic conditions for its vectors favoring transmission. However, to date, projections of the risk for WNV expansion under climate change scenarios are lacking. Here, we estimate the WNV-outbreaks risk for a set of climate change and socioeconomic scenarios. We delineate the potential risk-areas and estimate the growth in the population at risk (PAR).

METHODS
We used a supervised machine learning classifier, XGBoost, to estimate the WNV-outbreak risk using an ensemble climate model and a multi-scenario approach. The model was trained by collating climatic, socio-economic, and reported WNV-infections data (2010-22) and the out-of-sample results (1950-2009, 2023-99) were validated using a novel Confidence-Based Performance Estimation (CBPE) method. Projections of area-specific outbreak risk trends and corresponding PAR were estimated and compared across scenarios

RESULTS
Our results show that the risk of the virus is projected to increase by 0.3 to 5-fold depending on the geographical region and climate scenario during 2040-60 when compared with 2000-20. The proportion of disease-reported European land areas could increase from 15% to 23-30%, putting 161 to 244 million people at risk.

CONCLUSIONS
Across scenarios, Western Europe appears to be facing the largest increase in the outbreak risk of WNV. The increase in the risk is not linear but undergoes periods of sharp changes governed by climatic thresholds associated with ideal conditions for WNV vectors. The increased risk will require a targeted public health response to manage the expansion of WNV with climate change in Europe.

Keywords: West Nile virus, XGBoost, WNV risk projections, Climate change, CBPE method, Machine learning
ABSTRACT ID: 103
PRESENTED BY: Zia Farooq, Sweden / zia.farooq@umu.se

Communication and health promotion

Abstract

Knowledge, perceptions and practices related to mosquitoes and mosquito-borne viruses: survey in Belgium, 2022

V. Laisnez [1]
M. Hermy [2], R. Brondeel [3], A. Abourashed [4], P. de Best [5], T. Lernout [6], J. Rebolledo [7]

[1] Department of Epidemiology and Public Health, Sciensano, Brussels, Belgium | ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 6, 7] Department of Epidemiology and Public Health, Sciensano, Brussels, Belgium
[4] Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Blanes, Spain
[5] Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands

BACKGROUND
Effective preparedness for emerging mosquito-borne viruses (MBVs) relies on citizens having good knowledge and taking appropriate preventive measures. We assessed current knowledge, perceptions and practices related to mosquitoes and MBVs among adults in Belgium to guide future health promotion activities.

METHODS
In this cross-sectional study, we conducted an online survey among adults recruited via social media (One Health PACT's MosquitoWise survey using the Health Belief Model). We included questions on demographic variables; knowledge; perceptions, self-efficacy and cues to actions (Likert scales); and preventive measures. We assigned knowledge levels (low, medium or high depending on number of correct answers) and scores for perceptions, self-efficacy, cues to action and preventive measures.

RESULTS
We included 776 participants (62% females), of which 50% had a medium and 40% a high knowledge level. Participants scored high on questions related to mosquito ecology but lower on MBVs. Only 19% of participants correctly identified mosquitoes among pictures of insects.Participants perceived the severity of MBVs as high (mean score 6.0/7.0), but their susceptibility to MBVs and mosquitoes lower (4.3/7.0). Participants were most motivated to take preventive measures upon observing mosquitoes in and around the house (cues to action, 5.3/7.0). Participants had limited confidence in finding information on preventive measures and in recognizing and removing breeding sites (self-efficacy, 4.8/7.0).Ninety-seven percent of participants reported implementing at least one preventive measure, mainly to prevent bites (95%).

CONCLUSIONS
Together with the recent findings of tiger mosquitoes in Belgium, based on our study results we recommend to improve knowledge about MBVs and awareness about possible transmission in Belgium in the future. Information on recognizing mosquitoes and removing breeding sites should be easy to find.

Keywords: Mosquitoes, Vector Borne Diseases, Knowledge, Perception, Health Belief Model
ABSTRACT ID: 476
PRESENTED BY: Valeska Laisnez, Belgium / Valeska.Laisnez@sciensano.be

EMERGING AND VECTOR-BORNE DISEASES

Communication and health promotion

Abstract

Determinants of prevention measure use against mosquitoes and mosquito-borne viruses: inferences from MosquitoWise survey data in Spain and the Netherlands, 2022

P. de Best [1]
A. Abourashed [2], L. Doornekamp [3], R. Sikkema [4], E. van Gorp [5], A. Timen [6], J. Palmer [7], F. Bartumeus [8],
M. Koopmans [9]

[1] Erasmus University Medical Center | National Institute for Public Health and the Environment (RIVM)
[2] Erasmus University Medical Center |C entre d'Estudis Avançats de Blanes (CEAB-CSIC)
[3, 5, 9] Erasmus University Medical Center
[4] Erasmus University Medical Center|Netherlands Institute of Ecology (NIOO-KNAW)
[6] National Institute for Public Health and the Environment (RIVM)
Radboud University Medical Center | VU University Amsterdam
[7] Universitat Pompeu Fabra
[8] Centre d'Estudis Avançats de Blanes (CEAB-CSIC)|Centre de Recerca Ecològica i Aplicacions Forestals (CREAF)
Institució Catalana de Recerca i Estudis Avançats (ICREA)

BACKGROUND

In the last decade, Europe has seen an emergence of mosquito-borne viruses (MBVs). Understanding citizens' perceptions of and behaviours towards mosquitoes and MBVs is crucial to reduce disease risk through intervention campaigns. This understanding can be evaluated using European-tailored surveys, such as MosquitoWise. This study aims to investigate citizens' perceptions, knowledge, and behaviours towards mosquitoes and MBVs to identify determinants for public health interventions.

METHODS

Using the validated Health Belief Model (HBM)-based MosquitoWise survey, data was collected through an age- and sex-stratified panel in Spain (N=475) and the Netherlands (N=438). HBM scores (6 – 42) to measure behavioural intent and knowledge scores (0 – 9) were calculated. Confidence Interval-Based Estimation of Relevance was used to identify which determinants are most relevant in improving prevention measure use. Knowledge and the HBM constructs (Susceptibility, Severity, Benefits, Barriers, Self-Efficacy, and Cues to Action) were assessed as determinants.

RESULTS

Most participants in Spain (92.2%) and the Netherlands (91.8%) used at least one prevention measure. Spanish participants had a significantly higher median knowledge score than Dutch participants (4.88 and 4.39, respectively, $p < 0.001$). Spanish participants also had higher behavioural intent to use prevention measures compared to Dutch participants (29.1 and 28.2, respectively, $p < 0.001$). To improve prevention measure use in both countries, the Cues to Action construct was the most relevant determinant for intervention. Specifically for repellent use, the most relevant determinants were Knowledge, Benefits, and Cues to Action for both countries.

CONCLUSIONS

This study found differences in knowledge and behavioural intent between countries but similarities in determinants for improving prevention measure use. The identified determinants should be the focus for future public health campaigns to reduce MBV transmission risks.

Keywords: Surveys and Questionnaires, Vector Borne Diseases, Health Belief Model, Knowledge, Social Determinants of Health, Prevention and Control
ABSTRACT ID: 526
PRESENTED BY: Ayat Abourashed, Netherlands / a.abourashed@erasmusmc.nl

FOOD- AND WATERBORNE DISEASES AND ZOONOSE

Field epidemiology (e.g. outbreak investigations)

Abstract

An outbreak of Legionnaires’ disease linked to a municipal and industrial wastewater treatment plant in the Netherlands

S. Raven [1]
R. Pijnacker [2], S. Euser [3], A. Vahidnia [4], J. Limaheluw [5], C. Schout [6], G. Haj Mohammad [7], P. Brandsema [8]
[1] Department of Infectious Diseases, Public Health Service region Utrecht, Zeist, the Netherlands
[2, 8] Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[3, 4] Regional Public Health Laboratory Kennemerland, Haarlem, The Netherlands
[5] Institute for Risk Assessment Sciences, Utrecht University, Utrecht, The Netherlands
[6, 7] Department of Infectious Diseases, Public Health Service region Utrecht, Zeist, the Netherlands

BACKGROUND
Wastewater treatment plants (WWTPs) are increasingly identified as source of Legionnaires’ disease (LD) outbreaks. However, their role is likely still underestimated. Here we describe an outbreak investigation that was initiated after 5 LD cases were reported between 13-27 September 2022, living in the town Houten, the Netherlands.

METHODS
Case identification was based on the LD European case definition with symptom onset ≥ 1 September 2022, living in the town Houten, within 5km of Houten, or having visited Houten within the incubation period, without other likely sources. Environmental and clinical isolates were genotyped using sequence-based typing. A spatial source identification model and a spatio-temporal analysis based on wind direction were used to assess most likely sources of infection.

RESULTS
Between 13 September and 23 October 2022, 15 cases were registered. Two of six sampled possible source locations, an industrial and municipal WWTP, tested positive for Legionella, with the first discharging its water on the latter. Both locations tested positive for L. pneumophila (Lp) serogroup (SG) 1, sequence type (ST) 2678. The iWWTP also tested positive for Lp SG6, ST1326, and the mWWTP for Lp SG1, ST42, and Lg SG6, ST624. Lp SG1, ST42 was also found in one of three cases with available clinical isolates. Statistical modelling suggested the iWWTP and mWWTP as potential sources. Following preventive measures at both WWTPs, no more cases were observed.

CONCLUSIONS
Epidemiological, microbiological and environmental investigations together suggested the iWWTP and mWWTP as most likely sources of infection, underlining the potential public health risk of WWTPs. An inventory of WWTPs should be made available for public health authorities to enable a more rapid source identification in case of a LD outbreak.

Keywords: Legionellosis, Disease Outbreaks, Epidemiological Models, Environmental Exposure
ABSTRACT ID: 131
PRESENTED BY: Stijn Raven, Netherlands / sraven@ggdru.nl

FOOD- AND WATERBORNE DISEASES AND ZOONOSES

Microbiology (incl. novel methods in microbiology, such as e.g. new diagnostic tools)

Abstract

Development and Validation of a cgMLST for Yersinia enterocolitica: a Tool for Outbreak Management and Surveillance

J. Pires [1]
L. Brandal [2], U. Naseer [3]

[1] Department of Infection Control and Preparedness, Norwegian Institute of Public Health, Norway, EUPHEM
ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3] Department of Infection Control and Preparedness, Norwegian Institute of Public Health, Norway

BACKGROUND
Yersinia enterocolitica is the most frequent etiological agent of yersiniosis and has been responsible for several national outbreaks in Norway since 2017. Currently, a high-resolution molecular typing method for Y. enterocolitica that enables inter-laboratory comparison is lacking. In this study we aim to develop a standardized high-resolution core-genome Multilocus Sequence Typing (cgMLST) method for Y. enterocolitica to enable pathogen traceability for national and cross-border outbreaks.

METHODS
We designed a cgMLST scheme using 16 high-quality reference genomes in SeqSphere. Validation was performed on 563 genomes collected in Norway between 2012-2022 each assembled with different assemblers and on 261 genomes from public databases. The scheme was validated if at least 95% of the genes included were found across the phylogenetic diversity (13 sub-biotypes) of Y. enterocolitica, and not in other Yersinia spp. We analyzed retrospectively outbreaks to establish a threshold based on the number of gene allelic differences.

RESULTS
The cgMLST scheme included 2582 genes. A median of 97.9% genes (interquartile range 97.7-98.7%) were found across sub-types. The median gene presence percentage was 97.9% and 98.6% for Norwegian and public database genomes, respectively. No performance differences were observed between assemblers (x2-test, $p = 0.264$). Other Yersinia spp. had a median of 13.9% genes (interquartile range 13.2-18.9%). Retrospective analysis of outbreaks identified all strains within three allelic differences.

CONCLUSIONS
Our cgMLST scheme showed very good performance in typing Y. enterocolitica using diverse data sources and was able to identify outbreak strains. We recommend using three allelic differences for outbreak detection and the implementation of this scheme nationally and internationally to facilitate Y. enterocolitica surveillance and improve outbreak response in national and cross-border outbreaks.

