ESCAIDE

European Scientific Conference on Applied Infectious Disease Epidemiology

20 - 22 November 2024

HYBRID Stockholm and online

ESCAIDE

ABSTRACT BOOK

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 studens.

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

Welcome to ESCAIDE 2024! I would like to take this opportunity to introduce myself as the newly-appointed Chief Scientist of ECDC, and Chair of the ESCAIDE Scientific Committee. I hope this year's conference will offer you an exciting and fulfilling occasion to learn, discuss and connect with peers from across Europe and the world. Each ESCAIDE gives me a sense of connection and reunion with like-minded people whose aim and vocation are to prevent diseases and improving lives, and I'm confident this one will be no different.

As always, the scientific programme of ESCAIDE focuses on the latest research in infectious disease epidemiology, microbiology and related disciplines. We received a wealth of high-quality abstracts, which have been reviewed and selected to produce the sessions of the conference. I would like to thank each of the co-authors who have contributed to a submitted abstract, and especially the presenters who will share their work with others. Each year we also rely on the dedication of all the expert reviewers during the selection process, and on the moderators who guide the audience through the Fireside Sessions and Poster Tours – I would like say a big "thank you" to all of them.

The core of the programme are the five plenary sessions, which reflect broader themes and examine pressing issues relating to infectious disease prevention and control. The keynote session explores the balance between prevention and cure, bringing in insights from other disciplines and areas. Plenary B examines, from different angles, infectious disease preparedness and response in the context of the war in Ukraine. Plenary C asks how we can improve infectious disease surveillance using the latest advancements and best practices. Plenary D looks into the thought-provoking concept of Disease X and our readiness to face the next potential pandemic. The conference concludes with Plenary E, which takes a new look at the resurgence of known diseases, especially now in the wake of the COVID-19 pandemic.

My first year as Chair of the Scientific Committee has been an exciting and enriching experience. Throughout the past months, supported by the ECDC ESCAIDE Team, I have had the pleasure of collaborating with and getting to know the other members of the Scientific Committee, who I would like to very much thank for their dedication and insight. I would also like to express my appreciation for our esteemed guest speakers, whose expertise is key to shaping the scientific dimension of the conference.

We are pleased to once again bring you this conference in a hybrid format, with the aim of improving the sustainability and accessibility of the event. The past two editions of ESCAIDE have shown the many benefits of offering both in-person and online participation, which allows us to reach a much broader and more diverse audience. I invite you all to explore the conference online platform, to discover its many interactive features and make the most of your conference experience, both during and after the event. This year, special attention has also been given to sustainability and wellbeing during the conference, for example through a carbon offsetting initiative and activities to promote the wellbeing of participants.

Finally, I am excited to already invite you all to ESCAIDE 2025, which will take place in my home country, Poland. Preparations are already underway for what promises to be another exceptional edition of the conference in Warsaw. But first, let us focus on ESCAIDE 2024 – thank you all for your interest and enthusiastic participation; I hope you will all enjoy the event and that it will bring value and significance to your work in public health.

Piotr Kamarz
Chair, ESCAIDE
Scientific Committe

Piotr Kamarz

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09:20-10:20	**PLENARY SESSION A:** PREVENTION VS. CURE: WHAT CAN WE LEARN FROM CANCER, CRIME AND CLIMATE CHANGE? Chaired by the ESCAIDE Scientific Committee members Kateřina Šédová *(Loono, Czech Republic)* and Henriette de Valk *(Santé Publique France)* ***Speaker:*** Chris Dye *(University of Oxford, UK)* LEVEL 1 AUDITORIUM 1 MÄSSHALLEN	
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		12:45-13:45 EAN General Assembly (Closed event) *organised by: EPIET Alumni Network* LEVEL 1 AUDITORIUM 3 FOGELSTRÖM
		13:30-14:00 Follow the science: follow the song MEZZANINE ROOM TORNET
14:00-15:30	**FIRESIDE SESSION 3** Burden of disease LEVEL 1 AUDITORIUM 1 MÄSSHALLEN	**FIRESIDE SESSION 4** Food- and waterborne diseases LEVEL 2 AUDITORIUM 2 RIDDARSALEN
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17:00-18:30	**PLENARY SESSION B:** INFECTIOUS DISEASES IN TIMES OF CONFLICT: LEARNING FROM UKRAINE Chaired by the ESCAIDE Scientific Committee members John Kinsman *(ECDC)* and Piotr Kramarz *(ECDC)* ***Speakers:*** Ihor Kuzin *(Ministry of Health Ukraine)*, Olga Gvozdetska *(Public Health Center Ukraine)*, Katarzyna Drążek-Laskowska *(Ministry of Health Poland)* LEVEL 1 AUDITORIUM 1 MÄSSHALLEN	
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09:00-10:30	**PLENARY SESSION C:** SURVEILLANCE OF INFECTIOUS DISEASES: HOW CAN WE BETTER TELL WHAT'S GOING ON? Chaired by the ESCAIDE Scientific Committee members Alicia Barrasa *(EAN)* and Ágnes Hajdu *(National Center for Public Health and Pharmacy, Hungary)* ***Speakers:*** André Charlett *(UK Security Health Agency)*, Lieke van Alphen *(Maastricht University, Netherlands)*, Caterina Rizzo *(University of Pisa, Italy)* LEVEL 1 AUDITORIUM 1 MÄSSHALLEN	
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09:00-10:30	**PLENARY SESSION E:** THE NEW OLD: RETHINKING THE FUTURE OF KNOWN DISEASES Chaired by the ESCAIDE Scientific Committee members Nadine Zeitlmann *(Robert Koch Institute, Germany)* and Jacobo Mendioroz *(Public Health Agency of Catalonia, Spain)* ***Speakers:*** Nienke Beerlage-De Jong *(University of Twente, Netherlands)*, Tomasz Sobierajski *(University of Warsaw, Poland)*, Maria Wessman *(Statens Serum Institut, Denmark)* LEVEL 1 AUDITORIUM 1 MÄSSHALLEN	
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		12:45-13:45 **Side session 3: Career Compass** Organised by: *EPIET Alumni Network* ***Moderated by:*** Ioannis Karagiannis *(EAN)* and Bojana Mahmutović *(EAN)* ***Speakers:*** Marc-Alain Widdowson *(WHO EURO)*, Ricardo Mexia *(EUPHA-IDC)*, Tanja Charles *(ECDC)*, Natalie Fischer *(LSHTM)* LEVEL 2 AUDITORIUM 2 RIDDARSALEN
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- Nosocomial outbreak of Ralstonia pickettii infections linked to sodium chloride in Germany since September 2023 and challenges in medical product-related outbreak investigations, Mirco Sandfort
- Disparity in surgical site infection risk according to ethnicity and Index of Multiple Deprivation in England, Jan 2010 – Dec 2019, Miroslava Mihalkova
- Inclusion of Emergency Department attendance on onset status classification of Clostridioides difficile infections (CDI): A revised definition and implications on hospital-onset CDI cases in England, Antoine Salzmann
- Hybrid plasmid caused a rapid increase of OXA-48 K. pneumoniae in Lithuania, Paulius Greicius
- Reducing healthcare associated Gram-negative bloodstream infections: An England Perspective, Dimple Chudasama
- Are AI-based surveillance systems for Healthcare Associated Infections really ready for clinical practice? A systematic review and meta-analysis, Claudia Cozzolino

FIRESIDE SESSION 2

COVID-19

MODERATOR: **Gowri Gopalakrishna**

- Evaluation of the effectiveness of COVID-19 vaccination appointment letters on uptake across sociodemographic groups: A regression discontinuity analysis in Sweden, Georgios Varotsis
- Effectiveness of Omicron XBB.1.5 vaccine against SARS-CoV-2 Omicron XBB and JN.1 infection in a prospective cohort study in the Netherlands, October 2023 to April 2024, Anne Huiberts
- Effectiveness of COVID-19 vaccines against laboratory confirmed SARS-CoV-2 infection in the European Union multi-centre hospital healthcare worker cohort (VEBIS HCW), season 2023 – 2024, Camelia Savulescu
- COVID-19 vaccine effectiveness against severe outcomes for subgroups of immunosuppressed people in England, 2021 – 2022, Daniel Stewart
- The impact of non-pharmaceutical interventions implemented during the COVID-19 pandemic on the number of close contacts of SARS-CoV-2 cases in the Netherlands, Jizzo Bosdriesz
- Are there changes in parental attitudes towards the Dutch National Immunisation Programme after the COVID-19 pandemic? – preliminary results, Rosaline van den Berg

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FIRESIDE SESSION 3

Burden of disease

MODERATOR: **Ajibola Omokanye**

- Characterisation of the SARS-CoV-2 pandemic in healthcare workers within the United Kingdom: risk factors for infection across four distinct waves within a multicentre prospective cohort study (SIREN), Edward Monk
- High seropositivity and COVID-19 incidence among healthcare workers in Ireland: A prospective cohort study, 2022-2023, Louise Marron
- Using surveillance data to inform vaccination policy in Sweden - a comparison of ICU burden between COVID-19 and influenza during winter seasons 2022-2023 and 2023-2024, AnnaSara Carnahan
- Economic burden of Healthcare associated infections: case-control study, Katya Kruglova
- Emerging trends in hospital admissions for necrotising fasciitis in England, 2018-2023, Eleanor Blakey
- Unraveling the “indirect effects” of interventions against malaria endemicity: A systematic scoping review, Yura K. Ko

FIRESIDE SESSION 4

Food- and waterborne diseases

MODERATOR: **Nathalie Jourdan da Silva**

- Multi-country outbreak of Salmonella Enteritidis related to chicken meat from Poland in 2023 – the Danish perspective, Emily D. White
- Large outbreaks of Cryptosporidium linked to lamb contact events on working farms in England: A public health call to break the cycle, Luke McGeoch
- Nosocomial listeriosis outbreak in patients on oral glucocorticoids: time to rethink supply, preparation, and consumption of sausages and other deli meats in the health care setting in Germany, Anja Schoeps
- International data sharing linked fish products from a Danish producer to a long-lasting Danish Listeria monocytogenes outbreak, 2019-2024, Susanne Schjørring
- Unveiling the trichinellosis outbreak: pork contamination in a butcher’s shop in Jahliyeh, Lebanon, November 2023 – February 2024, Hawraa Sweidan
- Outbreak of botulism in Spain linked to a commercial refrigerated potato omelette, June–July 2023: A case-control study, Andrea Parisi

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Surveillance

MODERATOR: **Marc-Alain Widdowson**

- Temporal relationships between the sentinel community acute respiratory infection (CARI) programme and routine respiratory surveillance systems in Scotland: Exploring the potential for forecasting, Kehinde Akin-Akinyosoye
- Enhancing Public Health Surveillance at FIFA 2022 Qatar: A Collaborative Event Based Surveillance approach, Farida Abougazia
- Wastewater-based surveillance of SARS-CoV-2 has limited potential to predict the number of COVID-19 cases in Sweden, Anna Ohlson
- Correlation between SARS-CoV-2 RNA in wastewater and notified COVID-19 cases and intensive care unit admissions in North Rhine-Westphalia, Germany, 2022-2023, Rosanne De Jong
- Current surveillance system underestimated paediatric invasive Group A Streptococcal disease in Finland: a population registry-based study, 2014-2023, Joana Neto
- Exploring global trends in botulism neurotoxin A usage: implications for iatrogenic botulism surveillance and management, Tristan Learoyd

FIRESIDE SESSION 6

Modelling and biostatistics

MODERATOR: **Jose Canevari**

- Repetition in Social Contacts: Implications in Modelling the Transmission of Respiratory Infectious Diseases in Pre-pandemic & Pandemic Settings, Neilshan Loedy
- Waning observance of social distancing measures during the COVID-19 pandemic in Greece: insights for emerging epidemics, Vasiliki Engeli
- Modelling Hepatitis C virus infection and treatment impact through serological surveillance data, Conor Egan
- Multi-signal fusion modelling to integrate wastewater-based surveillance into pandemic monitoring, Daniele Proverbio
- The use of a Poisson hidden Markov model for automated detection of outbreaks with vancomycin-resistant Enterococci in routine surveillance data, Sophie van Kessel
- Increasing pertussis morbidity in Lviv Region, Ukraine, Karolina Shumylo

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FIRESIDE SESSION 7

Vaccine-preventable diseases

MODERATOR: **Sabrina Bacci**

- Measles epidemic in a middle-school with high vaccination coverage, in the Rhône valley, France, 2023, Erica Fougere
- Disproportionate impact of measles on deprived and ethnic communities in Birmingham, England, 2023-2024, Hannah Jary
- Re-emergence of Toxigenic Corynebacterium diphtheriae among people experiencing homelessness linked to a 2022 European diphtheria outbreak, Frankfurt am Main, Germany, 2023, Jonas Haller
- Implementation of whole genome sequencing-based typing for Corynebacterium diphtheriae in Norway, João Pires
- Seasonal 2023/24 influenza A vaccine effectiveness: VEBIS European hospital multicentre study, Angela Rose
- Motivational interviewing intervention reduced mothers' vaccine hesitancy and increased intention to vaccinate their children: a randomized control trial, southeastern France, 2021 to 2022, Lauriane Ramalli

FIRESIDE SESSION 8

Preparedness

MODERATOR: **Anne Vergison**

- International transport of a mock patient with high consequence infectious disease within the EU: a three-country simulation exercise for Ireland, Germany and Norway, Máirin Boland
- Integral Scientific Advice for Outbreak Response: Lessons learned from an Avian Influenza Simulation in the Netherlands, Charlotte Waltz
- Knowledge, Attitude and Practices towards Mosquito-borne Arboviral diseases in Public Health Offices in 10 Federal States in Germany: a cross-sectional questionnaire-based analysis, Aparna Dressler
- Performance of the Robert Koch Institute's outbreak task forces during COVID-19: An evaluation, Mario Martín Sánchez
- Using mobile phone connection data to contextualize epidemiological findings in Île-de-France during the 2024 Paris Olympic and Paralympic Games, Nelly Fournet

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Antimicrobial resistance

MODERATOR: **Umaer Naseer**

- The epidemiology of candidaemia in Wales, United Kingdom, April 2018 – March 2024: Preparation for the development of national surveillance, Rhiannon Johnson
- Investigating Carbapenemase Producing Enterobacterales Persistence and Potential Patient Acquisition From The Hospital Environment, Aneta Kovarova
- Epidemiology and control of an outbreak of Methicillin-resistant Staphylococcus aureus (MRSA) colonisation in a neonatal unit, England, May to September 2023, Katie Thorley
- Challenges in investigating a non-O157 Shiga-toxin producing E. coli (STEC) outbreak: an STEC O26 case study, Rosie Collins
- Novel multiplexed Nanopore sequencing-based approach: rapid detection of drug-resistance associated mutations in Mycobacterium tuberculosis, Maeve Grifhorst
- Impact of antimicrobial resistance on recurrence after community-onset bacteremia, Salam Abbara

FIRESIDE SESSION 10

Sexually transmitted infections

MODERATOR: **Lina Nerlander**

- Upsurges in sexually transmitted infections among men who have sex with men and young populations in the EU/EEA: analysis of 2018-2022 surveillance data, Otilia Mardh
- Outbreak of Hepatitis A associated with sexual transmission among men who have sex with men (MSM) in Portugal, October 2023 to April 2024, Sebastian von Schreeb
- Factors associated with late HIV diagnosis in England, 2015 to 2022, Joseph Jasperse
- Are we reaching the HIV targets? Modelling-based estimates to assess the first UNAIDS goal, Denmark, 2023, Roberto Croci
- Hepatitis B patients' adherence to treatment in relation to knowledge, attitudes, and practices (KAP) in the West Bank, Palestine, 2022-2023, Ayham Sawalmeh
- Syphilis outbreak among people who use drugs attending harm reduction settings, Luxembourg, December 2023-September 2024, Corinna Ernst

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FIRESIDE SESSION 11

Childhood vaccinations

MODERATOR: **Tarik Derrough**

- Effectiveness of nirsevimab for the prevention of RSV hospitalisation in infants under 1 year of age: a population-based case control study in Spain, October 2023 – March 2024, Susana Monge
- Effectiveness of nirsevimab administration in newborns to prevent RSV hospitalisation: A test-negative case control study with SARI sentinel surveillance data in Spain, Clara Mazagatos
- A reduction in geographical disparities in childhood vaccination coverage following the National 2018 mandatory vaccination law, Alpes-Maritimes, France, David Kelly
- Influenza vaccine effectiveness among children and adolescents: results from the European VEBIS primary care multicentre study in the 2022/23 and 2023/24 seasons, Héloïse Lucaccioni
- Evaluation of humoral immunogenicity to yellow fever vaccine in children younger than 2 years of age: a systematic review, meta-analysis, and meta-regression, Pietro Ferrara
- Interim analysis of pertussis outbreak in Croatia indicates the need for vaccine booster doses in adolescence, May 2023 – April 2024, Ivan Mlinaric

FIRESIDE SESSION 12

Late Breakers

MODERATOR: **Barbara Schimmer**

- Shiga toxin–producing Escherichia coli (STEC) O145:H28 outbreak linked to pre-packaged sandwiches in the UK, 2024, Amy Douglas
- Measles outbreak in a mass reception centre for refugees in Berlin, Germany, April-May 2024: A call for better protection of newly arriving refugees, Navina Sarma
- Automated detection of hospital outbreaks of antimicrobial-resistant bacteria in one Italian region, 2022 to 2024, Francesco Venuti
- Current resurgence of Bordetella pertussis in France, January-August 2024, Sara Mazzilli
- Rapid escalation of enterovirus D68 cases in northern Italy associated with respiratory infection, August-September 2024, Elena Pariani
- Outbreak of myocarditis in children in Germany, 2024: Rare complication of parvovirus B19 or something new?, Teresa Nygren

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POSTER TOUR 1

Healthcare associated infections

MODERATOR: **Tommi Karki**

- Identification of risk factors for hospital-onset bacteremia to inform a routine data based risk prediction– an umbrella review, Anna Bludau
- Healthcare associated infections in Intensive Care Units: prevalence and associated factors, Emna Mziou
- Identification of the main genomic clusters of carbapenem-resistant Klebsiella pneumoniae in the healthcare network by whole genome sequencing in Latvia, Baiba Niedre-Otomere
- Trends in critical care unit associated Gram-negative bloodstream infections and associated antibiotic resistance in England between 2017 and 2023: a data linkage study, Matt Wilson
- Acinetobacter baumannii PCR-based replicon typing and resistance genes among isolates from pneumonia and skin and soft tissue infections from patients in southern Poland, Tomasz Kasperski
- Nosocomial outbreak of Ralstonia pickettii linked to internationally distributed sodium chloride products, United Kingdom 2023-2024, Amy Weaver
- An outbreak of carbapenemase-producing Enterobacterales (CPE) in a new-build single bed-room specialist cardiothoracic hospital in England, 2024, Juliette Cavaye

POSTER TOUR 2

Epidemiology of food-and waterborne diseases

MODERATOR: **Taina Niskanen**

- Comparing Observed Iso- and non-isothermal Listeria monocytogenes Growth with Model Predictions Under dynamic Conditions, Patrizia Centorame
- ESBL-producing Salmonella Kentucky cluster linked to locally produced eggs, August 2023, Malta, Ariana Wijermans
- Come rain or shine? Outbreak of gastroenteritis after a swimming competition in open water, Esther Schol-van Puffelen
- Where the cooling water drifts: An outbreak of Legionella pneumophila serogroup 1 in Sydney, Australia, 2024, Eunice Stiboy
- Investigation of an acute watery diarrhea outbreak among students of a Police College in the Jericho district of Palestine, Subhi Alshaer
- A multi-country and intersectoral assessment of cluster congruence between different bioinformatics pipelines used in genomics surveillance of foodborne bacterial pathogens, Verónica Mixão
- Multi-organ complications identified ≥1 year after Shiga-toxin producing Escherichia coli O157 (STEC O157) infection and STEC- associated haemolytic uraemic syndrome (STEC-HUS), Wales, 1990-2020, Chris Williams

POSTER TOUR 3

Emerging and vector-borne diseases

MODERATOR: **Anna Maisa**

- Epidemiological investigation of a multistate leptospirosis outbreak linked to pet rats (Rattus norvegicus forma domestica) in Germany, 2022–2023, Jasmin Metz
- Unprecedented number of imported cases and autochthonous transmission in Northern France: was 2023 a tipping point for dengue in mainland France?, Lucie Fournier
- Five autochthonous dengue cases and the first local transmission in the Paris region in 2023, Nelly Fournet
- Orthohantavirus seroprevalence among high-risk adults in western Kazakhstan, 2023, Ulyana Gubareva
- Highly Pathogenic Avian Influenza A H5N1 infections in domestic poultry and human contacts in the Fraser Health region, British Columbia, Canada, Brigitte Ho Mi Fane
- Public Health Challenges in Contact Tracing of Leprosy, Ireland, August 2024., Rebecca Marshall

POSTER TOUR 4

HIV intervention strategies

MODERATOR: **Otilia Mardh**

- Integrating hepatitis C screening and treatment into routine HIV care in Cameroon is feasible, Liza Coyer
- Optimising HIV pre-exposure prophylaxis eligibility in men who have sex with men in 10 European countries: a modelling study and cost-effectiveness analysis, Boxuan Wang
- Prevalence and predictors of chemsex practice among people living with HIV in Serbia, Zoran Milosavljevic
- Evaluating the Impact of Healthcare Providers' Attitudes and Practices on the Prioritization of Patients with Recent HIV Infections on the Yield of HIV Testing Services in Rwanda, Sophia Chkonia
- Risk behaviour patterns among people who inject drugs and services provided in Lithuania: cross sectional study report from 2023, Evelina Pridotkiene
- Adjusting for seroconversion and migration in the CD4 back-calculation method for HIV incidence estimation, Peter Kirwan

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POSTER TOUR 5

Burden of disease

MODERATOR: **Jane Whelan**

- Individual and environmental determinants of differences in excess mortality between neighbourhoods in Amsterdam during the COVID-19 pandemic, Jizzo Bosdriesz
- Low impact of the autumn-winter COVID-19 seasonal booster campaign in averting severe COVID-19 cases in Italy (October 2023 - March 2024), Emmanouil Alexandros (Max) Fotakis
- Impact of diabetes and obesity on SARS-CoV-2 infection following vaccination: an epidemiological and immunological analysis within the SIREN study, Ana Atti
- Using SARS-CoV-2 Nucleoprotein antibodies to detect re-infection, Mirjam Knol
- COVID-19 Pregnancy and maternal outcomes in Slovakia, Ladislav Kovac
- Prolonged hospital outbreak associated with multidrug resistant Clostridioides difficile RT027 clone exhibiting reduced susceptibility to vancomycin, Joana Isidro
- Estimating the disease burden of respiratory syncytial virus (RSV) in older adults in England during the 2023/24 season, a new hospital-based surveillance system, Rebecca Symes

POSTER TOUR 6

Childhood vaccinations and disease outbreaks

MODERATOR: **Nathalie Nicolay**

- Pertussis vaccination status of patients during an ongoing outbreak in North Macedonia 2024, Enkela Pollozhani
- Outbreak of pertussis in Montenegro, November 2023 to January 2024, Milko Joksimovic
- MMR vaccination coverage decrease in the Netherlands from birth cohort 2008 to 2020 and its sociodemographic determinants, Joyce Pijpers
- Effectiveness of Universal Respiratory Syncytial Virus monoclonal antibodies in preventing Acute Respiratory Infections of patients admitted to a tertiary hospital in the 2023/2024 season, Raíssa De Fátima Silva Afonso Francisco
- The impact of routine prophylaxis through monoclonal antibodies and maternal immunisation on the respiratory syncytial virus burden in the Lombardy region, Italy, Danilo Cereda

POSTER TOUR 7

Surveillance systems

MODERATOR: **Timothee Dub**

- Evaluation of the European severe acute respiratory infection surveillance, October 2023: useful, acceptable, and meets its main objective, Diogo FP Marques
- Surveillance of severe acute respiratory infections associated with SARS-CoV-2, influenza virus and RSV using ICD-10 codes: a case definition accuracy study across five European countries, 2021-2023, Miguel Angel Sanchez Ruiz
- Protecting Scotland’s health: An evaluation of the Community Acute Respiratory Infection (CARI) surveillance programme, Catriona Oliver
- National surveillance system for invasive Haemophilus influenzae disease in Italy: evaluation of completeness and timeliness, 2016–2022, Miruna E. Rosu
- Strengthening molecular surveillance of ARIs in the federal state of Bavaria, Germany: Expansion of the Bavarian Influenza Sentinel (BIS+C), Hilde Angermeier
- Evaluation of the surveillance system for severe Clostridioides difficile infections in Germany 2017-2022, a mixed methods approach, Sofia Burdi
- Evaluation of the measles surveillance system in Tashkent, Uzbekistan, 2023, Shoxsanam Abdullaeva

POSTER TOUR 8

COVID-19

MODERATOR: **Maria Keramarou**

- XBB.1.5 COVID-19 vaccine effectiveness against hospitalisations and deaths during Omicron BA.2.86/JN.1 period among older adults in seven EU/EAA countries: ECDC VEBIS electronic health record network, Baltazar Nunes
- Effectiveness of XBB.1.5 vaccines against symptomatic SARS-CoV-2 infection in adults aged >=65 years during the JN.1 lineage-predominant period, European VEBIS primary care multicentre study 2023–2024, Lore Merdrignac
- Effectiveness of the XBB.1.5 COVID-19 vaccines against hospitalisation during the BA.2.86 variant-predominant period in adults aged >=65 years: VEBIS European hospital multicentre study, 2023/24, Madelyn Rojas
- Evaluation of an electronic health record-based multi-country network designed to monitor COVID-19 vaccine effectiveness in EU-EEA countries (October 2021 – February 2024), James Humphreys
- Pre-booked COVID-19 vaccination appointments vs. self-scheduling: assessing the effect on vaccination uptake during the 2023 autumn campaign in the Netherlands using a regression discontinuity design, Manon Haverkate
- Effectiveness of tiered restrictions in slowing down COVID19 in Portuguese municipalities in the winter of 2020-2021: a weighted matching differences-in-differences study, Rafael Vasconcelos
- Unpacking our SuITCases - Identifying travel-associated SARS-CoV-2 cases in England, Mary Sinnathamby

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MODERATOR: **Bojana Mahmutovic**

- Main determinants of vancomycin-resistant Enterococcus faecium (VREF) infection in bloodstream isolates: data from ARISS, the Italian national surveillance system on antimicrobial resistance, 2015-202, Chiara Sacco
- Community- and Healthcare associated bloodstream infections caused by extended-spectrum beta-lactamase-producing Escherichia coli in Finland in 2018-2023, Heikki Ilmavirta
- Carbapenem resistance in gram-negative bacteria in the Republic of Moldova, 2019-2023, Nadejda Morarescu
- Antimicrobial resistance and area-level socioeconomic position in Germany, 2010-2019, Regina Singer
- Comparing antibiotic consumption trends in Italian acute care hospitals: a propensity score matching analysis of two point prevalence surveys, Antonino Russotto
- Epidemiological description of carbapenemase-producing organisms (CPO) cases in Wales, April 2023 – March 2024: Initial results of a new surveillance system, Victoria McClure
- Molecular epidemiology and antimicrobial resistance of invasive Streptococcus dysgalactiae subsp. equisimilis isolates in Denmark 2020-2022, Jana Grüttner

POSTER TOUR 10
Diagnostics of food-and waterborne diseases

MODERATOR: **Theresa Enkirch**

- Possible impact of culture-independent diagnostic techniques on surveillance of gastrointestinal pathogens in Belgium, Wouter Van Dyck
- Association of Yersinia enterocolitica biotype 1A and gastrointestinal symptoms: an epidemiological and genomic study from 2021 to 2023 in Belgium, Elena Portell-Buj
- Enhanced echovirus 11 genomic surveillance in neonatal infections in Spain following a European alert reveals new recombinant forms linked to severe cases, 2019-2023, Maria Dolores Fernandez Garcia
- Added value of PCR on feces in two hepatitis A outbreaks in care facilities for the disabled in the Netherlands, Marloes Stradmeijer
- Development of a Nanopore DNA sequencing workflow for detection of zoonoses and antimicrobial resistance genes in avian faeces, Karen Keegan
- Surge in the number of STEC notifications in Germany in 2023 – A real increase in infections or a laboratory artifact?, Tanja Jung-Sendzik
- Opportunities and challenges of Integrated Genomic Surveillance based on Salmonella surveillance data from 2020 to 2023, Germany, Laura Giese

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Vaccination programmes and strategies

MODERATOR: **Kim Brolin**

- A new vaccine and two outbreak responses: a game-changer in meningitis control?, Joaquin Baruch
- Factors associated with Influenza vaccination uptake among frontline healthcare workers in Tunisia, 2022/2023 season, Fatma Ben Youssef
- Factors associated with influenza vaccine uptake among healthcare workers in Georgia, 2021-2024, Oksana Artemchuk
- One more reason to have a vaccination program for healthcare professionals in Lebanon, Zeina Farah
- Childhood vaccinations: Declining coverage and widening inequalities in England, Mary Sinnathamby
- Is the high-dose influenza vaccine better for everyone over 60 years of age in Germany?, Laura Colombo
- Missed opportunities for vaccination among Healthcare seeking children–Kyrgyzstan, 2023, Gulzada Dadanova

POSTER TOUR 12
STIs and related prevention

MODERATOR: **Marieke van der Werf**

- Prevalence of chlamydia, gonorrhoea, trichomoniasis, and syphilis in Europe: A systematic review and meta-analysis to inform prevention and control of sexually transmitted infections in Europe, Richard Pentz
- Rising incidence of congenital syphilis in Portugal: Implications for achieving WHO Europe targets, Filipa Canha
- Spatio-temporal trends and determinants of syphilis among heterosexual men and women in the Netherlands, 2011-2023, Laura Kayaert
- Antimicrobial resistance in Neisseria gonorrhoeae in Portugal: Results from the Portuguese National Laboratory Network for Neisseria gonorrhoeae Collection, Miguel Pinto
- Knowledge, attitudes and HPV vaccination intentions among different populations of unvaccinated young Israeli adults:a cross-sectional survey, Michael Edelstein
- Neonatal herpes simplex virus infections in the Netherlands (2016-2022): incidence, health outcomes and guideline adherence, Goncalo Matias
- Reduction of mpox vaccination hesitancy in clinics offering on-site vaccination, Raquel Eusébio

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MODERATOR: **Nathalie Girin**

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- Circulation of enterovirus types in Europe between January 2018 and August 2023: a retrospective multi-center surveillance study, Emiel Vanhulle
- Factors associated with severe outcomes among adult patients with Severe Acute Respiratory Infection admitted to Bishkek Hospital 2, Kyrgyzstan, 2022- 2024, Dinagul Otorbaeva
- Increase in invasive group A streptococcal infections (iGAS) in children and older adults in Norway, 2022-24, Beatriz Valcarcel
- A geospatial approach to identify possible sources of infection during an outbreak of Legionnaires' disease, Baden-Wuerttemberg, Germany, 2023, Juliana Klein
- Wastewater-based epidemiological studies and their use in public health decision making: a scoping review, Anne-Merel R. van der Drift

POSTER TOUR 14

Social and behavioural sciences

MODERATOR: **Sarah Earnshaw Blomqvist**

- The influence of the COVID-19 pandemic on influenza vaccination willingness among healthcare workers in Dutch nursing homes, Lisa Kolodziej
- Impact of the COVID-19 pandemic on parental behaviour towards Childhood Vaccination: A self-controlled matched Cross-Sectional Study, Mahmud Omar
- Knowledge, attitudes and practice towards routine vaccination among medical students, Kazakhstan, 2023, Arystan Balmagambetov
- Physicians' knowledge and practices on syphilis diagnosis and prevention in Armenia, Lusine Boryan
- Creating good career prospects for professionals in the infectious disease control in the Netherlands, Marije Hop
- Focus group on information-seeking and sharing on vaccination, Betina Kiefer Alonso

POSTER TOUR 15

Preparedness

MODERATOR: **Soledad Colombe**

- The first year of operations of the EU Health Task Force in the European Union and globally, Dorothee Obach
- "Bern, get ready" (BEready), a One Health population-based household cohort for pandemic preparedness: Pilot study about participation and feasibility, Eva Maria M. Hodel
- The state of the art of professional exchange visits in preparedness in the European Union/European Economic Area, Amelie Plymoth
- Preparedness of European critical infrastructure operators to vector-borne outbreak, Olga Hovardovska
- Lessons for future pandemic preparedness: The SIREN experience, Sarah Foulkes
- Food Security Recommendations Following Investigation of an Outbreak Linked to Oyster Consumption, Douglas Hamilton

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MODERATOR: **Jordi Borell Pique**

- Evaluation of whole genome sequencing versus emm typing for iGAS outbreak management in England, Fariya Abdullahi
- Use of Large Language Models to Analyse Text Responses in a National HIV Survey, Tom White
- INSaFLU-TELEVIR: an open web-based bioinformatics suite for viral metagenomic detection and routine genomic surveillance, Vitor Borges
- Epidemic Intelligence from Open Sources (EIOS) to detect international public health events – an evaluation in the scope of public health intelligence activities at the Robert Koch Institute, Germany, Mario Martín Sánchez
- Evaluation of the newly established automated surveillance system to detect severe acute respiratory infections (SARI) using electronic health records in Denmark, 2022-2023, Frederikke Lomholt
- Drafting a manual on standardized work processes for IHR- relevant biological events at the five IHR-designated airports in Germany in the StandAtRisk-project, Hannah Höglund-Braun
- Cluster identification from backwards contact tracing: a key toolbox component for control of pandemic respiratory agents with over-dispersed transmission, Graham Fraser

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International health and migration

MODERATOR: **Anastasia Pharris**

- Association of depression and anxiety with traumatic exposures in the pre- and post-migration periods among refugees from Ukraine in Moldova, 2023, Ivanna Haman
- Assessing Health Disparities and Access: Afghan Refugee Health in Pakistan through Data-Driven Analysis, Saeed Ahmad
- Enhancing public health response to newly arrived migrants: A community intervention in Catalonia, Helena Martínez Alguacil
- Piloting recruitment methods for a biobehavioural survey on viral hepatitis in Germany among people born in Türkiye and Romania, HepMig pilot study, May 2023 – March 2024, Anna-Lisa Behnke
- Spotlight on Corynebacterium (C.) diphtheriae and C. ulcerans: Results of enhanced diphtheria surveillance in Germany, 2017 – 2022, Lena Schneider
- Infectious diseases and malnutrition in Gaza - August 2024 - approaching 1 year of conflict, Laura Anne Paris

POSTER TOUR 18

Antimicrobial resistance

MODERATOR: **Pete Kinross**

- Characterisation and network analysis of plasmids associated with combined carbapenem and aminoglycoside resistance, Mark Maguire
- Community outbreak with Panton-Valentine Leukocidin-encoding livestock-associated methicillin- resistant Staphylococcus aureus in the Netherlands, Patrick Van Schelven
- Nosocomial transmission of methicillin- resistant Staphylococcus aureus (MRSA) between two neonatal and maternity units in Wales, Israa Mohammed
- Use of Antimicrobial Sensitivity Testing for Prescribing Antibiotics Among Production Animals in Armenia, Georgia, Moldova, and Ukraine, 2023, Svitlana Mandyhra
- Proximity to humans is associated with antimicrobial resistant enteric pathogens in wild bird microbiomes, Evangelos Mourkas
- Antimicrobial resistance patterns in Klebsiella pneumoniae strains isolated from a tertiary care hospital in Romania, Mihai-Octavian Dan
- Antibiotic Resistance in reported Shigella cases in Baden-Wuerttemberg, Germany: A Pilot Study on Resistance Patterns and Phylogenetic Links from March until August 2024, Julia Kuhn

POSTER TOUR 19

Surveillance of food- and waterborne diseases

MODERATOR: **Therese Westrell**

- Lessons learnt from a One Health stakeholder analysis and systems mapping workshop on avian and swine influenza surveillance in humans in Denmark, August 2023, Gudrun Witteveen-Freidl
- Increase of Salmonella enterica serovar Chester cases in Spain, 2023, Jasmin S. Kutter
- Reptile-Associated Salmonella Enteritidis cases in England following import ban on feeder-mice from an EU importer, Yanshi Yanshi
- National perinatal survey to estimate seroprevalence of Toxoplasma gondii infection among pregnant women in France, 2021, Sara Mazzilli
- The occurrence of hepatitis E virus in human patients from Slovakia, Bozena Kocikova
- Investigation of a significant Cryptosporidium hominis increase across England and Wales, August to September 2023, using a retrospective case-case study revealed associations with travel and swimming, Sarah Williams
- The rise in Shiga toxin-producing Escherichia coli (STEC) O26 and the role of farm and nursery settings, England, 2019-2023, Lucy Findlater

POSTER TOUR 20

Food- and waterborne disease outbreaks

MODERATOR: **Joana Gomes Dias**

- Shiga toxin–producing Escherichia coli (STEC) O145: H28 outbreak linked to unpasteurised cheese in England and Scotland, 2023, Orlagh Ingeborg Quinn
- Outbreak of the novel Cryptosporidium parvum subtype IIγA11 linked to mixed kale salad from salad bars in Sweden, December 2023, Ioana Bujila
- Listeria monocytogenes outbreak linked to artisanal blackened olives in Baden-Wuerttemberg, Germany 2023, Florian Burckhardt
- Enteropathogenic E. coli gastroenteritis outbreak in Agri Province, Turkiye, March 2023, Mahmut Akdag
- Brucellosis outbreak in northwestern Tajikistan in 2023: a matched case-control study, Emomali Kurbonov
- A large Cryptosporidium parvum outbreak associated with a lamb-feeding event at a working farm in South Wales, March-April 2024: a retrospective cohort study, Gethin Jones
- Cross-border outbreak of Yersinia enterocolitica bioserotype 2/O:9 infections linked to unpasteurized goat milk cheese produced in France, 2024, Fanny Chereau

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MODERATOR: **Erika Duffell**

- Chronic hepatitis B infections in the European Union/ European Economic Area countries: estimates of prevalence using the UNAIDS Workbook Method, Ana Paula Finatto Canabarro
- National investigation and response to a cluster of acute hepatitis B cases in Ireland 2023-24 – implications for Ireland's new national sexual health strategy, Celia O'Hare
- Assessment of mother-to-child-transmission of hepatitis B in Germany based on routine surveillance data, 2019–2023, Klara Röbl
- Eliminating mother to child transmission of hepatitis B virus (HBV): monitoring outcomes for infants born to mothers living with hepatitis B infection in England, 2014-2023, Sameera Lyons
- Effect of risk management and communication in vaccination during a hepatitis A outbreak in Portugal, Joana Cardoso
- Seroprevalence of HIV, Hepatitis B, and C infections among pregnant women in Libya, 2023-2024, Jebril Gebril
- Investigation of a cluster of adult acute hepatitis of unknown aetiology in Greater Manchester, January-July 2024, Eve Matthews

POSTER TOUR 22
Modelling

MODERATOR: **Bastian Prasse**

- Estimating excess mortality in the Nordics between 2020-23 using a multi-model approach, Sasikiran Kandula
- Modelling West Nile virus (WNV) seroprevalence and infection burden in Europe, Hailin Feng
- Forecasting Seasonal Influenza Hospitalisations in Ireland using a Population SLIR Transmission Model with Hamiltonian Monte Carlo (HMC), Jim Duggan
- Introducing RespiCast: the first European respiratory diseases forecasting hub, Nicolò Gozzi
- Integrating epidemiological modelling into the evidence-based methodology used in health-policy assessment. The example of the updated French vaccination strategy against invasive meningococcal disease, Laurene Peckeu-Abboud
- Factors of hepatitis C transmission in Ukraine: the impact of dental interventions, Nataliia Halushko

POSTER TOUR 23
Surveillance of respiratory diseases

MODERATOR: **Senia Rosales-Klintz**

- Tracking seasonal influenza trends in South Tyrol during season 2022-2023 using genomic surveillance data, Irene Bianconi
- Genomic evolution of human respiratory syncytial virus during a decade (2013–2023) in Barcelona: bridging the path to monoclonal antibody surveillance, Alejandra Gónzalez-Sánchez
- Usefulness of Syndromic Surveillance in Real-Time Influenza Monitoring, Albania, 2019-2022, Jonilda Sulo
- Implementation of the moving epidemic method for RSV season detection and timely public health response in the post-COVID era, Slovenia, 2015-2024, Maja Mrzel
- Change of influenza burden between Corona pre-pandemic and pandemic times from 2014 to 2023: Analysis based on FLUNET data in Europe, Manuela Harries
- Post-pandemic rebound of Group A streptococcal infections in children in Germany, 2017 to 2024, Julia Mutevelli
- Post-COVID-19 outbreak of Parvovirus B19 affecting pregnant women - A retrospective study of laboratory-confirmed human Parvovirus B19 congenital cases 2016-2024 in the Lyon Metropolitan area, Kaisa Jaakkola

POSTER TOUR 24
Surveillance of vaccine-preventable diseases

MODERATOR: **Marlena Kaczmarek**

- Invasive meningococcal disease serogroup B: spatiotemporal cluster identification using finetype data, The Netherlands, 2005-2023, Hester de Melker
- Uneven geographical distribution of invasive meningococcal disease in Spain, 1996-2022, Marta Soler Soneira
- Investigation the largest wave of pertussis since 2016 in Wales, UK, Joshua Menadue
- Seroprevalence of varicella zoster virus IgG-antibodies in newborns and children up to 2 years of age in Lower Saxony and Bremen, Germany 2003-2023, Mareike Wollenweber
- Pertussis outbreak centered among immunized adolescents in Luxembourg, 2024, Dritan Bejko
- Mpox vaccination and outreach in the Valencian Community, Spain: response to PHEIC and coverage of high-risk groups, Juan Juaneda

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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 (10 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 2024, chaired by the ESCAIDE Scientific Committee. The format of each varies from panel discussions, interviews and debates.

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Scientific Committee

PIOTR KRAMARZ

SWEDEN

*Deputy Head of Unit/ Deputy Chief Scientist |
Chair of ESCAIDE Scientific Committee | ECDC*

Piotr Kramarz is a physician by training, with a PhD in immunology of viral infections, and eight years of clinical practice experience in a teaching hospital in the field of infectious diseases. Between 1997-2000, he worked at the US Centers for Disease Control and Prevention (CDC) as part of the Epidemic Intelligence Service (EIS) and then as a medical epidemiologist. Since 2007, he has worked at the ECDC as a Deputy Head of the Unit (first of the Scientific Advice Unit and now of the Disease Programme Unit) and, since April 2011, as the Deputy Chief Scientist of the Centre. His research interests include burden of communicable diseases and vaccine-preventable diseases.

JOHN KINSMAN

SWEDEN

Expert Social and Behaviour Change | 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.

Scientific Committee

ÁGNES HAJDU

HUNGARY

*Senior Advisor | Unit of Infection Control and Hospital Epidemiology |
National Center for Public Health and Pharmacy, Hungary*

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.

ALICIA BARRASA

SPAIN

EAN Network

Alicia Barrasa is part of the EPIET Alumni Network which brings together more than 600 European field epidemiologists and public health microbiologists. She has a PhD and MSc in public health and epidemiology. She has worked on HIV focussing on factors associated with disease progression, and on field epidemiology training as Scientific Coordinator for the Spanish FETP (2004-2008), EPIET (2008-2020) and currently for the UK FETP. She has also been part of the TEPHINET Accreditation Working Group (2019-2023).

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NADINE ZEITLMANN

GERMANY

Senior epidemiologist | Robert Koch Institute

Nadine Zeitlmann is a senior epidemiologist at the Robert Koch Institute (RKI) in Berlin, Germany and a part-time Scientific Coordinator for the European Programme for Intervention Epidemiology Training (EPIET) for ECDC. She has a Master Public Health from the University of Munich and a Master of Science in Applied Epidemiology from the Berlin Charité. Between 2011 and 2013 she worked in the field of public health and infectious disease epidemiology in Denmark and completed her EPIET/PAE -fellowship between 2013 and 2015 based at the Bavarian Health and Food Safety Authority in Munich, Germany. In the subsequent 8 years she worked as an epidemiologist in different international programmes at the RKI where she supported partner countries in North Africa and the Balkan peninsula in building up surveillance, outbreak investigation and crisis management structures as well as in their IHR implementation. During this time, she also been deployed as an epidemiologist on different international assignments on the African and Asian continent and worked as a field epidemiologist in various COVID-19 outbreak investigations in Germany during the pandemic. Currently, next to her role as an EPIET Coordinator, she works in coordinating roles in the field of epidemic intelligence, early warning and outbreak coordination in the RKI's "Unit for crisis management, outbreak investigation and training programmes".

KATEŘINA ŠÉDOVÁ

CZECH REPUBLIC

Physician, CEO | Loono | Faculty Hospital Bukova

Kateřina Šédová 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.

ANGELIKI MELIDOU

SWEDEN

Principal Expert Respiratory Viruses | ECDC

Angeliki Melidou is a virologist with a PhD in molecular epidemiology of influenza. She is an Assistant Professor of Molecular Microbiology-Virology at the Aristotle University of Thessaloniki, Microbiology Department, Medical School in Greece with which she is affiliated since 2004. Since 2016, she has been working at the European Centre for Disease Prevention and Control (ECDC), initially as a Seconded National Expert and currently as a Principal Expert in Respiratory Viruses at the Respiratory virus and legionella (RVL) group. Her expertise lies in the areas of microbiology, disease surveillance, and scientific advice related to respiratory viruses. During the COVID-19 pandemic she was serving as a coordinator of the ECDC Public Health Emergency Microbiology team.

Plenary speakers

PLENARY A

Prevention vs. Cure:
what can we learn from cancer, crime and climate change?

CHRIS DYE
UNITED KINGDOM

Professor of Epidemiology | University of Oxford

Chris Dye trained as a biologist and ecologist (BA York) but postgraduate research on mosquitoes (DPhil Oxford) led to a career in epidemiology and public health. Based at Imperial College and the London School of Hygiene and Tropical Medicine from 1982-96, he did research on bloodsucking insects as vectors of leishmaniasis, malaria and river blindness in Africa, Asia and South America, and on the role of domestic and wild animals as reservoirs of human infection and disease. In 1996, he joined the World Health Organization where he developed ways of analyzing the vast quantities of routine surveillance data collected by government health departments worldwide – to better understand and control tuberculosis, malaria, and Ebola, HIV, SARS and Zika viruses. As WHO Director of Strategy 2014-18, he served as science advisor to the Director General, oversaw the production and dissemination of health information by WHO press and libraries, and coordinated WHO's work on health and the Sustainable Development Goals. He is now Professor of Epidemiology at Oxford University, a Fellow of The UK Royal Society, and of the UK Academy of Medical Sciences. His most recent book is Investing in Health and Wellbeing: When Prevention is Better than Cure (OUP 2024).

PLENARY B

Infectious diseases in times of conflict:
learning from Ukraine

IHOR KUZIN
UKRAINE

Deputy Minister | Ministry of Health

Ihor Kuzin is an epidemiologist who currently serves as Deputy Minister of Health of Ukraine and Chief State Sanitary Doctor of Ukraine. He was previously appointed as Deputy Director General of the Public Health Center of the Ministry of Health of Ukraine. In 2021 he was elected Vice-Chair of the European Network of IANPHI, and is the National Contact Person for Surveillance in Ukraine to the European Epidemiological Surveillance System (TESSy). He has previously worked as a doctor of public health and researcher in epidemiology, and as Head of the Center for Monitoring and Evaluation of the Implementation of Program Measures to Combat HIV/AIDS.

He holds a medical degree from Donetsk National Medical University with a speciality in medical and preventive care, an MSc in Public Health and Health Management from the Medical University of Varna (Bulgaria) and a Master of Public Management and Administration from the Odessa Regional Institute of Public Administration. He has also graduated from the South Caucasus Training Programme in Field Epidemiology and Laboratory Research.

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OLGA GVOZDETSKA

UKRAINE

Deputy Director General | Public Health Centre | Ministry of Health

Olga Gvozdetska is the Deputy Director General of the Public Health Center of the Ministry of Health of Ukraine. She has about 20 years of experience in public health, both private and state. Olga has broad experience in managing and coordinating health and social programs and projects; collaborating with NGOs, government representatives, and the scientific community; organizing international cooperation activities and developing methods for its implementation; and establishing contacts with foreign agencies, associations, institutions, and country offices in Ukraine. As Deputy Director General, she ensures the proper functioning of structural units of UPHC such as the Department of Viral Hepatitis and Opioid Dependence, Department for Coordination of HIV Diagnosis and Treatment Programs, Department of Coordination of TB Diagnosis and Treatment Programs, Department of Pharmaceutical Management and Inventory Management, Scientific Research Department, Department of Project Management and International Cooperation.

She has previously worked as a public health consultant for the World Bank and as the Innovations and Development Director for the All-Ukranian Network of People Living with HIV/AIDS. She holds a Masters degree in International Management from the Kyiv National Economics University.

KATARZYNA DRĄŻEK-LASKOWSKA

POLAND

Director | International Cooperation Bureau | Ministry of Health

Katarzyna Drążek-Laskowska is the Director of the Department of International Cooperation of the Ministry of Health in Poland. In 2022 she was appointed as the Plenipotentiary of the Minister of Health for the Continuation of Treatment Abroad for Ukrainian patients who came to Poland in connection with the armed conflict in Ukraine and who will continue treatment in other countries. She was also elected to the WHO Executive Board for a term of 2024-2027, where she works to prioritise digital health, the fight against tuberculosis and the reconstruction of health care systems after crises.

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PLENARY C

Advancements in surveillance: how can we better tell what's going on?

LIEKE VAN ALPHEN

NETHERLANDS

Medical Molecular Microbiologist | Department of Medical Microbiology, Infectious diseases and infection prevention | Maastricht University Medical Centre

Lieke van Alphen studied Medical Biology at the Utrecht University, specialising in infection and immunity. She continued into a PhD at this same university and completed her thesis in 2008 on "the virulence strategies of Campylobacter jejuni". After a 3-year postdoc in the Szymanski lab at the university of Alberta (Canada) investigating the interaction of Campylobacter with bacteriophages, she trained as a Public Health Microbiologist during the EUPHEM fellowship at Statens Serum Institute in Copenhagen, Denmark. Since then, she has been working as a member of staff at the Department of Medical Microbiology, Infectious diseases and Infectionprevention, Maastricht university Medical Centre. She specialised during a 2-year postgrad training as Medical Molecular Microbiologist, where she is head of the regional typing lab. Currently, her research work at the MUMC focusses on the spread of resistant bacteria and resistance genes and molecular epidemiology using next gen sequencing and rapid data sharing.

CATERINA RIZZO

ITALY

Professor of Hygiene and Preventive Medicine | University of Pisa

Caterina Rizzo, MD, is Full Professor of Hygiene and Preventive Medicine at the University of Pisa (Italy). She started her academic career in January 2001 as a researcher at the Univeristy of Bari. Between 2006 and 2018 she was first lead researcher at the National Center for Epidemiology and Health Promotion until 2016, and from January 2017 at the Infectious Diseases Department of the National Institute of Health (Istituto Superiore di Sanità). From 2013 to 2021 she was appointed by the Ministry of Health as National Focal Point for the surveillance programmes on vector-borne diseases, influenza and alternate NFP for food-borne diseases coordinated by the European Centre for Disease Prevention and Control (ECDC) in Stockholm. From 2018 to 2022 she worked at the Innovation Unit of the Ospedale Pediatrico Bambino Gesù in Rome, and in May 2022 she resumed her position in the Italian University, moving to Pisa, where she is teaching Hygiene and Preventive Medicine and Public Health at the School of Medicine. Since 2021 she has been member of the National Immunization Technical Advisory Group (NITAG) and of the NUCE (Nucleo permanente di coordinamento della comunicazione del rischio sanitario nelle emergenze). Her research activity has been focused on infectious disease epidemiology and prevention. She is has co-authored more than 200 scientific articles in peer-reviewed journals.

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ANDRÉ CHARLETT

UNITED KINGDOM

Head Statistics, Modelling and Economics | UK Health Security Agency (UKHSA)

André Charlett studied mathematics as an undergraduate and has postgraduate degrees in medical statistics leading to his first position as a medical statistician at the MRC Clinical Research Centre. He moved in the early 1990s to take up the role of principal statistician within the Communicable Disease Surveillance Centre at Colindale. He was initially involved in establishing hospital infection surveillance systems within England and retains an interest in combatting the rise of antimicrobial resistance.

For the past twenty years he has headed the Statistics, Modelling and Economics Division in which staff develop and deploy analytical methodologies focused on infectious disease control and elimination programmes, in addition to working on collaborations with academic and UKHSA colleagues across numerous infectious diseases. He sits on SPI-M, the UK Government advisory committee on pandemic modelling, a group awarded the Weldon Memorial Prize by the University of Oxford for its collective responsive work during the COVID pandemic. He has an academic appointment at King's College, London, where he is currently investigating the role that the faecal microbiome plays in Parkinson's disease.

PLENARY D

Disease X: are we ready?

MIKA SALMINEN

FINLAND

Director | Finnish Institute for Health and Welfare (THL)

Professor Mika Salminen, Ph.D., is the Director General of the Finnish Institute for Health and Welfare (THL). He has previously led the Public Health and Welfare department at THL, overseeing public health and welfare initiatives and the Health Security department, responsible for national vaccination programs, infectious disease surveillance systems, microbiological reference laboratories, and environmental health.