Keywords: Yersinia enterocolitica, Yersiniosis, cgMLST, Molecular Typing, Genomic Epidemiology, Outbreak
ABSTRACT ID: 273
PRESENTED BY: João Pires, Norway / jp.dcpires@gmail.com

FOOD- AND WATERBORNE DISEASES AND ZOONOSES

Surveillance

Abstract

Rapid decrease in the seroprevalence of toxoplasmosis: a 6-year study in pregnant women in Lyon, France, 2017-2022

Á. Roy [1]
L. Gaucher [2], B. Lina [3], M. Wallon [4]

[1] Hospices Civils de Lyon, Hôpital de la Croix-Rousse, Institut des Agents Infectieux, Laboratoire de Virologie, Lyon, France | ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2] Geneva School of Health Sciences, HES-SO University of Applied Sciences and Arts, Geneva, Switzerland|Hospices Civils de Lyon, Hôpital Femme Mère-Enfant, Bron, France | Research on Healthcare Performance (RESHAPE), Université Claude Bernard Lyon 1, INSERM U1290, Lyon, France
[3] Hospices Civils de Lyon, Hôpital de la Croix-Rousse, Institut des Agents Infectieux, Laboratoire de Virologie, Lyon, France
[4] Hospices Civils de Lyon, Hôpital de la Croix-Rousse, Institut des Agents Infectieux, Service de Parasitologie et de Mycologie Médicale, Lyon, France | Walking Team, Centre for Research in Neuroscience in Lyon, Bron, France

BACKGROUND
France has a congenital toxoplasmosis prevention program based on identifying women at risk at the beginning of pregnancy and monthly monitoring their serological status. However, national data on Toxoplasma seroprevalence in France is limited to six cross-sectional perinatal surveys carried out on a limited number of women between 1995 and 2021, showing a decreasing trend. The aim of this study was to evaluate longitudinally the Toxoplasmosis seroprevalence and seroconversion percentages in pregnant women from 2017 to 2022 in Lyon.

METHODS
We conducted a longitudinal retrospective cohort study including all pregnancies with known Toxoplasma status followed at Lyon's public maternity hospitals between 2017 and 2022. We calculated the seroprevalence per year by age-groups. A logistic regression model was used to identify factors (age-group, population density of living area and parity) associated with seropositivity.

RESULTS
A total of 65,001 pregnancies with known status were included (97%). The seroprevalence of toxoplasmosis decreased consistently from 26.8% in 2017 to 22.3% in 2022, and the percentage of seroconversions remained constant at 0.1%. The seroprevalence increased linearly from 18.3% in women aged 20-24 years to 39.2% in women aged ≥40 years ($p < 0.001$). The seroprevalence was higher in pregnant women living in high populated areas [adjusted prevalence ratio (aPR) = 1.31, 95% CI: 1.22-1.41] and in multiparous women (aPR = 1.19, 95% CI: 1.14-1.24).

CONCLUSIONS
This study confirms the decreasing trend of toxoplasmosis seroprevalence observed in previous national cross-sectional surveys, which implies an increase in the number of tests needed in seronegative women in the coming years. This finding is useful for medico-economic assessments of the prenatal screening program, and can inform intervention planning and tailoring of future Toxoplasma surveillance programs.

Keywords: Toxoplasmosis, Pregnancy, Serology, Prenatal screening, France
ABSTRACT ID: 342
PRESENTED BY: Álvaro Roy, France / alvaro.roy-cordero@chu-lyon.fr

FOOD- AND WATERBORNE DISEASES AND ZOONOSES

Field epidemiology (e.g. outbreak investigations)

Abstract

Association of Helicobacter pyroli Infection and New-Onset Diabetes: A Systematic Review and Meta-analysis of Cohort studies

P. Paramiraksa [1]
C. Chaichan [2], K. Pornchokchai [3], Kongjun [4]

[1] Faculty of Medicine Vajira Hospital, Navamindradhiraj University
[2] Faculty of Medicine Vajira Hospital, Navamindradhiraj University (Vajira Hospital), Dusit, Bangkok, Thailand
[3, 4] Faculty of Medicine Vajira Hospital, Navamindradhiraj University

BACKGROUND
Helicobacter pylori (H. pylori) affects human health worldwide. The estimated global prevalence of type II diabetes has increased in recent decades, posing substantial clinical and public health burdens. Several studies have suggested that H. pylori infection may increase the risk of diabetes. However, there were inconsistencies among studies. Although there were some systematic review and meta-analysis of cross-sectional and case-control studies, the study design of included studies has restricted the determination of causality. To the best of our knowledge, there is no prior systematic review and meta-analysis of cohort studies. We conducted a systematic review and meta-analysis of cohort studies to determine the causal association of H. pylori infection on the risk of diabetes.

METHODS
A systematic search of PubMed, Scopus, EMBASE, and medRxiv was performed to identify the relevant studies until October 2022. Screening, data extraction, and risk bias assessment were independently conducted by two reviewers; if consensus is required, a third reviewer will be consulted. Only cohort studies were included in a systematic review and only studies reported hazard ratio (HR) were analyzed in the meta-analysis. The random-effect model was conducted and the publication bias was determined by funnel plot.

RESULTS
A total of seven studies were included in systematic reviews; four of seven comprising 23,473 participants were eligible for meta-analysis. A pooled analysis revealed no association between H. pylori infection and new-onset diabetes (HR 1.16, 95% CI 0.78-1.74, P = 0.47, I2 = 78%).

CONCLUSIONS
There was no association between H. pylori infection and new-onset diabetes. H. pylori eradication therapy may not be necessary to prevent diabetes. The heterogeneity is partly due to the different statistical management of covariables and study design implemented.

Keywords: Helicobacter pylori, Diabetes mellitus, Systematic review, Meta-analysis
ABSTRACT ID: 371

PRESENTED BY: Parkin Paramiraksa, Thailand / 6401101073@nmu.ac.th

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FOOD- AND WATERBORNE DISEASES AND ZOONOSES

Field epidemiology (e.g. outbreak investigations)

Abstract

Outbreak of cryptosporidiosis among a cohort of business event participants at a Finnish hotel associated with a green salad-mix, September – October 2022

W. Kitowska [1]
C. González Pérez [2], K. Suominen [3], A. Vainio [4], R. Åberg [5], P. Hokkanen [6], E. Lääkkö [7], E. Särelä [8], S. Isosomppi [9], R. Rimhanen-Finne [10]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden|Finnish Institute for Health and Welfare (THL), Helsinki, Finland.
[2] ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
Finnish Institute for Health and Welfare (THL), Helsinki, Finland.
[3, 4, 10] Finnish Institute for Health and Welfare (THL), Helsinki, Finland.
[5, 6, 7] Food Safety Unit, City of Helsinki, Finland.
[8, 9] Epidemiological Operations Unit, City of Helsinki, Finland.

BACKGROUND

A gastroenteritis outbreak occurred among participants of a business event held 26–27.09.2022 at a hotel in Helsinki, Finland. We investigated the outbreak to characterize the pathogen, identify the source, and to enhance control measures.

METHODS

We conducted a retrospective cohort study. We defined a case as any person who participated in event meals and developed at least one of the following symptoms during 28.09–18.10.2022: diarrhoea, stomach pain, or nausea. We calculated food-specific relative risks (RR) and 95% confidence intervals (95%CI).Faecal specimens were collected for PCR and culture. We characterized Cryptosporidium-positive samples by species (RT-PCR) and gp60 type (nested-PCR and Sanger Sequencing). No food or environmental samples were available for testing.

RESULTS

Out of 85 participants, 66 (response rate 78%) completed the online questionnaire, of whom 35 (53%) met the case definition. Among cases, 97% (34/35) ate a ready-to-eat salad-mix during dinner on 26.09, while among non-cases the proportion was 71% (22/31). We found a positive significant association between consumption of this salad-mix and illness (RR: 6.0, 95%CI: 0.9–39.2, p-value: 0.005).Of thirteen collected faecal samples, seven were tested for Cryptosporidium and four were positive. Two were identified as subtype C. parvum IIdA21G1, one IIaA15G2R1, and one was not characterized further.

CONCLUSIONS

A green salad-mix was the suspected source of this C. parvum outbreak. This outbreak was challenging to investigate, as microbiological evidence was limited. We recommend that testing for Cryptosporidium be emphasized in clinical settings and routine species determination and subtyping for outbreak detection be considered. Additionally, the existing recommendation of storing frozen food samples at restaurants for later testing should be strengthened. Risk management measures should be developed for producing ready-to-eat salads.

Keywords: Cryptosporidium parvum, Outbreak, Green salad, Finland, Cohort study
ABSTRACT ID: 449
PRESENTED BY: Wioleta Kitowska, Finland / wioleta.kitowska@thl.fi

Field epidemiology (e.g. outbreak investigations)

Abstract

Timely outbreak signal detection – the role of a kindergarten heath officer in a norovirus outbreak investigation in a kindergarten in Zagreb, Croatia, March 2023

G. Sarajlic [1]
M. Kosanovic Licina [2], N. Lazic [3], Z. Lovric Makaric [4], B. Kolaric [5]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Croatian Institute of Public Health (CIPH), Zagreb, Croatia
[2, 3, 5] Andrija Stampar Teaching Institute of Public Health, Zagreb, Croatia
[4] Croatian Institute of Public Health, Zagreb, Croatia

BACKGROUND
A dedicated kindergarten health officer reported a cluster of children experiencing acute onset vomiting while in kindergarten, on 22 March 2023. A team, together with the health officer (a trained nurse), investigated the outbreak to determine its extent and identify the source.

METHODS
We defined a case as a child or staff who attended the kindergarten and experienced gastroenterocolitis symptoms between 17 and 24 March 2023. The officer instructed parents to bring child’s stool or vomit for analysis, and distributed questionnaires for parents and staff to identify unreported cases and test the hypothesis that a child or a teacher imported the infection. Contaminated food was excluded as a source since no cases in other kindergarten buildings occurred. Attack rates in percentage were calculated using attendance sheets.

RESULTS
We identified 15 cases. 4 of the 10 stools samples received were confirmed as norovirus. The attack rate amongst the children was higher (14/73, 19%) than amongst the teachers (1/10, 10%) and it was highest in the kindergarten class where the initial cluster was reported (10/12, 83%). 93% (14/15) of the cases were reported by the officer. One remaining case identified via questionnaires was a child who experienced diarrhoea the day before the outbreak onset and attended the class with the highest attack rate. This was suspected to be the index case.

CONCLUSIONS
Outbreak investigation suggests that a single infected child may have caused an outbreak of norovirus in a kindergarten, possibly because the parents were not aware of the relevance of the child's symptoms. We recommend advancing surveillance of diseases in kindergarten children by employing a dedicated healthcare worker, as is stated in the national law in Croatia.

Keywords: Norovirus, Disease Notification, Infection Control, Gastroenteritis
ABSTRACT ID: 454
PRESENTED BY: Gordan Sarajlic, Croatia / gordan.sarajlic@gmail.com

Field epidemiology (e.g. outbreak investigations)

Abstract

A multi-country outbreak of Salmonella enterica serotype Mbandaka ST413 linked to consumption of chicken meat – a case-case study in Finland, 2022 – 2023

C. Gonzalez Perez [1]
H. Landgren [2], A. Vainio [3], W. Kitowska [4], A. Pihlajasaari [5], E. Leinonen [6], T. Lienemann [7], R. Rimhanen-Finne [8]

[1] ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
Finnish Institute for Health and Welfare (THL), Helsinki, Finland
[2, 3, 8] Finnish Institute for Health and Welfare (THL), Helsinki, Finland
[4] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden | Finnish Institute for Health and Welfare (THL), Helsinki, Finland
[5, 6, 7] Finnish Food Authority, Helsinki and Kuopio, Finland

BACKGROUND

In September 2021, a multi-country outbreak of Salmonella enterica serotype Mbandaka ST413 started in the EU/EEA, Israel, and the United Kingdom (UK). Finland detected 97 S. Mbandaka ST413 cases during 04/2022–01/2023.Several national investigations and international traceability analyses suggested ready-to-eat products containing chicken as the likely source of infection. We conducted a case-case study and microbiological investigations to identify the vehicle, implement control measures and prevent new cases.