He is an Adjunct Professor at the University of Helsinki, a former member of the European Centre for Disease Prevention and Control (ECDC) and currently at EU Commissions DG HERA's scientific Advisory Forum. He is the Chair of the European Space Agency Planetary Protection Working Group. He has published widely on various infectious disease and public health topics.

Mika has actively contributed to the Global Health Security Agenda (GHSA) initiative and was intimately involved in developing the WHO led Joint External Evaluation process, fostering strong relationships with relevant organizations such as the WHO, US-CDC, and the World Bank. He led multiple IHR Join External Evaluation missions, including those of Germany, Switzerland, Australia, Afghanistan, Pakistan and Sudan.

Throughout the COVID-19 pandemic, Mika played a pivotal role in leading the response efforts at THL. For his achievements he received multiple awards such as the Presidential Medal First Class of the Order of the Knights of the Finnish White Rose, the Helsinki Medal and the Leader of the Year Award. He is especially proud of being awarded the title of the Caricature figure of the year in 2021.

ANA MARIA HENAO-RESTREPO

SWITZERLAND

Technical Lead for the R&D Blueprint for Emergency Response | World Health Organization

Dr. Henao-Restrepo serves as the technical lead for the R&D Blueprint for Epidemics at the Health Emergencies Programme (WHE) in WHO. During her esteemed career at WHO, she was assigned to the Ebola Research and Development Team and coordinated the Ring vaccination trial in Guinea and Sierra Leone. In addition, she contributed to the expansion of immunization programs and served as the WHO global focal point for measles and rubella control efforts. Notably, she also worked in the implementation and evaluation of strategies to eradicate poliomyelitis and eliminate measles and maternal and neonatal tetanus.

Dr. Henao-Restrepo was born and raised in Colombia, South America. After receiving her Medical Doctor and Surgeon degree from the University of El Rosario in Bogota, Colombia, she received a Master's degree in communicable disease epidemiology at the London School of Hygiene and Tropical Medicine.

CHRISTIAN DROSTEN

GERMANY

Director | Institute of Virology | Charité Universitätsmedizin Berlin

Christian Drosten studied medicine in Frankfurt am Main/Germany. From June 2000, Drosten joined the virology department at Bernhard Nocht Institute for Tropical Medicine in Hamburg. His group focused on virus discovery and molecular diagnostics of tropical viral diseases. From 2007, Drosten became full professor and chair at the Institute of Virology at University of Bonn Medical Center. In 2017, he moved to the Charité-Universitätsmedizin in Berlin, where he is currently the Director of the Institute of Virology. He was a member of the German Ministry of Health's International Advisory Board on Global Health from 2017-2019. Drosten co-discovered the SARS coronavirus (SARS-CoV), for which he developed the first diagnostic tests in 2003. He worked on Middle East respiratory syndrome coronavirus (MERS-CoV) for which he resolved many aspects of the natural history of disease in humans and animals. In January 2020, his team developed the first SARS-CoV-2 RT-PCR test that was approved by the WHO and globally applied. His subsequent work focused on characterizing essential disease traits and diagnostic approaches in COVID-19. During the pandemic, he has been advising German federal and state authorities and was appointed to the European Commission's advisory panel on Covid-19.

PLENARY E

The new old:
rethinking the future of known diseases

NIENKE BEERLAGE-DE JONG

NETHERLANDS

Assistant Professor of technology for planetary health behaviour | University of Twente

Nienke Beerlage-de Jong is an Assistant Professor of Technology for Planetary Health Behaviour, at the Technical Medical Centre of the University of Twente, the Netherlands. She also holds a guest appointment at the Medical Microbiology and Infection Prevention dept. of the University Medical Centre Groningen, the Netherlands.

Her research focuses on the interface between behaviour, technology and planetary health, much of it involving the participatory development, implementation, and evaluation of eHealth technologies to foster behaviour change in the face of the complex planetary health challenges.

In her work, she seeks to transcend disciplinary, sectoral, and national boundaries, integrating insights from e.g. behavioural science and infectious diseases, and fostering collaboration between academia, industry, and healthcare.

She coordinates and teaches bachelor- and master-level courses on eHealth at the University of Twente, for e.g. health sciences, technical medicine and biomedical engineering students. In addition, she is general chair of the international Supporting Health by Technology conference series, and co-editor of an international edited book on 'eHealth Research, theory and development – a multidisciplinary approach'.

Plenary speakers - Plenary E

MARIA WESSMAN
DENMARK

Epidemiologist, Head of Section | Statens Serum Institut (SSI)

Maria Wessman is a medical doctor and epidemiologist, specialised in Public Health. She holds a Ph.D in Infectious Diseases and her research concentrates within the field of HIV and sexually transmitted infections. She currently works as the Head of section of Blood-borne and Sexually Transmitted Infections and Digitization of the Infectious Disease Surveillance, at the Department of Infectious Disease Epidemiology and Prevention at Statens Serum Institut (SSI) in Copenhagen, Denmark.

She graduated with a medical degree in 2009 and has a background as a clinical doctor, mostly working at the Department of Infectious Diseases of Hvidore Hospital in Copenhagen, before joining SSI in 2017.

TOMASZ SOBIERAJSKI
POLAND

Health scientist, Sociologist and Professor | Sociomedical Research Centre | University of Warsaw

Tomasz Sobierajski is a health scientist, sociologist, methodologist, social vaccinologist, sociomedical researcher, interpersonal and medical communication trainer, socio-urbanist, evaluator, university lecturer, head of the Sociomedical Research Center, and professor at Warsaw University. He is the creator of the multidisciplinary scientific sub-discipline of social vaccinology. He has authored dozens of scientific publications in sociology, sociomedical, public health, and vaccinology, and 5 scientific monographs and 5 textbooks for health care professionals. He designs and coordinates research projects for Polish and international public institutions, NGOs, and private companies. He performs scientific project research in cooperation with, among others: Warsaw Medical University, Silesian Medical University, National Institute of Public Health - National Institute of Hygiene, National Institute of Medicines, Poznan Medical University, and Ankara Üniversitesi and the University of Alabama. He also supports the business sector with social research and analysis and business ethics. For over a decade, he has trained medical personnel in patient communication. He trains in cross-biking and squash and is a marathon runner.

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Plenary summaries

PLENARY A

Prevention vs. Cure:
what can we learn from cancer, crime and climate change?

Day 1 - Wednesday 20 November, 9:30-10:30

The debate between prevention and cure has long been discussed in the field of infectious diseases. The current paradigm places reactive medical treatment at the forefront of most research and financial investment, while public health emphasises the benefits of prioritising the prevention of avoidable illness and injury, thereby promoting better health and well-being for all. Lessons in prevention of infectious diseases can be learnt from both successes and failures in many fields: from non-communicable diseases, but also from engineering, gaming and gambling, climate change, and more.

In this session, Chris Dye, Professor of epidemiology at the University of Oxford, will draw from the principles outlined in his recently published book The Great Health Dilemma – Is Prevention Better than Cure? Through a presentation of key lessons that he has identified in different areas, he will consider what we can learn from past achievements and failures, how we can apply these to the field of infectious diseases, and how to strike a better balance between prevention and cure.

Chairs: Kateřina Šédová *(Loono, Czechia)*, Henriette de Valk *(Santé Publique France)*
Speaker: Chris Dye *(University of Oxford, UK)*

PLENARY B

Infectious diseases in times of conflict:
learning from Ukraine

Day 1 - Wednesday 20 November, 17:00-18:30

The ongoing full-scale Russian invasion of Ukraine has not only reshaped the geopolitical landscape of Europe, but it has also created considerable challenges for the prevention and control of infectious diseases. The Ukrainian health system and the health of its population has been drastically affected, with severe impacts on healthcare facilities, the interruption of critical medical treatments (including for HIV, viral hepatitis B and C, and tuberculosis), problems with accessing vaccinations, and the spread of antimicrobial resistance, among others. While the conflict has, to date, been contained inside Ukraine, the rest of Europe has had to manage the healthcare needs of large numbers of refugees, as well as face the possibility of the war – or at least the impact of the war – spreading into EU/EEA Member States.

In this session, the audience will hear from Ihor Kuzin, the Deputy Minister of Health of Ukraine, who will provide a framework for understanding the complex needs of a European public health system in times of armed conflict. Through reference to specific examples, Olga Gvozdetska, from the Public Health Centre of the Ministry of Health of Ukraine, will share lessons learned about ensuring continuity of care for patients with long-term infectious diseases; and Katarzyna Drążek-Laskowska will share her experiences in the Ministry of Health of Poland in providing effective care and immunisation services to those fleeing the conflict zone.

Chairs: John Kinsman *(ECDC)*, Piotr Kramarz *(ECDC)*
Speaker: Ihor Kuzin *(Ministry of Health Ukraine)*, Olga Gvozdetska *(Ministry of Health Ukraine)*,
Katarzyna Drążek-Laskowska *(Ministry of Health Poland)*

PLENARY C

Advancements in surveillance:
how can we better tell what's going on?

Day 2 - Thursday 21 November, 9:00-10:30

The COVID-19 pandemic has emphasised the importance of infectious disease surveillance and brought attention to the latest advancements in surveillance, from the increasingly widespread use of whole genome sequencing (WGS) to the use of automated tools and artificial intelligence (AI). These developments include improving signal detection algorithms to reduce false alerts and using WGS to more accurately identify infection clusters and manage outbreaks, thereby better informing public health actions. Moreover, besides automated surveillance of Healthcare associated infections (HAIs), developments in AI can now also be used to enhance traditional surveillance methods in hospitals and long-term care facilities, improving the way HAIs are monitored within and beyond healthcare settings.

This session aims to explore these advancements, evaluating the advantages, disadvantages and feasibility of these approaches, and how we can tackle the challenges associated with the vast amounts of data these tools generate. The PRESENTERs will be joined by a panel of experts, including Lieke van Alphen (Maastricht University), Caterina Rizzo (University of Pisa) and Andre Charlett (UK HAS), who will discuss and share examples of the post-pandemic adjustments and developments in signal detection algorithms, the issue of 'clusterdemics', and the potential of AI tools in surveillance.

Chairs: Alicia Barrasa *(UKHSA / EAN)*, Ágnes Hajdu *(National Center for Public Health and Pharmacy, Hungary)*

Speaker: Lieke van Alphen *(Maastricht University, Netherlands)*, Caterina Rizzo *(University of Pisa, Italy)*, André Charlett *(UK Health Security Agency)*

PLENARY D

Infectious diseases in times of conflict:
learning from Ukraine

Day 2 - Thursday 21 November, 17:00-18:30

The concept of "Disease X" has been adopted by the global public health community as a way to refer to a potential unknown pathogen that could cause the next pandemic. Despite the uncertainty surrounding the specific pathogen, it is still possible – and crucial – to proactively prepare for and work towards an effective response to potential pandemics. In order to understand our readiness to face the next disease X, we need to explore different facets of disease preparedness, prevention and response: from the need for research and global health infrastructures and collaboration, to developing surveillance strategies and preparedness measures, to the ability to accelerate a pandemic response when faced with emerging threats.

This session will discuss the comprehensive journey from pathogen X preparedness to pandemic response. Ana Maria Henao-Restrepo (WHO) will open with an introduction on the concept of disease X and its characteristics, as well as the current state of global readiness for unknown pathogens. Mika Salminen (THL, Finland) will explore the preparedness and prevention measures that can be put in place for disease X, including surveillance strategies, as well as public health interventions and the importance of international collaboration. Christian Drosten (Charité, Germany) will also discuss the importance of rapid responses to potential pandemics, emphasising the need to accelerate crucial processes such as genomic sequencing, vaccine and therapeutics deployment, and the upscaling of surveillance systems.

Chairs: Angeliki Melidou *(ECDC)*, Luísa Peixe *(University of Porto, Portugal)*, Chikwe Ihekweazu *(WHO)*

Speaker: Mika Salminen *(THL, Finland)*, Ana Maria Henao-Restrepo *(WHO)*, Christian Drosten *(Charité, Germany)*

PLENARY E

The new old:
rethinking the future of known diseases

Day 3 - Friday 22 November, 9:00-10:30

As the impact of COVID-19 diminishes, the world has seen a resurgence in various infectious diseases, possibly driven by ecological, behavioural and microbiological factors. Increased human encroachment into natural habitats and higher population densities are reviving diseases such as tuberculosis and spreading vector-borne viruses, aided by climate change. Behaviourally, for example a rise in unprotected sexual activity and decreased vaccination uptake are fuelling sexually transmitted infections and outbreaks of vaccine-preventable diseases like measles. Additionally, post-pandemic genetic changes in microbes are contributing to the resurgence of bacterial infections.

In this session, experts from these three areas will discuss the complex causes of the re-emergence of infectious diseases, and why understanding these causes can help public health professionals to effectively manage and prevent emerging health threats. Nienke Beerlage-De Jong, assistant professor at the University of Twente, will provide examples of rising vector borne diseases or zoonosis influenced by behavioural changes. The Polish sociologist Tomasz Sobierajski will examine how post-pandemic human behavioural and biological changes have influenced the rise of the transmission of diseases such as STIs, whooping cough or measles. Maria Wessman, Head of section bloodborne and sexually transmitted diseases at SSI, will explain for example how internal microbiological factors and genetic evolution, as well as post-pandemic microbiological interactions, may explain the resurgence of some diseases.

Chairs: Jacobo Mendioroz Peña *(Public Health Agency of Catalonia, Spain)*, Nadine Zeitlmann *(RKI, Germany)*

Speaker: Nienke Beerlage-De Jong *(University of Twente, Netherlands)*, Maria Wessman *(SSI, Denmark)*,
Tomasz Sobierajski *(University of Warsaw, Poland)*

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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.

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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 PRESENTER-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 PRESENTER-led discussion with the audience (~5 min).

Abstract review

Albania

Kujtim Mersini

Austria

Ziad El-Khatib

Belgium

Amber Litzroth
Javiera Rebolledo
Pieter-Jan Ceyssens
Tarik Derrough
Wesley Mattheus

Canada

Jane Buxton
Lisa Jensen
Lisa Hansen

China

Chang-Jun Bao

Croatia

Mirjana Lana Kosanovic Licina
Sanja Kurecic Filipovic
Zvjezdana Lovric Makaric

Czechia

Hana Orlíková
Michaela Špacková
Monika Liptakova
Vladimír Príkazský

Denmark

Ana Paula Coutinho Rehse
Andreas Petersen
Jussi Sane
Kåre Mølbak
Lasse dam Rasmussen
Pikka Jokelainen
Stine Nielsen

ECDC

Adam Roth
Agoritsa Baka
Amelie Plymoth
Andreea Badache
Angeliki Melidou
Angelo D'Ambrosio
Anke Kohlenberg
Anna Machowska
Barbara Albiger
Barbora Kinross
Bruno Christian Ciancio
Carlos Carvalho
Carmen Varela Santos
Diamantis Plachouras
Eeva Broberg
Emmanuel Robesyn
Ettore Severi
Francesco Innocenti
Francois-Xavier Lamy
Gaetano Marrone
Helena De Carvalho Gomes
Howard Needham
Ines Steffens
Irina Ljungqvist
Joana Gomes Dias
John Kinsman
Julien Beauté
Katie Palmer
Katriina Willgert
Konstantinos Koutentakis
Leah Martin
Luis Alves de Sousa
Luisa Hallmaier-Wacker
Maria Keramarou
Maximilian Riess
Nana Mebonia
Nathalie Nicolay
Netta Beer
Olov Svartstrom
Otilia Mårdh
Pawel Stefanoff
Phillip Zucs
Piotr Kramarz
Rene Niehus
Sabrina Bacci
Sarah Earnshaw Blomquist
Silvia Funke
Stefania De Angelis
Tamas Bakonyi
Theresa Enkirch
Tommi Kärki
Veronica Cristea

Egypt

Ahmed Zaghloul

Finland

Erika Lindh
Hanna Nohynek
Lotta Siira

France

Alexandra Septfons
Angie Rose
Henriette De Valk
Jean-Sebastien Casalegno
Jourdan Nathalie
Lauriane Ramalli
Noël Harold

Germany

Anita Plenge-Bönig
Annette Jurke
Ariane Halm
Bettina Rosner
Dagmar Rimek
Florian Burckhardt
Gamze Aktuna
Gerhard Falkenhorst
Hofmann Alexandra
Ivo Foppa
Jamela Seedat
Johann Fontaine
Johannes Dreesman
Julia Fitzner
Katharina Alpers
Klaus Jansen
Lutz Ehlkes
Maylin Meincke
Michael Brandl
Miriam Wiese-Posselt
Nadine Zeitlmann
Naomi Boxall
Philipp Zanger
Raskit Lachmann
Sandra Dudareva
Sing Andreas
Soeren Becker
Sofie Gillesberg Raiser
Sophie Rettenbacher-Riefler
Tanja Charles
Ute Rexroth
Viviane Bremer
Walter Jan

Abstract review

Greece
Andreas Mentis
Dimitrios Paraskevis
Georgia Gioula
Georgina Tzanakaki
Lemonia Skoura
Maria Exindari
Rengina Vorou
Vana Sypsa

Hungary
Agnes Hajdu

Ireland
Anne Carroll
Eve Robinson
Lisa Domegan
Patricia Garvey

Israel
Michael Edelstein

Italy
Antonietta Filia
Claudia Lucarelli
Domenico Martinelli
Enrico Girardi
Fortunato D’Ancona
Lara Ricotta
Loredana Ingrosso
Patrizio Pezzotti
Saverio Caini

Latvia
Dzintars Mozgis

Lebanon
Zeina Farah

Luxembourg
Anne Vergison
Cinthia Menel Lemos
Joel Mossong
Martine Debacker

Malta
Tanya Melillo

Namibia
Christian Winter

Netherlands
Alma Tostmann
Barbara Schimmer
Ingrid Friesema
Kimberley Benschop
Mirjam Knol
Sonia Boender
Susan Hahné
Zsofia Igloi

Nigeria
Aisha Ahmed Abubakar

Norway
Preben Aavitsland
Robert Whittaker
Umaer Naseer

Pakistan
Imran Nisar

Poland
Karolina Zakrzewska
Magdalena Ankiersztejn-Bartczak
Magdalena Rosinska
Maria Ganczak

Portugal
Ana Miguel Matos
Carlos Matias Dias
Claudia Palladino
João Paulo Gomes
Luisa Peixe
Raquel Sá-Leão
Sandra Guedes
Vitor Borges

Romania
Alina Daniela Zaharia
Delia Herghea
Gabriela Loredana Popa
Irina Brumboiu
Madalina Preda
Mircea Popa

Saudi Arabia
Bassel Molaeb

Slovenia
Maja Subelj
Mario Fafangel
Sanja Vuzem

Spain
Elsa Negro-Calduch
Jacobo Mendioroz
Margarita Riera
Maria Dolores Fernandez Garcia
Silvia Herrera León
Silvia Jiménez-Jorge
Zaida Herrador

Sweden
Emmi Andersson
Hong Fang
Moa Rehn
Nils Anders Tegnell

Switzerland
Hannah Lewis
Ranya Mulchandani
Sudre Philippe

Turkey
Fehminaz Temel
Levent Akin

Ukraine
Olena Nesterova

United Kingdom
Alison Sykes
Androulla Efstratiou
Aoife Doyle
Caoimhe Mckerr
Christopher Williams
Daniel Rhys Thomas
Gavin Dabrera
Giri Shankar
Louise Coole
Malorie Perry
Mari Morgan
Naomh Gallagher
Petra Manley

United States
Peter Gerner-Smidt
Richard Goering

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FIRESIDE SESSIONS

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FIRESIDE SESSION 1

Day 1 | 11.00 - 12.30

Healthcare associated infections

PRESENTER

Mirco Sandfort

ABSTRACT

Nosocomial outbreak of Ralstonia pickettii infections linked to sodium chloride in Germany since September 2023 and challenges in medical product-related outbreak investigations

M. Sandfort[1]
A. von Laer [2], I. Eichhorn [3], S. Wolf [4], M. Driller [5], V. Bajic [6], S. Fuchs [7], S. Kampmeier [8], S. Engelhart [9], N. Mutters [10], E. Cónsul-Tejero [11], J. Zündorf [12], M. Hogardt[13], T. Eckmanns [14], S. Haller [15]

[1] Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[2] Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
[3, 4, 5, 6 , 7] Genome Competence Centre (MF 1), Robert Koch Institute, Berlin, Germany
[8] Institute for Hygiene and Microbiology, University of Würzburg, Würzburg, Germany|Infection Control and Antimicrobial Stewardship Unit, University Hospital Würzburg, Würzburg, Germany
[9, 10] Institute for Hygiene and Public Health, University Hospital Bonn, Bonn, Germany
[11, 12] Non-Active Medical Devices, Federal Institute for Drugs and Medical Devices (BfArM), Bonn, Germany
[13] Institute of Medical Microbiology and Infection Control, University Hospital Frankfurt, Goethe University, Frankfurt am Main, Germany | German National Consiliary Laboratory on Cystic Fibrosis Bacteriology, Frankfurt am Main, Germany
[14, 15] Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND

In December 2023, WHO reported a nosocomial outbreak of Ralstonia pickettii in Australia by contaminated sodium chloride-solution from an Indian manufacturer, causing bacteraemia. Concurrently, the Antibiotic Resistance Surveillance, a Germany-wide voluntary laboratory network, had captured five R. pickettii-positive blood cultures since September 2023 versus 0-1 annually in 2019-2022. This prompted an outbreak investigation to identify the infection source.

METHODS

Case definition: A person with any material positive for R. pickettii (possible case). We implemented nationwide R. pickettii surveillance, performed Illumina whole genome-sequencing on isolates and core genome-multilocus sequence typing-based cluster detection (2499 target genes), and gathered case data, including common exposures to medical products.

RESULTS

Since September 2023, we have detected 24 possible cases and could sequence 16 isolates. Six isolates clustered within a 3-allele difference, differing from Australian outbreak sequences by ≥26 alleles. These cases were considered confirmed cases and occurred in three hospitals across three federal states between 10/2023-3/2024. Five cases suffered from severe infection. Exposure to sodium chloride-solution was the only common link between all cases. Patient files did not specify the products. Hospital purchase lists did not generally specify supplied wards. Comparing hospital-level purchases, two products by two manufacturers matched across the three hospitals. Lot number lists from two hospitals revealed one match per product. The third hospital's list is pending due to non-digitalized documentation. Sterility tests for both lots were requested from both manufacturers, with results still pending.

CONCLUSIONS

Surveillance in Germany sensitively detected an R. pickettii outbreak, possibly linked to sodium chloride-solution. Automated patient-level documentation of exposure to all medical product lots including saline solution and mandates for public retain sample testing could fasten identification of contaminated products in future outbreaks.

KEYWORDS: Ralstonia pickettii,Sodium Chloride,Disease Outbreaks,Cross Infection
ABSTRACT ID: 468
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FIRESIDE SESSION 1

Day 1 – 11.00-12.30
Healthcare associated infections

PRESENTER
Miroslava Mihalkova

ABSTRACT

Disparity in surgical site infection risk according to ethnicity and Index of Multiple Deprivation in England, Jan 2010 – Dec 2019.

M. Mihalkova[1]
S. Thelwall [2], P. Harrington [3], C. Wloch [4], T. Lamagni [5], I. Hiironen [6]

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BACKGROUND
The role of ethnicity and socio-economic status in surgical outcomes has been implicated in several studies. The UK Health Security Agency (UKHSA) SSI Surveillance Service (SSISS) data from National Health Service (NHS) hospitals in England were used to assess the evidence for differential risk of surgical site infection (SSI).

METHODS
SSISS data following hip replacement, knee replacement, large bowel, breast, coronary artery bypass graft (CABG) and cardiac (non-CABG) surgery between 2010 and 2019 were matched to Hospital Episode Statistics (HES) on NHS number to ascertain patient ethnicity and Index of Multiple Deprivation (IMD). Patients were prospectively followed up for up to 30 days or 1 year (if an implant is used) to detect inpatient and re-admission SSIs based on international standard case definitions. Multivariable logistic regression analyses were carried out to investigate association between the risk of SSI and ethnicity and IMD (white ethnicity being the reference group) adjusting for patient and surgery related risk factors.

RESULTS
Ethnicity and IMD data were available for 87.4% and 86.1% of 972,422 SSISS records, respectively. Patients with mixed ethnicity had increased adjusted odds of SSI following large bowel (aOR=2.04; 95%CI: 1.10-3.76) and breast surgery (aOR=4.53; 1.04-19.78); no significant difference in SSI risk was observed for other groups of ethnicity nor other surgical categories.Living in most deprived areas (IMD decile 1) was associated with increased adjusted odds of infection in breast surgery versus IMD 10 (aOR=3.78; 1.37-10.41). A crude association was observed in hip and knee replacement and cardiac (non-CABG) surgery; however these associations did not persist after adjustment.

CONCLUSIONS
These preliminary results provide suggestive evidence of the association between social determinants of health and SSI risk in some surgical categories.

KEYWORDS: Surgical Wound Infection, Risk Factors, Ethnicity, Epidemiology
ABSTRACT ID: 557

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FIRESIDE SESSION 1

Day 1 – 11.00-12.30

Healthcare associated infections

PRESENTER

Antoine Salzmann

ABSTRACT

Inclusion of Emergency Department attendance on onset status classification of Clostridioides difficile infections (CDI): A revised definition and implications on hospital-onset CDI cases in England

A. Salzmann[1]
O. Nsonwu [2], C. Bell [3], D. Chudasama [4], C. Brown [5], D. Jeyaratnam [6], R. Hope [7]

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BACKGROUND

Hospitalisations often occur after attendance to an Emergency Department (ED). Infection prevention control are a major challenge in EDs due to its high-paced and high-volume nature, with mounting pressure as ED activity continues to rise. Surveillance of Clostridiodies difficile infections (CDI) is mandated in England, with cases categorised as either Hospital-onset (HO) or Community onset (CO). Ensuring the accurate categorisation of cases is key in monitoring the source of these infections.

METHODS

CDI cases reported to UKHSA Mandatory Surveillance Data Capture System (DCS) between January 2020 and December 2023 were linked to the Emergency Care Dataset (ECDS) to identify ED attendances within 1 day of the DCS-recorded hospital admission date. We compared the existing definition of HO; greater than two days from hospital admission to positive specimen date, against a modified definition where ED arrival date is used as the start point, when cases are admitted from ED.

RESULTS

During this period, 58,084 CDI cases were reported to the DCS. Of these, we identified 34,911 (60.1%) with a prior ED attendance. Using the conventional onset definition, 25,014 (43.1%) were ascertained as HO CDI cases, which increases to 26,587 (45.8%) once ED attendance was included, 6.3% increase. We note more cases shifting to HO classification annually, 2020–4.0%; 2021–5.8%; 2022–7.3% and 2023 7.2%. This coincides with increased duration in EDs in our cohort, with 3.7% of attendances spanning over one day in 2023 compared to 0.23% in 2020.

CONCLUSIONS

We observe an increasing proportion of CDI cases reclassified to HO from CO when adjusting current definitions to include duration in ED prior to hospitalisation. Not only does this reclassification have implications on accurate reporting, but interventions.

KEYWORDS: Clostridioides difficile,Hospital-Acquired Infections,Emergency Service, Hospital,Infection Control
ABSTRACT ID: 498
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FIRESIDE SESSION 1

Day 1 – 11.00-12.30

Healthcare associated infections

PRESENTER
Paulius Greicius

ABSTRACT

Hybrid plasmid caused a rapid increase of OXA-48 K. pneumoniae in Lithuania

P. Greicius [1]
[1] National Public Health Surveillance Laboratory

BACKGROUND

In 2023 Lithuania noticed a rapid increase in OXA-48-like carbapenemase producing Enterobacterales. An initial genomic investigation revealed a multi-cluster multi-hospital OXA-48 K. pneumoniae outbreak affecting most regions of the country. Such a sudden emergence of multiple clusters of OXA-48 carriers prompted us to expect a plasmid outbreak. To identify the plasmid, long-read sequencing of cluster representatives was conducted.

METHODS

All clinical carbapenem-resistant Enterobacterales are referred to the National Reference Laboratory in Lithuania. K. pneumoniae isolates confirmed to carry OXA-48-like-encoding genes by PCR were sequenced using Illumina MiSeq. Clusters were determined with core-genome multi-locus sequence typing. Isolates with < 5 allelic differences were considered to belong to the same cluster. Cluster representatives were further sequenced using long-read Nanopore technology for plasmid determination.

RESULTS

A total of 162 K. pneumoniae isolates from at least 21 Lithuanian hospitals were confirmed to carry OXA-48 and three clusters were identified: ST45 (n=53), ST392 (n=47), and ST395 (n=43). Analysis of short read assemblies also revealed that 149 of these isolates also carried iucABCD, iutA genes coding for the virulence factor aerobactin. Follow-up long read sequencing demonstrated that the OXA-48 gene and aerobactin gene locus are located on a 303 kb IncH1B hybrid plasmid.

CONCLUSIONS

The sudden onset of a multi-cluster, multi-hospital outbreak of OXA-48 producing K. pneumoniae is attributed to the spread of an IncH1B plasmid carrying this carbapenemase gene. In addition, same plasmid also carries the gene locus for virulence factor aerobactin which likely contributed to the success of the pathogen. In light of these findings, an epidemiological investigation was launched to identify factors enabling the spread of this plasmid.

KEYWORDS: Klebsiella pneumoniae,Cluster Analysis,Plasmids,Carbapenem-Resistant Enterobacteriaceae,High-Throughput Nucleotide Sequencing,Nanopore Sequencing
ABSTRACT ID: 528
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FIRESIDE SESSION 1

Day 1 – 11.00-12.30

Healthcare associated infections

PRESENTER

Dimple Chudasama

ABSTRACT

Reducing healthcare associated Gram-negative bloodstream infections: An England Perspective

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[2, 3, 4, 5, 6] UKHSA

BACKGROUND
Reducing the infections associated with antibiotic resistance is paramount in the campaign to maintain the effectiveness of antibiotics. Hence, an initiative as part of the 2019-2024 UK Antimicrobial Resistance National Action Plan (NAP) set out to halve the number of Healthcare associated (HA) Gram-negative bloodstream infections (GNBSI), responsible for ~80% of AMR in infections caused by priority pathogens.
We review the challenges and progress in England.

METHODS
Data on the 3 priority GNBSIs (Escherichia coli, Klebsiella species, and Pseudomonas aeruginosa) meeting the HA definition are published through UKHSAs mandatory BSI surveillance reports. For earlier data (<2018/19) Hospital Episode Statistics (HES) and UKHSA's Secondary Generation Surveillance System (SGSS) were used to generate a proxy for the HA burden.

RESULTS
53,756 GNBSI were reported in 2016/17, of which we estimate 23,037 (42.9%) met the HA definition. We report in 2023/24 HA GNBSI counts to be 22,687. Incidence reached their peak in 2019/20 (24,363) before sharply declining by 19.7% (n=19,568) in 2020/21 coinciding with the COVID-19 pandemic, before resuming its upward trajectory, but remained below pre-pandemic levels. The sharp declines were mostly from reductions in E. coli cases.Multiple commitments and deliverables were developed to underpin the efforts to achieve reductions in HA GNBSI.

CONCLUSIONS
There is limited evidence on achievable reductions in HA GNBSIs, with some reports suggesting ~20% possible. We note substantial reductions in incidence, an indirect consequence of the COVID-19 pandemic. Furthermore, the disruption of the pandemic hindered efforts to implement targeted measures to support this initiative. Lessons and learnings from the last few years, including taking forward improvements achieved through deliverables and commitments will be instrumental in development of further initiatives.

KEYWORDS: National Action Plan, Gram-negative bloodstream infections
ABSTRACT ID: 562
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FIRESIDE SESSION 1

Day 1 – 11.00-12.30

Healthcare associated infections

PRESENTER
Claudia Cozzolino

ABSTRACT

Are AI-based surveillance systems for Healthcare Associated Infections really ready for clinical practice? A systematic review and meta-analysis

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S. Mao [2], A. Gagliani [3], V. Baldo [4]

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BACKGROUND
Healthcare associated infections (HAIs) are a global public health concern, causing significant clinical and financial burdens. Despite advances, surveillance methods are often manual and resource-intensive, leading to underreporting. Automation, particularly through AI, holds promise, yet adoption challenges persist. This review aims to evaluate the performance and impact of AI in HAI surveillance, considering technical, clinical, and implementation aspects.

METHODS
We conducted a systematic review of Scopus and Embase databases in accordance with PRISMA guidelines. Two independent reviewers performed study selection, data extraction, and quality evaluation. We synthesized information on AI-based models for HAI detection, including their development, performances, and impact. Accuracy, AUC, sensitivity, and specificity metrics were pooled using a random-effect model, stratifying by HAI type. Our study protocol was registered in PROSPERO (CRD42024524497).

RESULTS
Of 2,834 identified citations, 249 studies were reviewed. The performances of AI models were generally high, but with significant heterogeneity between HAI type. Overall pooled sensitivity, specificity, AUC, and accuracy were respectively 0.835, 0.899, 0.864 and 0.880. About 36.7% studies compared AI system performances with others, with most achieving better or comparable results than clinical scores or manual surveillance. Less than 7.6% measured AI real impact, with the majority finding benefits. Only 30 studies deployed the model in a user-friendly tool, 9 tested it in real clinical practice.

CONCLUSIONS
Although AI shows promising performance in HAI surveillance, its adoption in clinical practice remains uncommon. Despite spanning over a decade, retrieved studies offer scant evidence on reducing burden, costs, and resource use. This prevents their potential superiority over traditional or simpler automated surveillance systems from being fully evaluated. Further research is necessary to assess impact, enhance interpretability, and ensure reproducibility.

KEYWORDS: Artificial intelligence,Healthcare associated infections,Infection control,Surveillance,Machine learning
ABSTRACT ID: 340
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FIRESIDE SESSION 2

Day 1 – 11.00-12.30

COVID – 19

PRESENTER

Georgios Varotsis

ABSTRACT

Evaluation of the effectiveness of COVID-19 vaccination appointment letters on uptake across sociodemographic groups: A regression discontinuity analysis in Sweden

G. Varotsis[1]
U. Hammar [2], C. Bonander [3], P. Lundmark [4], B. Kennedy [5], M. Gomez [6], M. Martinell [7], O. Dyar [8], A. Sarkadi [9], R. Kristiansson [10],
H. Svaleryd [11], T. Fall [12]

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[2, 4, 5, 12] Department of Medical Sciences, Uppsala University
[3] School of Public Health and Community Medicine, University of Gothenburg
[6] Department of Clinical Sciences in Malmö, Lund University Diabetes Centre
[7, 10] Department of Public Health and Caring Sciences, Uppsala University
[8, 9] Child Health and Parenting (CHAP), Department of Public Health and Caring Sciences, Uppsala University
[11] Department of Economics, Uppsala University

BACKGROUND
Ensuring high vaccination coverage across sociodemographic groups is vital, particularly during a pandemic. However, assessing the impact of vaccination campaigns through observational data remains demanding. To address this, our study adopts a quasi-experimental methodology to evaluate the effect of pre-booked appointment letters on COVID-19 vaccine uptake across demographics.

METHODS
In Uppsala County, Sweden, those born between 1962 and 1971 received COVID-19 vaccination appointment letters, while younger residents were prompted to self-book via SMS. Using Regression Discontinuity Design, we leveraged the intervention cutoff at age 50 to compare the effectiveness of the appointment letters to the SMS campaign on vaccine uptake across sociodemographic groups. Our analysis included 93 855 individuals born between 1962-1981. Vaccination within 90 days post-eligibility served as the primary outcome. We also conducted analyses to assess household spillover effects between partners and negative control analyses using neighbouring counties.

RESULTS
We found evidence of a policy effect at the age 50 threshold, with adults just above the cutoff having 30% (95 % CI 10%– 53%) higher odds of receiving vaccination than those just below. On an absolute scale, this corresponded to a 1.97 percentage point rise (95% CI 0.45–3.50) in coverage. Subgroup analysis identified intervention effects among those in high-risk groups, males, individuals with lower educational attainment, foreign-born individuals from low-trust countries and >10 years in Sweden, and low-income earners. No effects were found in the control counties, nor did we find any household spillover effects.

CONCLUSIONS
Pre-booked appointment letters are more effective than self-booking for boosting COVID-19 vaccination uptake, particularly in sociodemographic groups with low immunization coverage. These findings advocate for prioritizing appointment letters over self-booking as they can foster equitable vaccine distribution amid a pandemic.

KEYWORDS: COVID-19,Immunization Programs,Appointments and Schedules,Sociodemographic Factors,
Regression Analysis
ABSTRACT ID: 105
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FIRESIDE SESSION 2

Day 1 – 11.00-12.30

COVID – 19

PRESENTER
Anne Huiberts

ABSTRACT

Effectiveness of Omicron XBB.1.5 vaccine against SARS-CoV-2 Omicron XBB and JN.1 infection in a prospective cohort study in the Netherlands, October 2023 to April 2024

A. Huiberts[1]
C. Hoeve [2], B. de Gier [3], J. Cremer [4], B. van der Veer [5], H. de Melker [6], J. van de Wijgert [7], S. van den Hof [8], D. Eggink [9], M. Knol [10]

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[7] University Medical Center Utrecht (UMCU)|National Institute for Public Health and the Environment (RIVM)

BACKGROUND

We estimated vaccine effectiveness (VE) of XBB.1.5 vaccination against self-reported SARS-CoV-2 infection between 9 October 2023 and 21 April 2024 among adults who had previously received primary vaccination and at least one booster vaccination.

METHODS

XBB.1.5 vaccine-eligible participants of an ongoing prospective cohort study (VAccine Study COvid-19; VASCO), collecting questionnaire and serology data, were included in the analysis. VE was estimated using Cox regression with XBB.1.5-vaccination as time-varying exposure and adjustment for age group, sex, education level, medical risk condition and infection history. The variant of infection was determined by sequencing of viral genetic material present in positive self-tests.

RESULTS

Of 24,728 included participants, 4,085 reported an infection. Variants identified in sequenced self-tests (n=661) were Omicron XBB (26%), Omicron BA.2.86 (71%, of which 402 [85%] subvariant JN.1), and other Omicron variants (2%). The proportion of BA.2.86 increased from 6% in the first week of the study period to 100% in January 2024. Overall VE was 37% (95%CI:27-46) in 18-59-year-olds and 42% (95%CI:37-46) in 60-85-year-olds. VE estimates were lower 7-12 weeks after vaccination compared to up to 6 weeks after vaccination among 18-59 year-olds (30% vs 44%) and 60-85 year-olds (32% vs 47%). Among 60-85-year-olds, protection against infection was highest after a prior infection <1 year ago either with (79%) or without (70%) XBB.1.5 vaccination. The same trend was seen in 18-59-year-olds (82% and 61%, respectively).

CONCLUSIONS

We showed that, during a period in which JN.1 became dominant, XBB.1.5-vaccination provided considerable protection against SARS-CoV-2 infection. Protection from prior infection in the last year was high, although SARS-CoV-2 infection still carries a risk of severe acute disease for vulnerable groups and of post-COVID condition, stressing the importance of COVID-19 vaccination.

KEYWORDS: COVID-19,SARS-CoV-2,cohort studies,vaccine effectiveness
ABSTRACT ID: 219
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FIRESIDE SESSION 2

Day 1 – 11.00-12.30
COVID – 19

PRESENTER
Camelia Savulescu

ABSTRACT

Effectiveness of COVID-19 vaccines against laboratory confirmed SARS-CoV-2 infection in the European Union multi-centre hospital healthcare worker cohort (VEBIS HCW), season 2023 – 2024

C. Savulescu[1],
A. Prats Uribe [2], K. Brolin [3], A. Uusküla [4], C. Bergin [5], C. Fleming [6], R. Murri [7], V. Zvirbulis [8], D. Zavadska [9], A. Machado[10], C. Popescu [11], R. Hrisca [12], M. Cisneros [13], M. Latorre-Millán [14], L. Lohur [15], J. McGrath [16], L. Ferguson [17], K. Gaetano Donato [18], I. Abolina [19], D. Gravele [20], V. Gaio [21], S. Florescu [22], M. Lazar [23], P. Subirats [24], L. Clusa [25], J. Sui [26], C. Kenny [27], R. Santangelo [28], D. Krievins [29], E. Barzdina [30], P. Amaral [31], A. Kosa [32], S. Pohrib [33], C. Muñoz-Almagro [34], A. Milagro [35], S. Bacci [36], A. Nardone [37], (GROUP) VEBIS HCW VE study group

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[10,21] National Institute of Health Doutor Ricardo Jorge, Lisbon
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[34] Hospital Sant Joan de Deu, Barcelona|Ciber of Epidemiology and Public Health (CIBERESP), Madrid|Universitat internacional de Catalunya, Barcelona

BACKGROUND

COVID-19 vaccination recommendations include annual (re)vaccination in healthcare workers (HCWs). COVID-19 vaccine effectiveness (VE) against SARS-CoV infection is still scarce. We measured the COVID-19 VE in hospital HCWs against laboratory confirmed SARS-CoV-2 infection, in the season 2023–2024.

METHODS

We conducted a prospective cohort study among HCWs from 13 hospitals in 7 countries. HCWs were tested weekly by PCR for SARS-CoV-2 in nasopharyngeal or saliva samples. We measured VE against infection overall, by recent infection (defined as a SARS-CoV-2 episode between 1 November 2022 and testing date) and by Omicron sublineage-dominated periods: XBB.1.5. (September – November 2023) and BA.2.86 (December 2023 – April 2024). Using Cox regression, we calculated VE as (1-hazard ratio of vaccination after September 2023)*100, adjusting for hospital, age, sex, underlying conditions, and recent infection.

RESULTS

We included in this analysis 1309 HCWs of whom 307 (23%) were vaccinated and the majority, 252 (82%), received the XBB monovalent vaccine. Of the 211 SARS-CoV-2 positive HCWs, 32 (15%) had been vaccinated. The VE was 28% (95%CI: -13; 54) overall; 36% (95%CI: -7; 62) in HCWs with no recent infection and 2% (95%CI: -138; 59) in HCWs with recent prior infection. The VE was 51% (95%CI: -7; 78) and -5% (95%CI: -86; 41) during XBB.1.5.- and Omicron BA.2.86-dominated periods, respectively.

CONCLUSIONS

The COVID-19 vaccine offered moderate to low protection against SARS-CoV-2 infection overall, higher in HCWs with no recent infection, and higher during XBB.1.5-dominated period (vaccine strain). For the low VE point estimate during BA.2.86-dominated period, we could not disentangle the effect of sublineage from that of longer time since vaccination. The VEBIS HCW cohort study provided a unique opportunity to contribute generating evidence of VE against infection.

KEYWORDS: SARS-CoV-2 Infection, Healthcare Workers, Vaccine Effectiveness, COVID 19 Vaccine, Active surveillance
ABSTRACT ID: 316
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FIRESIDE SESSION 2

Day 1 – 11.00-12.30

COVID – 19

PRESENTER

Daniel Stewart

ABSTRACT

COVID-19 vaccine effectiveness against severe outcomes for subgroups of immunosuppressed people in England, 2021 - 2022

D. Stewart[1]
H. Whitaker[2], M. Leston[3], R. Goudie[4], S. de Lusignan[5], J. Lopez-Bernal[6]
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[2, 6]Public Health Programmes, Clinical and Public Health Group, UK Health Security Agency
[3, 4, 5]Nuffield Department of Primary Care Health Sciences, University of Oxford

BACKGROUND

Studies suggest immunosuppressed patients develop a reduced antibody response to COVID-19 vaccination when compared to people who are immunocompetent. However, immunosuppression incorporates a diverse range of conditions and treatments across which vaccine effectiveness (VE) is likely to differ. Our objective was to estimate COVID-19 VE against severe outcomes (hospitalisation and death) among immunosuppressed subgroups to inform COVID-19 vaccination policy.

METHODS

We used English primary care, immunisation, death registration and hospitalisation data, to calculate adjusted VE (aVE) in three subgroups of immunosuppressed people (bone marrow compromised (BMC), solid organ transplant (SOT), immunodeficiency) and non-immunosuppressed people during winter and spring 2021/22, when immunosuppressed groups were eligible for COVID-19 vaccine dose three and four.We used a retrospective cohort study design to estimate aVE against severe outcomes: hospitalisation within 14 days or death within 28 days following a positive test for SARS-CoV-2. We adjusted for confounders including age, sex, region and deprivation classification.

RESULTS

aVE in the non-immunosuppressed group was 67.7% (95%CI 66.4%-68.9%) but was lower in all immunosuppressed subgroups. Between immunosuppressed subgroups aVE varied, with peak aVE higher in the BMC group (43.1%, 95%CI 28.8%-54.6%) than SOT (12.8%, 95%CI -25.9%-39.6%) and immunodeficiency subgroups (0.4%, 95%CI -52.1%-34.8%). Peak aVE was sustained for the BMC subgroup unlike SOT and immunodeficiency subgroups in which aVE declined with time post-vaccination.

CONCLUSIONS

Our findings suggest that COVID-19 vaccination offered the greatest protection against severe outcomes for the BMC subgroup. Variation of COVID-19 VE between immunosuppressed subgroups merits further investigation.Though limited by small numbers, these results suggest the importance of studying VE in immunosuppressed subgroups and the potential this has to inform vaccination policy, specifically around booster provision and schedules.

KEYWORDS: COVID-19, vaccine effectiveness, immunosuppression, booster vaccination
ABSTRACT ID: 201
PRESENTED BY: Daniel Stewart | United Kingdom | *danielstewart@nhs.net*

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FIRESIDE SESSION 2

Day 1 – 11.00-12.30
COVID – 19

PRESENTER
Jizzo Bosdriesz

ABSTRACT
The impact of non-pharmaceutical interventions implemented during the COVID-19 pandemic on the number of close contacts of SARS-CoV-2 cases in the Netherlands

A. Bellaar[1]
E. den Boogert[2], S. Campman[3], N. Dukers-Muijrers[4], E. Fanoy[5], H. Götz[6], I. Goverse[7], J. Heijne[8], S. van den Hof[9], I. Joore[10], T. Leenstra[11], M. Petrignani[12], S. Raven[13], K. Wevers-de Boer[14], M. Schim van der Loeff[15],
J. Bosdriesz[16]
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[2, 6, 8]Amsterdam University Medical Centers
[3, 4, 9]Public Health Service of Amsterdam|Amsterdam University Medical Centers
[5]Public Health Service of Amsterdam
[7]Municipality of Amsterdam

BACKGROUND
During the COVID-19 pandemic, various non-pharmaceutical interventions (NPIs) were introduced to curb infections, but their effectiveness has not been studied sufficiently. This study aims to assess the impact of NPIs on the number of close contacts of people who tested positive for SARS-CoV-2 during their infectious period in the Netherlands.

METHODS
This study analyzed contact tracing data from nine regional public health services (PHS) in the Netherlands between September 1st 2020 and March 28th 2021. The outcome was the number of non-household close contacts, reported by people who tested positive for SARS-CoV-2 in the infectious period before testing. The severity of NPIs measured by the Oxford COVID-19 Government Response Tracker (OxCGRT) was the main determinant (scale:0-10), with binary subscales for specific measures used in further analyses. To estimate the relative ratio of the mean number of contacts (RR) and 95%CI, we used zero-inflated negative binomial regression, adjusted for confounders.

RESULTS
232,330 cases were included (median age: 40 years [IQR:24-55], 52% female). Among them, 91,982 cases (39.6%) reported having ≥1 non-household close contact. The fully adjusted model including sex, age, country of birth, occupation, and PHS region, showed no association between the OxCGRT and number of close contacts (RR:0.99, 95%CI:0.98-1.00). However, significant effects were found for a curfew (RR:0.76, 95%CI:0.73-0.78) and primary school closing (RR:0.77, 95%CI:0.75-0.80).

CONCLUSIONS
We found significantly lower numbers of reported contacts associated with a curfew and primary school closings, but no association with the overall stringency of NPIs. Reporting bias, contact tracing capacity, and limited variance in the NPI stringency during the study period might have influenced these findings. These analyses will be expanded over a longer period to draw more generalizable conclusions.

KEYWORDS: Excess mortality, COVID-19, inequalities, individual determinants, environmental determinants
ABSTRACT ID: 450
PRESENTED BY: Jizzo Bosdriesz | Netherlands | *jbosdriesz@ggd.amsterdam.nl*

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FIRESIDE SESSION 2

Day 1 – 11.00-12.30

COVID – 19

PRESENTER
Rosaline van den Berg

ABSTRACT

Are there changes in parental attitudes towards the Dutch National Immunisation Programme after the COVID-19 pandemic? – preliminary results

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[2, 3, 4, 6]Public Health Service (GGD) Zuid-Holland Zuid, Dordrecht, the Netherlands
[5]Public Health Service (GGD) Zuid-Holland Zuid, Dordrecht, the Netherlands|National Institute for Public Health and the Environment - Centre for Infectious Disease Control, Bilthoven, the Netherlands

BACKGROUND
Vaccine uptake within the Dutch National Immunisation Programme (NIP) declined over recent years. This could be due to an increased vaccine hesitancy among parents. We hypothesized that the COVID-19 pandemic might have had a negative influence on parental attitude and participation in the NIP.

METHODS
On April 30 2024, residents of a Dutch region of approximately 460.000 inhabitants received an online questionnaire about attitudes (drivers and barriers) towards NIP, participation in the NIP and self-reported impact of COVID-19. The survey is open until May 21st; therefore, preliminary results are presented.

RESULTS
On May 13, 1186 residents with one or more child under 18 years had responded. Mean age was 42.4 years (SD 7.6), 77% female and 62% have a higher education level. Of the respondents, 187 parents (16%) had partially/not vaccinated their child(ren) within the NIP. Barriers were fear of side-effects (14%), belief of harmful substances in vaccines (13%) and distrust towards the government (12%). Drivers for NIP participation were protection of their child(ren) (83%), belief in effectiveness (78%) and preventing the spread of diseases (69%). Eighteen percent reported a change in their attitude towards NIP due to the COVID-19 pandemic. Of these, 60% indicated increased vaccine hesitancy, 38% indicated a negative influence (i.e. pre-COVID-19 positive towards NIP and after-COVID-19 negative towards NIP) and 2% indicated a positive influence.

CONCLUSIONS
Our preliminary data show that for the majority of parents the COVID-19 pandemic did not have a negative influence on parental attitude and participation towards NIP. For a select group of parents the COVID-19 pandemic increased their vaccine hesitancy. Targeted health promotion for this group is needed to regain trust and increase vaccine uptake within the NIP.

KEYWORDS: self-mastery,COVID-19,Pandemic,mental health,general population
ABSTRACT ID: 639
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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

Edward Monk

ABSTRACT

Characterisation of the SARS-CoV-2 pandemic in healthcare workers within the United Kingdom: risk factors for infection across four distinct waves within a multicentre prospective cohort study (SIREN)

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BACKGROUND
Healthcare workers (HCW) were at high risk of infection throughout the SARS-CoV-2 pandemic, compromising healthcare provision. We characterise the occupational, household and community risk factors for infection in HCW across the United Kingdom (UK), during four distinct waves.

METHODS
SIREN is a UK-based multicentre prospective cohort study of HCW, with fortnightly SARS-CoV-2 PCR testing. This analysis' observation period included the UK's second (10/2020-04/2021: alpha emergence), third (05/2021-11/2021: delta), fourth (12/2021-04/2022: omicron BA.1/BA.2) and fifth (05/2022-08/2022: omicron BA.4/BA.5) waves. Data on demographic, occupational and household characteristics were captured at enrolment, and exposure history from fortnightly surveys. Each wave's attack rate (SARS-CoV-2 positive PCR) was calculated, and adjusted odds ratio (aOR) of infection by characteristic/exposure estimated through logistic regression.

RESULTS
The second wave's attack rate was 9.1% (1,760/19,427: 9.0% of which reinfection): risk factors were working as a nurse/healthcare assistant/bedside therapist (aOR 1.29/1.39/1.41 respectively) and working on an inpatient ward (aOR 1.67). The third wave's attack rate was 6.6% (1,338/20,260: 13.1% of which reinfection): occupational risk factors were not significant, whilst living with others, particularly children (aOR 2.45), and deprivation quintile (aOR 1.42) were risk factors. The fourth wave's attack rate was 36.5% (4,356/11,937: 33.5% of which reinfection): living with others remained as the only risk factor (aOR 1.57/1.23 with/without children). The fifth wave's attack rate was 15.9% (1,035/6,503: 37.4% of which reinfection): no specific characteristics/exposures were associated with infection.

CONCLUSIONS
SARS-CoV-2 attack rates in HCW, particularly from reinfection, increased considerably after omicron emergence. Risk factors varied considerably in our population, reflecting shifting social distancing measures and population-at-risk. Understanding the impact of these measures is key to establishing how best to prevent Healthcare associated/occupational infection during future outbreaks and winter pressures.

KEYWORDS: COVID-19,Occupational exposure,Healthcare workers,SARS-CoV-2
ABSTRACT ID: 168
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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

Louise Marron

ABSTRACT

High seropositivity and COVID-19 incidence among healthcare workers in Ireland: A prospective cohort study, 2022-2023

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[6, 7, 8, 9, 10, 11]Cairde

BACKGROUND

Hospital healthcare workers (HCWs) have a high exposure risk to SARS-CoV-2 and are a high-risk population for SARS-CoV-2 infection, despite high rates of prior infection and COVID-19 vaccination. We aimed to identify factors associated with SARS-CoV-2 seropositivity and incident infection in HCWs in two hospital sites in Ireland.