METHODS

A case (n=23) was defined as laboratory-confirmed S. Mbandaka during 01/09/2022–16/01/2023 in Finland. A control-case (n=46) was laboratory-confirmed Salmonella of another serotype, during the same period from the same or neighboring hospital district as a case.We conducted a web-based questionnaire (36% response rate) including five suspected ready-to-eat products and ten control products. We performed whole genome sequencing (WGS) for S. Mbandaka isolated throughout the outbreak of human (n=48) and food (n=1) origin, and cluster analysis (Ridom SeqSphere+).

RESULTS

Suspected ready-to-eat products from Company A in Country X were identified as the probable source of infection (odds ratio, 13; 95% confidence interval, 1.3–139; p-value 0.01). S. Mbandaka was isolated from a suspected product and linked by WGS to the sequence of an isolate from a chicken product used as an ingredient by Company A. The chicken meat product originated from a non-EU country and was linked to the Finnish cases.

CONCLUSIONS

Epidemiological and microbiological investigations showed that Company A's ready-to-eat products containing chicken caused a Salmonella Mbandaka ST413 outbreak in Finland. After Company A ceased using the contaminated batch of chicken product and changed the supplier, no new cases were detected. This study illustrates the usefulness of international cross-sectoral collaboration to investigate and control cross-border threats.

Keywords: Salmonellosis, Multi-country outbreak, Foodborne, Chicken, Case-case study
ABSTRACT ID: 463
PRESENTED BY: Cristina Gonzalez Perez, Finland / cristina.gonzalezperez@thl.fi

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

Developing an integrated approach to investigating meteorological factors affecting foodborne pathogen outbreaks

S. Williams [1]
N. Cunningham [2], B. Eggen [3], R. Close [4], A. Douglas [5], H. Crabbe [6], S. Hopkins [7], L. Larkin [8], G. Leonardi [9]

[1] UK Health Security Agency (UKHSA), FETP | Environmental Epidemiology Group, Radiation, Chemical and Environmental Hazards Directorate, UKHSA
[2, 7] Chief Medical Advisor's Office, UKHSA
[3, 4, 6, 9] Environmental Epidemiology Group, Radiation, Chemical and Environmental Hazards Directorate, UKHSA
[5, 8] Gastrointestinal Infections and Food Safety (One Health) Division, UKHSA

BACKGROUND
Seasonality of foodborne gastrointestinal infections is multifactorial, including meteorological patterns and human behaviours, with climate change related cases likely to increase. In summer 2022, the UK experienced a prolonged dry hot spell, followed by very heavy localised rainfall; this unusual weather preceded a large outbreak of Shiga-toxin producing E. coli (STEC) O157. Understanding this complex relationship between weather and gastrointestinal illness is a public health priority. We aimed to define work programme priorities and coordinate efforts by holding a stakeholder workshop.

METHODS
We used a One Health whole systems approach to identify stakeholders, expertise, and define the work programme. A workshop was held to: Share expertise on analysis of data for evidence generation in gastrointestinal outbreak investigations incorporating weather data Identify priority work areas, stakeholder needs and facilitate an integrated approach

RESULTS
The workshop in February 2023 had 33 participants from 13 organisations including international experts, academics, UK public health agencies, UK Met Office, UK food safety agencies, Animal and Plant Health Agency and the new UKHSA Centre for Climate and Health Security. Risk assessment steps, data sources, evidence gaps and policy considerations to inform an integrated approach were established. Priorities were identified around policy, preparedness and resilience, knowledge, and data needs. Recommendations included incorporation of analysis of local weather data, such as rainfall and temperature, for evidence generation and to inform risk analysis in outbreak investigations.

CONCLUSIONS
A One Health approach is crucial in mitigating predicted increases in frequency of gastrointestinal foodborne outbreaks. This workshop initiated our integrated approach with recommendations to incorporate weather effects and animal movement data into the STEC outbreak analyses as a proof of concept to aid public health interventions.

Keywords: Climate change, Shiga-Toxigenic Escherichia coli, Environmental, Epidemiology, Weather, One Health
ABSTRACT ID: 547
PRESENTED BY: Sarah Williams, United Kingdom / Sarah.V.Williams@ukhsa.gov.uk

Field epidemiology (e.g. outbreak investigations)

Abstract

Investigation of Leptospirosis Outbreak at Chili and Chilla Villages, Hathin Block, Palwal District, Haryana, India, July to October 2021

D. Tanwar [1]
D. Kathuria [2], D. Dzeyie [3], I. Kaur [4]
[1, 2, 4] World Health Organization, country office, New Delhi, India
[3] World Health Organization | World Health Organization, country office, New Delhi, India

BACKGROUND
On 11 September 2021, the district health authorities were alerted about fever related deaths in Chilla-Chilli village, Hathin Block, Palwal District, Haryana, India. We described epidemiology, recommendations for public health actions.

METHODS
A 'suspected' patient was defined as acute febrile illness in a resident of Chilli-Chilla village, Palwal district from 30 July-30 October 2021. Health teams visited every home and interviewed cases using a semi-structured questionnaire spplimented by treatment records. Serum and nasopharyngeal samples collected for malaria, dengue, SAR-CoV-2, leptospirosis, and scrub typhus. Environmental and sanitary conditions were assessed, and entomological survey conducted. Data was analyzed using Microsoft Excel and Epi info version 7.2.

RESULTS
We identified 692 patients (63% female) including eight deaths (case fatality rate: 1.1%) with median age of 6 years (range: 6 months-14 years); 54 (8%) were hospitalized. All deaths had contact with domestic animals and 7 lived in households around waterlogged areas. When suspected patients tested negative for dengue (n=31), malaria (n=692) and SAR-CoV-2 (n=361), five samples were tested for leptospirosis and scrub typhus eight days post admission: 4 tested IgM positive for leptospirosis. All deaths were epidemiologically linked to laboratory positive patients. The village was surrounded by thick herbs, rice fields, poor drainage. Aedes mosquito larvae was detected in 123/342 houses (36%). Public health response initiated for treatment and chemoprophylaxis of all suspected patients, awareness campaigns and environmental measures resulting in no further deaths.

CONCLUSIONS
We report a confirmed leptospirosis outbreak with deaths in a rural setting. The death patients were likely exposed to infected animals and their diagnosis delayed. We recommended strengthening of existing surveillance system and laboratory services for timely diagnosis to initiate timely public health action and prevent mortality.

Keywords: Leptospirosis, Disease Outbreak, Epidemiology, India
ABSTRACT ID: 561
PRESENTED BY: Sanjeev Tanwar, India / stanwar@who.int

FOOD- AND WATERBORNE DISEASES AND ZOONOSES

Field epidemiology (e.g. outbreak investigations)

Abstract

Rice Consumption Identified as Source of Gastroenteritis Outbreak in High School Dormitory: Implications for Food Safety Measures in Communal Settings, December 2022, Turkiye

Z. Ozguler [1]
O. Koyu [2]
[1, 2] Communicable Diseases and Early Warning Department, General Directorate of Public Health, Ankara, Turkiye

BACKGROUND
Between December 19th-21st, 2022, an outbreak of gastroenteritis occurred among high school female dorm residents aged 13-18 years. Rapid spread of gastroenteritis among adolescents in communal settings poses a public health concern, especially when the cause of the outbreak is not immediately apparent. We conducted an investigation to identify the potential source and mode of transmission by assessing the association between food and drink consumption, including specific food items, and development of illness.

METHODS
We conducted a retrospective cohort study and calculated food-specific attack rates and risk ratios with 95% confidence intervals. Univariate analysis was used to identify meals and food items associated with illness, and multivariable logistic regression was conducted to predict the relationship between predictor variables and illness. Stool sample (n=1) was tested for bacterial, viral, and parasitic pathogens.

RESULTS
Of 127 students, 88 (attack-rate:69.3%) reported illness. Epidemic curve suggested a point source outbreak with a median incubation time of 19-hours (range 1-45). The dinner served on December 21st was the likely source of infection (RR:1.40, 95%CI:1.04-1.88), with rice consumption being the only food item significantly associated with illness (OR:6.07, 95%CI:2.08-17.75), furthermore this association was found to be dose-dependent. Norovirus was detected in the stool sample, while bacterial culture was negative.

CONCLUSIONS
Our study provides evidence linking rice consumption to the outbreak of gastroenteritis in the high school dormitory and emphasizes the importance of investigating outbreaks to guide interventions. We used the findings of this study to develop targeted food safety measures, such as proper food handling and hygiene practices, to prevent and control outbreaks in similar settings. Continued efforts are needed to improve food safety and quality in communal settings to protect public health.

Keywords: Disease outbreaks, Gastroenteritis, Norovirus, Epidemiology, Foodborne diseases, Cohort studies
ABSTRACT ID: 745

PRESENTED BY: Zeynep Ozge Ozguler, Turkey/ zeynepozgemd@gmail.com

HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

Surveillance

Abstract

Statutory health insurance-covered pre-exposure prophylaxis (PrEP) in Germany 2018-2021: changing trends during the COVID-19 pandemic

H. Prins [1]

A. Doerre [2], D. Schmidt [3]

[1] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, German
ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND

In 2019, Germany introduced a law to reimburse high-incidence populations for pre-exposure prophylaxis (PrEP), prescribed as tenofovir-disoproxil/emtricitabine (TDF/FTC), via statutory health insurance (SHI). We evaluated changes in TDF/FTC prescriptions after the law's implementation and during the COVID-19 pandemic.

METHODS

We performed an interrupted time-series approach involving regression models with monthly TDF/FTC prescriptions per defined time period as the outcome. We modelled SHI-covered PrEP in 2019 as an interruption, and considered four COVID-19 waves and two national lockdowns in 2020–2021 as explanatory variables. We linearly extrapolated prescriptions had the lockdowns not occurred, and compared this to the actual prescriptions during the same period. Sub-analyses were based on the five federal states with the highest proportion of PrEP users (Berlin-Brandenburg combined, Bavaria, Hamburg, Hesse, North Rhine-Westphalia), and single-month (i.e. PrEP initiation) versus three-month prescriptions. We assessed model fit based on the adjusted R-squared value using RStudio.

RESULTS

The best fitting linear regression model included SHI-covered PrEP and the first COVID-19 lockdown (April 2020). Both nationally and in the five federal states, the increase after SHI-covered PrEP and decrease during the first lockdown was most pronounced in single-month prescriptions. The first lockdown resulted in estimated reductions of 57.7% (95% prediction interval (PI): 23.0-92.4%) for single-month prescriptions, while 17.4% (95% PI: 0.28-34.5%) nationally, and 13.9% (95% PI: -3.67-31.5%) for three-month prescriptions.

CONCLUSIONS

PrEP use greatly increased after the start of SHI coverage, and dropped during the first lockdown, particularly treatment initiations, possibly due to reduced healthcare access. Safeguarding access to PrEP is of high importance during public health crises like COVID-19. Therefore, monitoring PrEP trends and expanding coverage must be prioritized, for instance via telemedicine, targeted communication, and low-threshold, outreach-based programs.

Keywords: Tenofovir disoproxil/emtricitabine (TDF/FTC), Pre-exposure prophylaxis (PrEP), Pharmacy prescriptions, COVID-19, Lockdown, Germany
ABSTRACT ID: 141

PRESENTED BY: Henrieke Prins, Germany / h.a.b.prins@gmail.com

HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

Surveillance

Abstract

The impact of COVID-19 on notifiable HIV infection numbers in Germany: An analysis of surveillance data during pre-and COVID-19 era

K. Schmidt [1]
K. Jansen [2], B. Gunsenheimer-Bartmeyer [3], V. Bremer [4], U. Koppe [5]

[1] Robert Koch Institute, FG16: Mycotic and Parasitic Agents and Mycobacteria, Berlin, Germany
ECDC fellowship Programme, Public Health Microbiology path (EUPHEM)
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5] Robert Koch Institute, FG34: HIV/AIDS, STI and Blood-borne Infections, Berlin, Germany

BACKGROUND
Timely diagnosis of HIV infection is crucial to prevent severe disease trajectories. COVID-19 pandemic disrupted sexual health services use with a fall in people accessing HIV testing. We analysed if certain groups were over- or underrepresented among individuals with new HIV diagnoses during the COVID-19 pandemic.

METHODS
We compared HIV surveillance data during COVID-19 pandemic (03.2020-12.2021) and a corresponding pre-COVID-19 period (03.2018-12.2019). Descriptive statistical and epidemiological analyses were conducted using chi-square test to assess changes in new HIV diagnoses between those periods regarding gender, age group, region, transmission route, and late diagnosis.

RESULTS
The overall number of new HIV diagnoses during COVID-19 decreased by 24% (4,188) compared to pre-COVID-19 (5,510). This decline ranged from 6-38% (103 vs 97)-(115 vs 71) in all federal states, except one (Schleswig-Holstein) showing an increase of 12% (104 vs 118). The proportion of male with new HIV diagnoses were comparable between both periods (78.1% vs 78.4%, missing: 0.5%, p=0.253). Among all new diagnoses age group 20-29 years was less frequently reported during pandemic (23.6% vs 20.7%, p=0.001) while the proportion of diagnoses for age group 60-69 years increased (4.6% vs 5.8%, p=0.009). The proportion of people who inject drugs (PWID) increased from 5.2% to 5.8% (p=0.007) during COVID-19. The proportion of MSM (48.4% vs 42.3%) and heterosexuals (24.9%vs 20.5%) decreased (overall missing: 25%). The proportion of late diagnosis increased from 15% to 18% (p<0.001, overall missing: 19.5%).

CONCLUSIONS
During the COVID-19 pandemic new HIV diagnoses among PWID, age group 60-69 years and individuals with late diagnosis were overrepresented compared to the pre-COVID era. Increased testing efforts are necessary to reach people across all transmission and age groups and provide early diagnosis.

Keywords: HIV, Sexually transmitted infections, Surveillance, COVID-19
ABSTRACT ID: 175
PRESENTED BY: Katarzyna Schmidt, Germany / katarzyna.schmidt@yahoo.com

HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

Field epidemiology (e.g. outbreak investigations)

Abstract

Molecular epidemiology of HIV among people who inject drugs (PWID) in Athens, Greece, over a period of 20 years (1998-2019): Evidence for a continuous spread among PWID due to injecting practices

E. Kostaki [1]

S. Roussos [2], A. Kefala [3], S. Limnaios [4], M. Psichogiou [5], E. Papachristou [6], G. Nikolopoulos [7], E. Flountzi [8], S. Friedman [9], P. Lagiou [10], A. Hatzakis [11], V. Sypsa [12], G. Magiorkinis [13], A. Beloukas [14], D. Paraskevis [15]

[1] Department of Hygiene, Epidemiology and Medical Statistics, Medical School, National and Kapodistrian University of Athens, Athens, Greece
[2, 4, 6, 8, 10, 11, 12, 13, 15] Department of Hygiene, Epidemiology and Medical Statistics, Medical School, National and Kapodistrian University of Athens, Athens, Greece
[3] Department of Biomedical Sciences, University of West Attica, Athens, Greece
[5] First Department of Internal Medicine, “Laiko” General Hospital, Medical School, National and Kapodistrian University of Athens, Athens, Greece
[7] Medical School, University of Cyprus, Nicosia, Cyprus
[9] Center for Opioid Epidemiology and Policy, Department of Population Health, New York University Grossman School of Medicine, New York City, USA
[14] Department of Biomedical Sciences, University of West Attica, Athens, Greece | National AIDS Reference Centre of Southern Greece, Department of Public Health Policy, University of West Attica, Athens, Greece

BACKGROUND

In Greece, during 2011-2013, Athens, the capital city, experienced the largest recent HIV outbreak in people who inject drugs (PWID) in Europe and North America. Although the number of newly HIV-1 diagnosed PWID in Greece declined after 2013, ongoing HIV transmission was documented during 2014-2020 in this population. Our aim was to provide a detailed analysis of the HIV transmission patterns among PWID over a period of 20 years (1998-2019) using molecular epidemiology methods.

METHODS

Our study sample consisted of all the available HIV-1 sequences from PWID sampled during 1998-2019 in Athens (N=1,054). This number accounts for 50.6% (1,054 of 2,084) of all PWID diagnosed with HIV-1 during 1998-2019 in Greece. The study sequences were analysed phylogenetically along with a great number of reference sequences from Greece or worldwide (maximum likelihood method, FastTree v2.1).

RESULTS

Analysis revealed the existence of 4 major PWID-specific phylogenetic clusters [CRF14_BG (N=476,45.2%), CRF35_AD (N=156,14.8%), B (N=121,11.5%), A1 (N=60,5.7%)]. Some smaller clusters were identified during the pre-outbreak [A, B, CRF02_AG (N=9,0.9%)] and post-outbreak period [A6 (N=5,0.5%)]. Unique recombinant forms (URFs) including partial genomic fragments from these clusters were also detected (N=76,7.2%). The proportion of clustered sequences (i.e., sequences from PWID belonging to clusters or being URFs) was very low (5.3%) during the pre-outbreak period (1998-2009), increased to 41.7% one year before the outbreak (2010), and remained high (range: 88.5%-100.0%) during the whole period after 2011, including the post-outbreak period (2016-2019).

CONCLUSIONS

Using data over 20 years, we provide evidence that HIV clustering patterns among PWID continue to be at high levels during the post-outbreak period (2016-2019) as during the outbreak (2011-2014). PWID continue to acquire infections due to injecting practices during the post-outbreak period.

Keywords: HIV-1, PWID, Transmission clusters, Molecular epidemiology, Greece, Outbreak
ABSTRACT ID: 420

PRESENTED BY: Evangelia Georgia Kostaki, Greece/ ekostakh@med.uoa.gr

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HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

Surveillance

Abstract

Recent infection role in HIV transmission dynamics in Mexico City 2021-2022: a molecular network study

S. Schulz Medina [1]

V. Davila Conn [2], M. Matías Florentino [3], C. García Morales [4], D. Tapia Trejo [5], J. Monreal Flores [6], V. Quiroz Morales [7], A. González Rodríguez [8], S. Ávila Ríos [9]

[1] National Autonomous University of Mexico | Centre for Research in Infectious Diseases | General Directorate of Epidemiology, FETP

[2, 3, 4, 5, 6, 7, 9] Centre for Research in Infectious Diseases

[8] Clinica Especializada Condesa

BACKGROUND

Identification of people with recent HIV infection (PWRHI) in molecular studies may impact prevention and control strategies. We aimed to analyze socio-demographic, clinical, and behavioral factors associated with PWRHI and the role of this group in the HIV transmission network in Mexico City 2021-2022.

METHODS

We collected metadata and sequenced HIV from people requesting an HIV diagnostic test in Mexico City's largest clinic. The network was inferred from HIV pol sequences using genetic distance methods set with a 1.5% Tamura-Nei genetic distance threshold. Recent infection was defined by antibody avidity test. Multivariable logistic regression models for recent infection were built including statistically significant variables from a bivariate analysis and theoretically relevant variables. The distribution of PWRHI in the network was assessed to identify their contribution to cluster formation.

RESULTS

561/6,697 individuals (8%) had recent infection. PWRHI had a higher frequency of cisgender men (93%), single persons (79%), drug users (69%), dating apps users (69%), persons who engage in commercial sex (2%), higher education (37%), recent sexual risk practices (81%) and higher clustering (66%)(all $p<0.05$). After adjustment by covariates, commercial sex (aOR 4.9), spending most time at school (aOR2.1), periodical HIV testing (aOR2.8), and dating app use (aOR 1.5) were associated to clusters with PWRHI ($p<0.05$). Clusters including PWRHI had shorter average genetic distance between nodes (<=0.05%) but no difference in average node degree or cluster size was observed compared to clusters not including PWRHI.

CONCLUSIONS

PLWRI are highly represented in transmission clusters in Mexico City’s network. PWRHI characterization might be used to focus prevention strategies, like PrEP and early treatment; and strengthen behavioral interventions by spreading targeted risk communication campaigns using dating apps platforms.

Keywords: HIV-1, Molecular Epidemiology, Genetic clustering, Transmission network
ABSTRACT ID: 825
PRESENTED BY: Samuel Ehacatl Schulz Medina, Mexico / samuel.schulz92@gmail.com

INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

Modelling, biostatistics, and health informatics

Abstract

Mapping the risks of avian influenza outbreaks across Europe via machine learning

J. Hilton [1]

S. Hayes [2], L. Brierley [3], C. Donnelly [4], M. Baylis [5], J. Mould-Quevedo [6]

[1, 3, 5] University of Liverpool

[2, 4] University of Oxford

[6] CSL Seqirus, USA

BACKGROUND

The current avian influenza outbreak is the largest epidemic of highly pathogenic avian influenza ever recorded in Europe. The impact on the European poultry sector has been devastating with more than 50 million birds culled. Avian influenza virus also has public health significance as a potential source of human pandemic influenza. Wild bird hosts maintain avian influenza viruses and transmission from wild birds is an important route of introduction into domestic poultry and wild mammals. Despite this, the dynamics of avian influenza within wild birds is poorly understood. In this study, we use species distribution models to estimate the spatial risk of avian influenza in wild birds across Europe with a focus on wild bird ecological traits, which are traditionally neglected at this scale.

METHODS

Over 20,000 geospatial records of avian influenza virus from more than 60 wild bird families have been obtained. Bayesian additive regression trees are used to model the presence/absence of avian influenza over a $1km^2$ resolution across Europe. Models incorporate the environmental and livestock variables that are well-established predictors of avian influenza, but also capture the dynamics of wild bird ecology, such as phylogenetic diversity, species richness and habitat and diet preference.

RESULTS

Predictions of the risk of avian influenza in wild birds across Europe are generated, demonstrating key mapped hotspots and their associated uncertainty. Variable contribution is calculated, highlighting the relative importance of wild bird ecology and environmental factors in predicting avian influenza dynamics.

CONCLUSIONS

These models provide a framework which can be adapted to specific subtypes of public health significance (e.g. zoonotic strains) and can be used as an aid in planning effective surveillance strategies for future avian influenza epidemics.

Keywords: Avian influenza, Machine learning, Spatial interaction model, Statistical model, Epidemiological model, Birds

ABSTRACT ID: 254

PRESENTED BY: Joe Hilton, United Kingdom / joe.b.hilton@gmail.com

INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

Surveillance

Abstract

Analysis of fatal influenza cases during the strong and early Influenza epidemic wave in 2022 in Germany with special focus on outbreak-related cases

T. Jung-Sendzik [1]
K. Prahm [2], U. Preuß [3], S. Buda [4]

[1] Unit for Respiratory Infections, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany | Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[2, 3, 4] Unit for Respiratory Infections, Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND
Influenza outbreaks with fatal outcomes in care facilities are a relevant public health issue. Influenza disproportionally affects the elderly. Germany has a vaccination recommendation for those 60 years and older. Using notification data from the national influenza surveillance, we describe laboratory-confirmed fatal influenza cases regarding age distribution and outbreak settings in the strong and unusual early A(H_3N_2) influenza epidemic wave (calendar weeks (CW) 43/2022-01/2023).

METHODS
We checked data of each notified fatal influenza case for plausibility and validity. We investigated the age distribution, calculating proportions for age groups 60+ and 80+, the overall case fatality ratio (CFR), and the proportions of fatal outbreak cases in hospitals, medical treatment facilities, elderly and nursing homes.