METHODS

In this prospective cohort study, hospital HCWs were followed from December 2022 to September 2023. SARS-CoV-2 anti-nucleocapsid (anti-N) antibodies were measured at study enrolment. An enrolment questionnaire recorded demographic data, underlying medical risk factors for severe SARS-CoV-2 infection, and history of previous infection. Monthly questionnaires recorded self-reported incident SARS-CoV-2 infection. COVID-19 vaccination status was verified using the national COVID-19 vaccination database in Ireland. To identify factors associated with seropositivity and incident infection, we calculated adjusted Odds Ratios (aOR) using multivariable logistic regression.

RESULTS

Among 1,260 participants, 80% were seropositive, 91% had received at least one COVID-19 booster vaccine and 22% reported incident infection. HCWs aged 50 years and older were less likely to be seropositive (aOR=0.41, 95%CI 0.22-0.74). Having at least one medical risk factor for severe infection was associated with incident infection (aOR=1.67, 95%CI 1.04-2.65), as was increased time (>180 days) since last SARS-CoV-2 infection (aOR=1.86, 95%CI 1.24-2.84).

CONCLUSIONS

Despite high rates of seropositivity and vaccination coverage, hospital HCWs had a high rate of SARS-CoV-2 incident infection. Our findings suggest that COVID-19 booster vaccination programmes for HCWs should target older age groups, those with underlying medical risk factors and those with increased time since last infection (>180 days). We recommend strengthening surveillance of SARS-CoV-2 infection in HCWs to enable targeted COVID-19 vaccination programmes.

KEYWORDS: COVID-19, SARS-CoV-2, healthcare workers, vaccination
ABSTRACT ID: 237
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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

AnnaSara Carnahan

ABSTRACT

Using surveillance data to inform vaccination policy in Sweden - a comparison of ICU burden between COVID-19 and influenza during winter seasons 2022-2023 and 2023-2024

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BACKGROUND

COVID-19 and influenza cause substantial morbidity and mortality in Sweden. Seasonal vaccination against both viruses is currently recommended to risk groups. Co-administration of influenza and COVID-19 vaccines is safe, facilitates delivery, and resulted in 69% and 70% uptake, respectively, among individuals 65 years and older in Sweden 2023. To inform decisions about timing of co-administration in autumn 2024, we compared disease burden and epidemic timing of COVID-19 and influenza. Here we present the burden of ICU admissions.

METHODS

We used weekly mandatorily-reported confirmed COVID-19 and influenza cases 2022-2024 to define timing of epidemic peaks. We calculated cumulative incidence of ICU admission per 100,000 individuals among ≥65 years during peak months for both diseases: October-March 2022-2024, and December-May 2017-2018 for influenza. We compared COVID-19 and influenza, within season, and to the vaccine-mismatched severe 2017-2018 influenza season using relative risk (RR) with 95%-confidence intervals (CI).

RESULTS

COVID-19 peaked simultaneously with influenza in 2022-2023 and seven weeks before influenza in 2023-2024. Cumulative incidence of ICU admission for COVID-19 and influenza was 20 and 5.3 in 2022-2023, 15 and 4.7 in 2023-2024, and 12 for influenza in 2017-2018. ICU incidence for COVID-19 was higher than for influenza in 2023-2024 (RR:3.20, 95%CI:2.55-4.03), 2022-2023 (RR:3.81, 95%CI:3.09-4.73) and when compared to 2017-2018 (2022-2023 RR:1.72, 95%CI:1.46-2.0 and 2023-2024 RR:1.29, 95%CI:1.08-1.53

CONCLUSIONS

Since COVID-19 has contributed to higher ICU incidence than influenza, poorly timed COVID-19 vaccination is likely more detrimental than mistimed influenza vaccination. Because concurrent peaks cannot be expected, this suggests that timing of co-administered seasonal vaccination should be guided by anticipated COVID-19 peaks. Given the benefits of co-administration and the delivery schedule for updated vaccines, joint vaccination in Sweden is proposed to start in mid-October.

KEYWORDS: coronavirus,influenza human,vaccination,epidemics,health policy
ABSTRACT ID: 567
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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

Katya Kruglova

ABSTRACT

Economic burden of Healthcare associated infections: case-control study

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BACKGROUND

Healthcare associated infections (HCAIs) impose a major burden in acute care facilities by creating additional patient care costs. Costs increase for consumption of medication, procedures, and testing, as well as for extended length of stays. The clinical best practices of infection prevention and control (IPC) are essential for patient safety and have been shown to be cost-effective.

METHODS

A case-control study was used to determine the costs of HCAIs in five Canadian hospitals. Patients hospitalized between November 1, 2018, and March 31, 2021, had their medical charts reviewed. Patients who contracted an HCAI (cases) were matched with those who did not (controls). Matching was based on hospital unit, age, sex, primary diagnosis, and comorbidity. Demographic characteristics, diagnosis, HCAIs, services received, comorbidities, and costs pertaining to the relative level of resources were collected. Descriptive and inferential analyses were performed.

RESULTS

To date, 190 case-control pairs have been identified. Preliminary analyses demonstrate excellent matching between cases and controls for: sex (both are 51% male), age (mean age is 71 years for both), principal diagnosis, and comorbidities. Mann-Whitney U tests indicated cases had significantly higher costs compared to controls (p=.001) representing a $1576 difference per patient stay. Of the HCAIs identified, Methicillin-resistant Staphylococcus aureus (MRSA) had the highest costs to treat compared to controls. Multivariate analyses controlling for length of stay confirm these findings.

CONCLUSIONS

This study revealed the economic burden attributable to HCAIs in patients with varying levels of complexity of care and services provided. Coupled with the avoided indirect costs of lowered quality of life, this information reinforces the need to invest in IPC programs.

KEYWORDS: innovation,long-term care,COVID-19,secondary data analysis
ABSTRACT ID: 371
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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

Eleanor Blakey

ABSTRACT

Emerging trends in hospital admissions for necrotising fasciitis in England, 2018-2023

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BACKGROUND

Following international and anecdotal domestic reports of post-COVID-19 pandemic increases in necrotising fasciitis (NF), we investigated trends, patient demographics and microbial aetiology of hospital admissions for NF in England utilising new data-linkage platforms.

METHODS

Using UKHSA's 'Unified-Infection-Database' linkage platform, NF hospital admissions (ICD-10: M72.6) between 01/01/2018 and 31/12/2023 were extracted and linked to microbiology specimen data within -1/+7 days admission. Percentage 30-day all-cause case-fatality rates (CFR) were determined. Trends were assessed by patient demographic, (residence-based) socioeconomic deprivation and species. Odds ratios (aOR) were adjusted by age, sex, and year (reference: 2018).

RESULTS

Between 2018-2023, 7,737 NF cases were identified; median age was 57.5y (range; 0-99y); 55.5% (n=4,300) were men. Patients living in the most deprived decile represented the highest percentage of admissions (16.1%, n=1,392).Incidence was 1.0/100,000 population per-year between 2018-2021, before increasing to 1.5/100,000 in 2023. Annual CFR declined from 14.3% (95%CI:14.1-14.4%) to 12.2% (95%CI:12.0-12.3%; aOR: 0.82, 95%CI:0.79-0.84; p<0.0001) between 2018-2023. Microbiology records were available for 2,672 (34.5%) cases; 40.7% (n=1,087) cases indicated polymicrobial infection. Group A Streptococcus (GAS) was the most frequently identified species (21.3%; n=1,222), followed by Escherichia coli (10.4%; n=597), and Staphylococcus aureus (10.3%; n=594).GAS NF increased over time, from 6.5% (2018) to 15.8% cases (2023). Substantial elevations in GAS NF occurred between June-2022 (19.5%; n=24) and August-2023 (31.5%; n=45), peaking in January-2023 (44.2%; n=80).

CONCLUSIONS

Marked increases in NF admissions were observed from 2021, a similar picture to other European countries. Microbial aetiology varied over time, with increases of GAS in NF noticeable during GAS upsurges (2022-2023). Further assessment of risk factors and of presentations to healthcare is needed to better understand these trends and opportunities for improved NF outcomes.

KEYWORDS: Epidemiology,Necrotising Fasciitis,Healthcare Admissions,Group A Streptococcus
ABSTRACT ID: 210

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FIRESIDE SESSION 3

Day 1 – 14.00-15.30

Burden of disease

PRESENTER

Yura K. Ko

ABSTRACT

Unraveling the "indirect effects" of interventions against malaria endemicity: A systematic scoping review

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[7, 9]Mount Kenya University
[8, 10]Karolinska Institutet

BACKGROUND
There is an urgent need to maximize the effectiveness of existing malaria interventions and optimize the deployment of novel countermeasures. When assessing the effects of interventions against malaria, it is imperative to consider the interdependence of people and the resulting indirect effects. For instance, in malaria-endemic settings, a decline in the number of malaria-infected individuals or mosquitoes will reduce parasite reservoirs and means of transmission in a community, leading to a lower possibility of infection among all community members. However, the scientific literature on malaria interventions that explicitly differentiate and thoroughly analyze their indirect effects is currently limited.

METHODS
Here, we conducted a scoping review of existing literature on the indirect effects of malaria interventions. We searched PubMed, Web of Science, and EMBASE by title and abstracts. In addition, for grey literature, we searched OAIster by keywords. Searches were conducted in June 2023.

RESULTS
We retrieved 31 articles and observed an increase in the number of studies that measured the indirect effects of malaria interventions in recent years. We outline eight comparative schemes by which indirect effects of malaria interventions can potentially be quantified, and propose standardized terms for describing indirect effects. We further support the use of mathematical models to inform the evaluation of indirect effects of malaria interventions.

CONCLUSIONS
Incorporating assessment of indirect effects in future trials and studies may provide insights to optimize the deployment of existing and new interventions, a critical pillar in the current fight against malaria globally. In addition, evidence about the cost-effectiveness of interventions, taking into account the indirect effects, will lead to better-informed decisions by policymakers.

KEYWORDS: malaria,indirect effects,spillover effects,community effects,Plasmodium
ABSTRACT ID: 159
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FIRESIDE SESSION 4

Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER

Emily D. White

ABSTRACT

Multi-country outbreak of Salmonella Enteritidis related to chicken meat from Poland in 2023 – the Danish perspective

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BACKGROUND

Despite Salmonella Enteritidis being eradicated from chickens in Denmark since 2013, the pathogen still causes significant foodborne illness in Denmark and Europe. In July 2023, Denmark and Austria concurrently reported two genetically distinct human outbreaks of Salmonella Enteritidis ST11. The Danish outbreak investigation aimed to identify the vehicle(s) in order to implement control measures.

METHODS

Cases were defined as persons with laboratory-confirmed S. Enteritidis, matching the Danish (outbreak-1) or Austrian (outbreak-2) strain (≤7 allelic differences), based on core genome Multilocus Sequence Typing (cgMLST) between 01.01.2023-01.10.2023 in European Union/European Economic Area and United Kingdom. The investigation included cgMLST comparison of human, environmental and food isolates collected in Austria and Denmark. Interviews with cases, traceback and sampling of food products were performed and analyzed descriptively.

RESULTS

Internationally, 257 cases across 12 countries fulfilled the case-definition. In Denmark, we identified one (outbreak-1) and 28 (outbreak-2) cases; 52% male, median age 29.5 years (Range: 9-98 years), distributed across the country. Interviews showed that 96% (24/25) Danish cases had consumed chicken products ≤7 days prior to disease onset. The outbreak-1 strain was detected in two chicken samples. Furthermore, samples from one restaurant matched both outbreak strains (environmental and food). All food samples were traced-back to Poland.

CONCLUSIONS

We identified imported chicken from Poland as the vehicle of widespread S. Enteritidis ST11 outbreaks. Effective international and cross-sector collaboration, was crucial to identifying the commonly consumed and widely distributed product. In Denmark, recall of specific chicken products from Poland were conducted and no S. Enteritidis outbreaks have been detected since. This investigation exemplifies how ongoing collaboration within European governments, regulatory bodies and industry is needed to mitigate Salmonella risks and safeguard public health.

KEYWORDS: Salmonella Enteritidis, Foodborne Outbreaks, Whole genome sequencing, Trace-back investigation, International, chicken
ABSTRACT ID: 464
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FIRESIDE SESSION 4

Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER

Luke McGeoch

ABSTRACT

Large outbreaks of Cryptosporidium linked to lamb contact events on working farms in England: A public health call to break the cycle

L. McGeoch[1]
D. McMichael[2], O. McManus[3], M. Bardsley[4], S. Suleman[5], A. Chirita[6], D. Ogunsumi[7], S. Bartlett[8], L. Chenciner[9], C. Sawyer[10], G. King[11], J. Banks[12], S. Balasegaram[13], A. Fernandes[14], J. DuqueminSheil[15], R. Chalmers[16], C. Chatt[17], C. Anderson[18], R. Puleston[19], C. Humphreys[20], K. Paranthaman[21]
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BACKGROUND
Contact with newborn lambs is a recognised risk factor for Cryptosporidium parvum infection. In recent years, working farms ordinarily closed to the public have invited visitors during the lambing season. These premises are not subject to the same oversight as farms permanently open to visitors. We assessed the public health burden and investigation findings of three of the largest recorded C. parvum outbreaks linked to lambing events on working farms in England, all occurring in 2023-24.

METHODS
Outbreak investigations included microbiological testing of visitors and animals, epidemiological investigations for case-finding and risk factors using online questionnaires, and environmental health inspections. In two outbreaks, analytical studies were undertaken to investigate exposure-disease associations. Key findings were collated.

RESULTS
The three farm events offered lamb contact and feeding, receiving 2,400-8,039 visitors. Cryptosporidium cases (probable or laboratory-confirmed) among visitors ranged from 264-767, with microbiological and epidemiological evidence for C. parvum transmission from lambs. Cases were predominantly women aged 18-49 and children aged <16 years. Across two outbreaks, 42% of cases reported seeking healthcare; overall, 4.6% were hospitalised. Visitors described cuddling and feeding lambs. Environmental investigators reported inadequate infection prevention and control (IPC) practices, including concerns regarding handwashing facilities, animal health, animal handling and feeding, and staff preparedness.

CONCLUSIONS
Investigations of these three large outbreaks, involving a high healthcare burden, highlighted inadequate IPC practices as the primary concern. Event organisers, particularly those newly diversifying into lamb contact events, may underappreciate the risk of Cryptosporidium transmission and IPC measures required. We recommend strengthened regulation, communication and planning with stakeholders to ensure organisers understand this risk and are compliant with standards, and public engagement to support safe event attendance and adherence to IPC measures.

KEYWORDS: Hemolytic-Uremic Syndrome,Escherichia coli,Shiga-Toxigenic Escherichia coli,Public Health Surveillance,Gastroenteritis
ABSTRACT ID: 342
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Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER

Anja Schoeps

ABSTRACT

Nosocomial listeriosis outbreak in patients on oral glucocorticoids: time to rethink supply, preparation, and consumption of sausages and other deli meats in the health care setting in Germany

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BACKGROUND
Listeria monocytogenes causes infections via contaminated food, posing low risk to the general population, but putting the immunocompromised at increased risk of severe illness. In March 2023, within eight days, L. monocytogenes was isolated from blood (n=2) or pleural fluid (n=1) of three febrile patients on synthetic glucocorticoids at one tertiary hospital in Germany. This study aimed to identify the infection source and assess implications for food safety guidelines for immunocompromised patients.

METHODS
We assessed dietary history to identify contaminated food sources and collected food and environmental samples from the hospital and its meat supplier. Whole genome sequencing of patient isolates and food samples was used to confirm the source of infection.

RESULTS
On sequencing, all three patient isolates showed no differences in the core genome (cluster type CT2834). Food supply records suggested ingestion of sliced scalded sausage as the likely source, and L. monocytogenes isolated from four retained packaged sliced sausage and ham samples clustered within zero to four allele differences to CT2834. However, bacterial counts in all samples fell below the legally established European threshold of 100 CFU/gram for listeria before the end of the shelf life in ready-to-eat foods.

CONCLUSIONS
Our observations, together with systematic research that links listeriosis risk to glucocorticoid intake and numerous outbreak reports in patient groups with other conditions associated with altered T-cell immunity, highlight that a universal 100 CFU/gram threshold is insufficient for the protection of high-risk groups. We advocate for greater caution in the supply, preparation, and consumption of deli meats in German hospitals and recommend the development of dietary recommendations. In these, levels of T-cell impairment (e.g. glucocorticoid intake, pregnancy) may be one criterion to define risk groups.

KEYWORDS: Listeria monocytogenes, Listeriosis, Immunocompromised Host, Glucocorticoids, Deli Meats, Food Safety
ABSTRACT ID: 94
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FIRESIDE SESSION 4

Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER
Susanne Schjørring

ABSTRACT

International data sharing linked fish products from a Danish producer to a long-lasting Danish Listeria monocytogenes outbreak, 2019-2024

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

BACKGROUND

Listeriosis is a severe foodborne infection caused by Listeria monocytogenes, which is known to persist in production environments. Since August 2020, we have investigated an outbreak of L. monocytogenes sequence type 1607, to identify and eliminate the source. We here describe the investigation, challenged by weak epidemiological evidence, and demonstrate how sharing of information internationally was crucial for identifying the source and implementing control measures.

METHODS

We identified the outbreak using core genome multi-locus sequence typing, performed hypothesis-generating interviews, traceback-investigations, control visits at production site, including product and environmental sampling, compared sequences, and informed relevant international authorities.

RESULTS

In total, 17 cases were identified as being part of the national outbreak in Denmark 2019-2024, seven in 2023. Two patients died within 30 days of testing positive. No strong hypotheses about the source could be established after interviews with 13 patients or relatives, with a maximum of eight reporting eating sliced spiced cold-cut meat and ready-to-eat (RTE)-fish products, including cold-smoked RTE salmon products (n=4). Traceback-investigation for six cases of RTE-fish products did not point to a specific brand or supermarket chain. In July 2023, a genetic link between the Danish outbreak and a salmon producer in Denmark was identified through the Rapid Alert System for Food and Feed (RASFF). Isolates from production environment and product with a genetic match to the outbreak were obtained at control visits hereafter.

CONCLUSIONS

This investigation underlines the importance of sharing information through EpiPulse and RASFF as well as the importance of sharing data in the “One Health WGS System”. As a source could not be identified through interviews and trace-back, these were crucial for identifying the probable source and implementing control measures.

KEYWORDS: Listeria monocytogenes, WGS, Epidemiology,outbreaks,Data sharing,Infectious disease
ABSTRACT ID: 620
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Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER
Hawraa Sweidan

ABSTRACT

Unveiling the trichinellosis outbreak: pork contamination in a butcher's shop in Jahliyeh, Lebanon, November 2023 – February 2024

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[3]Ministry of Public Health (MOPH)
[4]minis|Ministry of Public Health (MOPH)

BACKGROUND
On December 4, 2023, the local authorities notified a suspected outbreak of trichinellosis in Jahliyeh (Mount-Lebanon), having approximately 6000 residents. We investigated to identify the outbreak source, estimate the magnitude, and implement preventive measures.

METHODS
We defined a suspected case as a Jahliyeh resident who experienced at least three symptoms (fever, myalgia, oedema, and/or hyper-eosinophilia), or was diagnosed by a physician, after October 1, 2023. We inspected local butcher shops and searched for suspected cases who have visited health facilities for case management or medical advice. We described suspected cases by demographic characteristic, symptoms, and possible exposures. We tested leftover food samples at the Lebanese Agriculture Research Laboratory.

RESULTS
During November – December 2023, a total of 146 suspected cases were identified, with one case confirmed via a positive muscle biopsy. Of 44 cases tested, 20 had hyper-eosinophilia (> 500). 30% (n=43) cases were hospitalized. The median age of cases was 38 years (range: 2-82), 59% were female. Almost all cases (n=144) reported purchasing meat from local butcher shop, with 86% (n=126) consuming beef or lamb but abstaining from pork, and 12% (n=18) consuming pork. Additionally, 41% (n=60) reported consuming the meat uncooked, while 48% (n=71) consumed it either fried or barbecued. Inspection of the butcher shop revealed inadequate hygiene practices and improper meat storage. Both minced and sausage beef samples contained Trichinella.

CONCLUSIONS
Our preliminary investigation suggested that contaminated beef was the vehicle of infection. The butchers were likely mixing untested pork with other types of meat. We recommend trainings of butchers on food safety and meat handling along with regular inspections. Additionally, we recommend educating the local communities on the risk associated with raw meat consumption.

KEYWORDS: Trichinellosis, outbreak, investigation, epidemiology, Lebanon
ABSTRACT ID: 309
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FIRESIDE SESSION 4

Day 1 – 14.00-15.30

Food- and waterborne diseases

PRESENTER

Andrea Parisi

ABSTRACT

Outbreak of botulism in Spain linked to a commercial refrigerated potato omelette, June–July 2023: A case-control study

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BACKGROUND

On 11 July 2023, an EU member state reported via the Early Warning and Response System two cases of botulism outside Spain who had purchased and consumed a common food item in Spain - a commercial refrigerated potato omelette (tortilla). In the following months, cases of botulism were also detected in Spain. We conducted a matched case-control study to investigate the outbreak source.

METHODS

Cases were collected through national surveillance and defined as persons developing botulism-compatible symptoms between 1 June and 31 July 2023 and being visitors or residents in Spain during their 7 days prior to symptom onset. Controls were recruited from the same primary health care centre as their respective case in a 3:1 ratio and matched on place of exposure, sex and age. In tailored surveys, cases and controls were asked about food consumption in the cases' incubation period. Odds ratios (OR) with 95% confidence intervals (CI) for the most common food items were calculated in univariable and multivariable logistic regressions (adjusted for various food items).

RESULTS

Between June and July 2023, 12 cases of botulism (8 laboratory confirmed) meeting the case definition were reported in Spain. Of those, 10 (83.3%) reported having consumed the packed tortilla in the incubation period. In the univariable regression, only this product displayed a statistically significant OR: 14.9 (95% CI: 1.8–123). Similar results were observed in the multivariable regression (OR=13.7; 95% CI 0.96-194.7).

CONCLUSIONS

Commercially refrigerated and packed tortilla was the most-likely vehicle in this botulism outbreak, although potential contamination pathways remain unknown. In the absence of microbiological food positive results, our research highlights the importance of epidemiological studies in identifying the most probable vehicle in foodborne outbreaks.

KEYWORDS: Vaccination Hesitancy,Health Personnel,COVID-19,Influenza,Human
ABSTRACT ID: 126
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FIRESIDE SESSION 5

Day 2 – 11.00-12.30

Surveillance

PRESENTER

Kehinde Akin-Akinyosoye

ABSTRACT

Temporal relationships between the sentinel community acute respiratory infection (CARI) programme and routine respiratory surveillance systems in Scotland: Exploring the potential for forecasting.

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BACKGROUND

The community acute respiratory infection (CARI) programme is a surveillance system covering around a fifth of the Scottish population, and monitors respiratory pathogen activity across 180 sentinel general practice (GP) sites. The near real-time data from CARI could be used to notify secondary care (SC) providers of potential changes to infection activity. This study examines how temporal variations in CARI infection activity relate to trends in all routine testing (community and hospital), and emergency hospital admissions (EHA).

METHODS

Over a 30-week period in 2023-24, age-specific population trends for CARI swab positivity (proportion of swabs testing positive for a pathogen, %), were compared with subsequent routine testing rates (RTR) and EHA for specific pathogens. RTR and EHA were captured from the electronic communication of surveillance in Scotland (ECOSS) database.
The presence of visually observed weekly lags between CARI and other surveillance systems was validated using autoregressive integrated moving average (ARIMA) models. Associations are presented as regression coefficients (β).

RESULTS

Over the 2023-24 season, 57% of all CARI swabs (n=23,878) tested positive for at least one pathogen. In certain age groups, changes in CARI swab positivity preceded changes in RTR (range $\beta=0.033$ to 1.39, $p<0.04$) and EHA (range $\beta=0.01$ to 1.22, $p<0.03$). Strongest associations with the previous week's swab positivity were observed in the 1 to 4 age group testing positive for Respiratory syncytial virus (RTR $\beta=1.39$, EHA $\beta=1.22$, $p<0.001$), influenza (RTR $\beta=0.47$, EHA $\beta=0.79$, $p<0.001$) and seasonal coronavirus (RTR $\beta=0.43$, EHA $\beta=0.24$, $p<0.001$).

CONCLUSIONS

Sentinel GP data might serve as a critical advance warning tool for infection activity and hospital admissions. CARI provides an opportunity to inform timely, actionable information to support public health decision-making and healthcare planning.

KEYWORDS: Community-Acquired Infections,Sentinel surveillance,Time factors,Trends
ABSTRACT ID: 508
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FIRESIDE SESSION 5

Day 2 – 11.00-12.30

Surveillance

PRESENTER

Farida Abougazia

ABSTRACT

Enhancing Public Health Surveillance at FIFA 2022 Qatar: A Collaborative Event Based Surveillance approach

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BACKGROUND

Background: The World Health Organization (WHO) endorsed the Epidemic Intelligence from Open Sources (EIOS) initiative to enhance public health surveillance during the FIFA World Cup Qatar 2022. Collaborations with Qatar Ministry of Health, and the European Centre for Disease Prevention and Control (ECDC) aimed to monitor health threats potentially affecting the tournament. The objective was to assess collaborative efforts between WHO and partners in enhancing public health surveillance in mass gatherings using public health intelligence tools.

METHODS

Methods: A EIOS dashboard was created to screen articles from Qatar and the neighboring countries. The dashboard used open-source databases specific keywords related to the WORLD CUP 2022 (WC22) EIOS surveillance initiative. Screening included weekends and public holidays, focusing on detecting public health related signals.

RESULTS

Results: From November 6 to December 31, 2022, 51,836 articles across 1,037 pages were screened. 12 national-level signals were identified from 105 flagged articles, with three significant incidents at the national and EMRO levels. The process verified 75% of these signals, enhancing the tournament's public health response.

CONCLUSIONS

The EIOS initiative effectively identified public health threats during the FIFA World Cup, enhancing the collaborative efforts between WHO and partners within the mass gathering surveillance practice. The integration of artificial intelligence is recommended to streamline future processes, improve consistency, and reduce human effort and errors.

KEYWORDS: Event-Based Surveillance,Mass gathering,artificial intelligence ,Communicable diseases
ABSTRACT ID: 634
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FIRESIDE SESSION 5

Day 2 – 11.00-12.30

Surveillance

PRESENTER
Anna Ohlson

ABSTRACT

Wastewater-based surveillance of SARS-CoV-2 has limited potential to predict the number of COVID-19 cases in Sweden

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BACKGROUND

During the SARS-CoV-2 pandemic, wastewater-based surveillance was used worldwide with varying degrees of success. We assessed its potential as an early-warning indicator for COVID-19 in Sweden.

METHODS

We evaluated the levels of SARS-CoV-2 in wastewater as predictors of the number of reported COVID-19 cases in Sweden. We used weekly SARS-CoV-2 wastewater virus-levels collected by the Swedish University of Agricultural Sciences, including 18 wastewater treatment plants (WTP) in 14 of 21 regions, covering 11-52% of respective regional population. Regional weekly number of COVID-19 cases between July 24, 2023 and January 15, 2024 was obtained from the national surveillance system at the Public Health Agency of Sweden.For each WTP, we fitted four Poisson models to weekly COVID-19 cases. The models included virus-levels from either five or six weeks and lagged either one or two weeks with respect to cases. Each model predicted the number of cases one week ahead, with 95% prediction interval (PI) for a 20-week period. To assess the accuracy of the predictions, we calculated the proportion of weeks when the 95%PI included the observed number of COVID-19 cases (95%PI coverage) and mean square prediction error (MSPE).

RESULTS

For 15 WTP, the best model for predicting COVID-19 cases included virus-levels from five weeks lagged two weeks, as they had highest 95%PI coverage or the lowest MSPE. For these models, 95%PI coverage varied between 15-50%, median 25%.

CONCLUSIONS

The low 95%PI coverage indicates a low predictive power, suggesting that wastewater virus-levels cannot accurately predict the number of COVID-19 cases one or two weeks ahead. Other approaches should be investigated when assessing the potential of wastewater virus-levels as an early warning indicator in real-time surveillance of COVID-19 in Sweden.

KEYWORDS: Wastewater-based epidemiological surveillance, Epidemiological surveillance, prediction, early warning
ABSTRACT ID: 185
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FIRESIDE SESSION 5

Day 2 – 11.00-12.30

Surveillance

PRESENTER

Rosanne De Jong

ABSTRACT

Correlation between SARS-CoV-2 RNA in wastewater and notified COVID-19 cases and intensive care unit admissions in North Rhine-Westphalia, Germany, 2022-2023

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BACKGROUND

Statewide wastewater monitoring of SARS-CoV-2 in North Rhine-Westphalia (NRW), Germany, started in June 2022 to complement routine COVID-19 surveillance during the pandemic. We aimed to estimate the correlation between SARS-CoV-2 RNA in wastewater with COVID-19 notifications and intensive care unit (ICU) admissions between June 2022 and December 2023 in NRW.

METHODS

Wastewater samples were collected bi-weekly from fourteen wastewater treatment plants (WWTPs) covering circa 29% of NRW's population. SARS-CoV-2 RNA concentrations were quantified by RT-qPCR, normalized by WWTP flow and weighted by the number of people connected to the WWTP. We included laboratory-confirmed COVID-19 cases notified as per the Infection Protection Act and cases treated in ICU recorded in the DIVI Intensive Care Register. We compared wastewater concentrations of SARS-CoV-2 to the number of COVID-19 notifications and ICU admissions in all of NRW using correlation and linear regression analysis to determine the correlation (r), temporal alignment and trend comparisons at three phases with different COVID-19 testing policies.

RESULTS

Preliminary results show positive correlations up to r=0.95 between SARS-CoV-2 in wastewater with COVID-19 notifications and ICU admissions, with optimal correlation at no time-offset (0 days). We observed variations in lead and lag time and strength of correlation between wastewater, notification and ICU data over time. Although testing policy influenced testing frequency and thus the number of notifications, SARS-CoV-2 concentrations in wastewater remained stable. Comparing trends showed parallel periods of increases and decreases between wastewater, notification and ICU data.

CONCLUSIONS

Wastewater concentrations of SARS-CoV-2 provide a real-time indication of COVID-19 infection dynamics in the population served by the WWTPs. Wastewater monitoring of SARS-CoV-2 could inform the public of current trends and guide public health preparedness strategies, regardless of testing policy.

KEYWORDS: Methicillin-resistant Staphylococcus aureus, Panton-Valentine leucocidin, Community-acquired infections, Students, Outbreak, Public health
ABSTRACT ID: 403

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FIRESIDE SESSION 5

Day 2 – 11.00-12.30
Surveillance

PRESENTER
Joana Neto

ABSTRACT

Current surveillance system underestimated paediatric invasive Group A Streptococcal disease in Finland: a population registry-based study, 2014-2023

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BACKGROUND

Invasive Group A streptococcal infections (iGAS) in children have increased in several European countries after the COVID-19 pandemic. This trend was not observed in Finland, where iGAS surveillance is laboratory-based, Streptococcus pyogenes (GAS) findings confirmed by culture or PCR in blood or cerebrospinal fluid are notified to the National Infectious Disease Registry (NIDR). Other clinical presentations of iGAS are not under surveillance. Our aim was to identify paediatric clinical iGAS cases in the Hospital Discharge Registry (HDR) to assess the completeness of the current iGAS surveillance system.

METHODS

We conducted a population registry-based study, including laboratory-confirmed iGAS cases from NIDR and clinical iGAS cases from HDR, aged 0-17 years and reported during 01.01.2014-31.12.2023. To identify iGAS cases in HDR we selected eleven ICD10-codes according to literature, among them A40.0 (GAS sepsis) and B95.0 (disease due to GAS). We used personal unique identifiers to assess overlap of iGAS cases in both registries.

RESULTS

We identified 138 paediatric iGAS cases in NIDR and 135 cases in HDR. Of the HDR cases, 88 (65%) overlapped with NIDR cases. Of the 47 cases found only in HDR, 37 (79%) were coded as GAS sepsis, and 10 as other iGAS clinical presentations (pneumonia (n=4), arthritis (n=3), and cellulitis (n=3)). Combined, we identified 185 unique iGAS cases, representing an increase of 34% (47/138) compared to NIDR only.

CONCLUSIONS

Our study suggests that NIDR underestimated the number of paediatric iGAS cases during 2014-2023, especially for GAS sepsis. A comprehensive evaluation of the iGAS surveillance system is warranted to tackle underreporting and gain better insight into the paediatric iGAS burden in Finland. This might facilitate identification of at-risk groups and the implementation of targeted prevention measures.

KEYWORDS: Streptococcus pyogenes,Streptococcal Infections,Surveillance,Pediatrics,Public Health,Finland
ABSTRACT ID: 400
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FIRESIDE SESSION 5

Day 2 – 11.00-12.30

Surveillance

PRESENTER

Tristan Learoyd

ABSTRACT

Exploring global trends in botulism neurotoxin A usage: implications for iatrogenic botulism surveillance and management

T. Learoyd[1]
J. Pittman[2], L. Cochrane[3]
[1]Emergent
[2, 3]Emergent

BACKGROUND

Iatrogenic botulism received minimal attention in Europe until a notification from Germany to WHO/Europe on 7 March 2023 as part of 101 cases identified that year. Despite this, little is known about the global trends and correlations between cosmetic use of BoNT/A, the number of iatrogenic botulism cases cited in literature, and severe adverse events (SAEs) reported in the past decade leading up to this most recent outbreak. This study aimed to understand global trends of iatrogenic botulism.

METHODS

An eight-language systematic review of peer-reviewed articles and databases was conducted for iatrogenic botulism cases reported 2013-2023. SAEs associated with BoNT/A were collected during this timeframe from EudraVigilance's database. Global counts of BoNT/A for cosmetic use were obtained from the International Society of Aesthetic Plastic Surgery (ISAPS) and compared to SAE notifications and cited iatrogenic botulism cases in the literature. This comparison was performed using jackknifed datasets and least squares regression analyses.

RESULTS

ISAPS reports revealed a total of 59,686,020 procedures from 2013-2022, with an annual upward trend from 2015. EudraVigilance SAE notifications associated with BoNT/A totaled 4,902 cases, and a systematic literature review revealed 45 iatrogenic botulism citations. Positive correlation was shown between EudraVigilance SAE notifications and worldwide cosmetic BoNT/A use (Pearson CC: $r= 0.598$, $P<0.05$) but with wide variation in yearly reporting (least squares regression: $r=0.3577$). No correlation was found between BoNT/A use and iatrogenic botulism cases cited in the literature.

CONCLUSIONS

The annual numbers of SAEs associated with BoNT/A usage captured by EudraVigilance was positively correlated with the global rise in cosmetic BoNT/A procedures. Enhanced monitoring of iatrogenic botulism is advisable to bolster national readiness in response to the expanding availability and utilization of BoNT/A.

KEYWORDS: Botulism,database,systematic review,adverse event
ABSTRACT ID: 145
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FIRESIDE SESSION 6

Day 2 – 11.00-12.30

Modelling and biostatistics

PRESENTER

Neilshan Loedy

ABSTRACT

Repetition in Social Contacts: Implications in Modelling the Transmission of Respiratory Infectious Diseases in Pre-pandemic & Pandemic Settings

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BACKGROUND

The spread of viral respiratory infections is intricately linked to human interactions, and this relationship can be characterised and modelled using social contact data. However, many analyses tend to overlook the recurrent nature of these contacts. To address this gap, we reconstruct individuals' temporal contact patterns within different subgroups of the population to assess the potential impact of contact repetition on transmission dynamics.

METHODS

We describe individual contact patterns by characterising the interactions made with distinct individuals over a, without loss of generality, one week period, utilising data from social contact studies conducted in both pre-pandemic (the POLYMOD study) and pandemic settings (the Belgian CoMix study). Additionally, we use an age-structured individual-based model to gauge the implications of this reconstruction on the transmission of influenza-like and COVID-19-like diseases by juxtaposing it with the assumption of random mixing over time.

RESULTS

Failing to account for contact repetition results in an average overestimation of the weekly distinct physical contacts by up to 45% and 77%, for pre-pandemic and pandemic settings, respectively. Consequently, this can result in underestimating the transmission probability per contact by up to 23% and 45% for influenza-like and COVID-19-like diseases, respectively. This effect is dependent on pathogen characteristics and becomes more pronounced with lower reproduction numbers and longer infectious periods.

CONCLUSIONS

Our findings indicate the importance of accounting for contact repetition in epidemic models relying on social contact data, to suitably describe transmission dynamics and assess the transmission probability per contact. Moreover, we highlight how contact repetition and its effect on transmission varies in pre- and pandemic scenarios, providing valuable insights for shaping both local and global intervention measures to limit the spread of respiratory infections.

ABSTRACT ID: Infectious Diseases, Disease transmission, Epidemiological models, Social contact
ABSTRACT ID: 505
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FIRESIDE SESSION 6

Day 2 – 11.00-12.30

Modelling and biostatistics

PRESENTER

Vasiliki Engeli

ABSTRACT

Waning observance of social distancing measures during the COVID-19 pandemic in Greece: insights for emerging epidemics

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[2, 3, 4]Department of Hygiene, Epidemiology and Medical Statistics, Medical School, National and Kapodistrian University of Athens, Greece

BACKGROUND

During the COVID-19 pandemic, unprecedented social distancing measures were implemented. We aimed to identify determinants of social contacts and assess the impact of social distancing over time.

METHODS

We collected social contact data in Greece through repeated cross-sectional surveys using a contact diary approach. We covered one pre-pandemic period (January 2020), three lockdowns (March-April 2020, November-December 2020, April 2021) and four periods with relaxed measures (September 2020–October 2021). We estimated the mean daily number of contacts per individual. We fitted negative binomial generalised linear mixed models and estimated incidence rate ratios (IRRs) to assess determinants of contacts.

RESULTS

During lockdowns, participants of all ages reported low contact rates (2.8-5.9 contacts/day). During periods with relaxed measures, the highest number of contacts was observed among children/adolescents. Individuals ≥65-year-olds retained the fewest contacts during the pandemic (2.1-4.1). In 2021, a gradual increase in contacts emerged across all age groups, particularly among 18-64-year-olds, which persisted even during the third lockdown. Compared to the first lockdown, the second and third showed a higher number of contacts (IRR [95% CI]: 1.50 [1.27-1.76] and 2.19 [1.86-2.58], respectively). After the third lockdown, the largest increase in contacts was observed among children/adolescents. Overall, higher contact rates among adults were associated with male gender, higher educational level, living in larger household, being employed and having Greek nationality.

CONCLUSIONS

We provide evidence of waning observance of physical distancing policies after several months of mitigation measures. Effective communication of the risk in vulnerable populations alongside targeted adjustments to social distancing measures could be a viable alternative to repeated lockdowns, as emerging epidemics evolve.

KEYWORDS: COVID-19, social contacts, social distancing measures, lockdown
ABSTRACT ID: 454
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FIRESIDE SESSION 6

Day 2 – 11.00-12.30

Modelling and biostatistics

PRESENTER

Conor Egan

ABSTRACT

Modelling Hepatitis C virus infection and treatment impact through serological surveillance data

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[1]MRC Biostatistics Unit, University of Cambridge
[2]UK Health Security Agency
[3]MRC Biostatistics Unit, University of Cambridge

BACKGROUND

The introduction of new direct-acting antivirals for hepatitis C virus (HCV) has enabled a World Health Organisation (WHO)-led elimination strategy, targeting incidence reduction. Monitoring HCV incidence directly is challenging. However, cross-sectional bio-behavioural sero-surveys provide information on an individual's infection status and duration of exposure, and can be conducted serially to determine how these change over time.

METHODS

This study utilised annual HCV seroprevalence data from the unlinked anonymous survey of people who inject drugs, the main HCV transmission group in the UK. Flexible statistical models estimated incidence by exposure time and survey year. Antibody data were used to estimate incidence of primary infection, and the use of RNA data to estimate treatment and reinfection rates were explored via multistate models.

RESULTS

Incidence rates peaked in recent initiates of injecting drug use at approximately 0.20 infections per person-year, then reduced to approximately 0.05 infections per person-year in subsequent years. Recent survey years showed rising incidence among recent initiates. For those injecting longer, primary incidence rates remained stable. RNA data indicated high treatment rates, with RNA positivity reducing from 55% in 2015 to 22% in 2022. However, disentangling treatment and reinfection processes requires external information.

CONCLUSIONS

Seroprevalence and risk behaviour data can effectively estimate and monitor HCV incidence, providing insights into progress towards WHO-defined elimination of HCV. Previous studies of seroprevalence data have not considered reinfection or treatment effects. This limitation led to the development of a multistate model framework that describes the dynamics of HCV transmission, incorporating both antibody and RNA data. This model aims to jointly estimate the rates of primary infection, reinfection, and treatment uptake by time at risk and calendar period.

KEYWORDS: Hepatitis C; Cross-Sectional Studies; Reinfection; Drug Users; Incidence; Models, Statistical
ABSTRACT ID: 675
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FIRESIDE SESSION 6

Day 2– 11.00-12.30

Modelling and biostatistics

PRESENTER

Daniele Proverbio

ABSTRACT

Multi-signal fusion modelling to integrate wastewater-based surveillance into pandemic monitoring

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[7]University of Luxembourg|University of California San Diego

BACKGROUND

Predicting epidemic outbreaks is crucial for preparedness and intervention management. Wastewater-based epidemiology is emerging as a powerful complement to population sampling, but mostly remains at a qualitative level. Making more quantitative requires mapping viral load (in case of COVID-19) to a proportional number of shedding individuals, thus reconstructing disease diffusion within a population. Moreover, integrating wastewater-based epidemiology to pandemic surveillance based on case reporting is an open avenue, foreseen to drastically improve modelling and predictions.

METHODS

We proposed a causal model to quantify the infectious shedding population based on wastewater data. The CoWWAn (COVID-19 Wastewater Analyser) model embeds an epidemiological SEIR model, augmented by suitable compartments for viral shedding into wastewater, within a Kalman filter, to routinely calibrate the model and reproduce observed data. CoWWAn is designed to handle noisy data as inputs and was tested on global data sources. When both wastewater data and case numbers are available, it allows integrating both data sources to further improve the prediction of future pandemic trends.

RESULTS

CoWWAn successfully reconstructed case numbers from data and allowed predictions and “what-if” analysis. Its performance allows to use wastewater data to complement case numbers in epidemic modelling, forecasting, scenario modelling and outbreak anticipation. We also show that, by combining both data sources, the forecasting precision improves.

CONCLUSIONS

The CoWWAn model combines data from population sampling and WBE into a multi-signal model. The model is causal and based on verified epidemiological mechanisms, allowing for interpretability of the results and scenario modelling, on top of estimation of case numbers and forecasting. With this, we aim at fostering the development of fusion modelling and improve quantitative monitoring of epidemic diseases.

KEYWORDS: Wastewater,Pandemics,Wastewater-Based Epidemiological Monitoring,COVID-19,Information Sources,Virus Shedding
ABSTRACT ID: 290
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FIRESIDE SESSION 6

Day 2 – 11.00-12.30

Modelling and biostatistics

PRESENTER

Sophie van Kessel

ABSTRACT

The use of a Poisson hidden Markov model for automated detection of outbreaks with vancomycin-resistant Enterococci in routine surveillance data

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BACKGROUND

Early detection of outbreaks in hospitals, for instance with vancomycin-resistant Enterococci (VRE), is important for timely response measures. One of the objectives of the Dutch Infectious Disease Surveillance Information System-Antimicrobial Resistance (ISIS-AR) is being able to detect (multi-institutional) outbreaks. Here, we aimed to develop an algorithm to automatically detect in-hospital outbreaks with VRE in data on routinely performed antimicrobial susceptibility testing from ISIS-AR.

METHODS

ISIS-AR currently covers approximately 75% of Dutch hospitals, of which data on all VRE isolates, both screening and diagnostic, between 2013-2022 were obtained. The first isolate per patient per year was selected. A Poisson hidden Markov model (PHMM) was used to predict outbreaks based on weekly VRE counts at hospital level. Per week, the model provides the probability (p) that the observed number of cases arose from an outbreak. Different thresholds for detection of outbreaks were tested, being $p>0.5$, $p>0.7$, and $p>0.9$ for at least two consecutive weeks. We evaluated the model by comparing its results with outbreaks reported on a voluntarily basis to the national monitoring structure called SO-ZI/AMR.

RESULTS

Between 2013-2022, 110 outbreaks with known hospital identity were reported to SO-ZI/AMR by 44 hospitals. Eighty-six outbreaks had corresponding ISIS-AR-data. With the proposed thresholds, 85% (73/86), 83% (71/86), and 78% (67/86) of reported outbreaks were detected, respectively.

CONCLUSIONS

Further exploration into the number of false-positive detections in ISIS-AR will be done for optimal threshold selection. Also, improving ISIS-AR data quality can potentially reduce the number of false-negatives. To conclude, the PHMM is a promising tool, and we might be able to automatically detect VRE outbreaks based on routinely collected surveillance data in the future, which is valuable for taking early response measures.

KEYWORDS: Vancomycin-Resistant Enterococci, Disease Outbreaks, Epidemiological Monitoring, Infection Control
ABSTRACT ID: 291
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FIRESIDE SESSION 6

Day 2– 11.00-12.30

Modelling and biostatistics

PRESENTER

Karolina Shumylo

ABSTRACT

Increasing pertussis morbidity in Lviv Region, Ukraine

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BACKGROUND

Pertussis vaccination coverage has drastically decreased in the past few years. As a result, the number of pertussis cases in Ukraine has rapidly increased since 2023. One case was fatal—a one-month-old child.

METHODS

This research thoroughly analysed the data collected from statistical forms and medical cards of both inpatients and outpatients. The distribution of pertussis cases was evaluated by age and vaccination status.

RESULTS

According to the findings, 85 pertussis cases were reported in the Lviv region in 2023 (3,39 per 100,000 persons), compared to 1 case in 2022 (0,04 per 100,000 persons). Eighty-one cases were diagnosed in children: 28,4% infants, 22,2% aged 1-4 y.o., 32,1% aged 5-9 y.o., 14,8% aged 10-14, 2 cases - aged 15-17 y.o. Fifty-two children were not vaccinated (64,2%), and 29 had violations in their vaccination schedule (35,8%). In the first three months of 2024, an intensive indicator of morbidity was 4,96 per 100,000 persons (122 cases), compared to 0.16 in the same period in 2023 (4 cases). Pertussis was diagnosed in 114 children aged under 17 y.o.(93,5%), including 24,6% infants, 34,2% aged 1-4 y.o., 16,7% aged 5-9 y.o., 18,4% aged 10-14 y.o., and 6.1% aged 15-17 y.o. Having studied the vaccination status of patients with pertussis in the first 3 months of 2024, it appeared that only 4.4% of children were vaccinated according to the Vaccination calendar, 65% were not vaccinated, and 30.6% violated the Calendar.

CONCLUSIONS

It is crucial to understand that the most affected group is children between 1-4 years old, with 65% of patients not receiving the pertussis vaccine. It is urgent to revaccinate children at the age of 6, considering the high morbidity rate in this age group.

KEYWORDS: vaccine-preventable diseases,pertussis,children,morbidity,vaccination
ABSTRACT ID: 325
PRESENTED BY: Karolina Shumylo| Ukraine | *karolina.shumylo@gmail.com*

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FIRESIDE SESSION 7

Day 2 – 14.00-15.30

Vaccine-preventable diseases

PRESENTER

Erica Fougere

ABSTRACT

Measles epidemic in a middle-school with high vaccination coverage, in the Rhône valley, France, 2023

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BACKGROUND

In September 2023, a measles epidemic occurred in a middle-school in the Rhône valley; the index case was returning from Asia.

METHODS

Investigations consisted of validating the cases, tracing contacts, checking vaccination status with catch-up vaccination. Virological analyzes (sequencing, serologies) were done by the NRC MMR. The vaccination records were consulted on-site to assess measles vaccination coverage (VC) and determine attack rates. Vaccine effectiveness (VE) was estimated in sub-cohort of children for whom date of MMR vaccinations was collected (all cases and 309 non-cases), after binomial regression with bootstrap 95%CI, adjusted on gender, age and school level.

RESULTS

Among the 643 students, 49 measles cases occurred between 06/09-18/10/2023 (attack rate=7.6%). The 2-dose measles (MCV2) VC was 93.5% (601/643); 2 children had measles in childhood. Virological analyzes (n=27 cases) confirmed the clonality (genotype D8) and the concordance between the vaccination status and the immunological profile, with the exception of one case. In the sub-cohort, the measles rate was 100% in non-vaccinated; it was respectively 43.7%, 16.5%, and 3.2% among those vaccinated with 2 doses with the 1st dose at the age of <6-8 months (m), 9-11 m and ≥12 m. After multivariate analysis, the VE was estimated 96.4% (95% confidence interval [CI] 91.4-98.5%) after MCV2 with a 1st dose given at ≥12 m of age. The VE was 83.3% (95%CI:74.3-89.2%) after MCV2 when 1st dose given between 9-11 m and 60.7% (95%CI:10.6-82.7%) when given at 6-8 m of age.

CONCLUSIONS

This measles epidemic mainly affected children who were not vaccinated or fully vaccinated with a 1st dose was administered before 12 months of age and highlights the importance of catch-up vaccination if 1st dose was administrated before this age.

KEYWORDS: measles, cluster, vaccination coverage, vaccine effectiveness, epidemiological investigation
ABSTRACT ID: 283

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FIRESIDE SESSION 7

Day 2 – 14.00-15.30
Vaccine-preventable diseases

PRESENTER
Hannah Jary

ABSTRACT
Disproportionate impact of measles on deprived and ethnic communities in Birmingham, England, 2023-2024

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BACKGROUND
Measles disproportionately affects under-vaccinated communities, and there are known inequalities in vaccination coverage. In Birmingham, England, 406 cases of measles were notified to the UK Health Security Agency between 13 October 2023 and 12 April 2024. We describe the epidemiology of the outbreak and identify affected communities where control measures should be focussed.

METHODS
A case was defined as a Birmingham resident with laboratory confirmation (measles IgM in blood or oral fluid in the absence of recent vaccination or wildtype measles RNA in any clinical specimen). Using public health case management system data, we describe case demographics. Vaccination status and ethnicity data were enriched using primary care data. MMR vaccine eligible cases were >12 months of age.

RESULTS
The median age of cases was 5.5years (IQR 1-13). Three-quarters of cases (315/406 (78%)) occurred in the most deprived quintile, with none from the least deprived. The rate of measles was 47.4 per 100,000 in quintile 1 (most deprived) versus 29.0 and 13.4 in quintile 2 and 3 respectively. Ethnic origin was known for 339/406, (83%) of cases. The rates of measles in black, Asian, and white ethnicities were 75.6, 33.5 and 12.5 per 100,000 respectively. Of eligible cases, 306/350 (87%) had no MMR vaccination recorded. Cases of white ethnicity were more likely to have had at least one dose of vaccine (19/67, 28%) than cases of all other ethnic groups combined (44/243, 9%) (Chi-squared p=0.000).

CONCLUSIONS
In this large and ongoing outbreak, measles disproportionately affected individuals from socio-economically deprived backgrounds, and ethnic minorities, who were more likely to be unvaccinated compared to cases from white ethnicities. Targeted, data-driven catch-up vaccination campaigns should be used to protect vulnerable populations.

KEYWORDS: equity, inclusion,epidemiologic surveillance,communicable diseases
ABSTRACT ID: 377
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FIRESIDE SESSION 7

Day 2 – 14.00-15.30

Vaccine-preventable diseases

PRESENTER
Jonas Haller

ABSTRACT

Re-emergence of Toxigenic Corynebacterium diphtheriae among people experiencing homelessness linked to a 2022 European diphtheria outbreak, Frankfurt am Main, Germany, 2023

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BACKGROUND

In 2022, a Europe-wide Corynebacterium diphtheriae outbreak occured among minor refugees. In 2023, C. diphtheriae was detected in three intravenous drug users experiencing homelessness in Fankfurt am Main. We aimed to estimate the extent of C. diphtheriae infections and investigate a possible link with the 2022 outbreak to stop transmission.

METHODS

During 01/08/2023-31/10/2023, staff of medical aid organizations took wound and throat swabs from people experciencing homelessness presenting with pseudomembranes in the nose or thorat or with cutaneous lesions. We defined cases as persons with toxigenic C.diphtheriae without travel history 60 days prior to diagnosis. Cultivated C.diphtheriae isolates were sent to the Diphtheria National Consiliary Laboratoy, to verify toxigenicity (PCR; Elek test) and perform sequence typing (MLST and cgMLST via Next generation sequencing). We recommendes vaccination for thise with no vaccination or uncertain vaccination status.

RESULTS

Among 36 individuals tested, we identified three additional cases of cutaneous toxigenic C. diphtheriae; all suffered from alcohol use disorder. Non-toxigenic C.diphtheriae was detected in 7/36 (19 %) wound and 2/30 (6 %) throat swabs. Sequence type 574 was identified in 5 C. diptheriae toxigenic isolates same as in one predominant cluster in the 2022 outbreak among refugess. Direct contacts between the cases and minor refugees could not be ascertained.

CONCLUSIONS

The genomic investigation pointed towards a potential link between diphtheria cases among susceptible people experiencing homelessnee and regugees, due to a potential spatial overlap of both populations. Those findings underscore the need for increased awareness to detect cutaneous diphtheria and monitoring and bossting immunity against diphthiera in vulnerable groups.Genomic analysis is a valuable instrument to identify genetic relationships between outbreaks, even when the epidemiological data are scarce.

KEYWORDS: Corynebacterium diphtheriae,multi-locus sequence typing,outbreak,homelessness,refugees,molecular epidemiology
ABSTRACT ID: 302
PRESENTED BY: Jonas Haller | Germany | *jonas.haller@stadt-frankfurt.de*

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FIRESIDE SESSION 7

Day 2 – 14.00-15.30

Vaccine-preventable diseases

PRESENTER
João Pires

ABSTRACT

Implementation of whole genome sequencing-based typing for Corynebacterium diphtheriae in Norway

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[7]Department of Infection Control and Preparedness, Norwegian Institute of Public Health, Oslo, Norway

BACKGROUND

Diphtheria is a severe respiratory disease caused by toxin-producing Corynebacterium spp. In 2022, a European multi-country C. diptheriae outbreak was declared with 281 cases, including 1 from Norway. At the time, the Norwegian National Reference Laboratory (NRL) had not validated core-genome multilocus sequence typing (cgMLST) for C. diphtheriae outbreak investigations, and reagent batch variations hindered the toxin expression test (Elek) performance. Therefore, we aimed to implement cgMLST and genome-based toxin production inference at the NRL to support C. diphtheriae diagnostics and outbreak investigations.

METHODS

We sequenced 56 Norwegian C. diphtheriae isolates (20 toxin- and 36 non-toxin producers) collected between 2010-2023, comparing two available cgMLST schemes – SeqSphere and Pasteur. Performance was assessed based on the percentage of detected genes. Single-linkage clustering (SLC) at different allelic difference thresholds was performed to identify at which threshold clusters matched between schemes. Bioinformatic toxin gene detection was performed with Virulence Factor database. We visualized the distribution of toxin-producing isolates with a core-genome phylogenetic tree.

RESULTS

The Pasteur scheme performed better (median 98.9% genes, IQR [98.7–99.3]) than SeqSphere (median 98%, IQR [97.7%-98.3], Wilcox test $p<0.001$). SLC at 5 allelic differences (outbreak threshold) from Pasteur matched clusters obtained with 6 differences from SeqSphere (adjusted rand index 1). Bioinformatic toxin detection matched 100% with NRL diagnostics. However, toxin and non-toxin-producing isolates clustered together in the phylogenetic tree, hindering toxin-production inference using phylogenetic placement alone.

CONCLUSIONS

We recommend implementing the Pasteur scheme using SLC at 5 allelic differences in Norway and elsewhere for improved outbreak response in national and cross-border outbreaks, and harmonization of C. diphtheriae surveillance globally. Furthermore, given the importance of timely toxin detection, we recommend the NRL to keep current toxin diagnostics workflow.

KEYWORDS: Diphtheria,Molecular Typing,Core Genome Multilocus Sequence Typing,Toxin Detection
ABSTRACT ID: 265
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FIRESIDE SESSION 7

Day 2 – 14.00-15.30

Vaccine-preventable diseases

PRESENTER

Angela Rose

ABSTRACT

Seasonal 2023/24 influenza A vaccine effectiveness: VEBIS European hospital multicentre study

J. Howard[1]

F. Pozo[2], G. Pérez-Gimeno[3], I. Martínez-Baz[4], . Belgium SARI Surveillance Network (BelsariNet)[5], V. Gómez[6], S. Abela[7], R. Dürrwald[8], C. Popescu[9], G. Petrovic[10], G. Túri[11], L. Jancoriene[12], R. Duffy[13], L. Soucková[14], S. Bacci[15], M. Rumayor[16], J. Castilla[17], A. Machado[18], G. Xuereb[19], K. Tolksdorf[20], I. Loghin[21], Z. Lovric Makaric[22], B. Oroszi[23], M. Kuliese[24], M. Fitzgerald[25], P. Husa[26], N. Nicolay[27], A. Rose[28], on behalf of European Vaccine Effectiveness group[29]

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BACKGROUND

The 2023-24 influenza season was characterised by the predominant circulation of influenza A(H1N1)pdm09. We measured 2023/24 influenza vaccine effectiveness (IVE) against laboratory-confirmed influenza A(H1N1)pdm09 and A(H3N2) hospitalisation through the Vaccine Effectiveness, Burden and Impact Studies (VEBIS) multicentre European network.

METHODS

We conducted a test-negative case–control study among patients aged ≥18 years admitted with severe acute respiratory infection (SARI) swabbed ≤7 days after symptom onset from 69 hospitals across 11 study sites in 10 European countries. We defined cases as RT-PCR influenza A(H1N1)pdm09– or A(H3N2) –positive; controls as negative for any influenza. We estimated subtype–specific IVE using logistic regression, adjusting for study site, onset date, age and chronic conditions, both overall and stratified by age-group (18–64, ≥65 years), those with a severe clinical outcome (death, admitted to ICU or received respiratory support) and those within the country-specific influenza vaccination target group (IVTG), where sample size allowed.

RESULTS

Between week 41 2023 and week 10 2024, we included 767 influenza A(H1N1)pdm09 and 275 A(H3N2) cases and 5103 controls.IVE against influenza A(H1N1)pdm09 was 45% (95% CI: 35-54): 57% (95% CI: 36–72) among 18–64-year-olds, 42% (95% CI: 29–53) for ≥65-year-olds, 37% (95% CI: -13–66) among patients with severe outcome and 46% (95% CI: 36–55) in the IVTG. Against influenza A(H3N2), IVE was 17% (95% CI: -11–37): 10% (95% CI: -67–53) for ≥65-year-olds and 17% (95% CI: -11–38) among patients in the IVTG.

CONCLUSIONS

Our 2023/24 influenza season results show IVE of over 40% against hospitalisation with A(H1N1)pdm09 (except for severe outcomes, which had a lower point estimate though confidence intervals overlapped), and as low as 10% against A(H3N2).

KEYWORDS: Influenza, influenza vaccine, vaccine effectiveness, multicentre study, case control studies, test-negative design
ABSTRACT ID: 110
PRESENTED BY: Angela Rose | France | *a.rose@epiconcept.fr*

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Day 2 – 14.00-15.30

Vaccine-preventable diseases

PRESENTER
Lauriane Ramalli

PRESENTER

Motivational interviewing intervention reduced mothers’ vaccine hesitancy and increased intention to vaccinate their children: a randomized control trial, southeastern France, 2021 to 2022.

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BACKGROUND

Childhood vaccination coverage in France remains below the 95% target for most vaccines. Parental vaccine hesitancy is a challenge but was successfully reduced in Quebec by a public health program using motivational interviewing interventions in maternity wards. In South-eastern France, we aimed to evaluate if motivational interviewing reduces mothers’ vaccine hesitancy (VH) and increases their intention to vaccinate (VI) children.

METHODS

We conducted a randomized controlled trial to compare the impact of motivational interviewing (intervention arm) versus vaccination leaflet (control arm) on VH and VI after intervention and seven months later. Trained midwives randomly offered motivational interviewing or a leaflet to 733 postpartum mothers in two maternity wards from November 2021 to April 2022. We assessed their VH with a validated scale (13 items, 0-100 score) and VI (1 item, 1-10 score) using auto-questionnaires before, just after interventions and seven months after birth. We applied regression models to estimate the net impact of motivational interviewing versus leaflet on VH and VI right after interventions and seven months later and stratified by socioeconomic status.

RESULTS

Post motivational interviewing at the maternity ward, mothers’ VH decreased by 33% and VI increased by 8%, corresponding to a net VH decrease of 5.8 points ($p=0.01$) and a net VI increase of 0.6 point ($p=0.005$) compared to the leaflet. Seven months later, the impact was maintained (-7.2 points for VH; +0.8 point for VI) and observed across all socioeconomic status.

CONCLUSIONS

This study showed that motivational interviewing reduced VH and increased VI in mothers across all socioeconomic status and with a maintaining effect over 7 months. Motivational interviewing should therefore be considered as key strategy to reduce vaccine hesitancy in France.

KEYWORDS: Randomized Controlled Trial,Program Evaluation ,France,Vaccine Hesitancy,Motivational Interviewing
ABSTRACT ID: 301
PRESENTED BY: Lauriane Ramalli | France | *lauriane.ramalli@santepubliquefrance.fr*

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FIRESIDE SESSION 8

Day 2 – 14.00-15.30

Preparedness

PRESENTER

Máirin Boland

ABSTRACT

International transport of a mock patient with high consequence infectious disease within the EU: a three-country simulation exercise for Ireland, Germany and Norway

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[19]Health Security Programme, National Health Protection Office, HSE, Dublin
[21, 22]Clinic for Gastroenterology, Hepatology and Infectiology, University Hospital Duesseldorf

BACKGROUND

The EU is at risk from rapid international spread of virulent pathogens causing high consequence infectious diseases (HCID). As part of a wide-ranging Irish exercise, Ireland, Germany and Norway exercised contingency planning for safe end-to-end transfer of a HCID case from Dublin's to Duesseldorf's High Level Isolation Unit (HLIU) availing of the Norwegian NOJAHIP EU standing Civil Protection (rescEU) resource which uses the EpiShuttle to perform airborne HCID-patient transfer.

METHODS

A three-country planning group led by Ireland's HCID Steering Group defined common (tri-partite), bilateral and country-specific key performance indicators using WHO's strategic toolkit for assessing risk, and the ECDC HCID checklist. Duesseldorf's HLIU was chosen following discussion between Ireland and the STAKOB office.The simulation aimed to test interfaces in alert mechanisms, activation, communication and safe transfer processes end-to-end across the multinational teams with the NOJAHIP medevac retrieval of the patient in Ireland, and handover in Germany. Post-exercise debriefing evaluated performance.

RESULTS

The exercise took place across three days in March/April 2024. There was successful activation of the NOJAHIP-team using the Emergency Response Co-ordination Centre. The new Early Warning and Response System Sim3 Tool was used for secure document/information transfer. Pathways for communication between sending and receiving HLIU were established. Clinical and technical information needed by the NOJAHIP-team were communicated and integrated into preparational SOPs tested during the exercise. All partners' feedback was positive.

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CONCLUSIONS

This complex simulation exercise enabled alerting, activation and management processes to be strengthened and harmonised at European level, and improvements to existing country-specific processes were made. This first simulation using the RescEU resource has led to improved coordination and preparedness for safe end to end management of patients with HCID.

KEYWORDS: Preparedness,Communicable Disease,Simulation,Repatriation,Cross-border,HCID
ABSTRACT ID: 645
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FIRESIDE SESSION 8

Day 2 – 14.00-15.30

Preparedness

PRESENTER

Charlotte Waltz

ABSTRACT

Integral Scientific Advice for Outbreak Response: Lessons learned from an Avian Influenza Simulation in the Netherlands

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[3]Agence Nationale de Sécurité Sociale (ANSS)
[4, 6]Santé Plus
[5, 7]Georgetown University

BACKGROUND

The complexity of COVID-19 highlighted the need for involvement of social scientists alongside biomedical experts to develop advice. Future pandemics demand swift and effective collaboration across disciplines to address diverse consequences and priorities. The governance framework for outbreaks in the Netherlands requires different disciplines to provide advice separately to the government. We conducted an avian influenza outbreak simulation to explore development of integrated scientific advice in pandemics.

METHODS

We planned two simulation events on different phases of an outbreak on 17 April and 24 May 2024, in the Netherlands. During first simulation, the scenario depicted a variant of avian influenza spreading via pigs, triggering significant health implications for humans and animals. Scenario of the May simulation continues with human-to-human and cross-border transmission. On 17 April, 23 Dutch experts from biomedical, and social and economic sciences initially crafted their recommendations independently. Three interdisciplinary groups then converged, utilizing the WICID evidence-to-decision framework. Thematic analysis was conducted on notes of group and plenary discussions, and reflection and evaluation sessions.

RESULTS

Interdisciplinary discussions helped participants identify blind spots in disciplinary recommendations. Two interdisciplinary groups generated comprehensive recommendations, one required additional time for consensus. Agreement seemed to be swift in the animal husbandry but contentious regarding human measures, notably school closures. Various disciplines brought insights from respective sectors, informed by hard-earned lessons from past experiences, for example with outbreaks in animal husbandry, human health crises, and the repercussions of COVID-related school closures. Open dialogue and curiosity for alternate perspectives emerged as vital for integrated advice. Results of May will follow.

CONCLUSIONS

Simulations provide invaluable opportunities to prepare for national crisis responses, fostering understanding across disciplines, and further developing and refining integrated advisory approaches.

KEYWORDS: interdisciplinary, collaboration, scientific advice,emergency preparedness,decision making
ABSTRACT ID: 322
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FIRESIDE SESSION 8

Day 2 – 14.00-15.30

Preparedness

PRESENTER

Aparna Dressler

ABSTRACT

Knowledge, Attitude and Practices towards Mosquito-borne Arboviral diseases in Public Health Offices in 10 Federal States in Germany: a cross-sectional questionnaire-based analysis

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[2, 3]Department of Health Protection and Epidemiology, State Health Office, Ministry of Social Affairs, Health and Integration, Baden-Wuerttemberg, Germany

BACKGROUND
The invasion of Aedes albopictus (AA) and increased activity of native Culex species is driving mosquito-borne arboviral diseases (MBAD) in Europe. Since 2019, autochthonous West-Nile-Virus (WNV) infections have been reported in Germany. Awareness of MBAD in the Public Health System is crucial for preparedness and improving public health response. This ongoing survey assesses knowledge, attitudes, and practices towards MBAD among local Public Health Offices (PHOs) in 10 federal states in Germany.

METHODS
A web-based online survey was started in January 2024. Ten German federal states with documented AA populations and/or documented cases of autochthonous arboviral infections participated. Using EUSurvey, an open source, web-based survey-tool, we mailed online-questionnaires to 212 local PHOs (one questionnaire per PHO). We performed descriptive analysis on data collected from Jan 18, 2024 until May 14, 2024.

RESULTS
We included 144 local PHOs in this preliminary analysis. Knowledge of arboviral transmission routes was reported by 40% (N = 56). 73.6% (N = 106) desired more information on arboviral transmission routes. As regards autochthonous human WNV infections, 62.5% (N = 90) reported no infections in their district, 6.2% (N = 9) reported infections and 31.2% (N = 45) did not know. 32.6% (N = 47) reported AA populations in their district, 45.8% (N = 66) reported no AA populations and 21% (N = 30) did not know. 82% (N = 118) wanted information on mosquitoes in Germany that could potentially transmit arboviruses. Only 14.6% (N = 21) reported having public awareness campaigns on MBAD in their districts in the past 5 years.

CONCLUSIONS
A clearer understanding and increased awareness of the threat of emerging MBAD is needed in the Public Health System in Germany.

KEYWORDS: Arboviruses, Germany, Public health, Surveys and Questionnaires
ABSTRACT ID: 500
PRESENTED BY: Aparna Dressler | Germany | *aparna.dressler@sm.bwl.de*

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FIRESIDE SESSION 8

Day 2 – 14.00-15.30

Preparedness

PRESENTER

Mario Martín Sánchez

ABSTRACT

Performance of the Robert Koch Institute's outbreak task forces during COVID-19: An evaluation

M. Martín-Sánchez[1]
C. Siffczyk[2], A. Loenenbach[3], K. Kajikhina[4], N. Zeitlmann[5]
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[2, 3, 4, 5]Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

BACKGROUND

In Germany, local public health authorities (LPHA) are responsible for outbreak investigations and response. The Robert Koch Institute (RKI) on the national level can support them on official request. Between January 2020 – September 2021, 50 RKI task force teams (RKI-TF) were deployed to support LPHA and state public health authorities (SPHA) in COVID-19 outbreak investigations. We evaluated the main reasons for requesting or not requesting RKI-TF assistance, and the performance of the RKI-TF-deployments.

METHODS

We conducted a retrospective cross-sectional survey. We administered an online questionnaire to all LPHA (n=376) and SPHA (n=16) between 09/03/2023–12/05/2023 including closed-ended (e.g. Likert scale) and open-ended questions pertaining to satisfaction, timeliness, and benefits of the RKI-TF in case of deployment and barriers in case of non-deployment. We conducted a descriptive analysis of the responses.

RESULTS

146 authorities (136 LPHA and 10 SPHA) participated. Of those, 21 had requested RKI-TF-deployments. The most common reasons for requesting help were need for additional expertise (n=19) and lacking personnel resources (n=13). The main reasons for the 125 authorities not requesting help were no need for assistance (60%; 56/94) and lack of experience (31%; 29/94) or knowledge (29%; 27/94) about the official procedures of seeking RKI assistance.15 authorities provided information on 22 deployments. Their median duration was 4 days (range 1–26). Overall, the RKI-TF-deployments were rated as very satisfactory/satisfactory (n=20) and timely (n=19). Conducting analytical epidemiology (n=18) and transfer of scientific knowledge from RKI-TFs (n=16) were considered the biggest benefits of the RKI-TF-deployments.

CONCLUSIONS

LPHA and SPHA evaluated RKI-TF-deployments positively. We recommend further promotion of RKI-TF-deployments for future outbreaks. RKI should address knowledge gaps about request and deployment procedures through regular training and information dissemination.

KEYWORDS: Task Force,COVID-19,Crisis Management,Field Epidemiology,outbreak investigation,Disease Outbreaks
ABSTRACT ID: 189

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FIRESIDE SESSION 8

Day 2 – 14.00-15.30

Preparedness

PRESENTER

Nelly Fournet

ABSTRACT

Using mobile phone connection data to contextualize epidemiological findings in Île-de-France during the 2024 Paris Olympic and Paralympic Games

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[6]Santé publique France
[7]Laboratory of virology, Avicenne University Hospital, Assistance Publique-Hôpitaux de Paris, Bobigny, France

BACKGROUND

The 2024 Paris Summer Olympics and Paralympics Games (OPG) were held predominantly in Paris and seven surrounding Départements of Île-de-France (IdF) Région, from 26/07 to 08/09. To contextualize epidemiological findings, we estimated population denominators, accounting for vacationers' departures and international visitors' arrivals.

METHODS

We used daily population estimates produced by a specialized mobile phone company. These are modelled using antennae-mobile phone connection data (MPD). They were available for the period 01/07-08/09 and for each IdF Département, detailing the provenance in France or 180 other countries or territories where the SIM card was registered.

RESULTS

A total of 695,407,118 person-days were documented in IdF during the 69-day period. Of those present, 68.5% were IdF residents of any nationality, 5.7% were French non-IdF residents, 8.7% were non-French EU/UK/Swiss and 17.0% were non-EU/UK/Swiss residents. The estimated daily IdF resident population in IdF went from 8,315,318 to 7,464,350 with a minimum of 5,424,582 on 15/08 (-34.7% of baseline). Visitors from outside EU/UK/Swiss of any nationality went from 1,862,384 to 1,748,192 with a maximum of 1,862,384 on 01/07 and a minimum of 1,482,380 on 01/09.MPD-based population estimates were used to contextualize the end-of-summer rise in indicators, to redress the observed slowdown in SARS-CoV-2 circulation data in IdF and estimate the number of visitors from currently epidemic countries when influenza A virus was detected or Mpox was declared an international emergency.

CONCLUSIONS

Near-real-time, MPD-based population estimates were used as denominators to effectively and usefully contextualize and interpret epidemiological indicators in the 2024 summer and OPG period during which the IdF population was highly diverse and mobile. This system may constitute a legacy of the OPG.

KEYWORDS: Vector-borne disease, surveillance, mandatory reporting
ABSTRACT ID: 189
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FIRESIDE SESSION 9

Day 3 – 11.00-12.30
Antimicrobial resistance

PRESENTER
Rhiannon Johnson

ABSTRACT
The epidemiology of candidaemia in Wales, United Kingdom, April 2018 – March 2024: Preparation for the development of national surveillance.

R. Johnson[1]
R. Chandrasekar[2], M. Fallon[3], V. McClure[4], C. McKerr[5], M. Morgan[6]
[1]Public Health Wales (PHW)
[2, 3, 4, 5, 6]Public Health Wales (PHW)

BACKGROUND
Candidaemia is associated with high mortality in hospitalized patients but is not monitored nationally in Wales. To guide development of national surveillance, we described candidaemia cases in Wales over 6 years.

METHODS
Candida positive blood cultures from 01/04/2018-31/03/2024 were extracted from the laboratory information system. We excluded repeat episodes within 14 days. We linked to hospital admissions using NHS number, and to Welsh Index of Multiple Deprivation using residential postcode. Hospital onset was classified as specimens collected ≥3 days after admission and before discharge. ICU cases were identified from patient ward location at specimen collection. Mortality was death from any cause 28 days post-positive specimen.

RESULTS
740 episodes in 654 unique patients were identified. Half of episodes were C. albicans. Candidaemia was more common in men (59%) and in those aged 65+ (55%). 28% of episodes were from ICUs and 74% were hospital onset. Episodes increased as deprivation increased (9% (6.7–10.7 95%CI) in least deprived quintile vs 21% (17.9–23.7, 95%CI) in most deprived). Mortality was 35% overall, peaking at 43% in 2020/21. Mortality was 50% (43.1–57.4 95%CI) in ICU patients, compared to 28% for others (24.0-32.1 95%CI). Trend data suggests a seasonal pattern, with higher counts in Autumn. Annual population rates decreased from 4.5 per 100,000 in 2018/19 to 3.2 in 2023/24.

CONCLUSIONS
Results show candidaemia as a hospital issue, with poor outcomes for vulnerable ICU patients. It highlights the importance of comprehensive data in routine surveillance, particularly inclusion of mortality and deprivation, given the high percentage of deaths and trend with increasing deprivation. Incorporating cause of death and antifungal resistance into surveillance will be investigated to enhance understanding of these poor outcomes.

KEYWORDS: Surveillance, Candidaemia, Candida sp.,fungal surveillance
ABSTRACT ID: 495
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Day 3 – 11.00-12.30

Antimicrobial resistance

PRESENTER
Aneta Kovarova

ABSTRACT

Investigating Carbapenemase Producing Enterobacterales Persistence and Potential Patient Acquisition From The Hospital Environment

A. Kovarova [1]
M. Maguire [2], B. Hanahoe [3], F. Higgins [4], C. Clarke [5], A. Tuohy [6], A. Maczynska [7], J. Davitt [8], G. Miliotis [9], M. Cormican [10], L. Burke [11]
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[10] Antimicrobial Resistance and Microbial Ecology Group, School of Medicine, University of Galway, Ireland|Centre for One Health, University of Galway, Ireland|Galway University Hospitals, Ireland

BACKGROUND

Environmental surveillance has revealed that showers, sinks, and drains are key Carbapenemase Producing Enterobacterales (CPE) reservoirs. This study aimed to characterise CPE persistence in hospital environment and to evaluate the potential contribution of these reservoirs to the acquisition of CPE by inpatients.

METHODS

Environmental surveillance of sinks and showers was carried out 5 times from August to November 2023 in three hospital wards where patients were screened weekly for CPE. Established culture-based methods were used to isolate presumptive CPE, with confirmation by PCR/NG-Test® CARBA-5 immunoassay (NG-BIOTECH). Environmental isolates were compared by WGS to CPE from patients post-ward admission

RESULTS

Thirty-four CPE isolates were collected, comprising 7 species, with the Enterobacter genus (59%) and carbapenemase genes (CG) blaOXA-48 (n=20) and blaVIM-1 (n=11) dominant. Despite environmental decontamination, two older shared ward bathrooms (shower drains) remained CPE-positive for blaOXA-48 and/or blaVIM-1. The other (newer build) ward had single ensuite rooms which were intermittently positive for blaVIM-1 CPE, but not for blaOXA-48. The same VIM plasmid was detected in 6/7 isolates across 3 wards.Nine CPE isolates detected in patients following admission to the sampled wards, comprising 6 species. The same CG (blaOXA-48 and blaVIM-1) were newly detected in patients, but Klebsiella spp. (33%) and Escherichia coli (33%) were dominant. One Enterobacter hormaechei ST204 strain bearing both blaOXA-48 and blaVIM-1 was detected consistently in the environment and a patient on the same ward following admission.

CONCLUSIONS

Findings suggest hospital environment contamination contributes significantly to CPE acquisition by patients. Further characterisation of CG-bearing plasmids in this study may reveal their interplay between distinct Enterobacterales species in human and hospital environment niches.

KEYWORDS: Antimicrobial Resistance,Carbapenemase Producing Enterobacterales,Hospital Environment,Drain,Sink
ABSTRACT ID: 525
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FIRESIDE SESSION 9

Day 3 – 11.00-12.30
Antimicrobial resistance

PRESENTER
Katie Thorley

ABSTRACT

Epidemiology and control of an outbreak of Methicillin-resistant Staphylococcus aureus (MRSA) colonisation in a neonatal unit, England, May to September 2023.

K. Thorley [1]
J. Foster [2], S. Urquhart [3], J. Swinney [4], S. Kapadia [5], E. Heinsbroek [6]
[1] UK Health Security Agency (UKHSA)|UK Field Epidemiology Training Programme (UKFETP)
[2, 3, 4] Mid and South Essex NHS foundation trust
[5, 6] UK Health Security Agency (UKHSA)

BACKGROUND

During neonatal unit (NNU) outbreaks, analysing staff and cot/incubator movements is important. Routine MRSA screening in an NNU detected 12 MRSA colonisations, starting from May 2023, linked by Whole Genome Sequencing (WGS) suggesting transmission events. We describe the outbreak investigations.

METHODS

Cases were NNU inpatients from May 2023 with an MRSA-positive sample within the WGS-linked cluster. Concurrent screening of parents was conducted throughout; one-off screening of staff and environmental sampling was conducted in September. Cots were labelled and recorded in patient notes from week 25. We reviewed hospital record data for all NNU inpatients between May-September to support analytical investigations. Attack proportions (AP) for birth characteristics and clinical exposures were compared using Pearson's Chi-squared or Fisher's exact tests.

RESULTS

Of 89 NNU inpatients,14 were cases (12 colonisations, 2 non-invasive eye infections): AP 16%. There were two outbreak waves: 7 cases in weeks 21-27 and 7 cases in weeks 35-38. Median time between admission and first MRSA-positive swab was 10 days (range 3-24). The AP decreased as gestational age increased (28-<32 weeks:50%, 32-<37 weeks:21%, 37+ weeks:3%; $p<0.001$) and was higher among neonates receiving respiratory support (29%; $p=0.002$), having inserted lines (40%; $p=0.012$), and receiving gavage/enteral feeding (27%; $p=0.022$).Parental and environmental screening identified no MRSA-positives. Staff screening identified two outbreak-strain positives. Contemporaneous staff and cot/incubator movement analysis identified shared case exposures; data was not yet available for non-cases.

CONCLUSIONS

Neonates of lower gestational age and receiving invasive procedures were more at risk of MRSA colonisation. Continued case and positive staff identification in September confirmed ongoing transmission; readily accessible staff and cot/incubator movement data for cases, as available here, is crucial for rapid identification of potential reservoirs during NNU outbreaks.

KEYWORDS: Healthcare Associated Infections, Outbreak, Neonates, Methicillin-resistant Staphylococcus aureus, MRSA
ABSTRACT ID: 149
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FIRESIDE SESSION 9

Day 3 – 11.00-12.30
Antimicrobial resistance

PRESENTER
Rosie Collins

ABSTRACT

Challenges in investigating a non-O157 Shiga-toxin producing E. coli (STEC) outbreak: an STEC O26 case study.

R. Collins [1]
A. Douglas [2], L. Larkin [3], O. Quinn [4], C. Jenkins [5], E. Rodwell [6], B. Sims [7], F. Jorgensen [8], J. Thoulass [9], L. Browning [10], C. McCarthy [11], A. Nelson [12], L. Allison [13], A. Hoban [14], N. Chandra [15], V. Wong [16], S. Balasegaram [17]
[1] UK Health Security Agency (UKHSA)
[2, 3, 4, 5, 6, 7, 8, 14, 15, 17] UK Health Security Agency (UKHSA)
[9, 10, 11] Public Health Scotland (PHS)
[12] Public Health Wales (PHW)
[13] Scottish E.coli Reference Laboratory (SERL)
[16] UK Health Security Agency (UKHSA) |Cambridge University Hospitals NHS Foundation Trust

BACKGROUND

In October 2023, a multidrug-resistant outbreak of Shiga toxin-producing Escherichia coli (STEC) O26:H11 was detected by national gastrointestinal infections surveillance, characterised by unusually high clinical severity among young children. A multidisciplinary investigation was initiated to identify likely infection vehicle(s) and implement control measures.

METHODS

Enhanced Surveillance Questionnaires collected demographic, clinical, exposure and contact-tracing information. Primary cases were re-interviewed via exploratory or trawling questionnaires for hypothesis generation and testing. Cases were confirmed via whole genome sequencing; probable cases had gastroenteritis and epidemiological links to confirmed cases.

RESULTS

Overall, 36 confirmed and 3 probable cases were identified across 3 UK countries with a median age of 4 (range: 1-56 years); 72% of cases were aged under 6. Positive for stx2a and eae, 19 cases developed Haemolytic Uraemic Syndrome. Ten household clusters were identified, ranging 2-7 cases per household. Phylogenetic and drug-resistance analyses indicated a non-domestic lineage. The likely vehicle was identified as an imported, preserved fruit product in small packets, marketed to children. All cases reporting consumption were linked to a common, nationwide supplier. Microbiological testing of 110 samples were negative, although some implicated batches were unavailable.

CONCLUSIONS

This outbreak highlights the complexities in investigating small-to-medium-sized, non-O157 STEC clusters: distinguishing primary versus secondary/household transmission posing challenges for analytical studies; obtaining epidemiological data from parents of clinically severe cases; and confirming microbiologically with a high-volume, long-life, imported product and low infective STEC dose. Nonetheless, descriptive epidemiological, food-chain and phylogenetic investigations strongly evidenced the likely vehicle being an imported preserved fruit product. This underscores the importance of iteratively building multi-source evidence for timely identification of unexpected but plausible food vehicles for prevention and response – critical with UK non-O157 STEC emergence.

KEYWORDS: Shiga toxin-producing Escherichia coli, Disease outbreak, Gastrointestinal diseases, Foodborne illness, Epidemiology,STEC
ABSTRACT ID: 352
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FIRESIDE SESSION 9

Day 3 – 11.00-12.30

Antimicrobial resistance

PRESENTER

Maeve Grifhorst

ABSTRACT

Novel multiplexed Nanopore sequencing-based approach: rapid detection of drug-resistance associated mutations in Mycobacterium tuberculosis

M. Grifhorst[1]
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[1] Department of Infectious Diseases, Public Health Service Amsterdam (GGD Amsterdam), Amsterdam, The Netherlands
[2, 4] National Institute for Public Health and Environment (RIVM), Bilthoven, The Netherlands
[3, 5, 6] Department of Infectious Diseases, Public Health Service Amsterdam (GGD Amsterdam), Amsterdam, The Netherlands

BACKGROUND

Emerging drug resistance in Mycobacterium tuberculosis (Mtb) poses a great threat to public health worldwide. Early diagnosis, combined with appropriate treatment, is essential in reducing transmission of drug-resistant strains. Therefore, it is crucial to develop innovative methods for the early detection of Mtb infections with drug-resistant strains. In the Netherlands, drug susceptibility testing is done nationally using culture followed by sequencing of strains via Illumina-based Whole Genome Sequencing (WGS). Culturing and WGS introduces a delay and requires an expensive bio-safety level 3 laboratory. In this study, we aimed to develop a low-cost, Nanopore sequencing-based diagnostic tool for the rapid detection of resistance-associated mutations (RAMs) that can also be used in low-resource settings.

METHODS

We designed a multiplex PCR using 21 amplicons of 500bp, covering 12 genes associated with resistance to the following 11 drugs: rifampicin, isoniazid, ethambutol, pyrazinamide, streptomycin, bedaquiline, linezolid, moxifloxacin, levofloxacin, clofazimine and amikacin. We estimated the technical sensitivity by comparing the detected RAMs in 24 Mtb strains using Nanopore sequencing to corresponding Illumina data.

RESULTS

With this approach we were able to obtain an elaborate resistance profile for 90.3% (28/31) of the RAMs detected by Illumina-based WGS, with a turnaround time of approximately 1-2 days. The 3 missed RAMs were not included in our current PCR. For the RAMs detectable with our amplicon-based PCR sensitivity was 100%.

CONCLUSIONS

Our targeted Nanopore sequencing-based approach is a promising and flexible tool for the rapid detection of RAMs, potentially also suitable for low-resource settings. Targeted sequencing approaches could contribute significantly to the early detection of drug-resistance, in settings where this was previously not possible. Further research should focus on their application in current clinical diagnostic workflows.

KEYWORDS: Nanopore Sequencing ,Public Health ,Drug Resistance Microbial ,Mycobacterium tuberculosis
ABSTRACT ID: 536

PRESENTED BY: Maeve Grifhorst | Netherlands | *mgrifhorst@ggd.amsterdam.nl*

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FIRESIDE SESSION 9

Day 3 – 11.00-12.30
Antimicrobial resistance

PRESENTER
Salam Abbara

ABSTRACT
Impact of antimicrobial resistance on recurrence after community-onset bacteremia

S. Abbara[1], D. Guillemot[2], S. El Oualydy[3], M. Kos[4], D. RM Smith[5], C. Poret[6], S. Breant[7], C. Brun-Buisson[8], L. Watier[9]
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[2] Institut Pasteur Paris|Versailles Saint Quentin en Yvelines University (UVSQ)|Institut National de la Santé et de la Recherche Médicale (INSERM)|Assistance Publique– Hôpitaux de Paris (AP-HP)
[3,4] Plateforme de données de santé - Health Data Hub (HDH)
[5] University of Oxford
[6,7] Assistance Publique– Hôpitaux de Paris (AP-HP)
[8,9] Institut National de la Santé et de la Recherche Médicale (INSERM)|Versailles Saint Quentin en Yvelines University (UVSQ)|Institut Pasteur Paris

BACKGROUND
Clinical consequences of antimicrobial resistance (AMR) remain insufficiently documented. Here, we investigate the impact of AMR in incident community-onset (CO) bacteremia on the probability of bacteremia recurrence within 1 year.

METHODS
A multicenter retrospective cohort study was conducted using the clinical data warehouse of Europe's largest university hospital group in Paris, France. Adult patients hospitalized with an incident community-onset Staphylococcus aureus, Escherichia coli or Klebsiella spp. bacteremia between 2017 and 2019 were included. Recurrence was defined as any clinically significant episode of bacteremia occurring 7-365 days after the incident episode. Risk factors of 1-year recurrence were assessed using Fine Gray regression models, and subdistribution hazard ratios (HR) were calculated.

RESULTS
Of the 3,617 patients included, 291 (8.0%) had at least one recurrence episode. Third-generation cephalosporin (3GC)-resistance was significantly associated with increased recurrence risk after incident Klebsiella spp. (HR 3.91 [2.32 – 6.59]) or E. coli (HR 2.35 [1.50 – 3.68]) bacteremia. Methicillin resistance in S. aureus bacteremia had no effect on recurrence risk (HR 0.79 [0.29 – 2.19]). Fine-Gray models limited to recurrence to the same or a different species, and stratified analysis by bacteria found comparable results. In addition, certain comorbidities (cancer, renal disease, liver disease) and infection sources (absence of an identified infection source, device-related infection, digestive tract infection) were associated with increased recurrence risk, with HR ranging from 1.2 to 2.3.

CONCLUSIONS
Resistance to 3GCs in Klebsiella spp. and E. coli in community-onset bacteremia significantly increases bacteremia recurrence risk over time. This risk was highest for 3GC-resistant Klebsiella spp., for which increasing community dissemination represents an urgent public health problem.

KEYWORDS: Recurrence,Bacteremia,Community-Acquired infections,Drug resistance microbial
ABSTRACT ID: 288
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FIRESIDE SESSION 10

Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER

Otilia Mardh

ABSTRACT

Upsurges in sexually transmitted infections among men who have sex with men and young populations in the EU/EEA: analysis of 2018-2022 surveillance data

O. Mårdh [1]
L. Champezou [2], J. Gomes-Dias [3], L. Nerlander [4]
[1] ECDC
[2, 3, 4] ECDC

BACKGROUND

In 2022, several EU/EEA countries reported upsurges in sexually transmitted infections (STIs) notifications via ECDC's event-based surveillance platform. Untreated bacterial STIs can impact both individuals and society. We describe trends in case notification for chlamydia, gonorrhoea and syphilis and identify population groups at-risk to inform public health actions.

METHODS

Data on confirmed cases of chlamydia, gonorrhoea and syphilis from 2018 to 2022 were retrieved from The European Surveillance System, including demographic information and transmission mode. The overall EU/EEA notification rates (NR) were calculated using data from countries with comprehensive surveillance. Trends in transmission mode were described using data from countries with >60% completeness of this variable. Percentage change in age-specific NR was calculated from 2021 to 2022.

RESULTS

For 2022, 216 508 chlamydia, 70 881 gonorrhoea and 35 391 syphilis confirmed cases were reported in EU/EEA. Compared to 2018, the overall EU/EEA NR increased by 15%, 59% and 41% respectively. Between 2018 and 2022, notified cases of chlamydia, gonorrhoea and syphilis increased by 72%, 65% and 20%, respectively among men who reported transmission due to sex between men (MSM), by 8%, 47% and 31%, respectively among women reporting heterosexual transmission and by 2%, 30% and 29% respectively among men reporting heterosexual transmission. In 2022, compared to 2021, age-specific NR for all STIs increased across age-groups over 14 years. Notably, gonorrhoea rates for 20-24-year-olds increased by 63% in women and 50% in men.

CONCLUSIONS

Recent increases in STI notifications in EU/EEA are of concern. In addition to MSM, young people aged 20-24 years are emerging as increasingly vulnerable to STI. While further data are collected to understand the drivers of these increases, immediate prevention and control efforts are warranted.

KEYWORDS: Sexually transmitted infections; MSM; young people; surveillance; EU/EEA; upsurge
ABSTRACT ID: 119
PRESENTED BY: Otilia Mardh | Sweden | *otilia.mardh@ecdc.europa.eu*

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FIRESIDE SESSION 10

Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER

Sebastian von Schreeb

ABSTRACT

Outbreak of Hepatitis A associated with sexual transmission among men who have sex with men (MSM) in Portugal, October 2023 to April 2024

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BACKGROUND

Portugal is experiencing an outbreak of hepatitis A. Early notified cases raised suspicions of sexual transmission among men who have sex with men (MSM). We combined genotyping and epidemiological analysis to identify the at-risk population and inform public health actions.

METHODS

We conducted a retrospective case-case study using reported hepatitis A cases from the National Epidemiological Surveillance System, comparing case characteristics during the outbreak period (Oct 2023 to April 2024) with a baseline period (Jan 2020 to Oct 2023). Serum and/or stool samples were genotyped by the national reference laboratory, using the international HAVNet-network protocol.

RESULTS

A total of 71 confirmed cases were reported from 7 Oct 2023 to 24 April 2024, significantly surpassing the incidence rates of previous years. Outbreak cases were more likely to be men (OR=4.0, 95%CI:2.0-9.0), aged 18-44 (OR=9.0, 95%CI:3.2-32.6), reported from the Lisbon region (OR=4.0, 95%CI:1.8-9.5), and reported as suspected sexual transmission (OR=18.3, 95%CI:5.2-88.3). Genotyped samples from 25 out of 29 tested patients were identified as subgenotype IA and highly similar (99-100% nucleotide identity) to the VRD-521-2016 strain, circulating during the 2016-2018 multi-country MSM-associated hepatitis A outbreak. Outbreak cases linked by genotyping differed from baseline on the same characteristics as in the main analysis. Public health actions included targeted traditional and digital communication campaigns, such as Grindr notifications.

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CONCLUSIONS

Our results suggest mainly sexual transmission among a MSM-subgroup and indicate the resurge of a viral strain not detected since the 2016-2018 outbreak. Early detection enabled prompt implementation of targeted interventions, including promoting vaccination as recommended for MSM in Portugal. This outbreak likely poses a trans-border health risk and we advise other countries to be vigilant, especially within active MSM-communities, to limit further transmission.

KEYWORDS: Syphilis,Congenital,Epidemiology,Seuxal health,Reproductive health,Public health,Portugal
ABSTRACT ID: 556
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Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER

Joseph Jasperse

ABSTRACT

Factors associated with late HIV diagnosis in England, 2015 to 2022

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BACKGROUND
Late HIV diagnosis increases the risk of premature mortality and onward transmission. Despite a decline in new HIV diagnoses in England over recent years, the proportion diagnosed late increased from 34% in 2015 to 44% in 2022. We analysed factors associated with late diagnosis to inform future testing strategy.

METHODS
We extracted data from the national HIV surveillance system on all new HIV diagnoses in England residents aged >14 years reported between 2015-2022. Late diagnosis was defined as a CD4 count <350 cells/mm3 within 91 days of diagnosis and no evidence of recent infection. Using multivariable logistic regression, we estimated associations between late diagnosis and age, gender, ethnicity, deprivation, rurality, region of birth and residence, exposure route, and diagnosis year/setting.

RESULTS
A total of 13,662 diagnoses were included, of which 5,408 (40%) were late. In men who have sex with men (MSM), the number of late diagnoses fell while the proportion diagnosed late rose from 20% (363/1,798) to 39% (170/435) between 2015-2022. Year-on-year increases in the odds of late diagnosis were evident among MSM over the study period (adjusted odds ratio: 1.14 per year, 95% confidence interval: 1.10-1.18) but not in individuals acquiring HIV from sex between men and women. Time-invariant factors associated with late diagnosis included older age (aOR: 1.34 per 10 years, 95% CI: 1.29-1.38) and, for individuals born outside the UK, Black African (1.55, 95% CI: 1.37-1.75) and Asian (1.81, 95% CI: 1.52-2.15) ethnicity.

CONCLUSIONS
Targeted HIV testing strategies should be prioritised for older individuals and non-UK-born ethnic minority groups. Further research into the drivers behind the increasing proportion of late-diagnosed cases in MSM is needed to inform future testing strategy for this population.

KEYWORDS: HIV,Epidemiology,Public health surveillance,England,Logistic regression
ABSTRACT ID: 236

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FIRESIDE SESSION 10

Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER

Roberto Croci

ABSTRACT

Are we reaching the HIV targets? Modelling-based estimates to assess the first UNAIDS goal, Denmark, 2023.

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BACKGROUND

UNAIDS has set a target that by 2025, 95% of people living with HIV (PLHIV) should know their HIV status. To monitor this goal in all key populations, including migrants, high-quality modelling estimates are needed. Previous Danish estimates from 2021 surveillance data quantified this proportion at 91%. We aimed to assess whether Denmark reached the target for 2023 and to obtain updated estimates of PLHIV by migrant status.

METHODS

We calculated HIV notification rates by dividing the number of incident cases from surveillance data by publicly available national denominators. We used the ECDC HIV modelling platform to obtain yearly total estimated numbers and proportions of PLHIV from the onset of the HIV/AIDS epidemic in Denmark in 1983 to 2023. We reported rates, proportions and 95% Confidence Intervals (CI) generated from parametric bootstrap analyses.

RESULTS

In 2023, 105 incident HIV cases were notified in Denmark. The notification rates per 100,000 population were 0.6 for Danish nationals and 11.7 for migrants. According to the ECDC HIV modelling tool estimates, 96.3% of PLHIV in Denmark were aware of their status in 2023 (95%CI 95.5-96.6). The estimated cumulative prevalence of unaware PLHIV per 100,000 population in 2023 was 4.2 (95%CI 3.8-4.9) for Danish nationals and 0.8 (95%CI 0.6-0.9) for migrants.

CONCLUSIONS

Denmark met the UNAIDS target in 2023. Migrants appear to have higher notification rates and lower unascertained HIV rates than Danish nationals. This could result from targeted screening for migrants from high-endemic countries and increased testing attributable to higher proportions of individuals at increased behavioural risk. Obtaining comprehensive and comparable national-level HIV estimates is essential to guide public health strategies to end the HIV/AIDS pandemic.

KEYWORDS: Models, Theoretical,HIV Infections/prevention and control ,Transients and Migrants/statistics and numerical data
ABSTRACT ID: 198
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FIRESIDE SESSION 10

Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER

Ayham Sawalmeh

ABSTRACT

Hepatitis B patients' adherence to treatment in relation to knowledge, attitudes, and practices (KAP) in the West Bank, Palestine, 2022-2023

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BACKGROUND

Poor adherence to hepatitis B treatment can lead to severe sequelae and increased health costs. We aimed to assess the levels of knowledge, attitudes, and practices (KAP) amongst patients in the West Bank, Palestine and identify factors associated with good adherence.

METHODS

We conducted a cross-sectional study among randomly selected hepatitis B patients visiting primary healthcare from all West Bank regions during October-2022 to June-2023. We used an interviewer administered questionnaire covering KAP regarding hepatitis-B. We considered adherence as good if participants received >90% of their monthly prescription antiviral doses. We calculated mean scores and classified the overall KAP score as good if all the knowledge, attitude and practice scores were good/positive (>20/24(>75%)). We calculated adjusted prevalence ratios (aPR) using log-binomial regression.

RESULTS

Among 386 participants, median age was 45 years (range 20-81); 80% had good adherence to treatment. Mean knowledge score was 11.4 (on a 13-point scale); mean attitude score was 3.4 (on a 4-point scale); mean practices score was 6 (on a 7-point scale); the mean overall KAP score was 21.8 (on a 24-point scale). After adjusting for age, gender, income, and level of education, participants with good KAP scores had better adherence to treatment than those without (aPR:1.41, 95%CI: 1.10-1.84).

CONCLUSIONS

Our study identified a significant association between good adherence to treatment to hepatitis B and overall good/positive KAP after adjustment for other factors. We recommend investment in targeted education and awareness campaigns to improve adherence as a cost-effective method towards regional and global elimination of hepatitis B

KEYWORDS: Hepatitis,Public health ,Communicable diseases,Health knowledge, attitudes, and practices
ABSTRACT ID: 87

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FIRESIDE SESSION 10

Day 3 – 11.00-12.30

Sexually transmitted infections

PRESENTER
Corinna Ernst

ABSTRACT

Syphilis outbreak among people who use drugs attending harm reduction settings, Luxembourg, December 2023-September 2024

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BACKGROUND

In June 2024, specialists working in harm reduction settings (HRS) in Luxembourg reported a marked increase in primary infectious syphilis among people who use drugs and requested treatment access for cases without social security. We describe an ongoing syphilis outbreak to inform timely detection and treatment approaches.

METHODS

A primary syphilis case was defined as an individual attending one of five HRS in Luxembourg, diagnosed clinically via point-of-care test or laboratory confirmation (Treponema pallidum IgM-antibodies) between 28/11/2023-09/09/2024. Treating healthcare workers (HCWs) completed questionnaires on case demographics, clinical presentation, treatment, socioeconomic factors, including housing, occupation, drug use, sexual behaviour and documented sexually transmitted infections (STI) since 2020.

RESULTS

Twenty-two cases (median age: 31, range: 20-43; 36% female) were identified, with the peak (7 cases) in June 2024. Nineteen (86%) primary cases were notified, and 3 (14%) detected through active case-finding were not notified. Data completeness varied by variable (36%-100%). 8/10(80%) lacked social security, 8/9(89%) experienced homelessness, and 11/13(85%) used drugs, primarily via sniffing (4/8,50%), injection (2/8,25%) or both (2/8,25%). 8/22(32%) cases were incarcerated during the past 12 months. 13/18(72%) were symptomatic, 10/22(45%) had a prior STI, and 15/22(68%) reported heterosexual contact as probable transmission route. 6/12(50%) reported engaging in sex work and 3/8(38%) reported contact with sex workers. We provided Benzathine penicillin G treatment to 16/22(73%) cases, recommended treatment of contacts and closely collaborated with the HRS staff and HCWs on-site.

CONCLUSIONS

Our outbreak investigation in Luxembourg shows that populations in HRS are vulnerable to syphilis outbreaks. HRS need to provide rapid diagnostic testing with immediate treatment, which requires close collaboration between HCW and public health authorities to increase timely access to healthcare.

KEYWORDS: syphilis,people who use drugs,sexually transmitted diseases,sex work, prison, Luxembourg
ABSTRACT ID: 778
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FIRESIDE SESSION 11

Day 3 – 14.00-15.30

Childhood vaccinations

PRESENTER

Susana Monge

ABSTRACT

Effectiveness of nirsevimab for the prevention of RSV hospitalisation in infants under 1 year of age: a population-based case control study in Spain, October 2023 – March 2024

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BACKGROUND

Respiratory Syncytial Virus (RSV) causes significant morbidity in infants <1 year. From October 2023, Spain recommended the monoclonal antibody nirsevimab to all children born ≥1 April 2023, at birth or as catch-up (if born before October 2023). We estimated nirsevimab effectiveness in preventing RSV hospitalisations during the 2023-24 season.

METHODS

Cases were children born ≥1 April 2023 admitted to public hospitals in 16 of 19 Spanish regions with respiratory symptoms, apnea or sepsis, and RSV PCR-positive. For each case, we selected 4 community controls born on the same date (±2 days) and province. An Intention-to-treat analysis was performed, considering as exposure the administration nirsevimab in days 0-13 of life (for at-birth-immunisation) or within 30 or, alternatively, 45 days after the campaign start (for catch-up-immunisation). Odds Ratio (OR), effectiveness [(1-OR)x100] and 95% Confidence Interval (95%CI) were estimated using conditional logistic regression, adjusting by sex, gestational age, birthweight, comorbidities and previous non-RSV-related hospitalisation.

RESULTS

We included 376 cases and 1496 controls in the at-birth-immunisation group (64% and 89% immunised); 370 cases and 1478 controls in the catch-up-immunisation (40-42% and 64-67% immunized, using as threshold 30-45 days) with complete data. Respective median time (interquartile range) from immunisation to matching was 40 (25-60) and 56 (24-83) days. Non-immunised children included late nisevimab administrations: 5% of cases and 4% of controls, in at-birth-immunisation; 1-3% of cases and 3-6% of controls, in catch-up-immunisation. Effectiveness was 83% (95%CI:77-88%) for at-birth-immunisation, and 75% (95%CI:67-81%) or 79% (95%CI:71-84%), using 30 or 45 days threshold, for catch-up-immunisation.

CONCLUSIONS

Nirsevimab was an effective population-level intervention, including for children born before the respiratory season. Our results can inform nirsevimab recommendations in Europe and elsewhere. A per-protocol effectiveness analysis is underway.

KEYWORDS: Respiratory syncytial virus (RSV), Immunisation, Nirsevimab, Evaluation, Effectiveness, Pediatric
ABSTRACT ID: 335
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Day 3 – 14.00-15.30

Childhood vaccinations

PRESENTER
Clara Mazagatos

ABSTRACT

Effectiveness of nirsevimab administration in newborns to prevent RSV hospitalisation: A test-negative case control study with SARI sentinel surveillance data in Spain

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BACKGROUND
The sentinel surveillance of severe acute respiratory infections (SARI) in Spain monitors SARS-CoV-2, influenza and RSV hospitalisations and provides data to measure the effectiveness of available immunisation strategies. Spain was one in four countries globally that recommended administration of nirsevimab to healthy newborns for season 2023-24. We aimed to estimate the effectiveness of nirsevimab administration in newborns to prevent RSV infections requiring hospitalisation.

METHODS
Using a test-negative case control design (TND) and SARI surveillance data from 15 hospitals in 8 regions in Spain, SARI patients born 1 October 2023 onwards were tested for RSV and classified as cases (positives) or controls (negatives). We restricted to children without comorbidities. We estimated the Odds Ratio (OR), effectiveness (1-OR) and 95% Confidence Intervals (95%CI) for the administration of nirsevimab (before disease onset) using a penalised logistic regression, adjusted by admission week, sex and age on admission.

RESULTS
Between October 2023 and February 2024, 69 cases and 138 controls were included, of which 46% and 87% had received immunisation with nirsevimab, respectively. Cases had a more severe clinical course than controls, in terms of need for mechanical ventilation (4% vs. 1%) and ICU admission (27% vs.13%). Effectiveness was 84% (67%;92%) overall, and 96% (83%;99%), 67% (2%;89%), and 73% (-46%;95%) for children aged 0-30, 31-60 and 61-90 days on admission, respectively.

CONCLUSIONS
Nirsevimab prevented 84% of RSV hospitalisations in healthy children born 1 October onwards, similar to clinical trials estimates. TND with SARI surveillance data provided consistent results in this population group, although information was insufficient to assess the effectiveness accounting for comorbidities, or in children born before the respiratory season, who were targeted in Spain for catch-up immunisation.

KEYWORDS: RSV,respiratory infections,surveillance,hospitalisation,immunisation
ABSTRACT ID: 661
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FIRESIDE SESSION 11

Day 3 – 14.00-15.30
Childhood vaccinations

PRESENTER
David Kelly

ABSTRACT

A reduction in geographical disparities in childhood vaccination coverage following the National 2018 mandatory vaccination law, Alpes-Maritimes, France

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BACKGROUND
In response to suboptimal vaccination coverage rates, France implemented a vaccination mandate in January 2018 for 11 childhood vaccines against diphtheria-tetanus-polio (DTP), pertussis (PER), haemophilus influenzae B (HIB), hepatitis B (HEPB), measles-mumps-rubella (MMR), pneumococcal (PCV) and meningococcal C (MENC) infection. We evaluated if the vaccine mandate had any impact on vaccination coverage and on geographical disparities among schoolchildren born in 2017, 2018 and 2019 in Alpes-Maritimes, south-eastern France.