RESULTS
We analyzed 806 fatal cases out of 259,024 total notified influenza cases during calendar weeks (CW) 43/2022-01/2023 (259,024/806; CFR 0.3%). Of these 806 cases, 746 (93%) were 60 years or older, and 535 (66%) older than 80 years. Of all fatal cases, 68 (8%) were associated with outbreaks in care facilities; 48 (71%) of these fatal outbreak cases were 60 years and older, and died during an outbreak in elderly or nursing homes, and 16 (24%) within a hospital setting.

CONCLUSIONS
The elderly are at highest risk of dying from influenza. Rapid identification and control of outbreaks, especially in hospitals, elderly or nursing homes could reduce fatal courses. Increase in vaccination rates for people over the age of 60, and the option to use antiviral post-exposure prophylaxis could further decrease cases, especially in elderly or nursing homes. Our results likely are an underestimation, as due to the high workload at the reporting sites, underreporting of outbreaks is expected.

Keywords: Influenza, Surveillance, Fatal cases, Hospitals, Medical treatment facilities, Elderly and nursing homes, Outbreaks
ABSTRACT ID: 348
PRESENTED BY: Tanja Jung-Sendzik, Germany / jung-sendzikt@rki.de

INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

Surveillance

Abstract

Seroprevalence of protective antibodies against influenza and the reduction of the ILI incidence rate: annual repeated cross-sectional study between 2014 and 2019

R. Guiomar [1]

S. Pereira da Silva 2, I. Costa 3, P. Cristóvão 4, P. Conde 5, A. Rodrigues 6, B. Nunes 7, (GROUP) Portuguese Laboratory Network for Influenza and Ot

[1, 3, 4, 5] National Reference Laboratory for Influenza and Other Respiratory Viruses. National Institute of Health Dr. Ricardo Jorge, Lisbon, Portugal

[2, 6, 7] Department of Epidemiology, National Institute of Health Dr. Ricardo Jorge, Lisbon, Portugal

BACKGROUND

Seroepidemiological studies provides estimates of population-level immunity, prevalence/incidence of infections (symptomatic/asymptomatic), contributes to the evaluation of vaccination programs. We assessed the seroprevalence of protective antibodies against influenza virus and evaluated the correlation of seroprevalence with the cumulative annual influenza like illness (ILI) incidence rate.

METHODS

We conducted an annual repeated cross-sectional seroepidemiological survey, between 2014-2019, in Portugal. 4,326 sera were selected from all age groups, sexes and regions. Sera were tested by haemagglutination inhibition (HAI) assay; HAI titer ≥40 was considered protective. Seroprevalence and geometric mean titers (GMT) of protective antibodies against influenza vaccine strains and new drift strains, were assessed by age, sex, vaccine status. The association between annual seroprevalence and the ILI incidence rate was measured by Pearson correlation coefficient (r).

RESULTS

Significant differences in seroprevalence of protective antibodies against influenza A and B were observed in the population. Higher seroprevalence and GMT for A(H1N1)pdm09 and A(H3N2) was observed in children (5-14 years); for influenza B the seroprevalence in individuals 65+ was 1.6 to 4.4 times the seroprevalence in children (0-4). Seroprevalence and GMT was similar between sexes. Vaccinated participants (65+ years) showed significant higher seroprevalence/GMT for both influenza types compared to non-vaccinated. A strong negative and significant correlation was found between seroprevalence and ILI incidence rate for A(H1N1) in children between 5 and 14 (r=-0.84 (CI95% -0.98;-0.07); a weak negative correlation was observed for A(H3N2) and B/Yamagata (ρ ≤-0.1).

CONCLUSIONS

This study provides new insight into the relationship between the seroprevalence of protective antibodies against influenza and the reduction of the ILI incidence rate and the need for adjusted preventive health care measures to prevent influenza infection and transmission.

Keywords: Seroprevalence, Influenza, ILI incidence rate, Antibodies
ABSTRACT ID: 764
PRESENTED BY: Raquel Guiomar, Portugal / raquel.guiomar@insa.min-saude.pt

INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

DRIVEN Study: quaDRivalent Influenza Vaccines patient description and Efluelda® relative vaccine effectiveNess – 2021-22 season in France

H. Bricout [1]
M. Levant [2], O. Launay [3], A. Mosnier [4], L. Watier [5], B. Grenier [6], N. Assi [7], J. Gaillat [8], P. Crepey [9], G. Gavazzi [10], A. Chit [11]

[1, 2, 11] Sanofi Vaccines, France
[3] Inserm CIC 1417, Assistance Publique Hôpitaux de Paris, Hôpital Cochin, Université Cité Paris, Paris, France
[4] Open Rome, Paris, France
[5] Inserm at Centre for Epidemiology and Public health (CESP), Institut Pasteur, Paris
[6, 7] HEVA, Pôle Epidémiologie, Lyon
[8] Service de Maladies Infectieuses, Centre Hospitalier Annecy Genevois, Annecy, France
[9] Ecole des hautes études en santé publique, CNRS, Université de Rennes, ARENES - UMR 6051, Recherche sur les services et le management en santé – Inserm U 1309, Rennes, France
[10] CHU Grenoble Alpes, Service Universitaire de Gériatrie Clinique, CS 10217, Grenoble, France
Laboratoire T-Raig TIMC-IMAG CNRS 5525 Université Grenoble-Alpes, France

BACKGROUND

A randomized controlled trial demonstrated a superior relative efficacy of 24.2% (95%CI: 9.7;36.5%) of high dose (HD) vs standard dose influenza vaccine (SD) to prevent laboratory-confirmed influenza. In 2021/22 season, HD was introduced in France for 65+ individuals. The DRIVEN study objectives were to estimate HD vs SD relative vaccine effectiveness (rVE) against hospitalizations in a real-world setting in France.

METHODS

The study is a retrospective cohort from the national health insurance and hospital databases. Community dwellings 65+ with a reimbursed influenza vaccine in 2021/22 season were included and followed from the vaccination date up to 30 June 2022, nursing home admission or death. Socio-demographics and health characteristics were identified from medical records before vaccination. Hospitalizations due to influenza and other causes were collected from 14 days after vaccine dispensation to end of follow-up. After a 1:4 propensity score matching, the adjusted incidence rate ratios were estimated using regression models.

RESULTS

431,643 individuals received HD and 7,401,210 SD. In total, 405,385 HD were matched to 1,621,540 SD recipients. After matching, individuals had similar measured characteristics, although HD recipients were slightly sicker at baseline. In the matched cohorts, non-influenza specific hospitalizations post-vaccination were slightly more frequent in HD recipients, suggesting remaining residual confounding by indication. Despite this residual confounding, HD was associated with a 23.3% (95%CI: 8.4%;35.8%) decrease in influenza hospitalizations when coded as primary diagnosis compared with SD.

CONCLUSIONS

In a context of high SARS-CoV2 circulation in France and Health Care Professionals' likely prioritizing use of HD for frailer individuals in first year, this study showed lower rates of influenza hospitalizations in HD than SD recipients. This result is consistent with existing literature.

Keywords: Influenza, Relative vaccine effectiveness, Retrospective cohort study, France, High dose influenza vaccine
ABSTRACT ID: 771
PRESENTED BY: Hélène Bricout, France / helene.bricout@sanofi.com

Surveillance

Abstract

A review of deaths under community supervision of probation services in Wales between April 2018 and March 2021

G. Jones [1]
B. Gray [2], S. Perrett [3]
[1, 2 ,3] Public Health Wales

BACKGROUND
Figures published by the Ministry of Justice revealed that deaths among offenders within the community in England and Wales increased by 34% between 2019/20 and 2020/21. Unlike deaths in custody that undergo formal investigation, deaths occurring whilst under community supervision of probation services do not undergo the same scrutiny and therefore factors affecting the mortality of this group are poorly understood. This review aimed to understand the causes of these deaths to help prevent future premature deaths in this cohort.

METHODS
HM Prison and Probation Service in Wales provided Public Health Wales with identifiable data of 286 individuals who died whilst under the supervision of probation services in Wales between 01/04/2018 and 31/03/2021. NHS numbers were matched against the ONS Death Registry to obtain information regarding cause of death. Deaths were grouped using ICD-10 codes assigned as the underlying cause of death.

RESULTS
Drug and alcohol-related deaths, whether accidental or intentional, accounted for 44% of all the deaths reported between 2018-21, followed by diseases of the circulatory system (14%) and intentional self-harm (10%). Accidental drug-related deaths were the leading cause of death for those aged 18-49 (2.2/1,000), and for both males (1.7/1,000) and females (2.5/1,000). 72% of drug-related deaths involved poly-drug use. For those aged 50+, diseases of the circulatory system were the leading cause of death (2.2/1,000). The most deprived quintile saw over double the number of deaths (n=101) compared with the second most deprived (n=46).

CONCLUSIONS
The significant proportion of drug and alcohol related deaths highlight an urgent need for enhanced harm-reduction and substance use support for this cohort. A significant health divide is evident for those in the most deprived areas of Wales.

Keywords: Drug misuse, Alcohol misuse, Probation, Deprivation, Offender Health
ABSTRACT ID: 145
PRESENTED BY: Gethin Jones, United Kingdom / gethin.jones6@wales.nhs.uk

PUBLIC HEALTH SCIENCES

Modelling, biostatistics, and health informatics

Abstract

Unintended consequences: Disease avoidance and its influence on social isolation and social cohesion

H. Nunner [1]
V. Buskens [2], R. Corten [3], C. Kaandorp [4], M. Kretzschmar [5]

[1] University of Lübeck, Institute for Multimedia und Interactive Systems (IMIS)
[2, 3] Utrecht University, Department of Sociology
[4] Utrecht University, Research Data Management Support
[5] University Medical Center of Utrecht University, Julius Center for Health Sciences and Primary Care

BACKGROUND
Social networks play a crucial role in shaping the spread of infectious diseases. Clusters, for example, can impede transmission dynamics. However, much evidence is based on the assumption that social behavior remains unchanged during an outbreak. Regardless of the reason (imposed physical distancing, voluntary contact reduction), neglecting network dynamics may cloud our understanding of disease spread on social networks and create inaccurate conclusions.

METHODS
To gain insights into the impact of risk perception and self-imposed contact reduction on disease spread, we conducted a large-scale (2,879 participants), interactive, incentivized experiment in conjunction with an agent-based simulation. Both the experiment and simulation incentivized participants to maintain social relations (network degree) and structures (network clustering) while penalizing the acquisition of infections.

RESULTS
In the experiment, significantly fewer infections occurred than in the simulation. That is because participants disconnected from infectious neighbors more often and established fewer relations with infectious others than the artificial agents. This resulted in suboptimal network positions (too few relations, breaking up of clusters) and point rewards. Furthermore, participants avoided infected others regardless of personal disease state, although if infected or recovered, they were not at risk of re-infection.

CONCLUSIONS
Our findings suggest that individuals prioritize avoiding infection over maintaining social network positions. In addition, participants showed more sophisticated strategies for avoiding infection than we expected from our model design. These results could support the design of non-pharmaceutical interventions and highlight the importance of mitigating the risk of social isolation and loss of social cohesion during an outbreak.

Keywords: Disease dynamics, Social network dynamics, Risk perception, Health behavior, Incentivized experiment, Agent-based modeling
ABSTRACT ID: 252
PRESENTED BY: Hendrik Nunner, Germany / hendrik.nunner@uni-luebeck.de

TABLE OF CONTENTS

PUBLIC HEALTH SCIENCES (GENERAL)

Field epidemiology (e.g. outbreak investigations)

Abstract

Visual Network Analysis of a Hepatitis A Outbreak in a UK Educational Setting: Informing Public Health Interventions

E. Blakey [1]
J. Wilburn [2], R. Hams [3], L. Lambourne [4], W. Leung [5], S. Salimee [6]
[1, 2, 3, 4, 5, 6] UK Health Security Agency

BACKGROUND
In December 2022, the UK Health Security Agency responded to a Hepatitis A outbreak, originating from a household cluster and spreading within an educational setting. A visual network analysis was conducted to identify possible asymptomatic transmission and inform public health interventions.