METHODS
The Alpes-Maritimes council collects annual school vaccination records of children aged 3–4 years. For schoolchildren born in 2017, 2018 and 2019, we defined overall vaccination coverage as having received all age-appropriate doses according to the French National vaccine schedule, excluding MENC due to a recommendation update. We compared coverage for each vaccine and overall vaccination coverage between birth cohorts using a chi-squared test of homogeneity. We estimated the median overall vaccination coverage of the communes in Alpes-Maritimes and calculated the interquartile range to assess geographical disparities.

RESULTS
In total 9,584, 11,429 and 9,299 vaccination records were collected for schoolchildren born in 2017, 2018 and 2019. Comparing children born in 2017 versus 2019, vaccination coverage increased significantly ($p<0.001$) for HEPB (88.2% to 96.8%), MMR (88.1% to 94.1%), PCV (91.3% to 95.7%) and MENC (47.7% to 87.3%), and remained unchanged for DTP, PER and HIB. Overall vaccination coverage increased significantly from 75.9% to 82.8% ($p<0.001$). Median overall vaccination coverage of 98 communes progressively increased (74.3% to 83.3% to 88.3%), while the interquartile range decreased (16.9% versus 14.7% versus 13.8%) from 2017 to 2019.

CONCLUSIONS
Following the 2018 vaccination mandate, overall vaccination coverage among schoolchildren aged 3-4 years increased while geographical disparities in vaccination coverage reduced in Alpes-Maritimes, France.

KEYWORDS: vaccine-preventable diseases,vaccination coverage,mandatory vaccination,geographic disparities,France
ABSTRACT ID: 9
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Day 3 – 14.00-15.30

Childhood vaccinations

PRESENTER

Héloïse Lucaccioni

ABSTRACT

Influenza vaccine effectiveness among children and adolescents: results from the European VEBIS primary care multicentre study in the 2022/23 and 2023/24 seasons

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BACKGROUND

The World Health Organization suggests including children aged over 6 months in seasonal influenza vaccination campaigns may be beneficial; several European countries have implemented this guidance. The VEBIS primary care network conducted a multicentre test-negative case-control study in 10 European countries to measure influenza vaccine effectiveness (IVE) among children aged 6 months–17 years in the 2022/23 and 2023/24 seasons.

METHODS

General practitioners swabbed children presenting with acute respiratory infection, collecting information on demographics, vaccination and clinical characteristics. Cases were RT-PCR positive for any influenza virus; controls were negative. Using logistic regression, we calculated IVE adjusting for study site, age, sex, symptom onset date, and presence of chronic conditions. We estimated IVE overall and by age group.

RESULTS

In 2022/23 we included 10,368 patients; 3,286 were positive for influenza virus. In 2023/24, we included 6,016 patients; 1,353 were positive for influenza virus.In 2022/23, IVE against any influenza was 68% (95%CI: 59–76) among those aged 6 months–17 years. IVE was 78% (95%CI: 65–88), 68% (95%CI: 53–78) and 55% (95%CI: 26–74) among 6 months–4, 5–11 and 12–17 years, respectively.In 2023/24, IVE against any influenza was 71% (95%CI: 61–78) among those aged 6 months–17 years. IVE was 75% (95%CI: 63–84), 74% (95%CI: 55–86) and 53% (95%CI: 8–77) among 6 months–4, 5–11 and 12–17 years, respectively.Estimates were similar when restricting to children with comorbidities.

CONCLUSIONS

In both influenza seasons, high IVE among children supports their inclusion in routine influenza vaccination programmes. Further research on IVE across seasons and by (sub)type is warranted, to help provide evidence for countries considering inclusion of children in these programmes.

KEYWORDS: Influenza, influenza vaccine, vaccine effectiveness, multicentre study, case control studies, test-negative design,children
ABSTRACT ID: 103

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FIRESIDE SESSION 11

Day 3 – 14.00-15.30
Childhood vaccinations

PRESENTER
Pietro Ferrara

ABSTRACT
Evaluation of humoral immunogenicity to yellow fever vaccine in children younger than 2 years of age: a systematic review, meta-analysis, and meta-regression

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BACKGROUND
For individuals residing in or visiting endemic areas, the yellow fever (YF) vaccine is recommended from 9 months of age to prevent severe disease outcomes. However, previous evidence suggests that age under 2 years may compromise the immunogenicity of the YF vaccine due to the relative functional immaturity of the immune system. This study aims to synthesize existing evidence to elucidate the factors impacting the humoral response to primary YF vaccination in children below 2 years old.

METHODS
Studies examining the humoral response to primary YF vaccination in children aged 2 years or younger were reviewed through library databases and manual exploration of relevant literature. Meta-analysis employed a random-effects model to pool the proportion of children testing positive for vaccine-induced YF-specific neutralizing antibodies (referred to as humoral vaccine response rate, [VRR]). Additionally, subgroup and meta-regression analyses were conducted.

RESULTS
Based on studies conducted in YF-endemic areas, this research encompassed data from 23 articles involving 10,122 children. Within three months post-vaccination, the pooled VRR was 91.4% (95%CI 88.8–93.7). Meta-regression analysis demonstrated a higher VRR with the 17D-204 vaccine strain. No significant differences in immunogenicity were observed regarding administration method, concurrent vaccination, or fractional dosing. However, a decline in VRR over time was observed.

CONCLUSIONS
This systematic review and meta-analysis validate the robust immune response elicited by primary YF vaccination in children under 2 years old. The findings support previous evidence of a gradual decrease in humoral response to YF vaccination after 18 months, emphasizing the necessity of investigating long-term protection and the significance of cellular immunity in guiding potential booster strategies. Furthermore, this study opens new avenues for research, particularly concerning varying responses based on the vaccine strain.

KEYWORDS: Yellow Fever,Vaccination,Infant,Child, Preschool
ABSTRACT ID: 42
PRESENTED BY: Pietro Ferrara | Italy | *pietro.ferrara@unimib.it*

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FIRESIDE SESSION 11

Day 3 – 14.00-15.30

Childhood vaccinations

PRESENTER

Ivan Mlinaric

ABSTRACT

Interim analysis of pertussis outbreak in Croatia indicates the need for vaccine booster doses in adolescence, May 2023 – April 2024

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BACKGROUND

A rise in pertussis case numbers occurred in Croatia in 2023, resulting in the largest nationwide outbreak since 1958. Pertussis vaccination in Croatia is at 2, 4, 6, 15–18 months and 5 years. The aim of this study is to describe the outbreak and the cases as a basis for immunization program revision discussion.

METHODS

We analysed notifications received by the Croatian Notifiable Communicable Diseases Surveillance System. An outbreak case was defined using 2018 EU definition for surveillance of possible, probable or confirmed cases, living in Croatia with onset date from 15 May 2023 to 10 April 2024. We calculated age group specific incidences and described vaccination status.

RESULTS

Altogether 6400 cases (28 possible, 364 probable, 6008 confirmed) and no deaths were reported. The median age was 13 years (range 0–86 years, IQR 11–16 years), 52% (N=3338) were female. Overall incidence was 165 cases per 100,000 population. Incidence was highest in age groups 10–14 and 15–19 (1379 and 829 per 100,000, respectively). 24% of cases (N=1523) had unknown vaccination status, 54% were fully and 15% partially vaccinated. Among age groups 10–14 and 15–19, 62% and 71% of cases were fully vaccinated, respectively. Case numbers are steadily declining since January 2024.

CONCLUSIONS

Our analysis shows that the pertussis outbreak in Croatia affected mainly children aged 10–19 years, possibly due to expected waning immunity and low revaccination coverage. Different outbreak control immunization strategies (catch-up, cocooning and vaccination of pregnant women) have been applied mainly to protect the infants. Our results suggest the need to change the National immunization programme, adding new booster doses at ages 10 and 16.

KEYWORDS: Bordetella pertussis, outbreak, surveillance, Croatia
ABSTRACT ID: 190
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30

Late breakers

PRESENTER

Amy Douglas

ABSTRACT

Shiga toxin–producing Escherichia coli (STEC) O145:H28 outbreak linked to pre-packaged sandwiches in the UK, 2024

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BACKGROUND

Shiga toxin-producing Escherichia coli (STEC) is of public health concern due to the potential severity of illness, including sequalae such as Haemolytic Uraemic Syndrome (HUS). Non-O157 STEC serogroups cause large outbreaks of high severity. In May 2024 national gastrointestinal infections surveillance identified a fast-growing outbreak of STEC O145:H28 in England and Scotland.

METHODS

Confirmed cases across the UK were identified through routine whole genome sequencing. Routine surveillance questionnaires were used for descriptive analysis. A case-case study was undertaken for hypothesis generation using confirmed cases and non-outbreak English STEC cases. Hypotheses were tested using data from trawling questionnaires in an analytical case-control study. Market panel controls were recruited, frequency matched on age. Concurrent food-chain and microbiological investigations were undertaken.

RESULTS

There were 291 confirmed cases, with symptom-onset between 29/04/2024-16/08/2024; 58% of cases were female, the median age was 29 years (range 1-89 years), with 79% reporting bloody diarrhoea and 49% admitted to hospital. Nine cases developed HUS and two cases died. Case-case analysis identified pre-packaged sandwiches as a risk factor (OR=4.91, 95% CI=1.51-15.1, p=0.004).In the case-control study, eating a pre-packaged sandwich containing lettuce was identified as being associated with being a case (aOR=7.1, 95% CI=3.0-17.5, $p < 0.05$). Food chain investigations identified a lettuce product and a recall of affected products was initiated on 13/06/2024.

CONCLUSIONS

We report one of the largest outbreaks of STEC in the UK and demonstrate non-O157 STEC can cause clinically severe disease. Multiagency investigations led to rapid implementation of control measures. The risks associated with ready-to-eat products are highlighted, as well as the importance of effective control measures by manufacturers where the consumers are unable to implement risk mitigation.

KEYWORDS: Shiga toxin–producing Escherichia coli, STEC, gastrointestinal, UK
ABSTRACT ID: 824
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30

Late breakers

PRESENTER

Navina Sarma

ABSTRACT

Measles outbreak in a mass reception centre for refugees in Berlin, Germany, April-May 2024: A call for better protection of newly arriving refugees

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BACKGROUND

In spring 2024, a measles outbreak occurred in a reception centre for refugees from Ukraine and asylum seekers from other countries in Berlin, Germany. Unlike asylum seekers, refugees from Ukraine were not offered immunisation upon arrival. No transmission occurred outside the reception centre. We describe the outbreak focusing on the population at risk, transmission conditions, control measures, and public health lessons to improve protection for newly arriving refugees.

METHODS

We used data on socio-demographics, vaccination status, and clinical symptoms from the local health authority, the surveillance system, and administrative information from the centre operator. Cases were residents and staff with laboratory-confirmed or epidemiologically linked measles and symptom onset between 28/3-27/5/2024. The national reference centre performed laboratory confirmation and genotyping of clinical specimens.

RESULTS

52 cases were reported, including 51 refugees from Ukraine and one staff member, 54% females. Median age was 14.5 years (0-66, interquartile range: 5.75-33.2). Of these, 36 (69%) had no documented measles vaccination. 37 (71%) were PCR-confirmed, genotype D8 8782 was detected in 27 samples. All cases reported rash and fever, with 5 hospitalisations (2 for pneumonia). No deaths occurred. As a control measure, 2,541 of 6,922 individuals present during the outbreak were vaccinated due to lacking documented/presumed immunity.

CONCLUSIONS

The impact and duration of the measles outbreak was limited given the number of exposed people and crowded living conditions, underscoring the importance of prompt mass vaccination as a control measure. In the context of possible crisis-related low vaccination coverage in conflict settings and measles elimination goals, this outbreak highlights the need for host countries to offer recommended vaccinations to all reception centre residents upon arrival, regardless of their origin or residence status.

KEYWORDS: measles, refugees, vaccination,disease outbreaks,refugee camps
ABSTRACT ID: 705
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30

Late breakers

PRESENTER

Francesco Venuti

ABSTRACT

Automated detection of hospital outbreaks of antimicrobial-resistant bacteria in one Italian region, 2022 to 2024

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BACKGROUND

Antimicrobial resistance (AMR) is a critical public health issue. Automated tools for detecting hospital outbreaks of drug-resistant pathogens are essential for informing prevention and control interventions. For the first time in Italy, WHONET-SaTScan was used at a regional level in Lombardy to identify hospital outbreaks of pathogens associated with Healthcare associated infections (HAIs) beyond the EARS-Net priority pathogens.

METHODS

Microbiology data from the regional surveillance system, MICRO-BIO, covering 30 laboratories and 76 hospitals were analysed using WHONET-SaTScan to identify spatiotemporal clusters of drug-resistant pathogens. Cluster detection analyses were performed employing a simulated prospective analysis covering the first six months of 2024 and using the previous 24 months as historical data. A space–time uniform algorithm was used, and clusters were identified at three spatial levels: ward, groups of wards ('meta-wards'), hospital using a recurrence interval of 365 days for statistical significance.

RESULTS

The simulated prospective analysis included 41,435 isolates from 25,839 patients. Overall, 285 clusters were identified, with Enterococcus faecalis and Pseudomonas aeruginosa being the most frequently detected organisms. General medicine wards had the highest number of clusters detected (n=25, 6.9%). Clusters were primarily detected in large hospitals (92.9%) and at the meta-ward level (36.1%). There was no evidence for a difference in cluster length, cluster size, recurrence intervals, or days to first alert detected between the three spatial levels. Compared to small and medium-sized hospitals, clusters in large hospitals were larger ($p<0.001$) and accumulated cases for longer periods ($p=0.04$).

CONCLUSIONS

WHONET-SaTScan effectively identified clusters of drug-resistant pathogens consistent with hospital outbreaks. Its implementation as a real-time outbreak detection tool to support prevention and control interventions.would be particularly valuable in large hospitals.

KEYWORDS: Antimicrobial Resistance; Hospital-Acquired Infections; Drug Resistance, Microbial; Cluster Analysis; Surveillance
ABSTRACT ID: 776
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30

Late breakers

PRESENTER

Sara Mazzilli

ABSTRACT

Current resurgence of Bordetella pertussis in France, January-August 2024

Sara Mazzilli[1]
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[6]National Reference Center for Whooping Cough and other Bordetella infection, Institut Pasteur, Paris, France

BACKGROUND

Whooping cough (pertussis) can result in severe complications, including death, especially in infants. Following a period of low circulation in the EU/EEA, over 25,000 cases of pertussis were reported in 2023 and already 32,000 cases by March 2024. A similar resurgence occurred in France in early 2024. This analysis describes the pertussis resurgence and its burden in infants in France, January-August 2024.

METHODS

Pertussis is not a notifiable disease in France. Surveillance is conducted through multiple systems, including the RENACOQ network, a hospital-based sentinel system covering approximately 30% of hospitalized, laboratory-confirmed pertussis cases under 12 months (including demographic and vaccination data for children under six months only). Pertussis-related deaths were identified through electronic death certificates, covering about 66% of all deaths in children aged 0-14 years. We compared the number of pertussis hospitalizations and death in infants to the median case numbers for the same time period of 2019-2023.

RESULTS

Between 01/01-31/08/2024 RENACOQ reported 277 hospitalized infants, exceeding the previous years' numbers (median:34, range:1-55) and the numbers recorded during the last major outbreak in France in 2017-2018. Of the 220 (79%) cases under six months, 153 (55%) were too young for vaccination. Vaccination status was known for 38 of the 124 eligible infants, with 28 (74%) who received at least one dose. Twenty-one children died in 2024, 19 of whom were under 12 months, exceeding the previous years' numbers (median:3, range:0-5).

CONCLUSIONS

Our analysis revealed a significant rise in pertussis hospitalizations and deaths in France in 2024, primarily affecting infants under 12 months. These results underscore the importance of maternal vaccination as well as prompting health authorities to recommend a booster for professionals and other caregivers for infants.

KEYWORDS: Whooping Cough,Bordetella pertussis,Disease Outbreak,France
ABSTRACT ID: 724
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30
Late breakers

PRESENTER
Elena Pariani

ABSTRACT
Rapid escalation of enterovirus D68 cases in northern Italy associated with respiratory infection, August-September 2024

Elena Pariani[1]
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BACKGROUND
The emergence of enterovirus D68 (EVD68) as a notable respiratory pathogen with the potential to cause paralysis similar to poliomyelitis represents a significant public health concern. Nevertheless, no dedicated surveillance systems have been established in Europe to monitor EVD68. In response, a laboratory-based surveillance was conducted in Lombardy, Northern Italy, to assess the epidemiological and genomic features of enteroviruses.

METHODS
The study encompassed both outpatients presenting with influenza-like illness (ILI), identified within the respiratory virus surveillance system, and inpatients with severe acute respiratory infection (SARI) across 13 hospitals. Samples positive for EV were tested by a real-time RT-PCR assay for the detection of EVD68. The VP1/VP3 gene was sequenced.

RESULTS
A total of 506 respiratory EV-positive samples were collected between 1 January and 19 September 2024. Of these, 42.1% were from ILI outpatients and 57.9% from SARI inpatients. EVD68 was identified in 21.3% (n= 108) of EV-positive samples of which 79.6% in SARIs. The mean weekly EVD68 positivity rate was 4.4% (range: 0%–25%) up to 15 July 2024. Subsequently, a statistically significant increase was observed, reaching 49.4% (range: 5.6%-96.2%) as of 19 September 2024. From 19 August onwards, EVD68 constituted approximately 90% of EV cases. The median age of those testing positive for EVD68 was 39 years (interquartile range: 59 years), and 55.3% of these individuals were male. The preliminary sequence data indicate that the lineage is B3. Whole genome sequencing is ongoing.

CONCLUSIONS
The shift in the age profile, coupled with the high prevalence of EVD68, indicates that the outbreak predominantly affects adults. These findings emphasise the necessity for enhanced laboratory surveillance and rapid diagnostic capabilities for EVD68 to inform public health interventions.

KEYWORDS: respiratory infection; laboratory-based surveillance; genomic surveillance; enterovirus; enterovirus D68
ABSTRACT ID: 782
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FIRESIDE SESSION 12

Day 3 – 14.00-15.30

Late breakers

PRESENTER

Teresa Nygren

ABSTRACT

Outbreak of myocarditis in children in Germany, 2024: Rare complication of parvovirus B19 or something new?

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BACKGROUND

In July 2024, 4 children with myocarditis (aged 7–20 months) were admitted to one German hospital, 3 of whom died within 3 days. Parvovirus B19 (B19V) was detected in all 4 children, known to rarely cause myocarditis. We started investigating whether an outbreak of acute B19V-myocarditis occurred, locally or nationwide, and whether B19V virulence had increased.

METHODS

Cases were defined as children (<18 years) with acute myocarditis and PCR-confirmed B19V infection in myocardium or blood with disease onset since 01.01.2024 in Germany. We descriptively analysed case data from the paediatric myocarditis registry MYKKE with cardiopathological analyses of endomyocardial biopsies. As a B19V-activity proxy, we analysed B19V notifications in one federal state where detection is notifiable. B19V virulence assessment of clinical specimens was initiated.

RESULTS

The MYKKE registry showed an increase in B19V-myocarditis in 2024 compared to previous years, with 27 cases as of 26/08/2024 (median 2013–2023: 11 cases/year). There was only sporadic PCR co-detection of other routinely tested cardiotropic pathogens. Cases occurred nation-wide. Of cases with information available, 65% (17/26 cases) were <2 years old, 58% (15/26) were female, 85% (23/27) had histologically confirmed myocarditis, and 81% (21/26) occurred in April–July 2024. B19V-notification incidence in 2024 was 4.5-fold increased compared to the median incidence from 2016–2023, peaking in April 2024.

CONCLUSIONS

Investigations revealed a nation-wide increase of acute B19V-myocarditis, mainly affecting children <2 years of age. The strong post-pandemic B19V season may explain this myocarditis increase. Laboratory investigations on virulence are ongoing. B19V infection prevention is challenging, as it occurs pre-/asymptomatically. We have raised clinicians' awareness via paediatric professional societies and the MYKKE registry to speed up patient referral and harmonise treatment options and thus improve clinical outcomes.

KEYWORDS: Parvovirus B19,Myocarditis,Child,Incidence,Disease Outbreaks
ABSTRACT ID: 716
PRESENTED BY: Teresa Nygren | Germany | *nygrent@rki.de*

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POSTER TOURS

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POSTER TOUR 1

Day 1 – 15.30-16.30
Healthcare associated infections

PRESENTER
Anna Bludau

ABSTRACT

Identification of risk factors for hospital-onset bacteremia to inform a routine data based risk prediction– an umbrella review

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BACKGROUND
Hospital-onset bacteremia (HOB) places an enormous burden on affected patients, healthcare workers and society. It is important to identify patient groups – and ideally individual patients – with the highest risk of HOB in order to intensify infection prevention/control measures. The overarching goal of the national BMBF-funded project RISK PRINCIPE (RISK Prediction for Risk-stratified INfection Control and PrEvention, Grant number: 01ZZ2323A) is to develop and implement a data-driven, risk stratified infection control system to effectively and efficiently reduce HOBs. To understand infection-related risks, the aim of the umbrella review was to identify, classify, and potentially weigh already known risk factors for the onset of HOBs and support algorithm development.

METHODS
We searched CINAHL, Medline, Cochrane Library and Web of Science. Abstracts and full text were screened by two independent reviewers according to predefined criteria. Discrepancies were resolved by a third reviewer. We included systematic reviews reporting risk factors for the onset of HOB in all inpatients in OECD countries published since 2013. Risks of bias were assessed using AMSTAR2. The review was reported according to the Preferred Reporting Items for Systematic Review and Meta-analysis (PRISMA) guidelines. A narrative synthesis approach was used to interpret the results. PROSPERO registration: CRD42023480112

RESULTS
From 1668 screened records, 20 systematic reviews reporting 50 individual risk factors for different stages of HOB and patient populations were included. We categorized the risk factors into patient-related (e.g. immunosuppression, comorbidities, male sex, preterm birth, smoking, vitamin D deficiency), procedure-related (e.g. length of stay, regular admission, device utilization, catheter placement/type) and setting-related (multiple-bed rooms).

CONCLUSIONS
These findings support the development of routine data-based risk prediction for the targeted identification of high-risk patients and the corresponding resource allocation.

KEYWORDS: bacteremia, hospital, infection control, health care rationing, risk factors
ABSTRACT ID: 252
PRESENTED BY: Anna Bludau | Germany | *anna.bludau@med.uni-goettingen.de*

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Day 1 – 15.30-16.30

Healthcare associated infections

PRESENTER
Emna Mziou

ABSTRACT

Healthcare associated infections in Intensive Care Units: prevalence and associated factors

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BACKGROUND

Healthcare associated infections (HAIs) represent a serious and frequent problem in intensive care units (ICUs). Many factors could be potentially involved through invasive medical procedures which are required on patients who are most often in critical condition.In this context, our study aimed to determine the prevalence of HAIs in ICUs and to identify their associated factors.

METHODS

We conducted a cross-sectional survey between February and March 2023 in the ICUs of the two University Hospitals in Southern Tunisia.We included all patients who were present at 8:00 a.m. on the day of the survey. HAIs were defined according to the criteria of the Centers for Disease Control and Prevention. The ICUs included medical, surgical, and pediatric ICUs, emergency medical aid services, and neonatology departments.

RESULTS

We recorded 18 cases of HAIs among 90 patients investigated in the ICUs. The prevalence of HAIs was 20%. The sex ratio was 1.72. The median age was 58 years(Interquartile range(IQR)=[42.5-70.5]). The median length of stay was four days(IQR=[2-11]). Sepsis was the most common HAI(8 cases; 44.4%).A length of stay greater than or equal to seven days was significantly associated with the occurrence of HAIs(77.8% VS 22.2%;Odds ratio(OR)=6.58;p=0.001).In addition, HAIs were significantly more frequent in patients with hypertension(37.9% VS 11.5%;OR=4.71; p=0.003)and diabetes(35.7% VS 12.9%;OR=3.75;p=0.012). Moreover, HAIs were significantly associated with the installation of invasive medical devices, such as central venous vascular catheter(37.9% VS 25%;OR=4.71;p=0.003), intubation(41.2% VS 15.1%;OR=3.9;p=0.037), mechanical ventilation(30.8% VS 11.8%;OR=3.33;p=0.026),as well as bladder catheter(30% VS 12%;OR=3.14;p=0.034).

CONCLUSIONS

We noted high rates of HAIs in the ICUs in our hospitals. A global policy for the prevention and control of HAIs is urgent, the pillars of which will certainly be compliance by staff with hygiene precautions.

KEYWORDS: healthcare associated infection, intensive care units; ,prevalence
ABSTRACT ID: 626
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Day 1 – 15.30-16.30

Healthcare associated infections

PRESENTER

Baiba Niedre-Otomere

ABSTRACT

Identification of the main genomic clusters of carbapenem-resistant Klebsiella pneumoniae in the healthcare network by whole genome sequencing in Latvia

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BACKGROUND

The threat to the healthcare of carbapenem-resistant Klebsiella pneumoniae (CRKp) is amplified by the spread of convergent strains with acquired virulence determinants. Reports on carbapenem-resistance, convergence and genomic epidemiology of K. pneumoniae from the healthcare network in Latvia have been lacking. Submission of CRKp to the National Microbiology Reference Laboratory is mandatory. We used whole-genome sequencing (WGS) to identify genomic clusters, carbapenemases and convergence.

METHODS

We conducted a WGS-based retrospective study of 295 CRKp submitted from 9 laboratories covering 15 healthcare facilities from May 2022 to June 2023, matched with the isolation site, collection date and patient records. Clusters were identified by core genome multilocus sequence typing with maximal pairwise allelic difference (cgMLSTdmax) of 20. Sequence type (ST), capsular antigen locus (KL) type, carbapenemases and convergence were determined by Klebsiella spp. specific genotyping tool.

RESULTS

We identified a major cluster (91 cases; 108 isolates; cgMLSTdmax 20) of ST147 (KL64) spanning 11 healthcare facilities, most isolates (n=84) sustained CRKp spread in the Central tertiary care hospital 1. Majority co-produced carbapenemases OXA-48 and NDM-1 (n=72) and were convergent (n=105). The other cluster (30 cases; 32 isolates; cgMLSTdmax 17) of the non-convergent OXA-48 producer ST219 (KL114) was shared between the Central tertiary care hospitals 1 and 2.The introduction of the non-convergent KPC-3 producer ST512 (KL107) in the Central hospital 1 in March 2023 by migration from Ukraine advanced to establishment (27 cases; 29 isolates; cgMLSTdmax 7), one case from the Central hospital 2 had a preceding hospitalisation at the Central hospital 1 overlapping the introduction.

CONCLUSIONS

WGS spotted the genomic clusters in the healthcare network, including the migration-introduced source-isolate. The study has established a ground for continuing the genomic surveillance.

KEYWORDS: Carbapenem-resistant Klebsiella pneumoniae,Whole genome sequencing,Carbapenemase,Latvia
ABSTRACT ID: 230

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POSTER TOUR 1

Day 1 – 15.30-16.30
Healthcare associated infections

PRESENTER
Matt Wilson

ABSTRACT
Trends in critical care unit associated Gram-negative bloodstream infections and associated antibiotic resistance in England between 2017 and 2023: a data linkage study

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BACKGROUND
Rates of hospital-onset (HO) Gram-negative bloodstream infections (GNBSIs) in England reached their highest point in 2020/21, coinciding with the beginning of the COVID-19 pandemic. GNBSIs pose a large antimicrobial resistance (AMR) threat. There is limited national data on critical care unit (CCU)-associated GNBSI incidence and related AMR.

METHODS
Reports of HO Escherichia coli, Klebsiella spp. and Pseudomonas aeruginosa bacteraemia between 2017-2023 were extracted from UKHSA's mandatory bacteraemia surveillance system and linked to the Second-Generation Surveillance System to obtain AMR results, and to Hospital Episode Statistics to determine whether cases were CCU-associated. We estimated the incidence of CCU-BSIs over time and compared AMR in CCU-BSIs vs. other hospital-onset BSIs (HO-BSIs).

RESULTS
Of 70,867 HO GNBSIs identified during the surveillance period, 5,616 (7.9%) were determined to be CCU-BSIs. Incidence of E. coli, Klebsiella spp., and P. aeruginosa CCU-BSIs per 10,000 bed-days increased from average pre-pandemic rates of 3.4, 2.8, and 1.3, respectively, to 3.5, 6.3, and 2.6 in 2020/21, before decreasing to 2.5, 3.4, and 1.5 in 2022/23.AMR in CCUs increased in 2022/23 following reduced resistance in 2020-2022. For P. aeruginosa, across the surveillance period, CCU-BSIs exhibited higher resistance than HO-BSIs to carbapenems (19% resistant in CCU-BSI vs. 11% in HO-BSI), ceftazidime (15% vs. 9%), and piperacillin/tazobactam (17% vs. 10%). Elevated AMR in CCUs was also seen for E. coli to piperacillin/tazobactam (18% vs. 14%).

CONCLUSIONS
The COVID-19 pandemic saw increased rates of Klebsiella spp. and P. aeruginosa CCU-BSIs, which have since reduced towards pre-pandemic levels. Resistance to several antibiotics in CCU-BSIs is higher than in other hospital settings, particularly for P. aeruginosa. These findings underscore the importance of antimicrobial stewardship in CCUs.

KEYWORDS: Critical Care,Gram-Negative Bacterial Infections,Antibiotic Resistance,England,Public Health Surveillance,Bacteraemia
ABSTRACT ID: 63
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POSTER TOUR 1

Day 1 – 15.30-16.30

Healthcare associated infections

PRESENTER
Tomasz Kasperski

ABSTRACT

Acinetobacter baumannii PCR-based replicon typing and resistance genes among isolates from pneumonia and skin and soft tissue infections from patients in southern Poland.

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BACKGROUND
Acinetobacter baumannii (AB) is an opportunistic pathogen, dominant in Central/Southern Europe in Healthcare associated infections. In Polish hospitals, especially in intensive care units, there is a predominance of carbapenem-resistant AB, which in 2021 reached over 80% according to ECDC. The present study investigated AB resistance genes and the type of plasmids on which they are carried.

METHODS
In 2019-2020, 40 strains were collected from pneumonia (PNEU) and 40 strains from soft and skin tissue infections (SSTI) from patients from hospitals in the southern Poland. The antimicrobial susceptibility to 14 agents was studied and interpreted according EUCAST or CLSI criteria (cefiderocol and ampicillin/sulbactam). Resistance plasmids were typed by AB PCR-based replicon typing method which groups them into 19 homology groups (GRs). Screening for carbapenem resistance genes was performed by multiplex PCR.

RESULTS
All AB strains were resistant to carbapenems, fluoroquinolones, piperacillin/tazobactam, and tripetoprim/sulfamethoxazole. They showed the highest susceptibility to colistin (100%), cefiderocol (100%) and gentamicin (40%). No significant differences were found between the susceptibility of strains isolated from PNEU and SSTI.The presence of plasmids from the GR2 group was confirmed in 75 strains. Most strains with this type of plasmid (85.3%) carried the blaOXA24/40-like gene, 24% had blaOXA23-like, 4% had the blaNDM and 1.3% had the blaOXA58-like.

CONCLUSIONS
The susceptibility of carbapenems resistant strains to cefiderocol indicates its promising role but its place in the treatment of AB infections remains debated in the literature.The present study revealed that most strains carry GR2 plasmids with the blaOXA24/40-like gene, highlighting the epidemic nature of carbapenem-resistant AB and emphasizing the need for comprehensive genomic surveillance and targeted infection control strategies to identify multidrug-resistant pathogens.Founded by the National Science Centre, no.2020/39/O/NZ7/00145

KEYWORDS: Acinetobacter baumannii, plasmid replicon typing,resistance genes,pneumonia,skin and soft tissue infection
ABSTRACT ID: 278
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POSTER TOUR 1

Day 1 – 15.30-16.30
Healthcare associated infections

PRESENTER
Amy Weaver

ABSTRACT

Nosocomial outbreak of Ralstonia pickettii linked to internationally distributed sodium chloride products, United Kingdom 2023-2024.

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BACKGROUND
Ralstonia pickettii is an environmental waterborne bacteria known to cause opportunistic infections, with capacity to contaminate healthcare products. In late 2023, UKHSA were informed by Australian counterparts of a Ralstonia pickettii outbreak associated with contaminated saline products. We describe the detection and management of a linked outbreak of Ralstonia pickettii in the UK.

METHODS
Case finding was conducted using the national laboratory surveillance system and direct communication with hospitals. Isolates were submitted for whole genome sequencing analysis at the UKHSA national reference laboratory.Investigation comprised trawling questionnaires and targeted product sampling. Investigation and risk mitigation required a muti-stakeholder approach, including direct engagement between the manufacturer and UK medicines regulator.

RESULTS
Between September 2023 and January 2024 three confirmed and two probable cases were identified across the UK at separate hospitals. Confirmed case isolates were genetically indistinguishable from strains isolated in Australia with 0-4 single-nucleotide polymorphism differences over 4,218,213 sites, consistent with a common source.Cases were aged 4 to 63 years (median 51), 3 (60%) cases were male. Confirmed cases all had Ralstonia pickettii isolated from blood cultures, all had clinically significant infections and indwelling lines.Control measures included voluntary recall of the product and accompanying information for healthcare professionals and the public.

CONCLUSIONS
Ralstonia pickettii is a rare but important cause of healthcare product contamination. Public health institutions should adopt a low threshold for investigation of opportunistic pathogen clusters, including Ralstonia pickettii, with consideration for possible product contamination. Management of contamination events is complicated by global distribution chains; it is important to consider control measures may not be comprehensive. Our experience highlights the importance of intelligence sharing and international collaboration to protect patients and the public.

KEYWORDS: Ralstonia pickettii, healthcare associated infection, bacteraemia, epidemiology
ABSTRACT ID: 504
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POSTER TOUR 1

Day 1 – 15.30-16.30
Healthcare associated infections

PRESENTER
Juliette Cavaye

ABSTRACT

An outbreak of carbapenemase-producing Enterobacterales (CPE) in a new-build single bed-room specialist cardiothoracic hospital in England, 2024

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BACKGROUND
Globally, hospitals are experiencing increases in CPE (carbapenemase-producing Enterobacterales) bacteria that can cause antibiotic-resistant infections. Investigation into a CPE outbreak at a new-build single-bed-ward cardiothoracic hospital in England occurred after the detection of two clinical cases. Understanding transmission dynamics and the impact of control measures is crucial for preparation for increasing Healthcare based CPE outbreaks.

METHODS
A case was defined as a hospital in-patient testing PCR-positive for CPE (KPC-2 mechanism) from June 2024. Admission and weekly rectal screening was conducted for patients on the same floors as the clinical cases. Screening positivity rates were calculated before and after implementation of control measures. 35 environmental samples were collected. Whole-genome sequencing (WGS) of clinical and environmental samples was performed to understand relatedness. In-hospital movements of cases were plotted to identify common exposure areas.

RESULTS
33 cases were identified; 31 detected through screening and two in clinical samples. The clinical cases were closely related on WGS, indicating in-hospital transmission. Four environmental samples were CPE-positive; WGS ruled out relatedness for three samples; one sample (from a floor scrubber) was distantly related to the clinical samples. No common exposure areas among cases were identified. Control measures included increased screening, paused elective surgeries, cohorting positive patients, “double” chlorine cleaning, suspending floor scrubbers, staff education, and increased contact precautions. Screening positivity rates dropped from 11.9% to 0.4% after control measure implementation.

CONCLUSIONS
Despite the hospital's modern design, CPE spread rapidly across multiple areas. Comprehensive control measures contained the outbreak. A definitive link between clinical and environmental isolates was not found but cannot be discounted. With rising global CPE prevalence, our findings highlight the need for strict infection control, even in state-of-the-art hospitals, to prevent future outbreaks.

KEYWORDS: Carbapenemase-producing Enterobacterales,Health Care Associated Infections,Hospital Design and Construction,Outbreak
ABSTRACT ID: 761
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POSTER TOUR 2

Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Patrizia Centorame

ABSTRACT

Comparing Observed Iso- and non-isothermal Listeria monocytogenes Growth with Model Predictions Under dynamic Conditions

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BACKGROUND
With global food chains becoming increasingly complex, dynamic temperature fluctuations are more frequent and risks increase of allowing Listeria monocytogenes reach high levels of contamination and cause severe foodborne disease. In recent years, there has been substantial activity within the European Union (EU) to provide information on how to conduct shelf-life studies in ready-to-eat foods to ensure conformance to the EU microbiological criteria. Predictive microbiology has a central role in interpreting the results of challenge tests and extending their application.

METHODS
In this study a food-associated strain of L. monocytogenes was grown in broth under different temperature conditions, comparing isothermal (constant temperature) and non-isothermal (variable temperature) conditions that reflects real-world food storage scenarios. Isothermal conditions of 4, 8, 10 and 12°C and non-isothermal including growth at 4°C followed by a shift to 12°C, and vice versa, were used.

RESULTS
The non-isothermal data was used to estimate a secondary model and interpolate a growth rate for 8°C, which was similar to the isothermal result. Observations revealed that the L. monocytogenes growth rate was slightly higher under non-isothermal conditions than predicted from the isothermal-derived secondary model. This suggests the possibility of a 'hysteresis' effect: a phenomenon in which the output (growth rate) is not only dependent on the current input (temperature), but also its past (previous temperature).

CONCLUSIONS
This research contributes novel data, with full sets of data for both isothermal and non-isothermal growth, comparisons of predictions from both sets to the other, introducing a novel mechanism in predictive microbiological modelling. By incorporating real-world temperature dynamics, these findings add complexity to our understanding of bacterial growth and could enhance the accuracy of shelf-life predictions in food safety management.

KEYWORDS: Listeria monocytogenes,Isothermal,non-isothermal,Dynamic,Food safety,predictive microbiology
ABSTRACT ID: 251
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POSTER TOUR 2

Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Ariana Wijermans

ABSTRACT

ESBL-producing Salmonella Kentucky cluster linked to locally produced eggs, August 2023, Malta

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BACKGROUND
Emergence of multidrug-resistant bacteria is a public health concern worldwide. In August 2023, two hospitalised cases of Extended-spectrum beta-lactamases (ESBL) producing Salmonella Kentucky, were reported from the same locality in Malta. An outbreak investigation was initiated on 21/08/2023 to identify a common source.

METHODS
We conducted phone interviews (case investigations) to identify common food exposures. Based on these, further investigations included traceback investigations and health and veterinary inspections at affected retail points and suppliers. All positive Salmonella samples of humans, food and environment were further characterised by serotyping, antimicrobial susceptibility testing and subsequent whole-genome sequencing using Illumina (clusters: <10 Single Nucleotide Polymorphism (SNP)).

RESULTS
The cases' food history identified the consumption of eggs from the same farm. In the subsequent traceback investigations five farms supplying this farm were identified. The human isolates clustered phylogenetically with each other (0 SNPs) and were 23 SNPs related with a sample from a laying hen from one of these supply farms that tested positive for ESBL-producing Salmonella Kentucky. Several inconsistencies in the farm were identified including antibiotic misuse and improper separation of flocks irrespective of age. No culling/targeted measures could be implemented as presently within EU (Regulation No.2160/2003) and Maltese legislation (LN225 of 2012) Kentucky is not a target species. No additional related cases were identified through routine surveillance.

CONCLUSIONS
This outbreak investigation successfully linked human cases to a local egg-producing farm in Malta, highlighting the importance of One Health in the context of such outbreaks, and the possibility of ESBL-producing Salmonella transmission via food from laying hens to humans. We recommend adapting existing local/EU legislations to include relevant Salmonella strains or multidrug-resistant bacteria to prevent foodborne zoonotic transmission of these pathogens.

KEYWORDS: Foodborne Outbreaks,Salmonella Kentucky,ESBL,eggs,Whole Genome Sequencing
ABSTRACT ID: 439
PRESENTED BY: Ariana Wijermans | Malta | *ariana.wijermans@gov.mt*POSTER TOUR 2

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Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Esther Schol-van Puffelen

ABSTRACT

Come rain or shine? Outbreak of gastroenteritis after a swimming competition in open water.

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BACKGROUND

On September 12, 2022, the public health centre of West-Brabant, The Netherlands, received multiple signals of people getting ill, mainly vomiting and/or diarrhea, after attending a 2-day national swimming competition in open water. Therefore, we decided to conduct a retrospective cohort study and examined the environment of the swimming competition to get a picture of the magnitude and severity of the disease and to find the source.

METHODS

An online questionnaire was send to those who were present at the event in which presence, nature and extend of health complaints were asked as well as exposure to potential sources. Relative risks (RR) and adjusted odds ratios (aOR) were calculated with corresponding 95% confidence intervals (CI).

RESULTS

In total, 253 persons filled out the questionnaire of whom 193 were contestants (response 63%) and 60 were others present at the event. Of all respondents, 153 (60.5%) reported at least one gastro-intestinal symptom. The epidemiological curve is suggestive for a single point source. Four out of five fecal tests showed norovirus. Swimming was a significant risk factor for gastro-intestinal symptoms (aOR 5.86 [95%CI 2.24-15.34]). Subgroupanalyses of the contestants showed that swimming on Saturday was strongly associated with gastro-intestinal symptoms compared to swimming on Friday (aOR 26.97 [95%CI 8.42 – 86.39]). Environmental investigation showed sewage overflow after rainfall on Saturaday morning.

CONCLUSIONS

This outbreakstudy showed that the most likely source of this outbreak of gastro-enteritis amongst contestants of the swimming event in open water was sewage overflow after rainfall. These findings emphasize the need to explore on beforehand which factors might influence the quality of the water. It should also be determined per event which circumstances reduce the safety of the contestants.

KEYWORDS: Outbreak, event, swimming, gastroenteritis, epidemiology, sewer
ABSTRACT ID: 224
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POSTER TOUR 2

Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Eunice Stiboy

ABSTRACT

Where the cooling water drifts: An outbreak of Legionella pneumophila serogroup 1 in Sydney, Australia, 2024

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BACKGROUND

Legionnaires' disease causes severe pneumonia. Outbreaks are infrequent in Australia, with cooling water systems (CWS) regulated to reduce risk. In summer 2024, a Legionella pneumophila serogroup 1 (Lp1) outbreak was detected in visitors to the Sydney central business district (CBD). We investigated to identify cases and control the source.

METHODS

Case-patients were detected through routine laboratory notifications and classified as per surveillance case definitions. Case-patients were interviewed to determine symptoms, and environmental exposures 2-10 days prior to symptom onset. We mapped exposure sites and used a 500m radius buffer to identify overlapping areas for investigation. CWS in shared exposure areas were inspected and tested for Legionella. Historical results from routine CWS testing were reviewed. Genomic sequencing was performed on environmental and patient isolates. Clinician and public alerts were issued, and CBD building managers were requested to maintain CWSs.

RESULTS

The investigation identified 15 legionellosis case-patients; 2 had positive sputum cultures, 14 were hospitalised, 6 required intensive care. All case-patients visited the CBD between 12-26 December 2023. Between 3-12 January, 166 CWS across 118 sites, plus three water fountains were tested. Lp1 was isolated from one CWS. Genomic sequencing from five environmental and two clinical isolates showed a probable link. The positive CWS was decontaminated but continued to have Lp1 detected, possibly due to ongoing dust contamination, necessitating additional maintenance. Weeks later, a case-patient diagnosed in Europe was epidemiologically linked to the outbreak.

CONCLUSIONS

Our investigation indicates a contaminated CWS may have been the source of this outbreak, potentially precipitated by nearby construction. This emphasises the importance of strengthening Australian CWS regulations to reduce outbreak risk, and timely reporting under International Health Regulations to identify additional outbreak cases.

KEYWORDS: Legionnaires Disease,Legionella Pneumophilia,Legionella outbreak,Cooling tower contamination
ABSTRACT ID: 413
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Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Subhi Alshaer

ABSTRACT

Investigation of an acute watery diarrhea outbreak among students of a Police College in the Jericho district of Palestine

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BACKGROUND

On 12/11/2023 an outbreak of acute watery diarrhea at the Police College Training Centre in Jericho, Palestine was reported. The Ministry of Health's Preventive Medicine and Environmental Health Department (PMEHD) promptly investigated to identify the cause and implement control measures.

METHODS

On 12/11/2023, PMEHD conducted an inspection. We defined a case as a student or staff member experiencing vomiting and/or diarrhea starting from 01/11/2023. We conducted a retrospective cohort study and administered a web-based questionnaire to 145 individuals. Samples were collected from food stored in the college kitchen, water tanks, swabs from an external water cooler and internal water taps, and feces specimens from students, staff, and food handlers.

RESULTS

We identified 35 cases (attack rate=24.14%). Age range was 18-22 years with 91.42% (n=32) females. Vomiting and watery diarrhea affected 75.43% and 85.77% of cases, respectively. All were exposed to internal water taps. Fifty-five people (including all female cases) used an external water cooler near the female dormitory, 35 (63.63%) of whom became cases. Exposure to the external water cooler was associated with illness (RR=17.45, 95% CI=13.77-22.08). Laboratory analyses indicated mixed fecal contamination in the water cooler. Analysis of internal water taps, food contamination and stool testing yielded negative results for viral, bacterial, and parasitological profiles.

CONCLUSIONS

Mixed fecal contamination in an external water cooler was the likely source of the outbreak. Immediate replacement of the cooler and water chlorination were crucial to prevent further contamination. Community awareness campaigns on safe water practices and hygiene were implemented. The importance of regular monitoring of water quality, vigilance in stool testing, and prompt reporting of any new incidents will help mitigate the impact of similar outbreaks.

KEYWORDS: waterborne disease, outbreak, diarrheal, outbreak investigation, Palestine.
ABSTRACT ID: 654

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POSTER TOUR 2

Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Verónica Mixão

ABSTRACT

A multi-country and intersectoral assessment of cluster congruence between different bioinformatics pipelines used in genomics surveillance of foodborne bacterial pathogens

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BACKGROUND

Foodborne diseases surveillance requires Whole-Genome Sequencing (WGS)-based systems following a One Health approach. However, different laboratories employ different WGS workflows, casting doubt on the comparability of results and hindering effective communication at intersectoral and international levels. Through a collaborative effort involving nine European institutes across seven countries and spanning the food, animal and human health sectors, we aimed to assess the inter-laboratory comparability of WGS clustering results for four foodborne pathogens: Listeria monocytogenes, Salmonella enterica, Escherichia coli and Campylobacter jejuni.

METHODS

Each institute applied its routine surveillance pipeline over the same WGS datasets (>2000 isolates per species). Genetic clusters were identified at each possible allele/SNP distance threshold. Inter-pipeline clustering congruence was assessed by calculating a “Congruence Score” (relying on Adjusted Wallace and Adjusted Rand coefficients) across all resolution levels, followed by a comparison of cluster composition at outbreak level.

RESULTS

There is a general high congruence between allele-based pipelines at all resolution levels for all species, except for C. jejuni, where the different resolution power of available allele-based schemas led to discrepancies. Still, non-negligible differences were found in outbreak clusters detection, suggesting that a cutoff flexibilization is important for the detection similar outbreak signals by different laboratories. This data, together with the observation that different clonal complexes and serotypes exhibited remarkably different genetic diversity, should be considered in future threshold selections for outbreak case definitions.

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CONCLUSIONS

This study provides valuable insights into the comparability of pipelines commonly used for genomics surveillance, and reinforces the need, while demonstrating the feasibility, of conducting continuous and comprehensive WGS pipeline comparison studies. Our work contributes to a smoother WGS typing data communication towards an efficient One Health surveillance.

KEYWORDS: One Health,Genomics,Disease Outbreaks,Cluster Analysis
ABSTRACT ID: 459
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Day 1 – 15.30-16.30

Epidemiology of food- and waterborne diseases

PRESENTER

Chris Williams

ABSTRACT

Multi-organ complications identified ≥1 year after Shiga-toxin producing Escherichia coli O157 (STEC O157) infection and STEC-associated haemolytic uraemic syndrome (STEC-HUS), Wales, 1990-2020

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BACKGROUND

Information on chronic sequelae following Shiga-toxin producing Escherichia coli (STEC) infection is limited. We describe long-term complications experienced up to three decades after STEC O157 and STEC-associated haemolytic uraemic syndrome (STEC-HUS).

METHODS

We compared complications in individuals ≥1 year after STEC O157 or STEC-HUS to general population comparators. The exposed were residents in Wales registered with a General Practitioner (GP) practice with laboratory confirmed STEC O157 with earliest specimen date (study entry date) between 01/01/1990-01/01/2019. STEC-HUS was defined as hospitalisation (ICD-10: D59.3) within 28 days of entry date. The unexposed were age and sex equivalents (4:1 matching ratio) and assigned the same entry date. Follow-up was through multiple linked data sources until the first of: complication, emigration, death or study end (01/01/2020) ≥1 year after entry date. Complications were categorised as renal, neurological, cardiac, gastrointestinal or respiratory, and as mild (GP), severe (hospital) or either based on the data source. Hazard ratios (HR) and 95% confidence intervals (95%CI) were calculated for time-to-complication.

RESULTS

We identified 1,245 individuals with STEC O157, 53 of which developed HUS (4.2%). Renal (STEC O157: 26%), STEC-HUS: 36%), respiratory (STEC O157: 30%), gastrointestinal (STEC O157: 9.3%, STEC-HUS: 15%) and cardiac (STEC-HUS: 15%) complications were more common in the exposed vs unexposed. Individuals with STEC O157 were more likely to experience gastrointestinal (adjusted (a)HR: 1.6, 95%CI: 1.2-1.9) and respiratory (aHR: 1.3, 95%CI: 1.2-1.5) complications. HRs for all complications, except neurological, were elevated following STEC-HUS, ranging from 9.1 (95%CI: 2.4-35) for gastrointestinal to 1.8 (95%CI: 1.0-3.3) for respiratory.

CONCLUSIONS

Long-term complications were identified in up to one in three after STEC O157 and STEC-HUS. We recommend that individuals exposed to STEC be monitored for late-emerging complications.

KEYWORDS: STEC, STEC-HUS,Shiga-toxin producing Escherichia coli,long-term,chronic,complications
ABSTRACT ID: 170
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POSTER TOUR 3

Day 1 – 15.30-16.30

Emerging and vector-borne diseases

PRESENTER
Jasmin Metz

ABSTRACT

Epidemiological investigation of a multistate leptospirosis outbreak linked to pet rats (Rattus norvegicus forma domestica) in Germany, 2022–2023

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BACKGROUND

Leptospirosis is a bacterial infection that can be acquired through contact with the urine of infected rodents. In August 2023, the Bavarian Health and Food Safety Authority received reports of two severe human leptospirosis cases in Hesse, Germany, linked to pet rats from a Bavarian breeder. We initiated an investigation to determine the existence of an outbreak, assess the source, and establish control measures to prevent further cases.

METHODS

We alerted health and veterinary authorities at the breeder's county of residence and reviewed notified leptospirosis cases to evaluate potential links with the outbreak. We identified households that documents showed had potentially adopted infectious rats from the breeder, informed them about the infection risk, and sent each household an online questionnaire to assess risk factors. The national consultant laboratory for leptospirosis offered households free urine tests to assess acute infections in rats and serology tests (IgG/IgM) for household members.

RESULTS

Our investigation revealed two additional severe, hospitalised cases connected to the breeding site: one person who adopted a rat (symptom onset 06/2023), and the breeder (symptom onset 06/2022), who had not disclosed breeding of rats as possible infection source. We contacted 38 adopting households, of which 11 (29%) responded to our survey. Participants reported risk factors such as close physical contact with rats, bites, or exposure to rat urine. Of 56 rat urine samples, 9 yielded positive results. Serological testing of 30 household members revealed four additional cases of Leptospira infection (3 persons with IgM, 1 with IgM/IgG).

CONCLUSIONS

This outbreak underlines infection risks to humans posed by pet rats as carriers of Leptospira and a need for awareness among owners. We recommend owners consider testing rats before adoption.

KEYWORDS: leptospirosis,pet rats ,Rattus norvegicus forma domestica,outbreak,leptospira
ABSTRACT ID: 267
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Day 1 – 15.30-16.30

Emerging and vector-borne diseases

PRESENTER

Lucie Fournier

ABSTRACT

Unprecedented number of imported cases and autochthonous transmission in Northern France: was 2023 a tipping point for dengue in mainland France ?

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BACKGROUND
Aedes albopictus, a mosquito vector of dengue, was first established in mainland France in 2004. Since then its presence has considerably expanded, resulting in local dengue transmission. We set up an enhanced surveillance and response system to limit the risk of local dengue transmission. We describe the results of this surveillance for 2023.

METHODS
Epidemiological surveillance for dengue relies on mandatory notification. It is enhanced from May to November, when Aedes albopictus is active: to prevent or limit local transmission, awareness-raising campaigns targeting health professionals, daily monitoring of major laboratory platforms for active case finding and investigations to ascertain place of infection and of viremia are implemented. Vector control measures are implemented around both imported and autochthonous cases. Locally acquired cases trigger door-to-door cases-finding surveys, extensive vector control measures and community outreach.

RESULTS
In 2023, 2524 imported cases of dengue were identified, the highest number since surveillance began. Most imported dengue cases had travelled to the French Antilles where a dengue epidemic occurred. Nine autochthonous transmission events of dengue were detected, amounting to 45 cases. They were limited in size (11 cases for the largest) and in duration (9 weeks for the longest). For the first time, autochthonous dengue transmission was detected in the northern half of France, in the Paris region.

CONCLUSIONS
In 2023, we observed an unprecedented number of imported dengue cases and a high number of local transmission events. This data shows the ability of enhanced dengue surveillance to rapidly contain local transmission, highlighting the value of its continued implementation. We now face the following challenge: How can enhanced surveillance and vector control be maintained given the rising numbers of cases and limited resources?

KEYWORDS: Dengue,Public Health Surveillance,France,Autochthonous Transmission
ABSTRACT ID: 100
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POSTER TOUR 3

Day 1 – 15.30-16.30

Emerging and vector-borne diseases

PRESENTER

Nelly Fournet

ABSTRACT

Five autochthonous dengue cases and the first local transmission in the Paris region in 2023

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BACKGROUND

Aedes albopictus, a mosquito vector for dengue, was detected in Île-de-France (IdF: Paris and Greater Paris area) in 2015. It has since continuously expanded in the region, which, associated with population movements to and from dengue-endemic areas, results in an increasing risk of local transmission.

METHODS

Dengue is a mandatory notifiable disease year-round in mainland France. Autochthonous cases are those that develop signs with no travel history or 15 days after traveling. Active case finding aims to identify other cases and determines the extent of autochthonous transmission and control efforts.

RESULTS

In 2023, 5 autochthonous dengue cases were identified in IdF.A case suffered from homozygous sickle-cell disease, received multiple blood transfusions and kidney transplantation in 2020. He returned from Martinique 37 days before disease onset and had positive RT-PCR. It was impossible to conclude whether this fatal infection was acquired locally or imported.Another case presented fever 5 days following kidney transplantation, tested positive DENV-2 PCR and died 10 days later. Investigation found that the kidney donor returned from Martinique one month earlier, had a negative PCR on graft biopsy but positive IgM/IgG serology.Lastly, a family cluster of three confirmed dengue cases following autochthonous mosquito transmission with no travel history was detected in October 2023.

CONCLUSIONS

The first two cases illustrate the complexity of some investigations and suggest that a much longer incubation period than expected and a longer presence of the virus in the kidney of an imported donor are possible. The locally acquired cluster was the northernmost vectorial transmission of dengue in Europe. Immunocompromised and transplanted persons require particular vigilance. Early case detection, investigation and response are needed to contain dengue in Europe.

KEYWORDS: Vector-borne disease, surveillance, mandatory reporting
ABSTRACT ID: 690
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Day 1 – 15.30-16.30

Emerging and vector-borne diseases

PRESENTER
Ulyana Gubareva

ABSTRACT

Orthohantavirus seroprevalence among high-risk adults in western Kazakhstan, 2023

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BACKGROUND

Orthohantaviruses are emerging zoonotic pathogens with global distribution transmitted to humans primarily by small rodents. Western Kazakhstan is an endemic region, but infections are likely underdiagnosed due to limited testing and awareness in the community and among clinicians. We aimed to estimate antibody seroprevalence and identify associated factors.

METHODS

Using a cross-sectional design, we systematically sampled adults living in 14 villages in two endemic districts of Western Kazakhstan in June-July 2023. Investigators interviewed consenting participants and drew blood for orthohantavirus-specific IgG antibody and serotype testing. Poisson regression was used to estimate prevalence ratios (PR) for factors associated with orthohantavirus antibodies.

RESULTS

Among 921 participants, 63% were female, median age was 53 years, 72% resided in single-family houses, and 38% encountered with rodents. IgG antibody seroprevalence was 3.1% (95% confidence interval [CI]: 2.1-4.3). Among seropositive samples (n=28), 18 (64%) were consistent with Puumala orthohantavirus. Cross-reactivity with multiple orthohantavirus was observed in 12 (43%) samples, including one reactive for Hantaan and Dobrava-Belgrade viruses. Among seropositive participants, none reported a history of hantavirus diagnosis or had hantavirus-consistent illness in the past year. Seropositivity was associated with having a blue-collar job (PR=4.1, 95%CI=1.0–27.5), observing rodent activity indoors in the past year (PR=7.3, 95%CI=1.3–53.5), and living near a pond, which is an important rodent habitats (PR=11.5, 95%CI=1.6–54.7). Regular use of gloves for outdoor work was associated with reduced likelihood of seropositivity (PR=0.4, 95%CI=0.2–1.0)

CONCLUSIONS

We document that hantavirus infection is underdiagnosed in western Kazakhstan. Additional community and clinician awareness of hantavirus may improve routine case detection. Infection was associated with rodent activity and habitats, highlighting the importance of rodent control and precautions to reduce risk of hantavirus exposure.

KEYWORDS: Hantavirus infection,Orthohantavirus ,Kazakhstan,Seroprevalence ,Zoonoses,Occupational Exposure
ABSTRACT ID: 409
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POSTER TOUR 3

Day 1 – 15.30-16.30

Emerging and vector-borne diseases

PRESENTER

Brigitte Ho Mi Fane

ABSTRACT

Highly Pathogenic Avian Influenza A H5N1 infections in domestic poultry and human contacts in the Fraser Health region, British Columbia, Canada

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BACKGROUND

Since 2022, Highly Pathogenic Avian Influenza (HPAI) A (H5N1) virus infections, coinciding with migratory bird seasons, have affected farmed poultry in British Columbia (BC), Canada. Majority of Infected Premises (IP) were in the Fraser Health (FH) region. We compared HPAI activity over two seasons in FH and assessed public health interventions uptake for human contacts to identify changes in distribution of HPAI detections and understand implications for practice.

METHODS

We performed descriptive analysis on IP reported in the 2022-23 and 2023-24 seasons to assess geographic and temporal distribution of HPAI detections in farmed poultry. We calculated proportions of human contacts potentially exposed to HPAI A H5N1 for contacts management.

RESULTS

During the 2022-23 and 2023-24 seasons, there were respectively 72 and 49 HPAI infected poultry premises, accounting for 89% and 96% of notifications in BC. Compared with the prior season, 2023-24 season peaked earlier, was shorter, had fewer IP reported per week and was more widespread across FH. There were 146 and 103 human contacts identified in 2022-23 and 2023-24 seasons respectively. Seasonal influenza vaccine and post-exposure prophylaxis acceptance were low. Of the 4 symptomatic contacts reported in both seasons, no human cases were detected. In the 2023-24 season, 45% of contacts identified with high exposure risk were lost to or refused follow-up.

CONCLUSIONS

Our findings highlight the critical role of surveillance and characterization of human exposures to HPAI to swiftly identify cases, describe epizootics emergence, and inform risk assessment and interventions. Engaging with agricultural partners and swift information sharing from national to regional levels across public and animal health authorities are recommended for effective prevention and control strategies, more importantly given recent HPAI detections in livestock.

KEYWORDS: Avian Influenza,Surveillance,Emerging infectious disease,Zoonotic spillover
ABSTRACT ID: 607

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Day 1 – 15.30-16.30

Public health sciences (general)

PRESENTER

Rebecca Marshall

ABSTRACT

Public Health Challenges in Contact Tracing of Leprosy, Ireland, August 2024.

Rebecca Marshall[1]
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BACKGROUND
We present a case of multibacillary leprosy with neurological involvement in a Haitian male living in a congregate setting in Cork, Ireland. This was the first case of leprosy notified in the South of Ireland in the last decade and presented complex public health challenges with contact tracing given the highly stigmatising nature of this neglected tropical disease, and absence of Irish guidelines for this disease.

METHODS
Comprehensive contact tracing was undertaken in household and occupational settings, and among social networks of the index case. A rapid scoping review of international guidelines was undertaken. We defined a close contact as any person who had been in contact with the untreated index case for at least 20 hours/week, for at least three months in the preceding year. Chemoprophylaxis with single dose Rifampicin was offered to close contacts.

RESULTS
Three individuals were identified as close contacts and administered chemoprophylaxis. Ten other individuals were considered possible close contacts; two of whom had left the country. Contact tracing decisions for all exposed individuals needed to be weighed against the decision to disclose potentially stigmatising information. Most international guidance in relation to contact tracing is from low/middle income countries, including settings where leprosy is endemic, and was often not directly applicable in the Irish context. An extensive public health risk assessment informed our decision not to classify the remaining seven individuals as true close contacts.

CONCLUSIONS
This case presented significant challenges for contact tracing in a high-income setting and highlighted the relevance of EU countries to have their own guidance for the public health management of certain neglected tropical diseases, especially given recent trends of global migration.

KEYWORDS: Leprosy,Public Health,Contact Tracing,Risk Assessment
ABSTRACT ID: 749
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POSTER TOUR 4

Day 1 – 15.30-16.30

HIV intervention strategies

PRESENTER

Liza Coyer

ABSTRACT

Integrating hepatitis C screening and treatment into routine HIV care in Cameroon is feasible

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BACKGROUND

People with human immunodeficiency virus (HIV) and Hepatitis C virus (HCV) are vulnerable to worse clinical outcomes. Yet, HCV prevalence among people with HIV in Cameroon remains unknown, with diagnosis and treatment largely inaccessible. Integration of HCV services into routine HIV care by general practitioners could improve diagnosis and treatment coverage. We aimed to determine HCV screening acceptability, prevalence, and treatment cure rate among people with HIV attending 11 HIV clinics in the Centre Region of Cameroon.

METHODS

We offered HCV rapid antibody screening, and, if positive, an RNA test to all attendees of routine HIV counselling and treatment appointments between 20 April 2021 and 31 May 2022. Screening acceptability was measured in a sub-study in 5/11 clinics. HCV-RNA-positive participants received 12 weeks of pangenotypic sofosbuvir/velpatasvir (400/100mg). We calculated the cure rate as the proportion of participants with a sustained virological response 12 weeks after treatment completion (SVR12) among all starting and completing treatment.

RESULTS

We screened 8,266 (29.9%) of 27,606 individuals on HIV antiretroviral therapy known to receive HIV care from participating clinics as of December 2020. In the sub-study, 256/510 (50.2%) accepted screening. 316/8,266 (3.8%, 95%CI=3.4-4.3%) were anti-HCV positive. Among 286 sampled for HCV-RNA, 251 (87.8%) had detectable HCV-RNA. The cure rate was 93.6% (n=162/173, 95%CI=88.9-96.8%) among those enrolled for treatment and 98.2% (n=162/165, 95%CI=94.8-99.6%) among those completing treatment.

CONCLUSIONS

Our study demonstrates the viability of integrating HCV screening and treatment into routine HIV care in Cameroon, yielding new HCV diagnoses and high cure rates. Cameroon can use this strategy to achieve its HCV elimination goals, although improvements in screening acceptability, diagnosis and treatment access and laboratory capacity are needed.

KEYWORDS: Hepatitis C,Implementation Science,Diagnosis,Treatment,HIV,Africa
ABSTRACT ID: 374
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POSTER TOUR 4

Day 1 – 15.30-16.30

HIV intervention strategies

PRESENTER

Boxuan Wang

ABSTRACT

Optimising HIV pre-exposure prophylaxis eligibility in men who have sex with men in 10 European countries: a modelling study and cost-effectiveness analysis

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BACKGROUND

Men who have sex with men (MSM) remain at high risk for HIV in Europe, with significant disparities in Pre-exposure Prophylaxis (PrEP) eligibility and accessibility. This study evaluates the impact of various PrEP eligibility criteria on HIV prevention and the cost-effectiveness of PrEP interventions across ten European countries.

METHODS

We employed a network-based, dynamic, stochastic model to simulate HIV transmission within MSM populations, comparing different PrEP eligibility guidelines. The model integrated data on sexual behavior, PrEP adherence, and healthcare costs, projecting HIV incidence and the economic outcomes of PrEP policies over a 20-year period.

RESULTS

The analysis demonstrated that PrEP policies in the US and Belgium were most effective in reducing HIV cases and deaths, attributed to higher PrEP coverage. The WHO policy was identified as the most cost-effective, achieving significant health outcomes with minimal coverage. Notably, except in low-prevalence settings, all PrEP policies substantially reduced HIV transmission. Economic evaluations indicated that PrEP interventions are generally cost-effective, with the WHO policy consistently offering the greatest economic benefit.

CONCLUSIONS

The study underscores the importance of optimizing PrEP eligibility criteria and coverage to maximize HIV prevention efforts in Europe. High-coverage PrEP strategies, supported by comprehensive reimbursement policies, are crucial for enhancing PrEP accessibility and effectiveness. Our findings advocate for informed policy-making to leverage the full potential of PrEP in the global fight against HIV, albeit with consideration for the limitations of our modeling approach.

KEYWORDS: HIV,Agent-based Modelling,Policy comparison,Cost-effectiveness analysis,Pre-exposure prophylaxis
ABSTRACT ID: 552
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POSTER TOUR 4

Day 1 – 15.30-16.30

HIV intervention strategies

PRESENTER

Zoran Milosavljevic

ABSTRACT

Prevalence and predictors of chemsex practice among people living with HIV in Serbia

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BACKGROUND

Chemsex is characterized by the use of specific drugs—methamphetamine, gamma-hydroxybutyrate (GHB), and mephedrone—in sexualized settings. This behavior has been on the rise the past few years. The risk of contracting sexually transmitted infections and HIV, as well as drug-drug interactions, increases in chemsex parties with multiple sexual partners and, therefore, represents a serious emerging public health problem. The purpose of this study was to estimate the prevalence and factors associated with chemsex practice in people living with HIV (PLWH).

METHODS

We conducted a cross-sectional study with 326 PLWH living throughout Serbia. Participants responded to a questionnaire covering their demographic data, health behaviors, duration of having HIV, their viral load, and substance use with a focus on chemsex drugs. We used an adjusted logistic regression model to identify predictors for chemsex practice among PLWH.

RESULTS

Of the 326 participants living with HIV, 287 (88%) were male and 39 (12%) were female. 77.4% of males identified themselves as men who have sex with men (MSM). A total of 20.6% of men (59/287) and 5.1% of women (2/39) confirmed current chemsex practice. Among people who practiced chemsex, 88.5% were from the MSM population. Being younger (odds ratio [OR]=0.94; 95% confidence interval [CI] 0.84-0.99), knowing their current PCR result/viral load (OR=7.57; 95%CI 1.19-48.08), alcohol intake (OR=3.47; 95%CI 1.60-7.53), cocaine use (OR=6.56; 95%CI 2.15-20.00), and poppers use (OR=9.29; 95%CI 4.21-20.47) were associated with practicing chemsex among PLWH.

CONCLUSIONS

One in five PLWH in Serbia practices chemsex. Younger PLWH, as well as those who use other psychoactive substances, are more likely to engage in chemsex. Supporting PLWH to reduce psychoactive substance use is necessary to improve their well-being and prevent HIV transmission.

KEYWORDS: chemsex, people living with HIV, prevalence, predictors, Serbia
ABSTRACT ID: 595
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Day 1 – 15.30-16.30

HIV intervention strategies

PRESENTER

Sophia Chkonia

ABSTRACT

Evaluating the Impact of Healthcare Providers' Attitudes and Practices on the Prioritization of Patients with Recent HIV Infections on the Yield of HIV Testing Services in Rwanda

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BACKGROUND

The HIV/AIDS epidemic in Rwanda remains a significant challenge, with observed national progress towards UNAIDS 95-95-95 targets. The case-based surveillance program, featuring recent infection testing, seeks to enhance identification of HIV cases. This study aimed to examine the impact of healthcare provider (HCP) attitudes and practices on prioritizing recent infection cases on contact yield in Rwandan healthcare facilities.

METHODS

Data from 60 facilities in Rwanda were collected by ICAP at Columbia University. HCP attitudes and practices were assessed using self-administered questionnaires, and their impact on total contacts elicited per facility was evaluated. HCP demographics were assessed as covariates. The total of HIV-positive cases enrolled in index testing was assessed as a covariate and an effect measure modifier. Poisson regression and negative binomial regression was used due to overdispersion in count data. Statistical analyses were conducted with R Studio.

RESULTS

35% of HCPs believed index testing services should be prioritized for certain patients, most of whom were patients with recent results. Poisson regression analysis showed that facilities with at least one HCP reporting a belief in prioritization of cases with recent infections had 20% higher expected count of total contacts elicited (95% CI: 1.07, 1.35) compared to facilities where no HCP held this belief, adjusting for total indexes. No other significant findings were observed.

CONCLUSIONS

The significant findings imply that HCP attitudes may influence contact yield and impact HIV prevention strategies, pointing to interventions emphasizing the prioritization recent infection cases for triage and contact elicitation. However, there was a lack of significant findings in the negative binomial regression models. Future studies should consider a larger sample size, explore additional covariates, and a longitudinal study design to establish causal relationships.

KEYWORDS: HIV,Surveillance,Health Personnel,Rwanda
ABSTRACT ID: 382
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Day 1 – 15.30-16.30

HIV intervention strategies

PRESENTER
Evelina Pridotkiene

ABSTRACT

Risk behaviour patterns among people who inject drugs and services provided in Lithuania: cross sectional study report from 2023

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BACKGROUND

Substance use and injecting drug use in particular are related to health damages, reduced quality of life and life expectancy. Injecting drug use is a risk factor for acquiring infectious disease among people who inject drugs (PWID). The aim of the study was to assess the risk behaviour related to the use of intravenous psychoactive substances among PWID in Lithuania.

METHODS

In 2023 a cross sectional study using respondent driven sampling (RDS) of active intravenous drug users (n=370) was conducted in 5 different sites across Lithuania. RDS is a sampling methodology based on peer-referral in underserved populations that cannot be sampled randomly. Descriptive statistical and regression analyses were conducted using SPSS 23.0.

RESULTS

78% of the sample were males, 22%-females. Age mean is 40.6 years, SD-7.7. The first injecting drug was used at the age of 18 (mode). 69% of PWID received drug dependance treatment at least once in life. 70% of the PWID in harm reduction services are also in the substitution therapy programmes. Fentanyl is the main substance for every second respondent which is injected 3 times a day and commonly used with alcohol (64%). 79% of PWID during the last injection used sterile needles and syringes. 45% of respondents reported overdosing during the last 12 months and half of all PWID had naloxone for death prevention. Nearly 70% were tested for TB and syphilis during the last 12 months.

CONCLUSIONS

PWID are mainly males who began injecting drugs at 18 years. Unsafe injecting behaviour (frequency and mode), using alcohol were related to lower participation in health care services for PWID.

KEYWORDS: Health care services, injecting drug use, psychoactive substance use, PWID.
ABSTRACT ID: 506
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Day 1 – 15.30-16.30

International health and migration

PRESENTER
Peter Kirwan

ABSTRACT

Adjusting for seroconversion and migration in the CD4 back-calculation method for HIV incidence estimation

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2, 3, 4, 5, 6, 7, 8

BACKGROUND
Back-calculation is used to estimate unobserved incidence and undiagnosed HIV prevalence by linking a model of infection and disease progression to observed HIV diagnosis and CD4 count data. The model is implemented annually for gay and bisexual men (GBM) in the United Kingdom (UK) to assess progress towards HIV elimination, and was adapted for use in the ECDC HIV Modelling Tool. Two current limitations of the model are: 1) individuals are increasingly likely to be diagnosed during seroconversion, when a transient dip in CD4 count may occur, so an individual's progression towards AIDS may be incorrectly classified; and 2) estimates do not account for population migration, so the model is ill-suited to groups with large migrant populations. We aim to address these limitations by incorporating both a recent infection biomarker and migration information into the model.

METHODS
The existing (CD4-only) model was extended to a 'dual-biomarker' model by the inclusion of recent infection states, informed by serological tests for recent infection (RITA). Both models were applied to diagnosis data for UK GBM between 2011-2019 and compared.

RESULTS
Between 2011-2019, RITA information was available for 59% of HIV diagnoses among GBM. Estimated HIV incidence in 2019 was 1020 (95% credible interval (CrI) 540-1790) using the CD4-only model, and 960 (95% CrI 630-1570) using the dual-biomarker model. Estimates of undiagnosed HIV prevalence from the dual-biomarker model were significantly lower than those from the CD4-only model, particularly during earlier years.

CONCLUSIONS
Incorporation of additional biomarker information in the back-calculation model improved estimate precision, with undiagnosed prevalence estimates closer to those from other methods. Work is ongoing to include migration probabilities, informed by routine migration statistics, relevant to UK heterosexual populations.

KEYWORDS: HIV, Biomarkers, Incidence, CD4, Seroconversion, Transients and Migrants
ABSTRACT ID: 602
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POSTER TOUR 5

Day 1 – 15.30-16.30
Burden of disease

PRESENTER
Jizzo Bosdriesz

ABSTRACT
Individual and environmental determinants of differences in excess mortality between neighbourhoods in Amsterdam during the COVID-19 pandemic

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BACKGROUND
During the COVID-19 pandemic, excess mortality compared to previous years was observed in the Netherlands, while inequalities in COVID-19 incidence and mortality were apparent across individual and environmental indicators. We studied variability in excess mortality in Amsterdam during 2020 and 2021, and its association with individual and environmental factors.

METHODS
Municipal registry data were used, including date of death, age, sex, and migration background for all residents who died between 2018 and 2021. We calculated excess mortality ratios (number of deaths during the pandemic divided by the pre-pandemic number of deaths), and compared these between groups on age, sex, migration background, and city district. These ratios were merged on city district level with environmental data (neighbourhood demographics, population density, household size, healthcare availability, greenspaces, air pollution, socio-economic status, and vaccination coverage). We used multivariable Poisson regression to determine factors associated with pandemic mortality, adjusting for pre-pandemic mortality.

RESULTS
Excess mortality was highest amongst 70-89 year olds, men, and people with non-western migration backgrounds. Excess mortality varied between city districts (range: 1.09-1.37). Regression analyses showed that districts with a higher percentage of elderly residents, a larger household size, and more air pollution were significantly associated with higher pandemic excess mortality. Districts with more general practitioners nearby, more public greenspaces, and a higher neighbourhood-level socioeconomic status were associated with lower pandemic excess mortality.

CONCLUSIONS
We observed significant differences in excess mortality with individual factors such as migration background, that match known patterns of health inequalities, and environmental factors such as air pollution and availability of healthcare. When developing and targeting interventions to address inequalities in health, issues at both the individual and neighbourhood-level should be addressed.

KEYWORDS: Excess mortality, COVID-19, inequalities, individual determinants, environmental determinants
ABSTRACT ID: 307
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POSTER TOUR 5

Day 1 – 15.30-16.30

Burden of disease

PRESENTER

Emmanouil Alexandros (Max) Fotakis

ABSTRACT

Low impact of the autumn-winter COVID-19 seasonal booster campaign in averting severe COVID-19 cases in Italy (October 2023 - March 2024)

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BACKGROUND

ECDC recommended using monovalent XBB-adapted vaccines for the 2023/24 autumn-winter COVID-19 vaccination campaigns in older adults. Currently, evidence on the impact of the seasonal vaccination campaigns in European countries is scarce, hindering the evaluation of ongoing programs. We aimed to assess the impact of the 2023/24 vaccination campaign on the number of severe COVID-19 cases (i.e. hospitalisations or deaths) averted in Italy.

METHODS

We conducted a retrospective cohort analysis between October 2023-March 2024 in 15,558,207 persons aged 60ys and above (with at least one previous booster dose), eligible to receive the seasonal booster at the campaign start. Linking data from the Italian surveillance system to national vaccination registry data, we estimated adjusted relative vaccine effectiveness (rVE) of the seasonal booster against severe COVID-19 using Cox regression. We then estimated the number of severe cases averted as (N*VC*rVE)/[1-(VC*rVE)] (N, number of observed events; VC, vaccination coverage), also evaluating hypothetical VC scenarios.

RESULTS

The majority of severe events occurred in December (n=10,027;37%). During the study period VC reached 10.7%. Booster rVE decreased from 60% (95%CI:51-67) in October-November to 36.0% (95%CI:21-47) in February-March 2024. We estimated that 565 (95%CI:497-625) severe cases (i.e. 2.1% of those expected without a vaccination campaign) were averted during the seasonal campaign. In VC scenarios reaching 50% and 75%: 2,636 (9.7% of expected; 95%CI:2,320-2,914) and 3,954 (14.5% of expected; 95%CI:3,481-4,372) severe cases would have been averted, respectively.

CONCLUSIONS

Due to low VC the seasonal vaccination programme had a low impact on averting severe COVID-19 cases among persons aged 60ys and above. Considering the ongoing XBB-adapted vaccines' effectiveness against severe cases, our findings warrant vaccine communication campaigns increasing vaccination intention in Italy ahead of the 2024/25 seasonal rollout.

KEYWORDS: COVID-19,vaccination,impact,elderly population
ABSTRACT ID: 314
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POSTER TOUR 5

Day 1 – 15.30-16.30

Burden of disease

PRESENTER
Ana Atti

ABSTRACT

Impact of diabetes and obesity on SARS-CoV-2 infection following vaccination: an epidemiological and immunological analysis within the SIREN study

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BACKGROUND

Individuals with diabetes mellitus and obesity are at higher risk of COVID-19 related hospitalisation and mortality. We compared SARS-CoV-2 infection rates and anti-spike levels following COVID-19 vaccination in diabetic and non-diabetic participants stratified by Body Mass Index (BMI).

METHODS

We analysed PCR and antibody results from the SIREN healthcare worker cohort linked with demographic, comorbidities and vaccination data. We included participants who provided BMI (weight/height2) and were infection naïve before the second vaccine dose. SARS-CoV-2 infection rates were calculated at six-months after second (V2) and third (V3) COVID-19 vaccine doses, by diabetic status and BMI category. Anti-Spike levels were compared between groups at six-months post-V2.

RESULTS

There were 8,445 (97%) non-diabetics and 250 (3%) diabetic participants were infection naïve before V2. Diabetics had higher SARS-CoV-2 infection rates following V2 compared to non-diabetics within the same BMI category (BMI 18.5-24: 14.29 vs 3.20; BMI 25-34: 5.08 vs 3.42). No infections occurred in BMI ≥35 diabetic group. The same trend was observed following V3 for BMI 25-34 (diabetics 13.64 vs non-diabetics 11.92) and BMI ≥35 (23.08 vs 12.50). No infections occurred in diabetics with BMI 18.5-24. Among diabetics, infection rates increased with weight (BMI 25-34: 13.64 vs BMI ≥35: 23.08). Following V2, diabetics had lower anti-Spike levels than non-diabetics, except for BMI 18.5-24 (BMI 18.5-24: geometric mean 2190.43 vs 1350.38 p=0.9; BMI 25-34: 929.42 vs 1349.04 p=0.16; BMI ≥35: 810.95 vs 1064.17 p=0.71).

CONCLUSIONS

Following COVID-19 vaccination, diabetics had higher SARS-CoV-2 infection rates compared to non-diabetics at a similar weight. Lower anti-spike antibody response in diabetic participants with BMI>=25 may increase these individuals' susceptibility to COVID-19 infection. These findings have implications for planning vaccination strategies and prioritisation.

KEYWORDS: SARS-CoV-2,COVID-19 Vaccines,Diabetes Mellitus,Obesity
ABSTRACT ID: 205
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POSTER TOUR 5

Day 1 – 15.30-16.30

Burden of disease

PRESENTER
Mirjam Knol

ABSTRACT

Using SARS-CoV-2 Nucleoprotein antibodies to detect re-infection

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BACKGROUND
Monitoring SARS-CoV-2 infections remains important, for example to estimate vaccine effectiveness of COVID-19 vaccines. We assessed the validity of anti-Nucleoprotein (N)-antibodies to identify SARS-CoV-2 (re-)infections by estimating persistence of N-antibody seropositivity and boosting over time.

METHODS
From a Dutch prospective cohort study (VASCO), we included adult participants with ≥2 consecutive self-collected serum samples, 4-8 months apart, between May 2021-May 2023. Sample pairs were stratified by N-seropositivity of the first sample and subsequently by self-reported infection within the sampling interval. We calculated proportions of pairs with N-seroconversion and fold-increase (1.5, 2, 3, 4) of N-antibody concentration by determinants and by time since infection. 280 samples were measured twice to assess false-positive rates.

RESULTS
We included 67,632 pairs from 33,328 participants. In pairs with an N-seronegative first sample (69.8%), the N-seroconversion rate was 89% after reported infection and 11% when no infection was reported. In pairs with the first sample N-seropositive, a 1.5- or 4-fold increase was seen for 82% or 65% with a reported re-infection and 19% or 10% without a reported re-infection, respectively. Using seroconversion, 1.5 or 4-fold increase resulted in 24%, 112% and 59% more infections detected, respectively. At 50-59 weeks after first infection 83% were N-seropositive and after re-infection 93% showed a 1.5-fold increase and 61% a 4-fold increase. We found 3.0%, 1.5% and no false-positives using a 1.5-fold, 2-fold and 3-fold increase in duplicate samples. Odds for seroconversion and fold-increase were higher for unvaccinated participants, symptomatic infections, and Omicron infections.

CONCLUSIONS
N-seroconversion and fold-increase was high until a year after infection and re-infection. Using fold-increases detects many re-infections and few false-positives. Including N-serology in vaccine effectiveness analyses is important to reduce misclassification of infections.

KEYWORDS: COVID-19, SARS-CoV-2, serology, nucleoprotein, antibodies, reinfection
ABSTRACT ID: 36
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POSTER TOUR 5

Day 1 – 15.30-16.30
Burden of disease

PRESENTER
Ladislav Kovac

ABSTRACT
COVID-19 Pregnancy and maternal outcomes in Slovakia

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BACKGROUND
COVID-19 Pregnancy & Maternal Outcome initiative was established after the declaration of the global pandemic. Research part of the project consists of data collection and subsequent analyses of various subcategories: consequences of the infection on pregnancy, childbirth, puerperium, breastfeeding, occurrence/frequency of obstetric and non-obstetric complications and mental condition and wellbeing of affected.

METHODS
Pregnant women who tested positive for SARS-CoV-2 based on records of the National Public Health Office were approached as well as their primary care gynaecologists and facilities where they were treated or delivered. Data collection was first time conducted through purposefully developed web domains. Digital skeleton of the study is meant to exist as a hibernating research frame for eventuality of similar events in the future.

RESULTS
In a country of 5,46 million over the duration of declared global pandemics we encounter 1163 cases of SARS-CoV-2 infections during pregnancy. Composition of severe acute maternal mortality changed during pandemic: hypertension and pre-eclampsia (24%) overrun peripartum haemorrhage on a first place, there was slight increase in premature births (22% to previous 20%), cases of intrauterine growth retardation was on a rise as well, while incidence of pathological placentation decreased for half during pandemic compared to previous years. Due to the design of the study – one year follow-up, we expect overall results in August 2024. Maternal mortality significantly increased; cases linked to COVID-19 contributed up to 50% in the first year of pandemic.

CONCLUSIONS
Providing detailed insights into the dynamic of COVID-19 within as diverse a group as pregnant subpopulation might be the key for better pandemic preparedness as well as a tool to decrease still existing barriers in accessibility of pharmacological treatment options in pregnancy.

KEYWORDS: COVID-19,SARS-CoV-2 infection,pregnancy,maternal outcomes,severe acute maternal morbidity
ABSTRACT ID: 313
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POSTER TOUR 5

Day 1 – 15.30-16.30

Burden of disease

PRESENTER

Joana Isidro

ABSTRACT

Prolonged hospital outbreak associated with multidrug resistant Clostridioides difficile RT027 clone exhibiting reduced susceptibility to vancomycin

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BACKGROUND

Clostridioides difficile infection (CDI) remains a major burden to healthcare systems worldwide, being often associated with antibiotics exposure in hospitalized patients. In recent decades, the global increase in CDI incidence and severity was particularly associated with the epidemic PCR ribotype RT027, which was the leading cause of CDI in several countries. Here, we investigate a RT027 clone with reduced susceptibility to vancomycin causing a prolonged CDI outbreak.

METHODS

A CDI outbreak has been ongoing in a 669-bed tertiary-hospital since August-2023 in Portugal; 30 cases over five hospital wards were detected so far, with a 26% recurrence rate. Stool samples were sent to the National Reference Laboratory (NRL) for outbreak investigation, including PCR ribotyping, antimicrobial susceptibility testing and whole-genome sequencing (WGS).

RESULTS

The 13 samples sent to NRL were typed as RT027, tcdA+/tcdB+ and cdtA+/cdtB+, were resistant to MLSb, gentamicin, moxifloxacin, rifampicin, and exhibited an increased MIC (2mg/L) to vancomycin. WGS of 10 isolates confirmed the outbreak, and identified multiple determinants of resistance, among which: ermB (in Tn6189), point mutations R505K in RpoB, T82I in GyrA, and, importantly, T115A in VanR, a mutation recently associated with elevated vancomycin MICs. Integration within the global phylogeny showed that the closest strains were isolated between 2014-2018 in the USA, all harbouring the T115A mutation.

CONCLUSIONS

We describe a multidrug resistant RT027 clone with increased MIC to vancomycin, whose impact in the treatment is still unknown. Its proximity to 2014-2018 USA strains might point to recent transcontinental spread, similarly to the fluoroquinolone-resistant lineages. Despite the efforts for infection control leading to its recently decreased incidence in Europe, the hypervirulent RT027 is still a high cause of concern.

KEYWORDS: Clostridioides difficile,Antimicrobial Drug Resistance,Infectious Disease Outbreaks,Disease Burden,Health Care Associated Infections,Genomics
ABSTRACT ID: 663

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Day 1 – 15.30-16.30

Influenza and other respiratory viruses (except SARS-CoV-2)

PRESENTER

Rebecca Symes

ABSTRACT

Estimating the disease burden of respiratory syncytial virus (RSV) in older adults in England during the 2023/24 season, a new hospital-based surveillance system

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BACKGROUND

RSV is an important cause of acute respiratory infection (ARI) in older adults. In England, and across Europe, relatively little research has described the burden of RSV in older adults. This study aimed to describe the incidence of RSV associated illness requiring hospital admission in adults greater than 65 years and the mortality risk in these patients using a new, enhanced Hospital-based ARI Sentinel Surveillance (HARISS) system linked to National Health Service datasets.

METHODS

Setting: sentinel sites in England during the 2023/24 season. Retrospective data collection completed on 13th September 2024. Eligibility: patients aged 65 years or older, admitted to hospital for at least 24 hours with symptomatic RSV PCR-positive ARI. Data collection: an electronic data capture form was completed for all cases focusing on admission reason, symptoms, and severity. Analysis: incidence of RSV associated hospital admissions, RSV associated mortality and all-cause mortality are estimated in three age groups.

RESULTS

Between 30th October 2023 and 11th February 2024 across six sentinel sites in England, 470 RSV cases met the case definition. The RSV hospitalisation incidence rate in age groups 65 to 74 years, 75 to 79 years and 80 years and above were 32.3, 75.1, 108.1 per 100,000 persons respectively. In cases 80 years and above 8% died of as a result of an acute respiratory infection during admission, with an all-cause mortality of 20% at 90 days.

CONCLUSIONS

RSV is an important cause of admission and mortality in older adults. A new national RSV immunisation programme was introduced in September 2024. This new enhanced surveillance will provide critical information to monitor the programme and inform future policy.

KEYWORDS: Respiratory Syncytial Virus,Respiratory Tract Infections,Sentinel Surveillance,Incidence
ABSTRACT ID: 756
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POSTER TOUR 6

Day 1 – 15.30-16.30
Childhood vaccinations and disease outbreaks

PRESENTER
Enkela Pollozhani

ABSTRACT
Pertussis vaccination status of patients during an ongoing outbreak in North Macedonia 2024

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BACKGROUND
A pertussis outbreak has been ongoing in North Macedonia since 05/01/2024. During 2018-2023 pertussis vaccination coverage of the target population with 5 doses varied between 68.9%-88.5%. The investigation aimed to estimate patients' vaccination status and its role in the development of severe cases.

METHODS
Between 05/01/2024-31/03/2024 laboratory confirmed pertussis cases with demographic data, vaccination status, date of vaccination, and hospitalization were extracted from the national surveillance system. We conducted a cross-sectional study. Cases, having received all doses of pertussis vaccine for their age, were defined as fully vaccinated, while others with ≥1 doses as partially vaccinated. We used descriptive analysis for demographic data and logistic regression to estimate an association between vaccination status and the development of severe cases.

RESULTS
Totally 362 pertussis cases with a median age of 11 years (age range 1 month – 78 years) were reported during the study period. Less than 50% (n=165) were fully vaccinated with a median of 9 years since the last vaccine dose, 23% (n=83) partially vaccinated, while 24% (n=85) were unvaccinated (including 14 infants ≤2 months, who did not receive the first dose, scheduled at 2 months) and 8% (n=29) had unknown vaccination status. Totally 52 cases were hospitalized, with higher odds for hospitalization among infants ≤6 months vs cases >6 months old (OR=44.3; 95%CI: 19.8-107.0) and in unvaccinated vs fully vaccinated (OR=7.0; 3.4-15.0).

CONCLUSIONS
Fully vaccinated individuals could become infected with pertussis, and infants have a high probability to develop severe disease, highlighting the insufficient protection of the current vaccination schedule. Our results support the need for the introduction of maternal vaccination to protect newborns and further investigations to develop new immunization strategies for better pertussis control.

KEYWORDS: Pertussis,Outbreak,Vaccination status,Hospitalization
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Day 1 – 15.30-16.30

Childhood vaccinations and disease outbreaks

PRESENTER

Milko Joksimovic

ABSTRACT

Outbreak of pertussis in Montenegro, November 2023 to January 2024

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BACKGROUND

In the last two decades, no pertussis outbreaks have been reported in Montenegro but vaccine coverage with >=3 doses of pertussis-containing vaccines (PCV) has declined from 88.7% to 75.0% for birth cohorts 2018-2022. On November 20th 2023, the Montenegrin Institute for Public Health reported three cases of Bordetella Pertussis in persons who had not travelled abroad during the incubation period. This study includes pertussis cases interviewed from November 30th 2023 to January 31st 2024 and aims to describe the outbreak.

METHODS

Confirmed and probable cases were defined according to the Commission Implementing Decision (EU) 2018/945. All laboratories were asked to report confirmed cases. Probable cases were identified among cases' contacts. For cases born in 2000 onwards, data about PCV immunization were collected from the National Immunization registry; others were interviewed by epidemiologists.

RESULTS

In total, 434 cases (362 confirmed and 72 probable) were interviewed: 51.6% (n=224) were female, 52% (n=226) were aged 6-14 years, and 6.2% (n=27) were <1 year. Among 21 hospitalised cases 61.9% (n=13) were <1-year-old. No deaths were reported. Among all cases, 72.3% received >=3 doses of PCV and among those aged 6-14 years 95.5%. The median time between the last received PCV dose and the date of cough onset was 11 years (IQR: 8-13 years).

CONCLUSIONS

This was the largest pertussis outbreak in Montenegro in the last five decades. If the decline in vaccination coverage continues, similar pertussis outbreaks may occur periodically. Considering that most hospitalized cases were aged <1 year, implementing vaccination campaigns among pregnant women may be considered. The introduction of an additional dose to adolescents should also be considered since the vaccine immunity waned over time.

KEYWORDS: Pertussis, Whooping cough, Respiratory diseases, Infectious Disease Outbreaks, Vaccination, Montenegro
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Childhood vaccinations and disease outbreaks

PRESENTER

Joyce Pijpers

ABSTRACT

MMR vaccination coverage decrease in the Netherlands from birth cohort 2008 to 2020 and its sociodemographic determinants

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BACKGROUND
In the Netherlands, Measles-Mumps-Rubella (MMR) vaccination coverage has decreased, from 95% in cohorts 2008-2010 to 93% in cohorts 2015-2016 and 88% in cohort 2020. We studied sociodemographic determinants associated with MMR vaccination coverage.

METHODS
We conducted a retrospective database study including children born in the Netherlands in 2008-2020. MMR vaccination status at 2 years of age and sociodemographic variables (maternal education level, country of origin, income and income source, urbanisation level, family size and day-care attendance) were linked at individual level. Vaccination coverage for all levels of each (categorical) variable, stratified by birth cohort, was calculated. In cohort 2020, for each variable, differences in coverage were estimated using Poisson-regression while adjusting for all variables. We report those variables with >5% difference in coverage.

RESULTS
For most determinants a similar decreasing trend was observed, with notable exceptions. A steeper decrease was observed among children of Moroccan origin from cohort 2013 onwards (95% in 2008-2013 to 71% in 2020). Coverage remained relatively high among children with highly educated mothers (≥95% before 2020, 93% in 2020), with mothers in employment (≥95% before 2020, 93% in 2020), and those in the highest income households (≥95% before 2020, 94% in 2020). Preliminary Poisson-regression results showed a 6% lower vaccination coverage in the lowest versus highest income households; -9% in children from large versus small families; -12% in those not attending versus attending day-care and -18% in children of Moroccan origin versus children of Dutch origin.

CONCLUSIONS
Further analyses of changes in these associations over time will be conducted. Insights into subgroups with lower coverage is crucial for targeted public health interventions and prioritising vaccination access for vulnerable populations to protect public health equitably.

KEYWORDS: Vaccine-preventable diseases; Vaccination coverage; Measles; Epidemiology
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Childhood vaccinations and disease outbreaks

PRESENTER

Raíssa De Fátima Silva Afonso Francisco

ABSTRACT

Effectiveness of Universal Respiratory Syncytial Virus monoclonal antibodies in preventing Acute Respiratory Infections of patients admitted to a tertiary hospital in the 2023/2024 season.

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BACKGROUND

Spain's immunization schedule introduced universal Respiratory Syncytial Virus (RSV) prophylaxis for infants since October 2023. We evaluated monoclonal antibodies' (MA) effectiveness in preventing Acute Respiratory Infections (ARI) in infants during their first RSV season.

METHODS

A test negative case-control study was conducted at a Spanish tertiary hospital. Hospitalized patients with ARI symptoms, eligible for immunization either by birth date (from 1st of April 2023 to 31st March 2024) or risk factors for severe ARI under 24 months of age, were included. Cases had positive RT-PCR or antigen tests, while controls tested negative. To study the association between the development of ARI and the different possible associated factors, the crude odds ratio (OR) and adjusted OR were calculated using logistic regression. Effectiveness was determined by E = (1-OR) x 100, with 95% confidence interval.

RESULTS

Immunotherapy coverage in our Health Department (13 primary health centers and hospital) from October to January averaged 91.08%. From epidemiological weeks 40 to 18, 134 patients hospitalized for ARI were included, 28 (20.9%) cases and 106 (79.1%) controls. Antibody coverage was 75% (101/134), with 57.1% ^{16} cases and 80.2% ^{85} controls. The median age was 2 months (range 1-5), and the average birth weight was 3065 grams (range 2460-3430) with most infants born at 38 weeks (range 36-39). Risk factors were present in 41 patients (30.6%). The crude Effectiveness was 67.1% (CI 20.0-86.4), and adjusted Effectiveness for week of admission was 63.8% (CI 9.6-85.5).

CONCLUSIONS

The introduction of an effective MA to prevent ARI, combined with high coverage rates, has shown promising real life results and had a positive impact in reducing the burden of RSV in hospitals during the past RSV season.

KEYWORDS: Monoclonal Antibodies,Vaccine Effectiveness,Respiratory Syncytial Virus Infections,Hospitalization
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Childhood vaccinations and disease outbreaks

PRESENTER

Danilo Cereda

ABSTRACT

The impact of routine prophylaxis through monoclonal antibodies and maternal immunisation on the respiratory syncytial virus burden in the Lombardy region, Italy.

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BACKGROUND

Respiratory syncytial virus (RSV) stands as a leading cause of acute lower respiratory tract infections (LRTI) and hospitalisations in infants worldwide. Recent approvals by regulatory agencies for using monoclonal antibody (mAb) nirsevimab (Beyfortus, Sanofi and Astrazeneca) and maternal immunisation with RSVpreF vaccine (Abrysvo, Pfizer) offer promising approaches to mitigate RSV-associated morbidity.

METHODS

We applied a catalytic model to evaluate the effects of routine prophylactic campaigns based on mAbs or maternal vaccination on RSV hospitalisations in Lombardy, Italy. The model was informed by data on RSV-attributable cases and patients in the past, while accounting for changes in susceptibility caused by the lower RSV circulation experienced during the COVID-19 pandemic. Alternative scenarios were explored, considering the uptake levels observed in infancy and among pregnant women. The efficacy of nirsevimab and the RSVpreF vaccine in preventing the RSV infection was assumed between 62%-85% and 30%-75%, respectively.

RESULTS

Yearly administration of mAbs to 80% of infants, corresponding to uptake levels recently observed in Spain, was estimated to avert on average 41.5-56.6% hospitalisations in the overall population per year. Coverage levels close to those observed for childhood vaccines (95%) could result in an additional 18% reduction of hospitalisations. RSVpreF vaccine administered to 65% of pregnant women, resembling the Diphtheria, Pertussis, and Tetanus coverage for this target in the region, was estimated to avert on average 16.4-40.8% of hospitalisations. Considering a flu-like coverage (12%), less than 6% of hospitalisations could be averted by maternal immunisation.

CONCLUSIONS

Routine administration of nirsevimab in infants demonstrates significant potential to reduce the hospital burden associated with RSV. Maternal immunisation can play a complementary role in achieving high levels of protection in at-risk populations.

KEYWORDS: Respiratory Syncytial Virus,Monoclonal Antibodies,Respiratory Syncytial Virus Vaccines,Immunization Programs,Prevention and control,Maternally-Acquired Immunity
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Surveillance systems

PRESENTER
Diogo FP Marques

ABSTRACT
Evaluation of the European severe acute respiratory infection surveillance, October 2023: useful, acceptable, and meets its main objective

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BACKGROUND
Since 2020, ECDC has supported 27 EU/EEA and Western Balkans countries enhancing their severe acute respiratory infection (SARI) surveillance to monitor SARI trends, detect unexpected events, evaluate public health interventions, identify severe disease risk factors, and support vaccine effectiveness studies. Using diverse strategies, countries have implemented SARI surveillance and report data at national/European levels. In 2023, we evaluated this surveillance to provide recommendations for further enhancement.

METHODS
From July to October 2023, we administered an online questionnaire targeting representatives of SARI surveillance systems from 27 countries and ECDC/WHO staff to evaluate key surveillance attributes (meeting objectives, usefulness, acceptability, timeliness, representativeness) and to identify the main strengths, weaknesses, opportunities and threats.

RESULTS
The questionnaire response rate was 27% (54/198). Most respondents (76%; 41/54) reported that the system met its main objective of trend monitoring and considered it useful (89%; 48/54), acceptable (83%; 45/54), timely (56%; 30/54) and representative (46%; 25/54). Insufficient data completeness and data linkage were identified as reasons for not meeting the remaining surveillance objectives. High workload jeopardised timeliness, while inadequate geographical coverage limited representativeness. Multi-pathogen surveillance was identified as the main strength, heterogeneity of national SARI surveillance systems the main weakness, improvements of hospital information systems to allow data linkage/sharing the main opportunity, and lack of sustainable funding the main threat.

CONCLUSIONS
SARI surveillance was perceived as meeting its main objective and being useful and acceptable. To achieve additional objectives and enhance timeliness and representativeness, we recommend countries to improve data completeness, reduce workload, and expand geographical coverage. Such improvements would allow SARI surveillance to identify risk factors for severe outcomes, monitor the impact/effectiveness of public health interventions, and further contribute to pandemic preparedness and response.

KEYWORDS: Influenza, Respiratory syncytial virus (RSV),Surveillance,Severe acute respiratory infection (SARI),Evaluation,SARS-CoV-2
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PRESENTER

Miguel Angel Sanchez Ruiz

ABSTRACT

Surveillance of severe acute respiratory infections associated with SARS-CoV-2, influenza virus and RSV using ICD-10 codes: a case definition accuracy study across five European countries, 2021-2023

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BACKGROUND

Surveillance of severe acute respiratory infections (SARI) using ICD-10 codes from electronic health records (EHR) lacks consensus on the optimal SARI case-defining codes. We aimed to identify codes that maximise the sensitivity (Se) and positive predictive value (PPV) for the surveillance of SARI associated with SARS-CoV-2, influenza, and respiratory syncytial virus (RSV) in Denmark, Iceland, Malta, Norway, and Spain.

METHODS

We included hospitalisations in weeks 21/2021 to 39/2023, with first-three-character respiratory disease or four-character COVID-19 ICD-10 codes; and SARS-CoV-2, influenza virus or RSV tests. We assessed the Se and PPV of individual codes against laboratory confirmation and calculated the combined Se/PPV rank-sum. For each pathogen, we incrementally combined up to 10 codes based on their rank-sum, to identify code sets that maximised the Screening-Marker Index (SMI= Se*PPV): excellent (>=0.81), good (>=0.64), satisfactory (>=0.49), and poor (<0.49) utility.

RESULTS

We included 401,215 hospitalisations. For laboratory-confirmed SARS-CoV-2; code U07.1 (B34, B97 for Denmark) yielded excellent utility in Denmark, Malta, Norway and Spain (Se>=0.88, PPV>=0.90, SMI>=0.82) and good utility in Iceland (Se: 0.97, PPV: 0.81, SMI:0.79). For influenza virus; the utility of J09, J10, J11 was excellent in Denmark, Spain and Norway (Se>=0.84, PPV>=0.97, SMI>=0.83), satisfactory in Malta (Se: 0.56, PPV: 0.93, SMI: 0.52), and poor in Iceland (Se: 0.72, PPV: 0.60, SMI:0.43). For RSV, key codes included J12, J20, J21 and J96, but utility was poor (Se: 0.35-0.91, PPV: 0.25-0.71, SMI: 0.17-0.34).

CONCLUSIONS

Our findings recommend using codes U07.1, J09-J11 for identifying SARS-CoV-2 and influenza-associated SARI, and assessing the accuracy of four-character codes for RSV (e.g., J12.1). The applicability of our results may depend on surveillance systems' characteristics, coding practices, and the epidemiology of SARI. Therefore, context-specific assessments are recommended.

KEYWORDS: Electronic Health Records,International Classification of Diseases,Data Accuracy,SARS-CoV-2, Influenza - Human,Respiratory Syncytial Virus - Human
ABSTRACT ID: 148
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Surveillance systems

PRESENTER

Catriona Oliver

ABSTRACT

Protecting Scotland's health: An evaluation of the Community Acute Respiratory Infection (CARI) surveillance programme

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BACKGROUND

Public health surveillance is crucial for timely intervention. The Community Acute Respiratory Infection (CARI) surveillance programme, launched by Public Health Scotland (PHS) in 2021, follows WHO guidelines and is key to PHS's national infectious respiratory diseases plan for monitoring acute respiratory infections (ARI) in the community.The study aimed to evaluate CARI's performance during the 2023/24 season (2 October 2023 to 5 May 2024).

METHODS

CARI recruits sentinel general practitioner (GP) practices to identify ARI patients, for testing and trend monitoring of ten respiratory pathogens. The evaluation assessed key attributes: Simplicity and flexibility via daily operations and GP survey feedback; acceptability by recruitment/withdrawal rates; representativeness by demographic and geographic characteristics and data quality; timeliness and stability via publication speed and reliability; usefulness by data dissemination and its impact on decision making. Sensitivity/predictive value positive remains uncertain due to limited knowledge of true case numbers.

RESULTS

Across 215 GP practices, 24,512 samples were tested. The evaluation of CARI highlighted its simplicity, flexibility, and acceptability, with streamlined swab kit usage, adaptable processes, and positive GP feedback (92.3% overall satisfaction from 78 survey responses). Representativeness was generally satisfactory, although some health boards were over-/ under-represented. Data quality was high, with minimal lab rejections (8.4%). CARI mirrored European trends, detecting increased Mycoplasma pneumoniae and parainfluenza in early 2024. Timeliness was evident in weekly publications. CARI proved highly useful, disseminating information internally, externally, and contributing to alerts, and scientific papers.

CONCLUSIONS

This comprehensive evaluation demonstrates the usefulness and validity of CARI, generating critical data to guide local and national evidence-based actions and strategic decisions, informing effective interventions, ultimately protecting the health of Scotland's population.

KEYWORDS: Sentinel surveillance,Respiratory infections,Epidemiology,Public health
ABSTRACT ID: 354
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Surveillance systems

PRESENTER
Miruna E. Rosu

ABSTRACT

National surveillance system for invasive Haemophilus influenzae disease in Italy: evaluation of completeness and timeliness, 2016–2022

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BACKGROUND
The Italian national surveillance system (NSS) for vaccine-preventable invasive bacterial illnesses has monitored invasive Haemophilus influenzae disease (HID) since 2007. Except for a sensitivity analysis in 2016, the HID-NSS has never been evaluated before. We evaluated the completeness and timeliness of the HID-NSS in Italy from 2016 to 2022.

METHODS
We analysed HID cases reported to the NSS from 2016 to 2022 and measured completeness and timeliness per year, at national and regional level. Completeness was assessed as the percentage of missing data for: place and date notification, age, sex, vaccination status, comorbidities, infection type, serotype, place and date symptoms onset, outcome and sequelae. Timeliness was assessed as the time between symptom onset and first notification.

RESULTS
969 cases were notified between 2016 and 2022. The number of cases reported in 2020 and 2021 (94 and 65) was substantially lower than in other years (162 cases/year average). Place and date notification, date symptoms onset, comorbidities, sequelae, and infection type were complete; age and sex ranged from 97% to 100% annually. Completeness per year in vaccination status (range=39-72%), place symptom onset (47-87%), outcome (45-72%) and serotype (58-82%) improved or remained relatively stable over time. Depending on the reporting region, completeness in place symptom onset, outcome, and serotype was between 0% and 100%. The timeliness of reporting improved from 2016 to 2022 with an overall median of 7 days (IQR=3-21). Timeliness also varied substantially per region (median=3-27 days depending on region).

CONCLUSIONS
Our analysis identified gaps in crucial variables, and differences in both completeness and timeliness over time and across regions. Reducing the number of variables, and follow-up information sessions in regions with incomplete and untimely reporting may be beneficial.