METHODS
Case, contact, and school context information were extracted from the UKHSA case management system and visually represented using the open source Cytoscape software. This mapping illustrated the links between cases, contacts, families, and educational settings. The continuously updated network analysis was presented at multidisciplinary incident management team (IMT) meetings to inform the outbreak response.

RESULTS
By 21st April 2023, the network displayed 19 cases and 56 contacts across 19 different classroom/school contexts, with 11 in a single setting. The outbreak involved 13 family groups, two-thirds of which were specifically a complex family group. Adults accounted for 37% of cases (median: 29 years) while children comprised 63% (median: 5 years). Notably, all instances of possible asymptomatic transmission involved a potential child carrier (N=6). Household contacts represented 37% of cases. The findings from the visual network analysis supported direct public health interventions, including the decision to offer vaccination to all children and staff in the educational setting and their extended family contacts in the community.

CONCLUSIONS
The visual network analysis was highly valued by the IMT, enhancing understanding of the outbreak's dynamics, particularly the role of complex families and potential asymptomatic carriers, predominantly in younger children who are less likely to present with classic symptoms. In managing complex outbreaks, visual network analysis is an important, dynamic tool to aid public health interventions.

Keywords: Outbreak, Network analysis, Visualisation, Epidemiology
ABSTRACT ID: 336

PRESENTED BY: Eleanor Blakey, United Kingdom / eleanor.blakey@ukhsa.gov.uk

PUBLIC HEALTH SCIENCES (GENERAL)

Surveillance

Abstract

Identification and definition of attributes to evaluate international event-based surveillance using Epidemic Intelligence from Open Sources (EIOS) at the Robert Koch Institute, German

M. Martín-Sánchez [1]
S. Esquevin [2], A. Jansen [3], S. Raiser [4]

[1] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3] Centre for International Health Protection (ZIG), Robert Koch Institute, Berlin, Germany
[4] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND
Surveillance system evaluation (SSE) guidelines and attributes are generally designed for indicator-based surveillance. Adaptation to event-based surveillance (EBS) is needed, but rarely reported. Epidemic Intelligence from Open Sources (EIOS) is increasingly used worldwide to conduct EBS with publicly available information. We report on the definition of attributes and their formulation as indicators for the evaluation of EBS for international health events using EIOS at the Robert Koch Institute (RKI), Germany.

METHODS
We reviewed guidelines and publications on SSE to identify surveillance system attributes. We conducted stakeholder meetings between January and April 2023 to adapt the attribute definition from the literature to EBS for international health events using EIOS at RKI. We defined and developed new indicators to evaluate each adapted attribute based on the aim, components, and operation of the surveillance system.

RESULTS
We identified 14 attributes. Specificity and security were not considered applicable to EBS using EIOS. We defined various data collection methods to formulate the remaining attributes as indicators: eight attributes required quantitative data on system operation (completeness, cost-effectiveness, positive predictive value, sensitivity, stability, representativeness, timeliness and validity) and four required personal assessment by system operators through individual questionnaires (acceptability, flexibility, simplicity and usefulness). Some attributes are general and inherent to EBS systems using EIOS, while others depend on the settings implemented by operators.

CONCLUSIONS
Defining and implementing attributes for EBS can be challenging due to the scarcity of specific evaluation tools available. With the increasing importance of EBS as integral part of epidemic intelligence and surveillance, there is a need to establish best practices in this area. We recommend further inclusion of EBS in SSE guidelines and reporting attributes as part of evaluating EBS systems.

Keywords: Public Health Surveillance, Evaluation Studies, Epidemiologic Methods, Epidemics
ABSTRACT ID: 614
PRESENTED BY: Mario Martín-Sánchez, Germany / martin-sanchezm@rki.de

Preparedness (e.g. preparedness planning, simulation exercises, after action reviews)

Abstract

Assessment of planning and implementation of population-level non-pharmaceutical interventions for outbreaks of respiratory pathogens

O. Hovardovska [1]
R. Mwazighe [2], J. Nyirenda [3], I. Rodiah [4], T. Heinsohn [5], T. Wuebbelmann [6], C. Nam [7], L. Bouwer [8], B. Lange [9],
(GROUP) SUNRISE consortium

[1, 2, 3, 4, 5, 9] Department of Epidemiology, Helmholtz Centre for Infection Research (HZI)
[6, 7, 8] Climate Service Center Germany (GERICS), Helmholtz-Zentrum Hereon

BACKGROUND
In recent years, Europe has experienced several outbreaks of respiratory pathogens, including influenza and the SARS-CoV-2 pandemic. Population-level non-pharmaceutical interventions (PNPIs) for respiratory pathogen outbreaks could include limiting close physical interpersonal interactions such as isolation of symptomatic cases, quarantining contacts, shielding vulnerable populations, recommending 'social bubbles', as well as mobility-related measures. We assessed various PNPIs recommended to mitigate the spread of respiratory infections within a population.

METHODS
We assessed PNPIs in the available pre-pandemic influenza plans (2006-2012) of 10 European countries and in reports from the first wave of the SARS-CoV-2 pandemic (2020).

RESULTS
Of the 10 European pandemic plans assessed, all 10 plans provided hygiene recommendations; 6 recommended quarantine/isolation measures; 6 plans mentioned the closure of education facilities, while only 4 plans mentioned the closure of mass events; and 2 plans mentioned the closure of shops/venues. A few plans mentioned community-focused PNPIs, however, they were not described in detail. All PNPIs were implemented in the 10 countries. A general lockdown was not included in the plans, however, it was reported in all countries during the SARS-CoV-2 pandemic.

CONCLUSIONS
Our findings show that pandemic plans for respiratory infection outbreaks inadequately anticipated the measures taken and mainly focused on the healthcare system. Recommendations for the implementation of PNPIs for other critical infrastructures and essential services were mentioned only partially; a general lockdown was not anticipated. Changes in existing pandemic plans are needed to strengthen the preparedness of European countries for future respiratory pathogen outbreaks.

Keywords: Pandemic, Intervention, Respiratory Tract Infection, Outbreak
ABSTRACT ID: 653
PRESENTED BY: Olga Hovardovska, Germany / olga.hovardovska@helmholtz-hzi.de

TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

Surveillance

Abstract

Increase in group A streptococcal infections in young children in winter 2022/2023 in Germany

R. Singer [1]
S. Haller [2], M. Abu Sin [3], I. Noll [4], M. Schneider [5], M. van der Linden [6], S. Buda [7], A. von Laer [8]

[1] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
Postgraduate Training for Applied Epidemiology, Robert Koch Institute, Berlin, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 3, 4, 5 ,7, 8] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[6] German National Reference Center for Streptococci, Department of Medical Microbiology, University Hospital RWTH, Aachen, Germany

BACKGROUND
Late in 2022, clinicians and health authorities in Germany and other European countries reported a remarkable increase in scarlet-fever outbreaks and invasive group A streptococcal (iGAS) infections, especially in children. In Germany, non-invasive group A streptococcal (GAS) cases are only mandatorily notifiable for institutional outbreaks, mainly in schools and kindergartens. We investigated if there was an unusual increase in GAS and iGAS infections.

METHODS
We analysed routine diagnostic data of GAS and iGAS infections from a voluntary laboratory-based surveillance system, covering one third of the population, and scarlet-fever outbreaks notified through the German surveillance system, 2017–2023. Analyses focused on seasonal patterns of GAS and iGAS incidences (isolates/100,000 population) in children ‹15 years and numbers of scarlet-fever outbreaks.

RESULTS
After low incidences of GAS and iGAS infections among ‹15-year-olds at the start of the COVID-19 pandemic (3 and 0.003/100,000; quarter (Q)2/2020), incidences strongly increased again in Q4/2022 (14 and 0.5/100,000). In Q1/2023, GAS and iGAS incidences (34 and 0.9/100,000) increased 1.8-fold and 4.5-fold, compared to average incidences of previous peaks 2017–2019 (Q1 or Q2).1-4-year-olds were most affected by GAS and iGAS in Q1/2023 (51 and 1.7/100,000).In April 2023, the annual number of scarlet-fever outbreaks was already 3.5 times higher than in pre-COVID-19 years (n=1.980 vs. mean 2017–2019=560).

CONCLUSIONS
We found an early and sharp increase in GAS and iGAS infections in children in winter 2022/23, exceeding previous seasonal peaks. Reasons might include increased susceptibility after COVID-19 measures and increased risk of invasive bacterial infections facilitated by high influenza A and B circulation. To prevent new iGAS infections, understanding underlying reasons, rapid recognition, and treatment according to national recommendations are crucial.

Keywords: Streptococcus pyogenes, Scarlet Fever, Disease Outbreaks, Epidemiology, Germany
ABSTRACT ID: 195

PRESENTED BY: Regina Singer, Germany / singerr@rki.de

TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

Field epidemiology (e.g. outbreak investigations)

Abstract

Increase in invasive group A streptococcal infections in the Île-de-France region during the 2022/2023 season: a descriptive analysis of cases and outbreak control measures

A. Deslandes [1]

L. Mercuriali [2], C. Herber [3], A. Paty [4], S. Khouadhria [5], L. Reques [6], (GROUP) The ARS Ile-de-France iGAS working group

[1, 2, 3, 5, 6] Agence régionale de santé d'Ile-de-France, Saint-Denis, France

[4] Cellule Régionale de Santé publique France en Ile-de-France, Saint-Denis, France

BACKGROUND

Since September 2022, the number of invasive group A streptococcal infections (iGAS) increased in several countries in Europe, including France. The objective was to describe iGAS cases managed by the regional health agency (ARS) of the Ile-de-France region and the public health actions taken around these cases between 01/12/2022 and 31/03/2023.

METHODS

There is no mandatory notification of iGAS cases in France. Clinicians were temporarily instructed to notify all iGAS cases to the ARS, between 01/12/2022 and 15/02/2023. Afterwards, only cases linked to outbreaks or collective settings had to be notified. The ARS received iGAS notifications and enforced control measures around them, including contact tracing, chemoprophylaxis and active case finding in childcare and kindergartens. A dedicated database was created including demographic data, medical data (medical background, clinical presentation, department of admission, vital status) and public health measures decided around each case. Descriptive analyses were performed using R software (v4.3.0).

RESULTS

Overall there were 88 iGAS cases notified to the ARS between 01/12/2022 and 31/03/2023. Most cases were declared in December (42%) and January (17%). Among them, 43 patients were children (49%), with a median age of 16 years. 38 cases (43%) required intensive care (including 13 children) and nine (10%) died (including 4 children). Collective settings were involved in 28 (32%) cases, including 13 in childcare and 10 in elementary school. No secondary iGAS cases were identified in collective settings.

CONCLUSIONS

iGAS cases have a bad prognosis, including among children. Cases were frequently linked to collective settings, but no secondary cases were identified. Non-pharmaceutical and pharmaceutical interventions are key to prevent iGAS spread around cases. Complete characterisation of cases and contact tracing is ongoing.

Keywords: France/epidemiology, Disease Outbreaks/prevention & control, Streptococcus pyogenes, Public Health
ABSTRACT ID: 714

PRESENTED BY: Laura Reques, laura.reques@ars.sante.fr / laura.reques@ars.sante.fr

TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

Surveillance

Abstract

Emerging Trends in Invasive Group A Streptococcal Infections in Children: A Study of the Valencian Region, Spain (2018-2023)

J. Juaneda [1]
E. Vidal-Miñana [2], P. Ausina-Aguilar [3], B. Medina-Cortes [4], J. Roig-Sena [5]

[1] Epidemiologic Surveillance Department, General Directory of Public Health and Addictions, Valencian Region, Spain Hospital La Fe

[2, 3, 4, 5] Epidemiologic Surveillance Department, General Directory of Public Health and Addictions, Valencian Region, Spain

BACKGROUND
Since late autumn, an increase in scarlet fever has been reported by field epidemiologists in our region, along with cases of invasive Group-A Streptococcus (iGAS) infection which required hospitalization. Considering that iGAS notification is not a mandatory, the aim of this study was to compare 2023 with the previous periods (2018-2022).