KEYWORDS: surveillance, Italy, Haemophilus influenzae, Vaccine-Preventable Diseases
ABSTRACT ID: 421
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Surveillance systems

PRESENTER

Hilde Angermeier

ABSTRACT

Strengthening molecular surveillance of ARIs in the federal state of Bavaria, Germany: Expansion of the Bavarian Influenza Sentinel (BIS+C)

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BACKGROUND

In 2022, the Bavarian Ministry of Health decided to strengthen the Bavarian Influenza Sentinel (BIS+C). In BIS+C, primary care practices collect weekly nasopharyngeal swabs from patients with acute respiratory infections (ARIs) for virological diagnostics, resulting in molecular surveillance of ARIs.

METHODS

Since 2009, the BIS+C sentinel has focused on Influenza and Respiratory Synzytial Virus (RSV) diagnosis in children aged <5 years. Due to the pandemic, it has been extended to SARS-CoV-2 and RSV diagnostics in specimens from all age groups. Not only the sampling period was elongated from seasonal to year-round, but also the number of swabs taken per practice and week was increased. To achieve comprehensive coverage throughout Bavaria, additional practices were recruited per municipality through an extensive marketing campaign.

RESULTS

Sentinel participation has more than doubled, from 92 practices (2021/2022) to 197 (2023/2024) resulting in over 10.000 specimens since CW 40/2023. According to RKI definitions, the 2023/2024 season revealed an RSV epidemic caused mainly by the subtype RSV A (CW 45/2023 to 09/2024) in children <4 years. In addition, an Influenza A(H1N1)pdm09 epidemic was defined (CW 51/2023 to 13/2024), that primarily impacted children and middle-aged individuals. Notably, its onset was delayed compared to the previous Influenza A(H3N2) epidemic (CW 44/2022). In both seasons, Influenza B cases (Victoria lineage) occurred since the fiscal year's change1. SARS-CoV-2 affected mostly adults and the elderly > 60 years and peaked in CW 50/2023 (positivity rate of 33.8%).

CONCLUSIONS

The BIS+C sentinel network serves as a perfect means for monitoring ARI trends in the Bavarian primary health care sector. It thus constitutes a far-sighted molecular early warning system, enabling a rapid response to potential health threats.

KEYWORDS: Molecular Surveillance, Acute Respiratory Infections (ARIs), Sentinel, Epidemiology, Early Warning System
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Surveillance systems

PRESENTER
Sofia Burdi

ABSTRACT

Evaluation of the surveillance system for severe Clostridioides difficile infections in Germany 2017-2022, a mixed methods approach

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BACKGROUND

Severe Clostridioides difficile infections (sCDI) are notifiable by physicians to local public health authorities (PHA) and further reported to state PHA and national level in Germany. We aimed at evaluating sCDI surveillance regarding timeliness, completeness, representativeness, acceptability, simplicity and usefulness to adjust as necessary.

METHODS

Using national sCDI surveillance data from 01.01.2017–31.12.2022 we assessed timeliness, using median and interquartile range (IQR) for notification delay (date of diagnosis to date of notification) and reporting delay (local PHA to national level reporting, working days). We assessed completeness calculating percentages of available information for selected variables. Assessing representativeness, we compared incidences over time and age and sex distribution of notified cases with public databases (hospital surveillance, federal death cause and hospital discharge diagnoses monitoring, and state level notification data from Saxony for severe and non-severe cases). We conducted semi-structured interviews with PHA to understand their experiences of the system's acceptability, simplicity and usefulness, applying qualitative thematic analysis.

RESULTS

Altogether, 12,399 sCDI cases were reported to national level. Median notification and reporting delay were 4 days (IQR=1;9) and 1 working day (IQR=0;2), respectively. Completeness was sex=100%;12,397/12,399, age=100%;12,397/12,399, disease onset date=86%;10,709/12,399, hospitalization=98%;12,107/12,399, intensive care treatment=88%;10,891/12,399. Incidences over time and age and sex distribution were comparable between different databases. Main challenges identified through eight interviews were complex notification criteria (simplicity), low physician compliance and low perceived relevance (acceptability) and low usefulness in identifying epidemiological links.

CONCLUSIONS

While the system offers timely, complete, and representative data, it is perceived as complex, lacking acceptability, and having limited usefulness. More detailed information for PHA on notification criteria and training of physicians on notification processes is needed. The findings will guide possible revision of sCDI notification in Germany.

KEYWORDS: Clostridioides difficile Infection,Public Health Surveillance,Infectious Disease Reporting,Evaluation study
ABSTRACT ID: 121
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POSTER TOUR 7

Day 1 – 15.30-16.30

Surveillance systems

PRESENTER
Shoxsanam Abdullaeva

ABSTRACT

Evaluation of the measles surveillance system in Tashkent, Uzbekistan, 2023

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BACKGROUND

Measles is a highly contagious, vaccine-preventable disease. In 2023, in Uzbekistan, where reported measles vaccine coverage is 99%, there was an increase in measles incidence (8,670 cases; 24.1 per 100,000 population). We aimed to identify gaps in the measles surveillance system in Tashkent.

METHODS

We conducted a descriptive cross-sectional surveillance evaluation study in three healthcare facilities and the Committee for Sanitary-Epidemiological Welfare and Public Health of Tashkent City from January to April 2024. We reviewed case reports, medical and epidemiologic investigation cards from 200 patients registered for 2023.

RESULTS

Notification and case record forms are entirely paper-based. Knowledge of reporting norms and the standard case definition of measles among interviewed providers (n=50) was 65%. Of the reported cases (n=200), 22% were from polyclinics and 79% from an infectious disease hospital. Several data errors were found among reported cases: 2% (4/200) had incorrect sex, 3% were missing age or contact number, 5% were missing work/study place or had the wrong date of sampling, and 7% were missing the date of onset. Case notification reports were submitted late (>72 hours) in 19% of cases. Epidemiologic investigations were initiated late (>96 hours) in 21% of cases. The collection of blood samples for laboratory testing was late in 2% of cases. Among cases, 4% had documented previous measles vaccination, and 3% had no vaccine status. We identified no cases of measles that were not reported, and all reported cases met the case definitions (sensitivity and positive predictive value = 100%).

CONCLUSIONS

The surveillance system is accurately detecting measles cases. We identified important gaps in data quality and timeliness. Adoption of an electronic data system may help improve data quality and timeliness.

KEYWORDS: Measles,Surveillance evaluation,Uzbekistan,Data accuracy
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POSTER TOUR 8

Day 1 – 15.30-16.30

COVID-19

PRESENTER

Baltazar Nunes

ABSTRACT

XBB.1.5 COVID-19 vaccine effectiveness against hospitalisations and deaths during Omicron BA.2.86/JN.1 period among older adults in seven EU/EAA countries: ECDC VEBIS electronic health record network

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BACKGROUND

Monovalent XBB.1.5 vaccines were recommended for those aged >=65-years in EU/EEA countries in autumn 2023; however, since mid-December 2023, the BA.2.86/JN.1 variants became dominant. We aimed to estimate XBB.1.5 vaccine effectiveness (VE) against COVID-19-related hospitalisation and deaths in a period of BA.2.86/JN.1 predominance within a European multi-country study.

METHODS

We linked electronic health record data to create a multicentre two-stage historical cohort study, with data extracted in April up to the end of February 2024. We included individuals aged ≥65 years eligible for the autumn 2023 COVID-19 vaccines from seven study sites in Belgium, Denmark, Italy, Norway, Portugal, Sweden and Spain (Navarre). We designated the BA.2.86/JN.1 variant-predominant period starting when country-specific sequenced viruses BA.2.86/JN.1 were >=80% (start: 4/12/23 to 08/01/24 end: 26/02/2024). At the study site level, we estimated the vaccine confounder-adjusted (for age, sex, comorbidities and previous booster doses) hazard ratio (aHR) of COVID-19 hospitalisations or deaths between individuals 14-89 days after vaccination and individuals not vaccinated. VE was estimated as (1-pooled aHR)x100 with a random effects model.

RESULTS

At the end of study period we included, in the unvaccinated and vaccinated cohorts respectively, 13,679,119 and 5,106,110 persons, 3,674 and 1,838 hospitalisations and 782 and 475 death events.XBB.1.5 VE estimates against hospitalisations and deaths within 14-89 days since vaccination were, respectively, 51% (95%CI: 45;56) and 62% (46;74) in 65-79-years and 43% (37;48) and 49% (39; 57) in >=80-year-s.

CONCLUSIONS

Compared with the literature our XBB.1.5 VE estimates are lower than those observed during XBB.1.5 predominance. Despite the mismatch between variants, XBB.1.5 vaccine maintained a protective effect (>=40%) against severe COVID-19 likely caused by BA.2.86/JN.1 during the 2023/2024 winter, among those aged ≥65-years.

KEYWORDS: COVID-19, COVID-19 vaccines, Vaccine Effectiveness, Electronic Health Records, Cohort Studies
ABSTRACT ID: 215
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POSTER TOUR 8

Day 1 – 15.30-16.30

COVID-19

PRESENTER

Lore Merdrignac

ABSTRACT

Effectiveness of XBB.1.5 vaccines against symptomatic SARS-CoV-2 infection in adults aged >=65 years during the JN.1 lineage-predominant period, European VEBIS primary care multicentre study 2023–2024

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BACKGROUND

In autumn/winter 2023, COVID-19 vaccination campaigns in Europe predominantly administered XBB.1.5 vaccines. From November, JN.1 lineages began replacing XBB lineages and are now dominating worldwide. We conducted a multicentre test-negative study (VEBIS) at primary care level in 10 European countries to estimate COVID-19 vaccine effectiveness (VE) against laboratory-confirmed symptomatic SARS-CoV-2 infection during the JN.1 lineage-predominant period.

METHODS

Patients presenting to primary care with an acute respiratory infection were tested by RT-PCR for SARS-CoV-2. Those testing positive were cases; those testing negative were controls. The start of the JN.1 lineage-predominant period was defined by country when JN.1 exceeded 60% of weekly GISAID genetic sequencing data. Based on interim data up to end of February 2024, we estimated VE in adults aged >=65 years by time since last vaccination using logistic regression adjusted for study site, age, sex, onset date and comorbidities.

RESULTS

During the JN.1 lineage-predominant period estimated from week 47, we included 220 cases and 1733 controls. Median-age was 74 years for both cases and controls. Seventy-five cases (34%) and 753 controls (43%) received vaccination in the autumn/winter 2023 campaign. VE was 48% (95% CI: 12–71%), 23% (95% CI: -11–48%) and 5% (95% CI: -92–56%) among those vaccinated 1-5 weeks, 6-11 weeks and >=12 weeks before onset, respectively.

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CONCLUSIONS

Our interim results suggest that in adults aged >=65 years, XBB.1.5 COVID-19 vaccines provide moderate (48%) protection against symptomatic infection with the currently circulating JN.1 lineages within 5 weeks following administration. The VE point estimate decline from 6 weeks post-vaccination indicates a potential rapid waning of vaccine-induced immunity, although precision was low. Regular and timely COVID-19 boosters, where practical, may be key for optimal protection of the elderly.

KEYWORDS: COVID-19,SARS-CoV-2,vaccine effectiveness,test-negative design,COVID-19 vaccine,case control studies
ABSTRACT ID: 231
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POSTER TOUR 8

Day 1 – 15.30-16.30

COVID-19

PRESENTER

Madelyn Rojas

ABSTRACT

Effectiveness of the XBB.1.5 COVID-19 vaccines against hospitalisation during the BA.2.86 variant-predominant period in adults aged >=65 years: VEBIS European hospital multicentre study, 2023/24

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BACKGROUND

Adapted XBB.1.5 COVID-19 vaccines were authorised for use during the 2023 autumn/winter vaccination campaigns in Europe. SARS-CoV-2 XBB variants were then predominant in Europe until November 2023, when SARS-CoV-2 BA.2.86 variants started to predominate. We aimed to measure the vaccine effectiveness (VE) of XBB.1.5 vaccines against COVID-19 hospitalisation during the BA.2.86 variant-predominant period in Europe.

METHODS

The hospital Vaccine Effectiveness, Burden and Impact Studies (VEBIS) includes a multicentre, test-negative case-control study, across 11 participating European countries. We defined cases and controls as severe acute respiratory infection (SARI) patients testing positive and negative for SARS-CoV-2 by RT-PCR, respectively. We defined each country's variant-predominant period start when weekly sequenced samples reached >=60% for BA.2.86 in the ECDC-ERVISS database. We estimated VE for those aged 65+ years, by time since vaccination, using logistic regression adjusted by site, date of symptom onset, sex, age and presence of any chronic condition.

RESULTS

We included 499 cases and 4,328 controls from 22 November 2023 to 8 March 2024, of which 218 (44%) cases and 2,444 (56%) controls had been vaccinated in the 2023 autumn/winter campaign. VE was 46% (95%CI: 7;71) in the first 14–29 days post vaccination; 49% (95%CI: 32;63) at 30–59 days; 33% (95%CI: 14;49) at 60–89 days; and 22% (95%CI: -18;49) at 90–151 days.

CONCLUSIONS

Adapted COVID-19 XBB.1.5 vaccines provided protection during the BA.2.86 variant-predominant period among individuals aged >=65 years, halving the risk of COVID-19 hospitalisation among the vaccinated in the first 2 months post vaccination and one in five vaccinated at 3–5 months post vaccination. These results may indicate a potential waning of the vaccine effect. VE estimates will be updated with final season data.

KEYWORDS: COVID-19, XBB.1.5 COVID-19 vaccine, vaccine effectiveness, multicentre study, case control studies, test-negative design,BA.2.86 SARS-CoV-2 variant,Hospitalisation
ABSTRACT ID: 329
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Day 1 – 15.30-16.30

COVID-19

PRESENTER

James Humphreys

ABSTRACT

Evaluation of an electronic health record-based multi-country network designed to monitor COVID-19 vaccine effectiveness in EU-EEA countries (October 2021 – February 2024)

J. Humphreys[1]

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BACKGROUND

The ECDC-VEBIS electronic health record (EHR) network produced monthly estimates of vaccine effectiveness (VE) against COVID-19 related hospitalisation and death across seven EU/EEA study-sites since February 2022. This evaluation aims to describe and provide recommendations to improve the system according to several attributes of surveillance systems.

METHODS

We evaluated representativeness, completeness, timeliness, usefulness, acceptability, and flexibility via desk review and questionnaires. Internal validity was measured using four sensitivity analyses: i) level of confounding using change-in-point-estimate approach, ii) unmeasured confounding using negative outcomes (non-COVID-19 hospitalisations and deaths), iii) impact of model specification, and iv) misclassification bias due to EHR extraction timing.

RESULTS

The desk review demonstrated high study representativeness (range 57 to 100% of externally-sourced population estimates) and timeliness in line with equivalent systems (mean 77 days extraction to reporting). Survey results suggest high internal acceptability (100% of responses) and agreement that prioritising flexibility over stability of study design maximises its usefulness (75%).The change-in-point-estimate exercise indicates that, among currently-adjusted confounding candidates, previous booster dose count most influenced Hazard Ratio (HR) point-estimates (range -0.32 to +0.06) across all models and all but one site, while sex impact was negligible (range -0.01, +0.03). Evidence of association between vaccination and non-COVID-19 hospitalisations was found in two-thirds of study-sites (mean HR 0.66, range 0.42 to 1.01) and non-COVID-19 deaths in all study-sites (0.49, 0.35 to 0.7).

CONCLUSIONS

VEBIS-EHR showed good representativeness, acceptability, and timeliness. Despite extensive confounding adjustment, residual bias may persist based on negative-outcome analyses. These results show that regular evaluations of monitoring studies are key in understanding validity and usefulness of system outputs. Further investigations, including misclassification bias due to EHR extraction timing, are underway.

KEYWORDS: COVID-19 vaccines,COVID-19,Vaccine Effectiveness,Electronic Health Records, Evaluation,Implementation
ABSTRACT ID: 294
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POSTER TOUR 8

Day 1 – 15.30-16.30
COVID-19

PRESENTER
Manon Haverkate

ABSTRACT
Pre-booked COVID-19 vaccination appointments vs. self-scheduling: assessing the effect on vaccination uptake during the 2023 autumn campaign in the Netherlands using a regression discontinuity design

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BACKGROUND
During the COVID-19 vaccination campaign in the Netherlands in autumn 2023, from 02-10-2023 to 31-12-2023, persons aged >=60 years were personally invited by mail. Those born between 01-01-1934 and 01-05-1952 (i.e., age 71.7-90.0 on 31-12-2023) received a letter with a pre-booked appointment, while the others received a letter inviting them to self-schedule an appointment. We aimed to assess the effect of pre-booked appointments on uptake of COVID-19 vaccination during the 2023 autumn campaign.

METHODS
National registries of sociodemographic determinants and COVID-19 vaccination were linked by a unique personal identifier. A regression discontinuity design (RDD) was applied to estimate the local average treatment effect at 71.7 and 90.0 years of age, among non-institutionalised persons who had received at least one prior COVID-19 vaccination by the municipal health services (MHS).

RESULTS
The autumn 2023 vaccination coverage among 4.2 million non-institutionalised persons aged >=60 years with at least one prior COVID-19 vaccination by the MHS was 56.2%. Preliminary analyses showed a 1.3 (95% CI 0.5-2.0) and 4.4 (3.1-5.8) percentage point higher uptake in those with pre-booked appointments at 71.7 and 90.0 years, respectively. Estimates for persons who were also vaccinated during the 2022 autumn campaign were 1.6 (1.2-2.1) and 5.4 (4.1-6.7), respectively. Estimates were 2.7 (1.9-3.6) and 3.1 (1.3-5.0), respectively, for those who were not vaccinated in autumn 2022.

CONCLUSIONS
Preliminary results showed that pre-booked appointments were associated with a higher uptake of COVID-19 vaccination than self-scheduling at both age cut points. Since we used a RDD, this can be interpreted as a causal effect. Pre-booked appointments could be effective in increasing uptake. Further subgroup analyses are planned to assess the effect of pre-booked appointments on equity of the vaccination programme.

KEYWORDS: COVID-19 Vaccines, Vaccination Coverage, Registries, Evaluation Study
ABSTRACT ID: 361
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POSTER TOUR 8

Day 1 – 15.30-16.30
COVID-19

PRESENTER
Rafael Vasconcelos

ABSTRACT
Effectiveness of tiered restrictions in slowing down COVID19 in Portuguese municipalities in the winter of 2020-2021: a weighted matching differences-in-differences study

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BACKGROUND
The COVID-19 pandemic posed significant public health challenges worldwide, prompting the implementation of various non-pharmaceutical interventions to control virus spread. In Portugal, a tiered restriction system was introduced from November 2020 to January 2021, categorizing municipalities into four risk levels based on cumulative COVID-19 incidence. This study aims to evaluate the effectiveness of these tiered restrictions in reducing COVID-19 incidence at the municipal level.

METHODS
A quasi-experimental design employing a differences-in-differences approach was used to assess the impact of the tiered restrictions. Municipalities were classified into four risk categories: moderate, elevated, very high, and extreme. Data on 14-day cumulative COVID-19 incidence were collected for all 278 Portuguese municipalities from official open data. The analysis matched municipalities undergoing intervention with control municipalities based on demographic and socioeconomic covariates, using PanelMatch weighting. The primary outcome was the change in 14-day cumulative incidence.

RESULTS
The study found that municipalities transitioning from moderate to very high or extreme risk levels experienced significant reductions in 14-day cumulative incidence, when compared to the matched controls. Preliminary results show that the effect was most pronounced in the second and third weeks post-intervention, with decreases of -482.7 and -740.6 cases per 100,000 inhabitants, respectively. Sensitivity analyses restricted to municipalities with populations over 10,000 confirmed these findings, albeit with slightly reduced effect sizes.

CONCLUSIONS
The tiered restriction system effectively reduced COVID-19 incidence in municipalities at higher risk levels, demonstrating the value of targeted non-pharmaceutical interventions. These findings are in line with simillar studies, supporting the use of localized measures in managing outbreaks, balancing public health benefits with socioeconomic impacts. Future studies should include geospatial modeling, explore long-term effects and adherence variability to refine these strategies further.

KEYWORDS: COVID-19, Non-Pharmaceutical Interventions, Quasi-Experimental Studies, Public Health, Epidemiology, Portugal
ABSTRACT ID: 553
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POSTER TOUR 8

Day 1 – 15.30-16.30
COVID-19

PRESENTER
Mary Sinnathamby

ABSTRACT
Unpacking our SuITCases - Identifying travel-associated SARS-CoV-2 cases in England

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BACKGROUND

The emergence of SARS-CoV-2 and its variants manifested the need for implementing an integrated travel surveillance system, to identify travel-associated COVID-19 cases in England. A novel COVID-19-episode-level dataset, Surveillance of International COVID-19 Cases (SuITCases) was created using complex data-linkage to integrate four data sources with travel-associated information (1) Passenger Locator Forms (PLFs) from all persons entering and returning to the UK from any country, (2) data from cases/contacts from contact tracing (the Contact Tracing & Advisory Service, CTAS), (3) laboratory reported data via the national laboratory surveillance system (SGSS) and (4) data from interviews with cases/contacts by health protection teams (HPT). This enabled each episode (including variant episodes) to be assigned a travel status of being imported, sporadic or unknown

METHODS

We calculated the proportions of travel-associated COVID-19 episodes by each data source of report between 01 December 2020 and 30 April 2022.

RESULTS

517,988 travel-associated SARS-CoV-2 episodes (3.0% of all episodes) were identified through SuITCases, where 38.3% and 37.8% were identified from a combination of the two and three sources respectively; and for cases identified from a single source, 16.9% were from PLF, 4.1% from CTAS, 3.0% from SGSS and 0.1% from HPT investigations. When assessing the sources individually, PLFs proved to be the most reliable data source and contributed to assigning 39.8% of travel-associated episodes, followed by 27.6% by CTAS, two enhanced systems which were established for the COVID-19 pandemic

CONCLUSIONS

Our unique integrated SuITCases system played a vital role in the rapid identification of travel-associated COVID-19 cases to reduce transmission and inform public-health actions. The implementation/use of the PLFs, and contact-tracing data should be considered as potential tools for future enhanced investigations and pandemic preparedness.

KEYWORDS: SARS-CoV-2, travel, surveillance, pandemic, COVID-19
ABSTRACT ID: 262
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POSTER TOUR 9

Day 2 – 15.30-16.30

AMR: National surveillance studies

PRESENTER

Chiara Sacco

ABSTRACT

Main determinants of vancomycin-resistant Enterococcus faecium (VREF) infection in bloodstream isolates: data from ARISS, the Italian national surveillance system on antimicrobial resistance, 2015-202

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BACKGROUND

Several countries have reported an increase in the proportion of VREF, listed by WHO as a high-priority pathogen for Healthcare associated infections and in-hospital mortality. This study aims to identify factors associated with the increased proportion of vancomycin resistance among E.faecium isolates in Italy.

METHODS

Italian hospitals routinely test E.faecium isolates for resistance to vancomycin. We analysed data on 14,254 bloodstream E.faecium isolates systematically collected by ARISS (within the EARS-Net ECDC framework) from 2015 to 2022. We performed a multilevel logistic regression model (vancomycin-resistant vs vancomycin-susceptible as outcome), including time variables (year, season), patient variables (age, sex, geographical area, hospital ward), and hospital-level variables (level of care complexity, bed-turnover index, number of hospital beds) as fixed covariates, with the hospital as random effect.

RESULTS

We observed a continuous increase in VREF proportion over time (odds ratios (OR)=5.15; 95%CI:2.63-10.08 in 2022 vs. 2015). Age had no significant effect, while males had a lower odd (OR=0.89, CI:0.82-0.97). Central and North-West areas showed higher odds compared to the North-East (OR=2.37, CI:1.77-3.16, OR=1.64, CI:1.24-2.16). Patients in intensive care units (OR=1.46, CI:1.21-1.75) and medical wards (OR=1.39, CI:1.17-1.65) had higher odds vs emergency wards. At the hospital level, VREF samples were more likely to be associated with hospitals with low bed-turnover (OR=1.4, CI:1.07-1.84 vs medium bed-turnover) and with medium-high bed capacity (hospital beds 401-800 OR=1.56, CI:1.30-1.88; >800 OR=1.55; CI:1.22-1.95 vs low bed capacity).

CONCLUSIONS

The proportion of VREF is continuously increasing in bloodstream infections in Italy. Several risk factors at both the individual and hospital level have been identified, highlighting the need for improved implementation of infection prevention and control measures in high-risk situations to mitigate VREF spread in healthcare settings

KEYWORDS: Enterococcus faecium, Vancomycin resistance, Antimicrobial resistance, Surveillance, ARISS
ABSTRACT ID: 356
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Day 2 – 15.30-16.30

AMR: National surveillance studies

PRESENTER

Heikki Ilmavirta

ABSTRACT

Community- and Healthcare associated bloodstream infections caused by extended-spectrum beta-lactamase-producing Escherichia coli in Finland in 2018-2023

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BACKGROUND

Escherichia coli bloodstream infections (BSI) cause increasing morbidity and mortality, and emergence of resistance is concerning. During 2008-2019, the proportion of extended-spectrum beta-lactamase-producing E. coli (ESBL+Ec) BSIs more than tripled in Finland, but the increasing trends reversed during the COVID-19 pandemic in 2020-2022. However, it is unclear whether these changes were similar for community-acquired (CA) and Healthcare associated (HA) infections. Here, we evaluated changes in incidence and case fatality in CA and HA BSIs caused by ESBL+Ec in Finland before, during, and after the pandemic in 2018-2023.

METHODS

ESBL+Ec BSIs were identified from the National Infectious Disease Register, deaths from the National Population Information System, and hospitalisations to classify infections as CA or HA from the National Hospital Discharge Register. Case fatality was calculated based on deaths occurring within 30 days after a positive ESBL+Ec blood culture.

RESULTS

A total of 1916 ESBL+Ec BSIs were identified: 1499 (78%) were CA (4.52 cases/100,000 population) and 417 (22%) HA (1.26/100,000). The overall annual incidence of ESBL+Ec BSIs decreased from 6.7-7.2/100,000 in 2018-2019 to 4.9-5.0/100,000 in 2022-2023 and the proportion of HA-ESBL+Ec BSIs from 23-28% in 2018-2019 to 16-19% in 2022-2023. The 30-day case fatality varied during 2018-2023, being lower for CA-ESBL+Ec BSIs than for HA-ESBL+Ec BSIs (10% vs. 22%).

CONCLUSIONS

Majority of ESBL+Ec BSIs were CA. Despite the decrease in incidence during the pandemic, the proportion of CA-ESBL+Ec increased. This increase did not affect the overall 30-day case fatality, suggesting that the patient populations affected and predisposing factors for invasive infections may have changed. Our results can help to evaluate potential sources of ESBL+Ec and to improve prevention and control efforts in the community and healthcare settings.

KEYWORDS: Escherichia coli,Bacteremia,Drug Resistance Bacterial,epidemiology,mortality
ABSTRACT ID: 632
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Day 2 – 15.30-16.30

AMR: National surveillance studies

PRESENTER

Nadejda Morarescu

ABSTRACT

Carbapenem resistance in gram-negative bacteria in the Republic of Moldova, 2019-2023

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BACKGROUND

Carbapenem resistance can indicate gaps in infection prevention and control practices in hospitals, as well as inappropriate antibiotic use. Moldova established the National Antimicrobial Resistance Surveillance System in 2018 to gather data per international standards. Our aim was to describe carbapenem resistance among gram-negative bacteria from 2019 to 2023 to inform future strategies for antimicrobial stewardship and infection control.

METHODS

We included all isolates of gram-negative bacteria from hospitalised patients blood cultures between 2019 and 2023, which were tested and confirmed for carbapenem resistance at the national reference laboratory. We used polymerase chain reaction (PCR) to determine the genes encoding carbapenemases in these microorganisms, with specific primers including blaOXA-23, blaOXA-48, and blaNDM. We assessed the proportion and distribution of resistant strains by bacterial species and resistance genes.

RESULTS

Of 978 isolates tested, 644 (65.8%) were resistant to imipenem and meropenem. The highest proportion of carbapenem-resistant strains was in A. baumannii (219/232; 94.4%), P. aeruginosa (95/101; 94.0%), K. pneumoniae (323/495; 62.2%), and E. coli (7/150; 4.6%). The most common resistance genes were: blaOXA-23 in A. baumannii (111/232; 47.8%), and blaOXA-48 in K. pneumoniae and E. coli isolates (257/495 [51.9%] and 7/150 [4.6%], respectively). The blaNDM gene was common in P. aeruginosa isolates (12/101; 11.8%).

CONCLUSIONS

We found a significant proportion of carbapenem resistance among tested gram-negative bacteria. Since carbapenems are considered antibiotics of last resort, such widespread resistance may signal excessive and indiscriminate use of these antimicrobials. We recommend using detection of resistance genes for prompt implementation of control measures. Also, we recommend implementing stringent infection control protocols and promoting antibiotic stewardship practices to mitigate further spread of carbapenem resistance.

KEYWORDS: Carbapenem resistance, gram-negative bacteria, resistance gene.
ABSTRACT ID: 378
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POSTER TOUR 9

Day 2 – 15.30-16.30

AMR: National surveillance studies

PRESENTER

Regina Singer

ABSTRACT

Antimicrobial resistance and area-level socioeconomic position in Germany, 2010-2019

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BACKGROUND

Studies suggest a link between socioeconomic position (SEP) and antimicrobial resistance (AMR) prevalence, but comprehensive studies on this correlation in Germany are lacking. Our aim was to assess the association between area-level SEP and AMR incidence in Germany, in order to provide adapted recommendations.

METHODS

We used an ecological study design to analyse statutory notifications of invasive Methicillin-resistant Staphylococcus aureus (MRSA, n=34,440), 2010–2019, and of colonisations and infections with carbapenem-resistant Acinetobacter spp. (CRA, n=1,979) and Enterobacterales (CRE, n=10,825) 2017–2019. Area-level SEP was measured by the German Index of Socioeconomic Deprivation (GISD), incorporating data on education, employment, and income. AMR cases were linked to GISD via district identifiers. A multilevel Poisson regression analysis was conducted to examine the association between AMR incidence and GISD, adjusting for age, gender, year of notification, and degree of urbanization.

RESULTS

MRSA incidence (yearly mean incidence: 0.1–17.5/100,000 population) was higher in districts with lower average SEP (Incidence Rate Ratio, IRR=4.8; CI95%: 2.8–8.2). In stratified analysis, this association was strongest in large cities (IRR=9.1; CI95%: 2.7–30.9), and sparsely populated rural districts (IRR=6.5; CI95%: 2.8–15.0). There was no statistically significant association of CRA and CRE with SEP (CRA: IRR=0.9; CI95%: 0.5–1.6 and CRE: IRR=1.0; CI95%: 0.7–1.7).

CONCLUSIONS

Lower regional SEP was associated with about five times higher MRSA incidence. The strength of this association was also dependent on degree of urbanisation, pointing to not yet understood mechanisms. Further individual-level research will help to differentiate if health behaviours or living conditions can explain these associations and differences between pathogens. The strong association between SEP and MRSA underscores the need to consider SEP for improving AMR prevention efforts.

KEYWORDS: Antimicrobial drug resistance, Acinetobacter, Enterobacteriaceae, Methicillin-Resistant Staphylococcus aureus, Socioeconomic factors
ABSTRACT ID: 99
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AMR: National surveillance studies

PRESENTER

Antonino Russotto

ABSTRACT

Comparing antibiotic consumption trends in Italian acute care hospitals: a propensity score matching analysis of two point prevalence surveys.

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BACKGROUND
Antimicrobial resistance (AMR) is a significant public health concern, necessitating vigilant surveillance of antibiotic consumption patterns. To investigate this, the European Centre for Disease Prevention and Control (ECDC) promotes point prevalence surveys (PPS) repeated over time. We utilized data from surveys conducted in 2017 (PPS2) and 2022 (PPS3) in Italian acute care hospitals, employing a sample of 140 and 325 hospitals respectively, to evaluate potential differences.

METHODS
To mitigate potential biases stemming from unequal sample sizes and the presence of COVID-19 in PPS3, we implemented propensity score matching (PSM) based on patient characteristics (age, sex, and McCabe score) to create a matched population of 57,810 individuals. We assessed differences in antibiotic consumption using prevalence ratios (PRs), confidence intervals (CIs), and corresponding p-values.

RESULTS
Patients of PPS3 exhibited higher prevalence ratios for central venous catheter (PR 1.27, 95% CI: 1.22 – 1.32), urinary catheter (PR 1.19, 95% CI: 1.16 – 1.22), intubation (PR 1.31, 95% CI: 1.20 – 1.42), and surgery performed on admission (PR 1.08, 95% CI: 1.05 – 1.11). Subsequently, we observed higher consumption of ceftriaxone and piperacillin (PR 1.26, 95% CI: 1.20 – 1.33 and PR 1.24, 95% CI: 1.18 – 1.31, respectively). Meanwhile, consumption of amoxicillin decreased (PR 0.69, 95% CI: 0.64 – 0.74). Additionally, we found increased antibiotic prescription for hospital-acquired infections (PR 1.32, 95% CI: 1.26 – 1.38), and decreased prescription for both medical (PR 0.56, 95% CI: 0.53 – 0.59) and surgical prophylaxis (PR 0.91, 95% CI: 0.87 – 0.96). All analyses had a p-value <0.001.

CONCLUSIONS
PPS promoted by ECDC are crucial for monitoring antibiotic consumption. Comparing trends via PSM could contextualise sample differences and personalize intervention strategies to fight AMR.

KEYWORDS: antibiotics,surveillance,italy,hospitals
ABSTRACT ID: 196
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Day 2 – 15.30-16.30

AMR: National surveillance studies

PRESENTER

Victoria McClure

ABSTRACT

Epidemiological description of carbapenemase-producing organisms (CPO) cases in Wales, April 2023 – March 2024: Initial results of a new surveillance system

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BACKGROUND

Carbapenemase-producing organisms (CPO) are bacteria with acquired enzymes causing resistance to carbapenem antibiotics. CPO pose an increasing threat to effective healthcare provision. Hospital screening is conducted based on risk assessment and exposure. Using routine data linkage, we established surveillance from April 2023. We aimed to describe CPO in Wales, based on first year of data collection.

METHODS

Carbapenemase genes are identified by rapid test in local laboratories, or by the Public Health Wales Specialist Antimicrobial Reference Unit. We extracted test results from 01/04/2023-31/03/2024 from laboratory databases and linked them to patient administrative data. We excluded repeat specimens for same patient, organism and gene within 12 months. Counts and proportions were calculated by specimen type (screening/clinical); organism; gene; demographics; and care home residence. Mortality from any cause was calculated 28 days post-positive specimen to measure severity.

RESULTS

We identified 125 cases across the Wales population (~3131640); 62% were from screens. Most common organisms were Escherichia coli (43%) and Klebsiella pneumoniae (27%). The OXA-48-like gene was found in 52%, then NDM-type (28%). More cases were male (54%), and most commonly aged 50-74 years (49%). 5% were care home residents and mortality was 10%. Differences between screen and clinical cases included: in screens, a higher percentage NDM-type (34% vs 17%) and higher mortality (12% 95%CI=5-22 vs 6% 95%CI=1-18); in clinical cases, more female (56%) and older cases (35% 75+).

CONCLUSIONS

Routine CPO surveillance is important to better understand the epidemiology of infection and direct interventions to control transmission. Our surveillance identifies common CPO, describes CPO cases and demonstrates the utility of hospital screening in identifying asymptomatic carriage. Continuation of surveillance will allow further identification of risk groups to target interventions.

KEYWORDS: carbapenemase,carbapenem,healthcare,public health
ABSTRACT ID: 546

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Day 2 – 15.30-16.30
AMR: National surveillance studies

PRESENTER
Jana Grüttner

ABSTRACT
Molecular epidemiology and antimicrobial resistance of invasive Streptococcus dysgalactiae subsp. equisimilis isolates in Denmark 2020-2022

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BACKGROUND
The incidence of invasive Streptococcus dysgalactiae subsp. equisimilis (iSDSE) and antimicrobial resistance (AMR) in iSDSE isolates have been increasing worldwide. In Denmark, iSDSE surveillance is based on voluntary submission of isolates to Statens Serum Institut. Since 2013, submitted iSDSE isolates have increased. We analyzed the genetic structure of the Danish iSDSE population (2020-2022) including AMR to understand the molecular epidemiology and occurrence of resistances that could lead to treatment failure.

METHODS
All iSDSE isolates (n=1226, August 2020 - September 2022) were whole-genome sequenced (WGS). Phenotypic antibiotic susceptibility to penicillin, erythromycin and clindamycin was determined. Core-genome single-nucleotide polymorphism analysis was used to infer relatedness and phylogenetic clades were deduced using Bayesian hierarchical clustering (fastbaps). Acquired AMR genes, multi-locus sequence typing and M protein gene (emm) types were inferred from WGS data. We describe key epidemiological characteristics of genetic clades and AMR genes.

RESULTS
We identified 14 distinct genetic clades which were evenly distributed across Denmark. Three clades represented 61% of the population comprising sequence/emm types ST20/stG62647.0, ST17/stG480.0/stG2078.0 and ST17/stG485.0. Acquired AMR genes were detected in 21% of isolates. All isolates were phenotypically susceptible to penicillin, the first-choice treatment option. Only two isolates harbored beta-lactam resistance genes. One clade showed a high proportion of macrolide resistance genes (57% (n=39)), a second-choice treatment option. 3/14 clades showed high proportions of tetracycline resistance markers (96% (n=22), 64% (n=7), 45% (n=31)).

CONCLUSIONS
Denmark has a heterogeneous iSDSE population with genetic clusters characterized by high proportions of AMR markers. Continuous genomic iSDSE surveillance can monitor the occurrence and expansion of genetic clades and AMR genes, e.g. beta-lactam resistance genes, and thereby indicate possible treatment failures and outbreaks of resistant clonal lineages.

KEYWORDS: Whole Genome Sequencing, Streptococcal Infections, Epidemiology, Surveillance, Antimicrobial Drug Resistance
ABSTRACT ID: 225
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POSTER TOUR 10

Day 2 – 15.30-16.30
Diagnostics of food- and waterborne diseases

PRESENTER
Wouter Van Dyck

ABSTRACT
Possible impact of culture-independent diagnostic techniques on surveillance of gastrointestinal pathogens in Belgium

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BACKGROUND
Culture-independent diagnostic techniques (CIDT) are increasingly used to detect gastrointestinal pathogens as they offer short turnaround times, high sensitivities and specificities, and ultimately improve patient care. However, the absence of clinical isolates may hamper epidemiological investigations and public health surveillance. In Belgium, CIDT for gastrointestinal pathogens are not widely used yet, but a change in the reimbursement conditions might affect laboratory practices.

METHODS
In the context of the project United 4 Surveillance, whose main objective is to strengthen surveillance of infectious diseases in Europe, we carried out an online survey in April 2024 among medical laboratories in Belgium. The aim was to (i) estimate current diagnostic practices, (ii) assess future diagnostic practices in light of the upcoming change in test reimbursement and (iii) estimate the interest of laboratories for public health questions for Salmonella, Shigella, Yersinia, STEC and Campylobacter.

RESULTS
The participation rate was 80% (90/113). For STEC, up to 55% of the laboratories are currently using CIDT with an increase to 85% when CIDT will be added to the reimbursement conditions. For the other four pathogens, 75 to 95% of the laboratories currently perform culture, but a change in diagnostic practice towards CIDT is foreseen (55-70%) when included to the reimbursement conditions. More than 80% of the laboratories intend to perform reflex cultures or send samples to the national reference centers.

CONCLUSIONS
A switch in diagnostic practices towards CIDT for gastrointestinal pathogens is expected but there is a strong intention of the laboratories to participate to surveillance activities. The impact of this change will be monitored closely to maintain a comprehensive view on circulating strains for public health surveillance.

KEYWORDS: gastrointestinal bacteria,culture-independent diagnostics,United 4 Surveillance
ABSTRACT ID: 111
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POSTER TOUR 10

Day 2 – 15.30-16.30

Diagnostics of food- and waterborne diseases

PRESENTER

Elena Portell-Buj

ABSTRACT

Association of Yersinia enterocolitica biotype 1A and gastrointestinal symptoms: an epidemiological and genomic study from 2021 to 2023 in Belgium

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BACKGROUND

Yersinia enterocolitica is the main etiological agent of yersiniosis and includes 6 biotypes (1A/B, 2-5). Biotype 1A (BT1A) is generally regarded as non-pathogenic despite evidence of pathogenic potential and ystB and ymoA virulence gene carriage, which encode an enterotoxin and modulator, respectively. We aimed to assess the association between BT1A and gastrointestinal symptoms.

METHODS

Laboratories provided Y. enterocolitica cultures to the National Reference Centre for characterization. We collected epidemiological data from positive BT1A cultures (n=183) by questionnaires to clinicians. We included questions on symptoms; etiology of gastrointestinal symptoms; hospitalization and immunosuppression status. Whole-genome sequencing (Illumina) was performed on 57/183 strains. The genotyping was performed by core-genome multilocus sequence typing (cgMLST) (Galaxy) and screening for virulence genes (BIGSdb). Association between reported etiology of gastrointestinal symptoms and genotype was assessed calculating the virulence genes-specific odds ratio (OR) and 95% confidence intervals (95%CI).

RESULTS

Among patients, 99/183 were female (53.80%); 60 (32.79%) were ≥65 years old and 16 (8.75%) were ≤4 years old. Overall, in 103 (56.28%) BT1A was reported as the etiological agent of gastrointestinal symptoms; 24 (13.11%) required hospitalization and 18 (9.84%) were immunosuppressed. In total, 53/57 strains (92.98%) contained ystB and ymoA. However, these were not significantly associated with being reported etiological agent of gastrointestinal symptoms (OR:4.81, 95%CI:0.35-267.11, p=0.19). It was not possible to determine the association with a certain cgMLST genotype or virulence gene involved.

CONCLUSIONS

We demonstrate the potential ability of BT1A strains to cause gastrointestinal symptoms, including in immunocompetent patients. Our genotyping results might be explained by the small number of strains studied. To elucidate the burden of gastrointestinal disease it is crucial to implement a system for routine identification and characterization of BT1A.

KEYWORDS: Yersinia enterocolitica, Biotype 1A, Gastrointestinal symptoms, cgMLST, Genomic epidemiology
ABSTRACT ID: 264
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Day 2 – 15.30-16.30

Diagnostics of food- and waterborne diseases

PRESENTER

Maria Dolores Fernandez Garcia

ABSTRACT

Enhanced echovirus 11 genomic surveillance in neonatal infections in Spain following a European alert reveals new recombinant forms linked to severe cases, 2019-2023

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BACKGROUND

On June 2023, French authorities informed EU/EEA Member States through the Early-Warning-System of an increase in Echovirus-11 (E11) severe neonatal infections (E11-SNIs). The rise was associated with an emerging lineage (new-lineage-1) circulating from 2022 onwards. We investigated whether E11-new-lineage-1 has circulated in Spain associated with SNIs to assess the risk for the neonatal population.

METHODS

Retrospective molecular epidemiology study with clinical and genomic data collected from 1255 patients between 2019-2023 at the Spanish Enterovirus Reference Laboratory. E11-SNIs cases were defined as neonates (<28 days), ICU-admitted from 2019 to 2023 with E11 laboratory-confirmed diagnosis. Available samples from 2022-23 (n=10) were subjected to metagenomic Sequencing (mNGS) for detection of recombinant forms and coinfecting pathogens. Doctors were emailed to fill incomplete E11 clinical-forms.

RESULTS

Overall, 98 patients (33 neonates) were E11-positive. As in the French study, E11-new-lineage-1 strains were first detected in Spain in 2022, predominating during 2022-2023 including severe and non-severe infections. Contrary to the French study, we observed no significant difference in the proportion of E11-SNIs between 2019-20 (40%) versus 2022-23 (27.7%) periods (p=0.7). mNGS revealed three novel E11 recombinant genomes associated with severe (n=2) and non-severe (n=1) cases from 2022-23 clustering outside new-lineage-1. Coinfecting pathogenic viruses were present in 40% of E11-positive samples. For E11 neonatal cases, completeness of clinical information was 60%.

CONCLUSIONS

In Spain, emergence of new-lineage-1 is not linked with an increase of E11-SNIs. However, the detection of two novel E11 recombinant genomes associated with severe disease warrants enhancing genomic surveillance in E11-SNIs in further Member States. Co-infections should be thoroughly investigated as they could contribute to E11 severe outcomes. There is need to improve the recording of E11 clinical information when requesting sample testing.

KEYWORDS: Enterovirus,Neonatal Diseases,Recombination,Echovirus 11,Genomic Surveillance
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Day 2 – 15.30-16.30
Diagnostics of food- and waterborne diseases

PRESENTER
Marloes Stradmeijer

ABSTRACT
Added value of PCR on feces in two hepatitis A outbreaks in care facilities for the disabled in the Netherlands

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BACKGROUND
In 2023 two outbreaks of hepatitis A virus (HAV) emerged in three daycare centers for disabled children/young adults of one organization in the Netherlands. Clients, healthcare workers and family members were affected and a risk of transmission to other care facilities and schools existed. Outbreak investigations were initiated to control the outbreaks, confirm the source(s) and understand how cases were linked.

METHODS
The outbreaks were descriptively studied, focusing on the added value of HAV-PCR on feces for detecting infections, as due to disabilities and young age of clients a reluctancy for blood sampling existed. Cases were diagnosed using HAV-feces-PCR or serology; probable cases were identified based on clinical symptoms and/or epi-links. If possible, sequencing was performed. Source and contact tracing was conducted; people at risk were offered vaccination and information on HAV and preventive measures.

RESULTS
In total 38 cases were identified (35 lab-confirmed, 3 epi-links). Transmission occurred most frequently among clients (n=15) and families (n=17), but also 6 healthcare workers got infected. Due to the outbreaks 7 other care facilities and 5 schools were at risk. HAV-feces-PCR was used 40 times and identified 14 cases. Sequencing identified two different HAV-strains, matching HAV-endemic travel destinations mentioned during source tracing, and confirmed epi-links of subsequent cases.

CONCLUSIONS
These outbreaks illustrate the known high risk of infectious disease outbreaks among disabled due to reduced hygiene awareness and behavioral problems. The use of HAV-feces-PCR appeared a low-key and well-accepted alternative for blood sampling. It contributed significantly to source tracing, mapping and limiting the outbreak. HAV-infections among healthcare workers pose a threat of further transmission among vulnerable groups that can be reduced by offering them vaccinations at enlistment.

KEYWORDS: Hepatitis A virus, outbreak, care facility for the disabled, feces PCR
ABSTRACT ID: 233
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POSTER TOUR 10

Day 2 – 15.30-16.30
Diagnostics of food- and waterborne diseases

PRESENTER
Karen Keegan

ABSTRACT
Development of a Nanopore DNA sequencing workflow for detection of zoonoses and antimicrobial resistance genes in avian faeces

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BACKGROUND
Waterfowl can act as reservoirs for zoonotic pathogens, including the foodborne bacteria Campylobacter and Salmonella, which are shed via faeces. Waterfowl also disseminate antibiotic resistant bacteria, posing a threat to global health. Metagenomic analyses, using long read sequencing platforms, enable the comprehensive identification of species and antimicrobial resistance (AMR) genes in a sample. This may offer advantages over conventional targeted methods for 'One Health' surveillance of zoonoses and AMR and support the investigation of wildlife species as reservoirs and potential vectors.

METHODS
In this study, a Nanopore DNA sequencing workflow as a tool for zoonoses and AMR surveillance of goose faeces was developed. Firstly, quality and quantity of DNA isolated using seven DNA extraction methods was assessed. DNA from each method was subsequently sequenced on a MinION (Nanopore sequencer), with several metrics evaluated, including sequencing yield (number of DNA bases). Metagenomic outputs were compared, using a custom bioinformatics pipeline that included BLASTn searching against nucleotide databases, specifically the NCBI nucleotide database for taxon assignment and the CARD database for AMR gene identification.

RESULTS
DNA quality and quantity was similar across extraction methods, yet DNA isolated from Qiagen MagAttract® HMW DNA extraction kit yielded the highest sequencing output (247,870,850 bases) compared to the next best method (MP Biomedicals FastDNA™ SPIN Kit; 47,606,274 bases). Also, the highest diversity of bacterial species was observed using the MagAttract® kit and, when applying strict BLASTn filtering criteria, high confidence identification of Campylobacter and Salmonella spp., as well as AMR genes was achieved.

CONCLUSIONS
A bespoke Nanopore sequencing workflow, from DNA extraction to metagenomic analyses, was successfully used to investigate avian faecal samples for the presence of specific zoonotic pathogens and AMR genes.

KEYWORDS: One Health,Nanopore,avian diseases,DNA sequence,computational biology,zoonoses
ABSTRACT ID: 200
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POSTER TOUR 10

Day 2 – 15.30-16.30

Diagnostics of food- and waterborne diseases

PRESENTER

Tanja Jung-Sendzik

ABSTRACT

Surge in the number of STEC notifications in Germany in 2023 – A real increase in infections or a laboratory artifact?

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BACKGROUND

In 2023, 4,354 cases of Shiga toxin-producing E. coli (STEC) infections were notified in Germany, a 1.7-fold increase compared to the median in pre-pandemic years 2015-2019 (2,638 cases). Similar trends have been observed in Denmark and Norway, driven by changes in laboratory diagnostic methods. We investigated if the increase in Germany was also related to changes in laboratory methods.

METHODS

We compared notification data from the national database of notifiable diseases in 2023 to the prepandemic median 2015-2019. We looked at changes in case numbers over time, by age group, sex, hospitalization status, origin of cases, and numbers of haemolytic-uremic syndrome (HUS) cases. Additionally, we conducted a survey on diagnostic methods among 25 clinical laboratories in Lower Saxony, one of the federal states with the highest increase in case numbers.

RESULTS

The surge in STEC notifications was not uniformly distributed across Germany. Notifications increased in all age groups, with the strongest surge in those older than 60 years (2.6-fold). We did not detect major changes in gender distribution, number of imported cases, proportions of hospitalized cases or a rise in HUS cases. 10 of 17 laboratories reported the use of multiplex-PCR, six introduced it in 2023. Four of the 10 laboratories introduced multiplex-PCR before 2023.

CONCLUSIONS

The increase in STEC notifications was likely due to more frequent testing by multiplex-PCR rather than a true rise in infections. In Germany, it is not recommended to routinely test adults with gastroenteritis for STEC. With multiplex-PCR, especially older patients may now be detected as “bycatch”. Our findings underscore the importance of monitoring diagnostic practices when evaluating trends in surveillance data. We recommend extending surveys to other federal states to consolidate results.

KEYWORDS: STEC,multiplex-PCR,notification system,HUS,laboratory artifact,survey
ABSTRACT ID: 187
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POSTER TOUR 10

Day 2 – 15.30-16.30

Diagnostics of food- and waterborne diseases

PRESENTER

Laura Giese

ABSTRACT

Opportunities and challenges of Integrated Genomic Surveillance based on Salmonella surveillance data from 2020 to 2023, Germany

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BACKGROUND

Since 2020, integrated genomic surveillance (IGS) has been gradually introduced to the surveillance of human salmonellosis in Germany with routine sequencing of the most common serovars (Salmonella Enteritidis and Salmonella Typhimurium) and event-based sequencing of other serovars. In order to identify future opportunities and challenges of IGS, we analysed aggregated molecular and epidemiological Salmonella surveillance data from 2020-2023.

METHODS

Data basis are WGS clusters detected at the Robert Koch Institute from 2020-2023. Clusters were defined as 4 strains forming a main node and its satellites with ≤3 allelic differences (EnteroBase cgMLST scheme). We performed descriptive analyses focusing on cluster size, dynamics, multinationality and genetic matches from food, animal or environmental isolates supported by the German National Reference Laboratory for Salmonella.

RESULTS

From 2020-2023, we detected 154 WGS clusters with Salmonella Typhimurium and Salmonella Enteritidis accounting for the largest proportion (66%). The total number of clusters increased from 21 in 2020 to 53 in 2023, whereas the average cluster size decreased from 33 to 12 isolates per cluster. Altogether, 64/154 (42%) clusters show recurring patterns over ≥2 years and 26 clusters were confirmed as multinational. For 71/139 (51%) clusters genetic matches from food, animals or the environment were detected.

CONCLUSIONS

With further establishment of IGS in Germany, we are able to detect more clusters at an earlier stage resulting in higher total numbers and smaller cluster sizes. Matches from food, animals or the environment as well as multinationality and recurrence of clusters can help to identify possible vehicles and sources of infection. At the same time, it highlights the need for precise resource allocation, clear communication and collaboration on local, national and international level and across sectors.

KEYWORDS: Integrated Genomic Surveillance, Foodborne diseases, Salmonella, Outbreak investigations, Whole Genome Sequencing
ABSTRACT ID: 515
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POSTER TOUR 11

Day 2 – 15.30-16.30

Vaccination programmes and strategies

PRESENTER

Joaquin Baruch

ABSTRACT

A new vaccine and two outbreak responses: a game-changer in meningitis control?

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BACKGROUND

In 2023, WHO pre-qualified the first vaccine to target the most common circulating serogroups of Neisseria meningitidis (A, C, W, Y, and X) in the meningitis belt (Men5CV).

METHODS

Nigeria and Niger experienced large outbreaks of meningococcal meningitis during the 2023-2024 meningitis season. In March and May 2024, Nigeria and Niger pioneered the use of Men5CV, targeting over two million people aged 1-29 years. A post-campaign vaccination coverage survey was organised, a surveillance system was set up at the health facility level to report adverse events following immunisation (AEFI), and two cohort studies with 50,000 people were conducted to assess vaccine safety. Lastly, a vaccine effectiveness study was set up in Niger.