METHODS
A descriptive study was conducted on microbiology-confirmed pediatric iGAS cases in the Valencian Region. Pharyngeal and sterile samples (blood, cerebrospinal fluid, pleural fluid, articular fluid, or peritoneal fluid) from the entire Valencian Health System were included between 01-01-2018, and 15-05-2023. Trends over epidemiological weeks and years were assessed by age and microbiological sample.

RESULTS
There were a total of 69024 positive samples in the period 2018-2023 (16344, 16968, 8136, 5448, 11136 and 10992). Sterile samples represented 2.35%, 3.25%, 1.47%, 1.32%, 2.37% and 9.83% of the total samples, respectively ($p<0.0001$). In the current year of 2023, it doubled the maximum reached in 2019 (56 vs 25 cases). The predominant age groups in 2018-2019 were <5 years (76% of isolations) with few isolations above 10 years, whilst in 2023 <5 years and 10-14 years were barely similar (46.4% vs. 42.9%). Blood culture represented 68-100% of positive sterile samples in the period 2018-2022, while in 2023 pleural fluid (50%) overcame blood isolations (46.4%).

CONCLUSIONS
An unexpected increase in the total number of iGAS isolations and invasive disease was observed during the last autumn-winter period, with a changing pattern in age groups and sample types. This alarming trend raises concerns about the spread and impact of iGAS infections in the region. It is crucial to consider implementing surveillance measures for this disease.

Keywords: Surveillance, Streptococcus pyogenes
ABSTRACT ID: 782
PRESENTED BY: Juan Juaneda, Spain / juaneda.juan@gmail.com

TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

Field epidemiology (e.g. outbreak investigations)

Abstract

Surge of lower respiratory tract Group A Streptococcus infections in winter 2022: epidemiology and clinical profile

K. Wrenn [1]
P. Blomquist [2], C. Inzoungou-Massanga [3], O. Olufon [4], R. Guy [5], D. Hatziioanou [6], L. Findlater [7], I. Smith [8], M. Mirfenderesky [9], K. Luyt [10], T. Williams [11], S. Stoianova [12], M. Dickinson [13], M. Pietzsch [14], T. Lamagni [15], D. Kumar [16]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 13, 14, 15, 16] UK Health Security Agency
[10, 11, 12] National Child Mortality Database, Child Mortality Analysis Unit, Bristol Medical School, University of Bristol

BACKGROUND
Following low incidence of invasive group A Streptococcus (iGAS) infections during the COVID-19 pandemic, marked increases were noted in England during 2022, particularly in paediatric cohorts. In November 2022, severe presentations of lower respiratory tract infections (LRTIs), including empyema, were notified by clinicians. UKHSA investigated this group to inform clinical management and incident response.

METHODS
LRTI-associated iGAS cases in children aged <15y in England reported between October 01 and December 21, 2022, were identified using laboratory data (GAS detected in LRT specimens) and notifications by clinicians/ Health Protection Teams. Symptoms, diagnoses, healthcare interactions, and outcomes were described based on case management notes, the National Child Mortality Database, and the national Emergency Care Dataset.

RESULTS
147 paediatric cases of LRTI iGAS were reported across England; 52% male and with a median age of 4 (IQR 2-6). Most frequently reported symptoms were fever (76%; n=90/119) and cough (50%; n=60/119). 48% (71/147) of cases had a confirmed respiratory viral coinfection, including hMPV and RSV, although not all were tested. Where known, 93% (106/114) of cases attended an emergency department, 32% (36/114) at least twice. 25% of cases died (n=37/147), with a median of 4 days from symptom onset to death, and 62% (13/21) of deaths occurred in the community.

CONCLUSIONS
Cases of iGAS rose in 2022 across England in paediatric cohorts, including LRTI and empyema. Investigations using multiple data sources found that iGAS LRTIs were associated with high levels of viral co-infection and increased mortality. Among those who died, deterioration was rapid and mostly occurred in the community. This work highlights the importance of a rapid response and the need to further investigate risk factors for death and establish effective mitigations.

Keywords: iGAS, Incident response, Outbreak, LRTI, Empyema, Surveillance, Paediatric
ABSTRACT ID: 809
PRESENTED BY: Katie Wrenn, United Kingdom / katiewrenn95@gmail.com

VACCINE PREVENTABLE DISEASES

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

HPV vaccine awareness but not vaccine trust as the main determinant of HPV vaccination uptake in the urban female population of Marseille, France in 2022

D. Kelly [1]
A. Fruleux [2], A. Dutrey Kaiser [3], Y. Attalah [4], F. Franke [5], P. Chaud [6], P. Malfait [7], J. Gaudart [8], S. Rebaudet [9], L. Ramalli [10]

[1] Santé publique France, French National Public Health Agency, Marseille, France
ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 4] Santé Environnement Pour Tous, Marseille, France
[3] Association Corhesan, Marseille, France
[5, 6, 7, 10] Santé publique France, French National Public Health Agency, Marseille, France
[8, 9] Aix Marseille Université, IRD, INSERM, SESSTIM, Aix Marseille Institute of Public Health, ISSPAM, Marseille, France

BACKGROUND
Universal HPV vaccination is a public health priority in France, recommended for adolescents aged 11 years since 2021. County vaccination uptake rates however remain suboptimal for females (34%) and males (6%) in Marseille. We aimed to measure vaccination trust and awareness among the urban population of Marseille, to inform interventions for improving HPV vaccination uptake.

METHODS
We conducted a cross-sectional study of Marseille residents in September 2022. We interviewed 2,647 participants face-to-face on sociodemographic characteristics, awareness and uptake of HPV vaccination for those aged 18–35. We tested the association of being HPV unvaccinated with: country of birth, native language, education level, health insurance, employment status, and awareness of HPV vaccination using multivariate logistic regression, at a significance level of 0.05. We measured vaccination trust using the 7C vaccination scale (confidence, complacency, constraints, calculation, collective responsibility, compliance and conspiracy) to produce a linearised score of 0–100. We compared the mean 7C scores according to HPV vaccination status using a Kruskal-Wallis test of statistical significance.

RESULTS
Among participants, 33% (784/2370) were aware of HPV vaccination (43% of females versus 17% of males), while 24% (111/457) of females and 6% (18/304) of males were HPV vaccinated. Among females, being HPV unvaccinated was significantly associated with unawareness of HPV vaccination (OR=14.8, 95% CI 6.94–36.1). None of the sociodemographic characteristics were significantly associated with HPV vaccination uptake. We observed no significant difference in the mean 7C score among HPV vaccinated (56.6) versus unvaccinated (52.8) females (p=0.4).

CONCLUSIONS
Interventions to increase low HPV vaccination coverage in Marseille should aim to improve awareness of the HPV vaccine. Vaccine trust does not appear to be a determinant of HPV vaccination uptake in this female population.

Keywords: Papillomavirus vaccines, Cervical cancer, Primary prevention, Vaccine hesitancy, Social determinants of health
ABSTRACT ID: 10
PRESENTED BY: David Kelly, France / david.kelly@santepubliquefrance.fr

VACCINE PREVENTABLE DISEASES

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

Different proportion of types of influenza virus explains the lower influenza vaccine effectiveness in hospitalised patients than in outpatients, 2022/23

I. Martínez-Baz [1]
I. Casado [2], A. Echeverria [3], C. Trobajo-Sanmartín [4], A. Navascués [5], C. Ezpeleta [6], J. Castilla [7]
[1, 2, 3, 4, 7] Instituto de Salud Pública de Navarra – IdiSNA - CIBERESP, Pamplona, Spain
[5, 6] Hospital Universitario de Navarra, Pamplona, Spain

BACKGROUND
The 2022/23 influenza season has been characterised by circulation of influenza A(H3N2) until January, being displaced by influenza B and A(H1N1) since then. We estimated influenza vaccine effectiveness (IVE) in preventing outpatient and inpatient cases in the 2022/23 season.

METHODS
A test-negative design was performed in Navarre. Nasopharyngeal swabs from outpatient and inpatient cases with influenza-like illness were tested by PCR from October 2022 to April 2023. Influenza vaccination status of confirmed influenza cases was compared with test-negative controls. Vaccination status of the current and 3 previous seasons was obtained from the vaccination register. Multivariate logistic regression was used and IVE was calculated as (1-adjusted odds ratio)x100.

RESULTS
Of 629 outpatients tested, 222 (35%) were influenza-positive: 54% A(H3N2), 10% A(H1N1) and 30% B. Overall IVE to prevent outpatient cases was 51% (95% confidence interval: 14 to 72), and 52% (-6 to 74), 23% (-184 to 79) and 89% (11 to 98) against influenza A(H3N2), A(H1N1) and B, respectively. Of 2923 hospitalised patients tested, 12% were influenza-positive: 65% A(H3N2), 16% A(H1N1) and 7% B. Overall IVE to prevent hospitalisation was 23% (-7 to 44), and 6% (-43 to 38), -25% (-183 to 45) and 86% (57 to 95) against influenza A(H3N2), A(H1N1) and B, respectively. IVE estimate was similar by age groups and not decreased in 2023 compared to 2022. Vaccination history didn´t modify IVE and no residual effect was observed.

CONCLUSIONS
IVE in 2022/23 was high to prevent influenza B, moderate to low against influenza A(H3N2) and near null against influenza A(H1N1). A lower proportion of influenza B cases explain the lower IVE in hospitalised patients than in outpatients.

Keywords: Influenza, Vaccine, Vaccine effectiveness, Test-negative design
ABSTRACT ID: 460
PRESENTED BY: Iván Martínez-Baz, Spain / imartinba@navarra.es

VACCINE PREVENTABLE DISEASES

Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Abstract

Preparing for the EU Regulation on HTA and joint clinical assessments of vaccines

N. Largeron [1]
P. D'Agostino [2], D. Danko [3], J. Eskola [4], P. Godrfroid [5], R. Hanley [6], G. de Pouvourville [7], M. Postma [8], J. Puig-Barberà [9], J. Schmitt [10], C. de Waure [11], A. Vicere [12], E. Beck [13]

[1] Sanofi, Lyon
[2] CSL Seqirus, Munich
[3] Ideas&Solutions, Budapest
[4] National Institute for Health and Wellfare, Helsinki
[5] Janssen pharmaceutical companies of Johnson&Johnson, Diegem
[6] Takeda Pharmaceuticals GMBH, Glattpark
[7] ESSEC Business School, Cergy Pontoise
[8] Department of Health Sciences, University of Groningen | Department of Economics, Econometrics & Finance, University of Groningen | Center of Excellence in Higher Education for Pharmaceutical Care Innovation, Universitas Padjadjaran, Bandung
[9] Vaccines Research Area, FISABIO (Fundación para el Fomento de la Investigación Sanitaria y Biomédica de la Comunitat Valenciana), Valencia
[10] Global Health Press
[11] Department of Medicine and Surgery, University of Perugia, Perugia
[12] Vaccines Europe, EFPIA, Bruxelles
[13] GSK, Wavre

BACKGROUND

Clinical assessment of vaccines in the European Union (EU) currently involves many different bodies and processes. It requires an understanding of vaccine characteristics and vaccine-specific criteria for evaluating e.g., safety, efficacy. The urgency of harmonising the clinical assessment of vaccines was heightened by the adoption of the EU's Regulation on Health Technology Assessment (HTA) in 2022, which will apply to vaccines as of 2025 with joint scientific consultations (JSC) and as of 2030 with joint clinical assessments (JCA).

METHODS

Three complementary literature reviews were conducted to capture the current guidelines and recommendations for vaccine appraisals, identify methods used to assess evidence and outline the differences in recommendations for four selected vaccines. An expert consultation meeting was held to discuss the literature review findings, reflect on vaccine-specific considerations in HTAs and obtain insights into the EU's future JCAs of vaccines.

RESULTS

Significant variation exists across the EU in the decision-making processes and criteria for vaccines clinical evaluation with vaccine specificities being rarely considered by HTA bodies across EU member states. The literature review findings together with expert recommendations were codified in three guiding principles (use of appropriate terminology and measurements for vaccines, vaccine-specific assessment process, and data collection) and thirteen recommendations to foster development of new decision-making frameworks and facilitate the successful implementation of the EU Regulation on HTA for vaccines.

CONCLUSIONS

The review of the literature and discussion with experts raised concerns that JCA for vaccines may not be able to appropriately capture the broad value of vaccination. Guiding principles for clinical HTA were developed to help inform the discussion and development of vaccines-specificities within the EU joint clinical HTA frameworks until 2025 and 2030 respectively.

Keywords: Vaccines, Biomedical, European Union, Process Assessment, Technology Assessment, Health Policy, Healthcare
ABSTRACT ID: 575
PRESENTED BY: Joan Puig-Barberà, France / jpuigb55@gmail.com

Abstract

Outbreak of meningococcal infections in Dushanbe, Tajikistan, 2022

R. Sharifov [1]
R. Horth [2], Z. Tilloeva [3], M. Olimov [4], D. Nabirova [5]

[1] Central Asia Field Epidemiology Training Program | Disinfection Center of Dushanbe City, Tajikistan
[2, 5] Central Asia Field Epidemiology Training Program | Asfendiyarov Kazakh National Medical University
U.S. Centers for Disease Control and Prevention, Central Asia Office, Almaty
[3] Disinfection Center of Dushanbe City, Tajikistan | Central Asia Field Epidemiology Training Program
[4] Disinfection Center of Dushanbe City, Tajikistan

BACKGROUND
Bacterial meningitis is a debilitating vaccine preventable inflammation with high death and disability. In March of 2022 in Dushanbe, weekly epidemiological surveillance showed that the threshold for meningitis had been surpassed. We conducted an investigation to find additional cases and determine characteristics of patients to inform outbreak control measures.

METHODS
We used semi-structured questionnaires to interview patients and abstract medical data from two large hospitals in Dushanbe, March-June 2022. Meningoccal disease was defined as suspected for patients with fever (>38.0°C), headache, nausea, vomiting, rhinitis; probable for patients meeting suspected criteria plus stiffness of occipital muscles and/or hemorrhagic rash and contact with a case in <10 days; and confirmed for patients meeting probably critieria plus laboratory diagnosis.

RESULTS
We identified 132 cases of meningococcal infection (incidence 11/100k population). Of these, 92% had invasive disease, 71% meningococoxemia, 0.5% purulent meningitis, 19% mixed forms infection, and 8% noninvasive form. Also, 65% had Neisseria meningitidis and 5% Streptococcus pneumoniae. Median age was 10 years (range: 2 months-72 years); 65% were ≤14 years old. Most (91%) were hospitalized in serious condition and 6% had moderate disease; 2% died. Of 6 genotyped samples, 3 were serotype W135, 1 serotype C, 1 serotype 29E, and 1 non-agglutinating strain. Just 16% (21/132) were direct contacts of known cases. Of these, 15 (71%) were family, 2 (1%) school and 4 (19%) university contacts. One in four (23%) lived outside of Dushanbe. No cases had ever received a meningococcal vaccine.

CONCLUSIONS
The primary preventive measure against meningococcal infection is vaccination. Vaccination against meningococcal infection is not included in the national immunization schedule in Tajikistan. Results demonstrate need to add meningococcal vaccination to the immunization schedule.

Keywords: Neisseria meningitidis, Meningococcal Infections, Disease Outbreaks, Tajikistan, Field epidemiology, Vaccine preventable disease
ABSTRACT ID: 610

PRESENTED BY: Rajabali Sharifov, Tajikistan / sharifovraj@gmail.com

VACCINE PREVENTABLE DISEASES

Microbiology (incl. novel methods in microbiology, such as e.g. new diagnostic tools)

Abstract

Largest European Corynebacterium diphtheriae outbreak in 50 years: phenotypic and genomic analysis

A. Hoefer [1]
L. Freschi [2], D. Palm [3], J. Borrell Pique [4], S. Funke [5], S. Bacci [6], S. Brisse [7], A. Egli [8], H. Seth-Smith [9], F. Palma [10], A. Sing [11], S. Schindler [12], R. Mariman [13], (GROUP) Pan-European Diphtheria Research group

[1, 2, 3, 4, 5, 6] ECDC
[7, 10] Instituto Pasteur
[8, 9] University of Zurich
[11] Bayerisches Landesamt für Gesundheit und Lebensmittelsicherheit (LGL)
[12] Ages
[13] RIVM

BACKGROUND
Increased numbers of cases of Corynebacterium diphtheriae infections were diagnosed in migrant related facilities of Europe since summer 2022. Most cases involved cutaneous diphtheria, although some respiratory cases and fatalities were reported. A pan-European consortium assessed the genetic relatedness and the antibiotic susceptibility the of the isolates from the outbreak.

METHODS
All 366 toxigenic C. diphtheriae isolates from ten European countries underwent WGS analysis. A combination of cgMLST and SNP-based methods were used to outline phylogenetic relationships of outbreak isolates. Sequence, integron, toxin and antimicrobial resistance (AMR) typing were performed with diphtOscan. Phenotypic resistance testing was performed according to EUCAST guidelines.

RESULTS
cgMLST analysis identified four genomic multicountry outbreak clusters (GC): GC795 (ST574, n=134), GC817 (ST377, n=116), GC671 (ST377, n=19), and GC217 (ST384, n=80). Notably, GC671 carried ermX and blaOXA-2 genes on an integron. Strains harboring ermX were phenotypically resistant to erythromycin; isolates carrying pbp2m were resistant to penicillin, but susceptible to amoxicillin, and those carrying blaOXA-2 remained susceptible to all beta-lactams.SNP analysis within the four genomic clusters showed root-to-tip SNP distances of maximum 14 SNPs. The multi-country distribution of each cluster, with some smaller scale genetic clusters observed within countries, demonstrated recent transmissions, likely occurring during travel and within migrant facilities.

CONCLUSIONS
The increased number of C. diphtheriae cases among migrants is a cause for concern, particularly considering the presence of antimicrobial resistance genes that threaten the efficacy of first-line treatments and lack of DAT global supply. To reduce further transmission, we recommend: Increased clinical suspicion, prompt treatment, vaccination, ability for a laboratory confirmation and high routine vaccination coverage. Continute monitoring using molecular typing and genomic approaches can support identification of identify potential spillover events.

Keywords: Diphtheria, Migrants, Outbreak, AMR, WGS
ABSTRACT ID: 744
PRESENTED BY: Andreas Hoefer, Sweden / andreas.hoefer@ecdc.europa.eu

Abstract

Epidemiological profile of bacterial meningitis, Hambol health region, Côte d'Ivoire, 2019-2021

T. Badian Baba [1]
S. Moussa Pegnontaye [2], W. Pierre [3], J. Otshudiandjeka [4], I. Tiembre [5], V. Beni Bi [6]
[1] AFENET | FETP
[2, 5, 6] MOH | FETP
[3, 4] AFENET

BACKGROUND

The Hambol region experienced epidemic outbreaks of meningococcal A meningitis in 2008 and pneumococcal meningitis in 2016 with an average attack rate of 14 cases/100,000 inhabitants. To deal with these outbreaks, Côte d'Ivoire joined the meningitis control program with the introduction of MenAfriVac in 2014. Thus, to assess the progress of this fight, we analyzed surveillance data bacterial meningitis in the Hambol region over a three-year period.

METHODS

A descriptive cross-sectional study was conducted in September 2022, covering surveillance data from the period of 2019 to 2021. The data was obtained from the health information management system of the epidemiological surveillance service. The analyzes were done on Epi-Info 7.2, calculating measurements of frequencies and rates.

RESULTS

A total of 52 suspected cases of meningitis were notified over the period. Lethality was 6%. About 64% were male. The median age was 6 years (0-49). The age group of 0-9 years was the majority in 42% of cases. Indeed, 49 cerebrospinal fluid samples were analyzed with 38% positivity. The germs isolated were Streptococcus pneumoniae (46%) and Neisseria meningitidis A (15%). In 2019, the incidence rate was 4 cases/100,000 inhabitants; This rate was 2 cases/100,000 inhabitants in 2020 and 5 cases/100,000 inhabitants in 2021.

CONCLUSIONS

Meningitis down in the Hambol health region since the introduction of MenAfrVac. Thus, strengthening case-by-case surveillance and improving routine vaccination coverage against meningococcal and pneumococcal disease in children will help achieve the goals of eliminating meningitis in the region

Keywords: Profile, Epidemiological, Meningitis, Hambol, Ivory Coast
ABSTRACT ID: 836
PRESENTED BY: Toure Badian Baba, Côte d'Ivoire / tourebadian@gmail.com

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VACCINE PREVENTABLE DISEASES

Communication and health promotion

Abstract

An exploratory analysis of potential caregiver acceptance of malaria vaccination and associated factors for children under 5 years of age in Guinea and Sierra Leone, May – August 2022

K. Röbl [1]
H. Fischer [2], A. Delamou [3], A. Mbawah [4], G. Burger [5], B. Geurts [6], L. Feddern [7], V. Diaconu [8], H. Baldé [9], I. Kaba [10], A. Dörre [11], C. El Bcheraoui [12]

[1] Department of Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany
Postgraduate Training for Applied Epidemiology (PAE), Robert Koch-Institute, Berlin, Germany
ECDC Fellowship Programme, Field Epidemiology path (EPIET),
European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[2, 5, 6, 7, 8, 9, 10, 12] Unit for Evidence-based Public Health, Centre for International Health Protection, Robert Koch-Institute, Berlin, Germany
[3] Centre d'excellence africain pour la prévention et le contrôle des maladies transmissibles (CEA-PCMT), Conakry, Guinea | Faculté des sciences techniques de la santé (FSTS), Université Gamal Abdel Nasser de Conakry (UGANC), Conakry, Guinea
[4] College of Medicine and Allied Health Sciences (COMAHS), University of Sierra Leone, Freetown, Sierra Leone
[11] Department of Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany

BACKGROUND
Malaria vaccination for children in Guinea (GN) and Sierra Leone (SL) is not yet implemented and evidence of acceptance to guide roll-out is scarce. This analysis aimed to assess potential caregiver malaria vaccine acceptance and identify associated factors to inform future vaccine implementation.

METHODS
We conducted a cross-sectional household survey using lot quality assurance sampling in three regions per country between 05/2022 and 08/2022. The first respondent in each household provided sociodemographic information. A household member responsible for childcare shared their likelihood of accepting malaria vaccination for their children <5 years and details on children's health. We calculated the prevalence of caregivers' vaccine acceptance and explored associated factors using multivariable logistic regression modelling calculating odds ratios (OR) with 95% confidence intervals (CI).

RESULTS
Among 717 included households in GN and 576 in SL, 74% and 81% of caregivers were accepting of potential vaccination for their children. In both countries, acceptance was lower in remotest areas compared to urban counterparts (GN: OR 0.20 [95%CI 0.09-0.46], SL: 0.27 [0.11-0.58]) and among households adopting more preventive measures against malaria (GN: 0.38 [0.24-0.60], SL: 0.53 [0.32-0.90]). In GN, acceptance was lower among richest households compared to poorest (0.10 [0.04-0.22]) and if children received malaria testing when febrile (0.57 [0.36-0.89]), but was positively associated with caregivers' malaria knowledge (5.57 [1.76-16.20]). In SL, households with highest educated first respondents stated higher acceptance than least educated ones (2.29 [1.08-4.89]).

CONCLUSIONS
In both countries, vaccine acceptance seems promising. For optimization, policymakers should consider regional differences, sociodemographic factors, and levels of knowledge about malaria. Raising awareness about the benefits of comprehensive control efforts – including vaccination and other preventive measures – requires attention in future vaccination campaigns.

Keywords: Malaria Vaccines, Surveys and Questionnaires, Child, Cross-Sectional Studies, Guinea, Sierra Leone
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PRESENTED BY: Klara Röbl, Germany / roeblk@rki.de

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