RESULTS

Between weeks 1 and 16, 2024, 2,012 cases with 123 deaths and 2,377 cases with 227 deaths were reported in Niger and Nigeria, respectively. The main circulating serogroup in Nigeria was C, whereas Niger reported a combination of serogroups C, W, and X, further highlighting the need for a pentavalent vaccine. While administrative data on vaccination coverage surpassed 100% in both Nigeria and Niger (except for two districts in Nigeria, where the administrative coverage was 46%), the coverage survey indicated that most districts had vaccination coverage of around 90%, with the two with 46% having 76% and 94% coverage. The number of AEFIs from the surveillance system (minor and severe) was within the safety standards. The data from the cohort event monitoring and the vaccine effectiveness study are currently being collected.

CONCLUSIONS

The deployment of the new Men5CV can substantially impact the control of meningococcal meningitis. The first introduction of Men5CV presented multiple opportunities to assess its safety and effectiveness.

KEYWORDS: meningitis, Outbreak response,Men5CV,Vaccination campaign
ABSTRACT ID: 579
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POSTER TOUR 11

Day 2 – 15.30-16.30

Vaccination programmes and strategies

PRESENTER

Fatma Ben Youssef

ABSTRACT

Factors associated with Influenza vaccination uptake among frontline healthcare workers in Tunisia, 2022/2023 season

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BACKGROUND

The worldwide target for influenza vaccine (IV) uptake among healthcare workers (HCW) is 75% and the Tunisian national IV program recommends free vaccination for HCWs. We aimed to estimate IV uptake in 2022/2023 among HCWs in Tunisia and identify associated factors.

METHODS

We conducted a cross-sectional survey (January 2024) among HCWs using purposive sampling. We measured IV uptake with 95% confidence intervals (CI) and the association between various factors assessed with a comprehensive face-to-face survey (including socio-demographics and different behaviors, perceptions, and attitudes toward vaccination) and using logistic regression.

RESULTS

We included 906 HCWs (response proportion: 98%) from 46 primary healthcare centers (89.9%, n=815 were paramedics). Sex-ratio F/M was 4.2 and mean age was 41.8 ± 8.9 years. IV uptake was 16.9% (n=151) (95%CI=14.6-19.4%). In multivariable analysis, higher odds of IV uptake was associated with: IV uptake prior to the COVID-19 pandemic (adjusted odds ratio (aOR)=12.4; 95%CI=7.1-21.9), annual IV uptake over all of the previous five years (aOR=7.7; 95%CI=4.2-14.2), being aware of the national IV program (aOR=3.9; 95%CI =2.1-7.2), perception of IV as safe (aOR=2.5; 95%CI=1.3-5), having >14 years' professional experience (aOR=2.1;95%CI=1.2-3.5), having at least one underlying disease (aOR=1.9; 95%CI=1.1-3.2), perception of influenza as severe (aOR=1.8; 95%CI=0.9-3.5), and living in an urban area (aOR=2;95%CI=0.7-5.5). HCWs from the northern region had a lower IV uptake (aOR=0.8; 95%CI=0.2-0.8) compared to the south.

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CONCLUSIONS

IV uptake among HCWs was low. Our results identified regional disparities and several factors associated with higher uptake, including perceptions of IV safety and influenza severity. We recommend promoting the importance of IV in healthcare settings, addressing regional disparities and ensuring similar access to vaccines among HCWs with lower vaccine uptake.

KEYWORDS: Influenza Vaccine, Tunisia, Healthcare workers
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POSTER TOUR 11

Day 2 – 15.30-16.30
Vaccination programmes and strategies

PRESENTER
Oksana Artemchuk

ABSTRACT
Factors associated with influenza vaccine uptake among healthcare workers in Georgia, 2021-2024

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BACKGROUND
Healthcare workers (HCWs) are prioritised to receive influenza vaccine annually in Georgia. We aimed to determine factors associated with influenza vaccine uptake among Georgian HCWs.

METHODS
We used three seasons of self-reported influenza vaccination coverage data (2021-2024) along with 2023 re-enrolment survey data about attitudes towards influenza from a prospective cohort study among HCWs in six hospitals in Georgia. We calculated adjusted odds ratios (aORs) and 95% confidence intervals (CI) using multivariable logistic regression to identify factors associated with influenza vaccination uptake among HCWs. We compared HCWs who received influenza vaccine in at least one of the three study years with those who were not vaccinated in any of the three years

RESULTS
Of 445 participants, the median age was 46 (IQR = 36-54), 400 (90%) were female, 182 (41%) were nurses, 111 (25%) were support staff, 90 (20%) were doctors, and 62 (14%) were janitorial staff. Overall 289 (68%) participants received influenza vaccine in ≥ 1/3 seasons, while 139 (32%) participants did not receive influenza vaccine in any season.
In the multivariable analysis, there was no difference in vaccine uptake by site, age, sex or occupation. Among 14 sociodemographic, occupational and attitudinal variables evaluated in the univariate analysis, only two factors remained significant in the multivariable analysis. HCWs who did not believe in influenza vaccine safety (aOR: 0.13, 95%CI 0.07-0.25) and influenza vaccine effectiveness in preventing missing work (aOR: 0.41, 95%CI 0.22-0.75) were less likely to get vaccinated

CONCLUSIONS
We found that Georgian HCWs who had doubted influenza vaccine safety and vaccine effectiveness in preventing missing work had lower odds of influenza vaccination. Future campaigns to promote influenza vaccine among HCWs should address these concerns

KEYWORDS: influenza vaccination, healthcare workers, Georgia
ABSTRACT ID: 298
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POSTER TOUR 11

Day 2 – 15.30-16.30

Vaccination programmes and strategies

PRESENTER

Zeina Farah

ABSTRACT

One more reason to have a vaccination program for healthcare professionals in Lebanon

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BACKGROUND

Healthcare workers are priority groups for influenza and COVID-19 vaccination. In Lebanon, the Ministry of Public Health recommends seasonal influenza vaccination for high-risk groups. Evidence is needed to mobilize resources for healthcare workers' vaccination. The main objective of this study is to determine the role of influenza vaccination uptake as a predictor of COVID-19 vaccine uptake.

METHODS

A cross-sectional study was conducted targeting clinicians working in Lebanon. Data was collected on Kobo Toolbox using an online questionnaire developed based on the Health Belief Model. A random sample of physicians was selected from the Order of Physicians database. The link to the questionnaire was sent by email or message. Data management and analysis were performed using R(4.2.2) and R studio(2023.12.0).

RESULTS

The total responses were 1019. Two-thirds(65%) have ever received influenza vaccine before COVID-19 pandemic while half(49%) received it in the 2022-2023 season, yet, 73% intend to get the vaccine if recommended and offered. For the COVID19 vaccine, 920(96%) participants completed the primary doses, of whom, 73% received at least one booster dose whereas 42% are willing to be annually vaccinated. The history of receiving at least one COVID-19 booster dose was associated with influenza vaccine uptake before COVID-19 pandemic (adjusted-OR=1.88, 95%CI:1.29-2.75). A positive association was found between intention to take annual shots of both vaccines(adjusted-OR=4.56, 95%CI:3.02-7.05). Recommending annual COVID19 vaccination to patients was associated with recommending the flu vaccine (adjusted-OR=3.23, 95%CI:1.21-9.97) and intention to take COVID-19 vaccine annually (adjusted-OR=43.8, 95%CI: 26.7, 76.1).

CONCLUSIONS

Influenza vaccination among healthcare workers is associated with COVID-19 vaccine uptake. We recommend advocating for a vaccination program in Lebanon that could set the stage for other vaccines to be administered in future pandemics.

KEYWORDS: Health Personnel, COVID-19 Vaccines, Influenza Vaccines, Lebanon
ABSTRACT ID: 646
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POSTER TOUR 11

Day 2 – 15.30-16.30

Vaccination programmes and strategies

PRESENTER

Mary Sinnathamby

ABSTRACT

Childhood vaccinations: Declining coverage and widening inequalities in England

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BACKGROUND

We describe the longer-term trend of coverage of childhood immunisation programmes and inequalities over a ten-year period in England.

METHODS

Data on vaccine coverage (%) for routine childhood immunisation were collected via the COVER (Cover Of Vaccinations Evaluated Rapidly) programme and deprivation quintiles assigned using the Index of Multiple Deprivation 2019 local authority scores. Aggregate data from GP systems, including ethnic group were also analysed for some immunisation programmes where available. (%)

RESULTS

A longer-term decreasing trend in coverage over the past decade was observed, with coverage declining between 1.8% (Men B) and 6.0% (pre-school booster) . There were regional variations, with the largest declines observed in London. When comparing coverage by IMD quintile across the ten-year period, there has been a widening of inequalities in coverage. For two-doses of MMR, coverage at 5 years of age in the most deprived quintile decreased by 9.8% compared to an increase of 0.5% in the least deprived quintile. The gap between the most and least deprived has reversed from 2.2% higher in the most deprived quintile versus the least deprived, to 8.1% lower over the study period. Analyses of ethnicity data, indicate a disproportionate decline amongst ethnic groups who already had the lowest coverage. Coverage of the MenB programme increased by 0.4% in White-British children and decreased by 4.6% in Black-Caribbean children, widening the gap from 7.5% to 11.5% between the two groups.

CONCLUSIONS

Overall declines in coverage were observed and inequalities by deprivation and ethnicity have widened over the past decade. These translate to a risk of outbreaks such as the measles and pertussis incidents in England in 2024, and the potential to disproportionately impact those most disadvantaged.

KEYWORDS: Immunisation programmes; Vaccines; ,Ethnicity,Vaccination coverage,Disease outbreaks,Inequalities
ABSTRACT ID: 676

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POSTER TOUR 11

Day 2 – 15.30-16.30
Vaccination programmes and strategies

PRESENTER

Laura Colombo

ABSTRACT

Is the high-dose influenza vaccine better for everyone over 60 years of age in Germany?

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BACKGROUND

Elderly population is more susceptible to seasonal influenza, with increasing mortality and decreasing seroprotection with age. German STIKO guidelines exclusively recommend high-dose influenza vaccine (HD-IV) for individuals ≥ 60 years old.A recent meta-analysis showed increased relative vaccine effectiveness (rVE) of HD-IV vs standard-dose (SD-IV) with age, with people ≥75 years old better protected than people 65-74 years old.We analysed real-world evidence comparing the effectiveness of HD-IV and SD-IV, focusing on age subgroups data.

METHODS

Qualitative literature search was performed to identify the articles describing the rVE of HD-IV vs SD-IV against hospitalization for influenza, and lab-confirmed influenza cases within the elderly population, specifically, within age sub-groups (65-74; 75-84; >85).

RESULTS

Of 39 articles retrieved, 5 matched our criteria (Izurieta, Thadani et al. 2015, Richardson, Medvedeva et al. 2015, Young-Xu, Van Aalst et al. 2018, Lu, Chillarige et al. 2020, Doyle, Beacham et al. 2021). Results show rVE of HD-IV in preventing influenza or pneumonia-associated hospitalization, reducing hospital admissions and ER visits, consistently increased with age, and was more effective than the SD-IV for people ≥ 85. However, subgroup analysis from one study did not show any difference between age groups 65-74 and ≥75 (Doyle, Beacham et al. 2021).

CONCLUSIONS

Given that the most benefit of the HD-IV is seen in ≥75 years and older, it would be appropriate to recommend it for this age sub-group, thereby allowing the SD-IVs to be used for 60-74 age group. With such prioritization, the existing resources could be used optimally to increase vaccination coverage in Germany in the ≥65 years old group without sacrificing the protective effect of the population.

KEYWORDS: Influenza Vaccines,hospitalization,Elderly,Germany,Comparative Effectiveness Research
ABSTRACT ID: 422
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Day 2 – 15.30-16.30

Vaccination programmes and strategies

PRESENTER

Gulzada Dadanova

ABSTRACT

Missed opportunities for vaccination among Healthcare seeking children–Kyrgyzstan, 2023

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BACKGROUND

In Bishkek, Kyrgyzstan (population: 1.15 million), coverage for many childhood vaccines had dropped to <90% in 2022. Opportunities for vaccination were being missed at child healthcare visits. Understanding the burden and reasons for these missed opportunities was needed to increase coverage.

METHODS

We conducted a cross-sectional study in Bishkek in 2023 using the Missed Opportunities for Vaccination (MOV) World Health Organization protocol. We interviewed 20 caregivers of <30 months olds from 33 primary care clinics and abstracted medical records. MOV was the number of children not receiving a vaccine among those eligible for vaccination (missing a dose at visit onset and no contraindications). The p-values from Poisson regression Wald tests are shown.

RESULTS

Of 660 candidates, 69% (448/650) met the inclusion criteria. MOV prevalence was 86% (386/448). MOV was 81% (195/240) among children 0-11 months old and 92% (191/208) among 12–30-month-olds. Vaccine-specific MOV was lowest for hepatitis B (8%; 52/648) and highest for diphtheria-pertussis-tetanus (50%; 52/103). Among eligible children (n=448), 62% had >4 annual clinic visits, 6% had never been immunized, and 84% were missing vaccine cards. Healthcare providers did not check immunization status in 53%. Half (53%, 71/133) of those visiting for vaccination had a MOV. MOV did not differ by sex, district, or number of annual visits. MOV was higher among children with never-vaccinated vs vaccinated caregivers (98% vs 85%, p=0.03) and caregivers with self-reported negative vaccine attitudes vs positive (94% vs 83%, p=0.01).

CONCLUSIONS

Nearly nine in ten children missed an opportunity to be immunized while seeking healthcare services. Training for healthcare workers, to check immunization status of all children at each visit, and strategies that address caregiver barriers can help increase immunization coverage.

KEYWORDS: Vaccination coverage,Kyrgyzstan,Delivery of Health Care,Primary Health Care,Cross-sectional Studies,Child
ABSTRACT ID: 443
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POSTER TOUR 12

Day 2 – 15.30-16.30

STIs and related prevention

PRESENTER

Richard Pentz

ABSTRACT

Prevalence of chlamydia, gonorrhoea, trichomoniasis, and syphilis in Europe: A systematic review and meta-analysis to inform prevention and control of sexually transmitted infections in Europe

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BACKGROUND

Routine surveillance of sexually transmitted infections (STIs) organised by the European Centre for Disease Prevention and Control is impacted by variations across countries in national testing practices and surveillance systems characteristics. To better describe the epidemiology of the four curable STIs (chlamydia, gonorrhoea, trichomoniasis, syphilis) in Europe, we conducted a systematic review of prevalence estimates for the general population and populations of special interest.

METHODS

From seven databases and a grey literature search, we systematically retrieved prevalence studies from European countries published between January 2012 and February 2024 with data for the general population, suitable proxy populations, men who have sex with men (MSM), sex workers, and/or people who inject drugs (PWID). Study quality was assessed using the Joanna Briggs Institute checklist and pooled prevalence estimates were calculated using random effects models.

RESULTS

We included 97 studies from 25 countries. Prevalence estimates in women are 2.81% (95%CI 1.71–3.91) for chlamydia, 0.29% (95%CI 0.05–0.54) for gonorrhoea, 0.69% (95%CI 0.41–0.98) for trichomoniasis, and 0.16% (95%CI 0.02–0.30) for syphilis. In men, prevalence estimates are 2.67% (95%CI 0.65–4.69) for chlamydia, 0.27% (95%CI 0.00–0.64) for gonorrhoea, and 0.13% (95%CI 0.00–0.34) for trichomoniasis. Prevalence estimates varied for young people, women in antenatal care, MSM, sex workers and PWID. However, interpretability of pooled results is limited by low number of estimates, heterogeneity in study design, and different sampling timeframes.

CONCLUSIONS

Variations in STI prevalence across populations in Europe warrant targeted public health actions. Recent and high-quality prevalence estimates are rare and unevenly available across European countries. Enhancing data collection efforts at the national level is needed to track progress towards the elimination of STIs as a public health concern.

KEYWORDS: Chlamydia infections, Gonorrhoea, Trichomonas Infections, Syphilis, Systematic review, prevalence
ABSTRACT ID: 372
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POSTER TOUR 12

Day 2 – 15.30-16.30
STIs and related prevention

PRESENTER
Filipa Canha

ABSTRACT

Rising incidence of congenital syphilis in Portugal: Implications for achieving WHO Europe targets

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BACKGROUND
The incidence of congenital syphilis in Portugal has been increasing over the past years. World Health Organization (WHO) Europe has established targets for the elimination of mother-to-child transmission (MTCT) of syphilis for 2030 and interim targets for 2025. Our objective was to analyze Portugal's progress towards these targets.

METHODS
Cases of congenital syphilis notified between 2018 and 2023 were extracted from the Portuguese National Epidemiological Surveillance System. Descriptive analysis was conducted, and the rates per 100,000 live births were calculated for Portugal, mainland Portugal and its autonomous regions. The difference between the WHO Europe targets for 2025 and 2030 and the rates of congenital syphilis for each year and region was also calculated.

RESULTS
Between 2018 and 2023, there was a four-fold increase in the rates of confirmed cases of congenital syphilis per 100,000 live births in Portugal. In the time-period studied, Madeira reported zero cases but the rate of confirmed cases in Azores was higher than in the mainland in the years 2019 and from 2021 to 2023. In 2023, Portugal had an excess of 8.6 cases per 100,000 live births compared to the interim target for 2025, and in Azores the excess was 87.9 cases per 100,000 live births.

CONCLUSIONS
Portugal is failing to meet the targets set by the WHO Europe, highlighting the urgent need for further research on missed opportunities for the prevention of MTCT of syphilis and the implementation of region-specific measures to reverse this trend. Congenital syphilis can be prevented with adequate prenatal healthcare and treatment, making its increase in Portugal particularly relevant as a public health issue.

KEYWORDS: Syphilis Congenital,Public Health,Health Policy,Epidemiology,Health Services Accessibility
ABSTRACT ID: 590
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POSTER TOUR 12

Day 2 – 15.30-16.30

STIs and related prevention

PRESENTER

Laura Kayaert

ABSTRACT

Spatio-temporal trends and determinants of syphilis among heterosexual men and women in the Netherlands, 2011-2023

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BACKGROUND
Syphilis is increasing among heterosexual men and women in Europe and other Western countries. In the Netherlands, there has been an increase in syphilis positivity and diagnoses in the last 10 years. Research on syphilis among heterosexuals and on spatio-temporal syphilis trends in the Netherlands is limited. We aimed to assess these spatial and temporal trends and identify determinants of syphilis among heterosexuals in the Netherlands.

METHODS
This study used national surveillance data of the Sexual Health Centres (SHC) and included consultations among heterosexual men and women tested for syphilis in 2011-2023. Syphilis was defined as an infectious syphilis diagnosis (primary, secondary, or early latent). Spatial autocorrelation was assessed using the Global Moran's I statistic. Spatio-temporal trends were assessed using SaTScan, adjusting for demographic and behavioural factors. We performed a multivariate logistic regression to identify (demographic and behavioural) determinants of syphilis.

RESULTS
We identified 686 syphilis diagnoses among heterosexuals and found an increase in syphilis positivity in 2011-2023. The Global Moran's I identified spatial clustering (I statistic: 0.35, p-value: 0.004). The SaTScan identified two space-time clusters, one in the north (2019-2023) and one in the southwest (2020-2023) of the Netherlands. Being HIV-positive (OR: 19.50, 95%-CI: 12.90-28.40), being male (OR: 2.55, 95%-CI: 2.13-3.06), being older than 25 (OR: 2.47, 95%-CI: 2.05-2.99), and having symptoms (OR: 2.89, 95%-CI: 2.44-3.45) were the most associated with syphilis.

CONCLUSIONS
We found an increasing trend of syphilis among heterosexuals diagnosed at SHC in the Netherlands and two ongoing clusters, warranting increased syphilis testing among heterosexuals living in those areas. Since being HIV-positive was the strongest risk factor for syphilis, increased testing among HIV-positive heterosexuals, both at SHC and HIV treatment clinics, is recommended.

KEYWORDS: syphilis,sexually transmitted diseases,spatio-temporal analysis,determinants
ABSTRACT ID: 516
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POSTER TOUR 12

Day 2 – 15.30-16.30

STIs and related prevention

PRESENTER

Miguel Pinto

ABSTRACT

Antimicrobial resistance in Neisseria gonorrhoeae in Portugal: Results from the Portuguese National Laboratory Network for Neisseria gonorrhoeae Collection

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BACKGROUND

Neisseria gonorrhoeae, the bacterium responsible for the sexually transmitted disease gonorrhea, has shown an extraordinary ability to acquire antimicrobial resistance (AMR) to multiple classes of antibiotics after the introduction of each different treatment regimens. With no available vaccine, managing gonorrhea infections relies on preventive measures, effective antibiotic treatment and surveillance. In 2010, the Portuguese National Institute of Health (NIH) created the Portuguese National Laboratory Network for Neisseria gonorrhoeae Collection (PTGONONET) in order to monitor and manage the spread of antimicrobial-resistant N. gonorrhea in our country.

METHODS

Currently, the PTGONONET enrolls 35 countrywide spread public and private laboratories that voluntarily participate in providing N. gonorrhoeae isolates. Isolates are anonymously sent to the NIH were they are sub-cultured before detection of β-lactamase production and antimicrobial susceptibility testing (using commercial E-tests) for azithromycin, benzylpenicillin, cefixime, ceftriaxone, ciprofloxacin, gentamicin, spectinomycin, and tetracycline.

RESULTS

A total of 6781 N. gonorrhoeae isolates, collected from 1983 to 2023, were tested for antimicrobial susceptibility. Data revealed that since 2016 ~80% of isolates present resistance to penicillin and tetracycline. Ciprofloxacin resistance has remained high in the last decade (ranging from 40% to 60% of resistant isolates) contrasting with data from the 1980s and 1990s. Cephalosporins resistance was only sporadically observed (total of seven cases). While azithromycin resistance was observed ~10% in the 2000s, a marked increase was observed from 2019 onwards, reaching ~40% in both 2022 and 2023.

CONCLUSIONS

This study compiles N. gonorrhoeae AMR data from the last four decades and highlights the advantages of a nationwide collection network for AMR testing to respond to supranational requirements (e.g. the European Gonococcal Antimicrobial Surveillance Programme) while providing unprecedented AMR surveillance data in Portugal.

KEYWORDS: Neisseria gonorrhoeae,Antimicrobial Resistance,Surveillance,Drug susceptibility testing
ABSTRACT ID: 507
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POSTER TOUR 12

Day 2 – 15.30-16.30

STIs and related prevention

PRESENTER
Michael Edelstein

ABSTRACT

Knowledge, attitudes and HPV vaccination intentions among different populations of unvaccinated young Israeli adults: a cross-sectional survey

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BACKGROUND

In Israel, The Human Papilloma Virus (HPV) vaccine is offered to both genders at school and recommended until age 26. Many young adults missed the opportunity for school vaccination and barriers to vaccination are unclear. We described HPV knowledge, attitudes and vaccination intentions among unvaccinated Israelis from different population groups aged 18-26

METHODS

We recruited participants through a survey panel and collected information about demographics and HPV knowledge, attitudes and vaccination intentions using yes/no questions and likert scales in an anonymous digital survey distributed 12/23-02/24. We calculated weighted mean knowledge and attitude scores according to age, gender, ethnicity and sexual orientation. We determined factors associated with vaccination intention using multivariate linear regression.

RESULTS

Of 4,324 respondents, 36% were vaccinated. Of 1,994 unvaccinated respondents in the final analysis, overall weighted HPV knowledge score was of 10.1/15 (95% CI 9.9-10.3). Older participants, Jewish non-Ultra-Orthodox, and those with higher education levels reported higher knowledge. HPV vaccination attitudes were positive overall (mean score 2.9/5), with little variation across groups. Vaccination intention was low with <15% overall, and a minority in all subgroups indicating intention to vaccinate over the next year. Being Arab, older, female, having multiple sexual partners and being a student were significantly associated with a higher vaccination intention. There was no association between sexual orientation and intention. Notably, Arab participants exhibited the least knowledge but the greatest vaccination intention.

CONCLUSIONS

Young adults in Israel demonstrate a lack of HPV awareness and low vaccination intention, with slight variations in attitudes across different demographics. Simply providing more information may not enhance vaccine uptake in all groups. Identifying specific barriers and tailoring interventions in different groups is essential to increase intention to vaccinate.

KEYWORDS: vaccines,human papillomavirus viruses,Health Knowledge, Attitudes, Practice,cross-sectional studies
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POSTER TOUR 12

Day 2 – 15.30-16.30

STIs and related prevention

PRESENTER

Goncalo Matias

ABSTRACT

Neonatal herpes simplex virus infections in the Netherlands (2016-2022): incidence, health outcomes and guideline adherence

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BACKGROUND

Neonatal herpes simplex virus (nHSV)-infection is an invasive disease of newborns with high morbidity/mortality. Because it is non-notifiable in the Netherlands as in most European countries, incidence is monitored through reiterated surveys. We estimated nHSV-incidence, health outcomes, and guideline adherence in the Netherlands between 2016-2022.

METHODS

Online questionnaires on nHSV-infections were distributed to hospitals through pediatric, obstetric, and microbiology associations. Questions included diagnostics, health outcomes and self-reported guideline adherence. We estimated nHSV-incidences per 100,000 live births (2016-2022) and compared them with registry-data from Dutch Hospital Data (DHD, 2016-2020).

RESULTS

Overall, 22 (19%) pediatric, 20 (65%) obstetric, and 39 (30%) microbiology departments returned the questionnaire; 66 nHSV-infections were reported for 2016-2022 (5.5/100,000 live births), and 48 in DHD for 2016-2020 (5,6/100,000).; slightly higher than the previous survey in 2012-2015 (4.6/100,000). For 51 cases with health outcomes available, 47% (24/51) were nHSV-1, 29% (15/51) nHSV-2, and 24% (12/51) of unknown type. Case fatality was 6.7% (3/51), and 67% (16/24) of cases had symptoms of the central nervous system or disseminated disease. 65% of neonatologists and 70% of obstetricians reported using nHSV guidelines. Among those using guidelines, 71% of obstetricians used the national STI guideline, while 47% of neonatologists used adapted/other guidelines. Preliminary results show high adherence to guidelines in diagnostics, treatment, and prevention.

CONCLUSIONS

Our results indicate that nHSV-incidence in the Netherlands is at least as high as in previous years. Yet incidences are difficult to compare between surveys and registry-data due to variation in study design, time periods, and lack of unique identifiers across data. As nHSV is severe, more awareness and prevention might diminish the burden. Systematic monitoring is needed through surveillance or by making nHSV notifiable

KEYWORDS: herpes simplex virus ,neonatal herpes,surveillance,guidelines
ABSTRACT ID: 513
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POSTER TOUR 12

Day 2 – 15.30-16.30
STIs and related prevention

PRESENTER
Raquel Eusébio

ABSTRACT
Reduction of mpox vaccination hesitancy in clinics offering on-site vaccination

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BACKGROUND
The sustained spread of mpox primarily occurs within networks engaging in high-risk sexual behaviours. Pre-exposure vaccination emerges as a critical strategy for controlling outbreaks. This study evaluates the impact of on-site vaccination services in clinics on reducing vaccination hesitancy among individuals eligible for mpox pre-exposure vaccination.

METHODS
We did a retrospective cohort study involving 3,062 individuals considered eligible for mpox pre-exposure vaccination by healthcare professionals in 15 clinics at the Lisbon region, Portugal. We compared the time from vaccination eligibility to actual vaccination between clinics offering vaccination services (n=1,608, 52.5%) and those without these services (n=1,454, 47.5%). Individuals not vaccinated within 60 days of eligibility were categorized as hesitant. We performed a time-to-event analysis utilizing Cox proportional hazards regression to assess the risk of vaccination hesitancy.

RESULTS
The median time from eligibility to vaccination at clinics with vaccination services was significantly shorter (4 days, IQR 0-12) compared to clinics without vaccination services (20 days, IQR 10-38). The risk of hesitancy was 2.55 times higher (HR 2.55; 95% CI 2.35-2.77) at clinics without vaccination services. The risk remained significant after adjusting for age and eligibility criteria.

CONCLUSIONS
The presence of on-site vaccination services in clinics substantially decreases the risk of vaccination hesitancy among individuals eligible for mpox vaccination. Integrating vaccination services into existing healthcare settings could significantly enhance vaccine uptake. These findings support the development of targeted interventions by policymakers to improve vaccination access and reduce barriers.

KEYWORDS: mpox,vaccination hesitancy,vaccination access,healthcare integration
ABSTRACT ID: 380
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POSTER TOUR 13

Day 2 – 15.30-16.30
Surveillance studies

PRESENTER

Sophie Campman

ABSTRACT

SARS-CoV-2 infection and vaccination status in six ethnic groups in Amsterdam, the Netherlands, May-November 2022

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BACKGROUND

Ethnic minority groups have been at increased risk of SARS-CoV-2 infection, while vaccination uptake remained low in certain groups, potentially leading to varying immune statuses. Hybrid immunity, which is immunity through both vaccination and prior infection, protects most effectively against severe COVID-19. We studied the SARS-CoV-2 infection and vaccination status among six ethnic groups in Amsterdam, the Netherlands.

METHODS

We analysed participants of the HELIUS cohort who were tested for SARS-CoV-2 spike protein antibodies using WANTAI ELISA between May 17 and November 21, 2022 as part of a three-visit COVID-19 substudy. We categorized participants with antibodies as only infected, only vaccinated (≥1 dose), or both infected and vaccinated, based on self-reported prior infection and vaccination status, and seroprevalence data from previous substudy visits (June-October 2020, November 2020-June 2021). We compared infection and vaccination status between ethnic groups using multivariable, multinomial logistic regression.

RESULTS

Of 1,482 included participants [median age 58 years (IQR=48-65), 57% female], 98.5% had SARS-CoV-2 antibodies (P between ethnic groups=0.899). Being previously infected and vaccinated ranged from 44.7% (n=122/273) in the African Surinamese to 65.7% (n=117/178) in the Turkish group. Compared to participants of Dutch origin, [1] participants of African Surinamese [adjusted OR (aOR)=8.19, 95% confidence interval (CI)=3.93-17.06] or Moroccan (aOR=9.21, 95%CI=4.05-20.92) origin were more likely to be only infected and [2] participants of Turkish origin (aOR=0.51, 95%CI=0.28-0.95) were less likely to be only vaccinated, than infected and vaccinated.

CONCLUSIONS

SARS-CoV-2 infection and vaccination status varied across ethnic groups, particularly regarding non-vaccination. As hybrid immunity is most protective against COVID-19, future vaccination campaigns should encourage vaccination uptake in specific demographic groups with only infection.

KEYWORDS: SARS-CoV-2,vaccination,seroprevalence,antibodies,immunity,ethnicity
ABSTRACT ID: 289
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POSTER TOUR 13

Day 2 – 15.30-16.30

Surveillance studies

PRESENTER

Emiel Vanhulle

ABSTRACT

Circulation of enterovirus types in Europe between January 2018 and August 2023: a retrospective multi-center surveillance study

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BACKGROUND

Enteroviruses (EV) are an increasing public health concern, most recently due to the increase in severe neonatal echovirus 11 (E11) infections and acute flaccid myelitis clusters linked to enterovirus D68 (EV-D68). Although prevalent, EV infections are not notifiable in most European countries, resulting in substantial variation in surveillance between countries. We assessed EV data from the European Non-Polio Enterovirus Network (ENPEN) and from National Focal Points to understand the epidemiological and clinical landscape of EV over the past six years in European countries.

METHODS

We requested aggregated numbers on the detection and typing of EV cases. The information included monthly counts, specimen type, age group, and clinical presentation of the top ten most detected types between January 2018 and August 2023.

RESULTS

26 institutions from 13 countries participated, 28,014 EV-positive samples were reported during the study period and 16,037 (57%) were successfully typed, identifying 43 types. Echovirus 30 (E30) was the most frequent EV type (n=1303), followed by coxsackievirus A6 (CVA6), enterovirus D68 (EV-D68), E9, E11, CVB5, E18, EV-A71, CVB4, and E25. For 9,529 EV infections with available age information, 6,868 cases (72%) occurred in children under 5 years. Neurological symptoms were reported for 1,367 cases. E30 and EV-D68 demonstrated fluctuating numbers with surges in autumn 2018, and in autumn/winter 2021 and 2022, respectively.

CONCLUSIONS

These results emphasize the continued widespread circulation and distribution of EV among young children, and their association with neurological infections. E30, a common cause of viral meningitis outbreaks, was the most frequently identified type. Despite individual countries collecting extensive EV data, inconsistencies in case definitions and reporting parameters poses challenges to surveillance efforts. Encouraging harmonization of case definition for EV surveillance is recommended.

KEYWORDS: Enterovirus,Laboratory detection,Typing,Europe,Outbreak
ABSTRACT ID: 128
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POSTER TOUR 13

Day 2 – 15.30-16.30

Surveillance studies

PRESENTER
Dinagul Otorbaeva

ABSTRACT

Factors associated with severe outcomes among adult patients with Severe Acute Respiratory Infection admitted to Bishkek Hospital #2, Kyrgyzstan, 2022- 2024

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[5,6,7]World Health Organization, Regional Office for Europe

BACKGROUND

Understanding in-hospital severity of Severe Acute Respiratory Infections (SARI) patients is critical for healthcare planning and resource allocation. We evaluated surveillance data from adult SARI pattients (≥ 18 years old) admitted to Bishkek Hospital #2 from Week 40, 2022-Week 11, 2024 period to better understand which kinds of patients were at risk for severe outcomes.

METHODS

All SARI patients were tested by RT-PCR for SARS-CoV-2 and influenza. We defined severe outcome as a composite outcome that included being admitted to the intensive care unit (ICU), requiring oxygen, or in-hospital death. We performed descriptive statistics to assess the epidemiology of SARI patients, and multivariable analyses to assess factors associated with severe outcome.

RESULTS

We included 634 SARI patients. The median age was 61 years (interquartile range:46-72), 335 (53%) were female, 166 (26%) received at least one COVID-19 vaccine dose and only 7 (1%) received influenza vaccine during 2023-2024 season. Overall, 316 ^{51}% patients required oxygen, 166 (26%) patients were admitted to the ICU, and 7(1%) died. In total, 34 (6%) patients had PCR confirmed Influenza, 24 (4%) patients had SARS-CoV-2. Being female (adjusted odds ratio (aOR): 1.5; 95% confidence interval (CI): 1.0–2.3), being an older adult [41-55 years old (aOR: 2.7; CI: 1.5–4.6) and ≥ 56 years old (aOR: 4.6; CI: 2.8–7.4)] compared to adults aged 18-40, smoking (aOR: 2.2; CI: 1.3–3.5) and having fever ≥ 39°C at admission (aOR: 4.3; CI: 1.3–14.0) were significantly associated with severe outcome.

CONCLUSIONS

SARI patients who were female, older, smokers, admitted with high-grade fever were more likely to have severe in-hospital outcomes. These subgroups should be targeted for interventions, such as vaccination and antiviral treatment, to reduce severe outcomes.

KEYWORDS: Kyrgyzstan, Intensive Care Units, Hospital Mortality, patients
ABSTRACT ID: 310
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POSTER TOUR 13

Day 2 – 15.30-16.30
Surveillance studies

PRESENTER
Beatriz Valcarcel

ABSTRACT
Increase in invasive group A streptococcal infections (iGAS) in children and older adults in Norway, 2022-24

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BACKGROUND
During the first half of 2023, an increase in invasive group A streptococcus (iGAS) notifications was observed in Norway, followed by a new surge in early 2024. We aimed to evaluate the epidemiological characteristics of iGAS cases before and after the COVID-19 pandemic to better interpret surveillance trends.

METHODS
Data on laboratory-confirmed iGAS cases was extracted from the Norwegian Surveillance System for Communicable Diseases. We calculated incidence for two post-pandemic periods (March 2022 – February 2023 and March 2023 – February 2024) and compared with a pre-pandemic period (March 2015 - February 2020). Descriptive epidemiology was performed, including age, sex, region, clinical presentation, and emm-types. Using 10 years (2010 - 2019) as baseline, generalized linear models were performed to estimate the post-pandemic expected incidence. Excess incidence was calculated as the difference between the observed and expected incidence.

RESULTS
We observed a large increase in the number cases during the second post-pandemic period (n=530) and estimated an excess of 266 cases (PI: 212-320) during this period. All age groups were affected, but most notably children <10 years (n=85) and adults >70 years (n=194). During the post-pandemic period a larger proportion of cases were males (56%) compared with the pre-pandemic (51%). An increase in the severity of cases, especially in children <10 years, was also detected in the second post-pandemic period. No changes in emm-type distribution were observed across study periods.

CONCLUSIONS
The ongoing increase in iGAS notifications globally is of concern. Continued monitoring of the epidemiological situation is essential to detect new surges and identify changes associated with severe outcome. We recommend clinicians should be on alert and familiar with recommendations for a prompt identification and treatment of GAS.

KEYWORDS: Group A Streptococcus, iGAS, invasive, outbreak, Streptococcus pyogenes
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POSTER TOUR 13

Day 2 – 15.30-16.30
Surveillance studies

PRESENTER

Klein Juliana

ABSTRACT

A geospatial approach to identify possible sources of infection during an outbreak of Legionnaires' disease, Baden-Wuerttemberg, Germany, 2023

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BACKGROUND

During autumn 2023, a legionellosis outbreak with 35 confirmed cases was investigated in a large city in Baden-Wuerttemberg, Germany. Epidemiological investigations pointed towards a common environmental source in the city center. We used a geospatial approach to narrow down the exposure area for further testing and identification of suspected cooling towers (CT).

METHODS

All laboratory-confirmed cases were interviewed about their whereabouts and movement profiles during the incubation period. We visualized cases' geolocation data using ArcGIS-Pro (version-3.0.3.;ESRI) and added data from all cooling systems recorded in the national registry of evaporative cooling systems (KaVKA-42.BV). We applied 2/3/5 km buffer polygons for all cases and CTs to identify the risk area for exposure (RA), considering topography and meteorological data (wind direction). The outbreak investigation team investigated the CTs in the RA with legionella test-results exceeding the action value (10,000 CFU/100 ml) or without testing three months prior. The national reference laboratory further typed human and environmental legionella positive specimens using Mab-typing.

RESULTS

Of the 141 CTs registered in KaVKA-42.BV, 69 were located inside the RA. Of those, two remained suspicious due to high Legionella contamination and time overlap with human infections. Upon additional testing, one suspected CT was no longer contaminated, but the other one still indicated contamination with Legionella serogroup 1 of >100,000 CFU/100ml. No more cases were identified during the three-month period following the shutdown of the suspected CT. Human outbreak specimens were identical to the specimens taken from the suspected CT (Mab-type Allentown/France).

CONCLUSIONS

The use of geospatial tools supported the localization of the exposure area and facilitated the detection of suspected sources. We recommend the use of GIS-tools to control future legionellosis outbreaks.

KEYWORDS: Legionella,Legionnaire Disease,Outbreaks,Geospatial Analysis,Spatial Cluster,Hotspot
ABSTRACT ID: 249
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POSTER TOUR 13

Day 2 – 15.30-16.30
Surveillance studies

PRESENTER
Anne-Merel R. van der Drift

ABSTRACT
Wastewater-based epidemiological studies and their use in public health decision making: a scoping review

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BACKGROUND
This study aims to provide the first overview of wastewater surveillance studies on pathogens and the key study characteristics to support public health decision making. Many of the studies on monitoring the circulation of pathogens (e.g. SARS-CoV-2 and poliovirus) in human populations refer to the value of wastewater surveillance in public health decision making processes. However, whether and how this is embedded in the study design widely varies.

METHODS
A scoping review was conducted by searching PubMed and Scopus to identify relevant studies describing wastewater surveillance with the aim to monitor circulation in human populations. Abstract screening was performed using the active learning tool ASReview, and data extraction was independently conducted by two reviewers.

RESULTS
655 out of 2436 records are included in this review. Based on preliminary data analysis, 8% (26 out of 317) of the studies describe the communication of data to health professionals, of which 69% (18 out of 26) also initiated interventions, such as contact tracing, vaccination campaigns or communication to the public. These studies monitored several viral pathogens, namely SARS-CoV-2 [23], poliovirus [3] and influenza virus [1]. Most of the studies were conducted in non-European regions.

CONCLUSIONS
Although many wastewater surveillance studies are published, only a fraction describes the actual communication to or use by health professionals in public health decision making processes. The findings of this study help to learn from existing use cases and aid in setting up effective wastewater surveillance studies that are targeted towards public health impact.

KEYWORDS: Wastewater-Based Epidemiological Monitoring,Decision Making,Public Health,Epidemiological Monitoring
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POSTER TOUR 14

Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER

Lisa Kolodziej

ABSTRACT

The influence of the COVID-19 pandemic on influenza vaccination willingness among healthcare workers in Dutch nursing homes

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BACKGROUND

During the pandemic, COVID-19 vaccination coverage was high among healthcare workers (HCWs) in nursing homes (NHs). We aim to study the influence of the COVID-19 pandemic on vaccination willingness for influenza among this group.

METHODS

In this mixed-methods study, online questionnaires were distributed to gain insight into vaccination status, barriers to vaccination and the influence of the COVID-19 pandemic on influenza vaccination willingness. Facilitators and barriers of vaccination willingness were identified in ten in-depth interviews and a focus group.

RESULTS

Almost all HCWs (94%; 280/298) received the primary COVID-19 vaccination(s). Influenza vaccination coverage was 41.7% (123/298) before the COVID-19 pandemic, 56% (168/298) in 2021-2022, and 54.7% (162/296) of the HCWs intended to receive an influenza vaccination in 2022-2023. Perceived urgency was identified as an important reason for the increase of influenza coverage during the pandemic and for the difference between COVID-19 and influenza vaccination willingness. Knowledge gaps and (dis-)beliefs were identified regarding vaccine efficacy, the role of preventive measures, and the immune system. Participants suggested that information should be transferred in an open, neutral and non-persuasive manner in order to build trust. Other identified facilitators to vaccination willingness were reducing practical issues such as flexible scheduling, on site provision, and combined COVID-19 and influenza vaccinations.

CONCLUSIONS

NH HCWs were more willing to get vaccinated against COVID-19 than against influenza due to the severity of the pandemic compared to the low perceived urgency of influenza. The pandemic's impact on willingness to get vaccinated against influenza appears to be temporary, underscoring the importance of addressing practical barriers to vaccine access. To optimize vaccination uptake, transparent, non-persuasive communication and education is important to increase trust and fill knowledge gaps.

KEYWORDS: Nursing Homes; Health Personnel; Vaccination Coverage; Vaccination Hesitancy; Influenza, Human; COVID-19
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POSTER TOUR 14

Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER

Mahmud Omar

ABSTRACT

Impact of the COVID-19 pandemic on parental behaviour towards Childhood Vaccination: A self-controlled matched Cross-Sectional Study.

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BACKGROUND

The long-term impact of the COVID-19 pandemic on routine childhood vaccination remains unclear. We aimed to determine changes in vaccination attitudes and behavior among parents with at least 2 children: one born before and one after the pandemic.

METHODS

Using a self-controlled, matched design, we measured changes in vaccination attitudes and practices among Israeli parents recruited February-May 2024 through an online survey panel including population groups comprising Israeli society. We measured changes in attitudes and vaccination using Paired t-tests and McNemar's tests, and factors associated with change in vaccination behaviour using logistic regression. Fisher's Exact Test assessed the association between decreases in trust and vaccination.

RESULTS

We recruited 1046 participants (56% female). Compared with pre-covid, 9.3% did not vaccinate a child born post-COVID with either MMR or pentavalent vaccines when their child born pre-COVID was vaccinated; 2.4% vaccinated post-COVID but not pre-COVID: an overall net decrease in vaccination rates of 6.9% ($p < 0.01$). The drop was larger for MMR than pentavalent. Compared with participants from the secular Jewish majority, non-Jewish (i.e mainly Arab) participants were significantly more likely to stop vaccinating for either MMR or pentavalent post-COVID (Odds Ratio = 3.2, $p < 0.001$). Compared to pre-pandemic levels, 37% of parents reported a decline in vaccine confidence post-pandemic, 18% an increase, and the remainder no change. Decrease in confidence did not correlate with a decrease in vaccination ($p = 0.43$).

CONCLUSIONS

Using an innovative, bias-reducing approach, we show the pandemic has significantly decreased vaccine uptake and confidence. The study is ongoing, and interventions will be required to restore optimal collective immunity. Improving attitudes to vaccination may not be sufficient to improve coverage.

KEYWORDS: COVID-19, Childhood Vaccination
ABSTRACT ID: 176
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Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER

Arystan Balmagambetov

ABSTRACT

Knowledge, attitudes and practice towards routine vaccination among medical students, Kazakhstan, 2023

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BACKGROUND

In Kazakhstan, childhood immunization coverage has decreased. Healthcare workers can increase vaccine coverage if they are sufficiently trained. To assess whether interventions are needed, we aimed to understand current vaccine knowledge, attitudes and practices (KAP) in medical students.

METHODS

We conducted a cross-sectional study among senior medical students in 3 universities in Karaganda, Astana, and Almaty, from March to May 2023. We used multivariable logistic regression to test association with adequate KAP; the threshold for adequate scores for questions in each domain was 70%.

RESULTS

We interviewed 3,956 students: 1,716 (43%) in Astana, 1,313 (33%) in Almaty, and 927 (24%) in Karaganda. Of these, 74% were female, and 65% were 21-23 years old. Additionally, 89% were studying general medicine, 8% pediatrics, and 3% public health. Fewer than half (38%) reported having received training on vaccination. Adequate KAP scores were 11% for knowledge, 55% for attitudes, and 17% for practices. Most (74%) believed common myths about routine vaccinations, including 62% believing that the flu vaccine causes flu. Inadequate knowledge was associated with inadequate attitude (odds ratio [OR]: 1.72; 95% confidence interval [CI]=1.37–2.17) and inadequate practice (OR: 1.66; CI=1.30–2.11). Inadequate attitude was associated with being male (OR: 1.25; CI=1.07–1.47), living with someone <18 years old vs not (OR: 1.37; CI=1.08–1.73), and living in Astana vs Karaganda (OR: 1.69 CI=1.41–2.03). Inadequate practice was associated with living with someone >65 years old vs not (OR: 1.32; CI=1.03–1.72), Islam religion vs none (OR: 2.03; CI=1.65–2.50), and having inadequate attitude (OR: 2.99; CI=2.45–3.66).

CONCLUSIONS

Our study revealed markedly low levels of correct KAP related to routine immunizations. These results demonstrate the need to increase training on vaccination among medical students.

KEYWORDS: Vaccination, Students, Kazakhstan, Influenza Vaccines, Health Personnel
ABSTRACT ID: 415
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POSTER TOUR 14

Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER

Lusine Boryan

ABSTRACT

Physicians' knowledge and practices on syphilis diagnosis and prevention in Armenia

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BACKGROUND

The diagnosis of new cases of syphilis is not reliable in Armenia. In 2022, 29% cases were diagnosed as latent, 21% as secondary syphilis. We aimed to assess the knowledge and practice of syphilis diagnosis and prevention among primary care physicians to inform early identification of primary cases.

METHODS

In February-March 2024, we conducted a cross-sectional survey among doctors working in outpatient clinics. We randomly selected 24 clinics located in six regions. Then we sent an online questionnaire to physicians randomly selected from employee registries. We assigned 1 or 2 points to correct answers, and 0 points to incorrect or unknown answers, and classified knowledge and practice as good (80-100%), moderate (60-79%), and poor (<60%). We compared the scores between groups using non-parametric tests (Wilcoxon, Kruskal-Wallis, Spearman correlation tests).

RESULTS

Of 413 physicians contacted, 345 (83%) responded; 74% were female; median age was 46 years; 188 (54%) had >16 years work experience; 163 (47%) worked as general practitioners. Respondents had poorest knowledge on risk groups (56%), symptoms (49%) and disease transmission (8%). Knowledge did not improve with the number of years of practice ($p<0.31$). As for practice, respondents could easily interpret laboratory results (86%), but expressed difficulty to prescribe additional laboratory tests based on clinical symptoms (51%), and struggled with reporting diagnosed syphilis cases (66%). Respondents' knowledge did not correlate with their practice scores ($r=0.23$, $p<0.001$).

CONCLUSIONS

Knowledge of primary care physicians was not positively associated with improved practice of syphilis diagnosis and prevention. This highlights the need to improve healthcare workers' education, and implement an efficient screening program to detect and treat asymptomatic, late latent, congenital infections as well as preventing complications, transmission, and reinfection.

KEYWORDS: knowledge, practice, syphilis
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POSTER TOUR 14

Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER

Marije Hop

ABSTRACT

Creating good career prospects for professionals in the infectious disease control in the Netherlands

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BACKGROUND

A strong public health system in the Netherlands requires sufficient and motivated professionals. In preparation for new large outbreaks and pandemics, a strong workforce is essential. Addressing barriers and facilitators for good career prospects is essential to attract, engage and retain public health professionals at the 25 Dutch Regional Public Health Services (RPHSs) for pandemic preparedness. However, it is unclear what barriers and facilitators professionals experience concerning their career prospects in the infectious disease control.

METHODS

We aimed to identify these barriers and facilitators using focus groups with infectious disease medical doctors, nurses and assistants, infection preventionists, and administrative assistants. Tangible solutions to address barriers and strengthen facilitating factors were gathered using in-depth interviews with key figures within the board, management, training coordinators and human resources of the RPHSs.

RESULTS

Forty-six professionals participated in six focus groups. Barriers and facilitators for good career prospects included whether or not professionals experienced: job crafting (freedom), personal development opportunities, achievement appreciation, and opportunities for (financial) growth. Interviews with key figures identified solutions to career prospect barriers, which were grouped into five themes: 1) Engage in conversations about career prospects, 2) Provide sufficient achievement appreciation, 3) Ensure connectivity between RPHSs, 4) Develop a perspective on career prospects, 5) Improve the image of RPHSs.

CONCLUSIONS

Career prospects can be improved by developing and communicating a perspective on career prospects, increasing achievements appreciation, and improving the image of working in public health. A guideline focused on these goals was developed for RPHSs including 17 recommendations. Implementation of these recommendations is essential to captivate, engage and retain public health professionals for pandemic preparedness.

KEYWORDS: Work Engagement, Training Support, Vocational Guidance, Pandemic Preparedness, Public Health Professional, Job Satisfaction
ABSTRACT ID: 280
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Day 2 – 15.30-16.30

Social and behavioural sciences

PRESENTER
Betina Kiefer Alonso

ABSTRACT

Focus group on information-seeking and sharing on vaccination

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BACKGROUND

This qualitative study aimed to better understand how the general public seek, use and share information about vaccines/vaccinations, and how healthcare professionals (HCPs) share this information with the general public.

METHODS

The study comprised two sets of focus groups: ten focus groups with members of the general public (n = 60) and ten focus groups with HCPs (n = 59). The focus groups were conducted online between 16th and 25th of January 2024 in ten EU Member States and the data was aggregated and analysed in May-June 2024. Participants were selected to include a balanced mix of genders, age groups and education levels to capture a broad range of opinions and behaviours. Focus groups covered the following topics: 1) interest, knowledge and information needs, 2) information seeking/sharing strategies, 3) information seeking/sharing challenges and 4) information engagement/information sources.

RESULTS

General public participants most often reported searching information on side effects, age-specific recommendations, and benefits/risks. HCPs reported being most asked on necessity, safety, and practicalities. Participants from the general public generally reported that in-person advice from HCPs was their most important source on vaccines. They also mentioned public health authorities' and scientific institutes' websites, and news outlets, as key sources. The general public cited source trustworthiness as essential to address information-seeking challenges. HCPs generally reported sharing information face-to-face with patients to create trust and tailor information. The information-seeking challenges most reported by the general public were over-abundance of information, assessing trustworthiness of sources, understanding technical language, conflicting information, and assessing information accuracy. HCPs cited misinformation, vaccine hesitancy, and cultural factors.

CONCLUSIONS

The findings aim to contribute to communications efforts on vaccines and vaccination at the national and European levels.
"

KEYWORDS: Vaccines,vaccination hesitancy,Communication,Information Seeking Behavior,Health Behavior
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POSTER TOUR 15

Day 2 – 15.30-16.30
Preparedness

PRESENTER
Dorothee Obach

ABSTRACT
The first year of operations of the EU Health Task Force in the European Union and globally

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BACKGROUND
The EU Health Task Force (EUHTF) was created in January 2023 under the Regulation (EU) 2022/2370 to offer support to European Union (EU) and third countries during communicable disease crises, and to strengthen their emergency preparedness. It is operational since May 2023, is coordinated by the ECDC Coordination Team and composed of three EUHTF pools: ECDC Experts, ECDC Fellows and External Experts. We report on the assignments undertaken during the first year of EUHTF operations.

METHODS
For each assignment, we collected information on objective, dates of interest (request received, actions taken, end of assignment) and outcome. We descriptively analysed the EUHTF assignments conducted from 1-5-2023 to 30-4-2024.

RESULTS
The EUHTF carried out 13 assignments in support of 10 countries (seven EU/EEA and three third countries) involving ECDC experts, one ECDC Fellow and one External Expert. Four countries received response support for outbreak/emergency response (n=3) and rapid risk assessment [1], with a median time for initiation of 1 (IQR 1-3) day. Preparedness assignments were in support of six countries and related to after-action reviews (n=3), mass gathering events [2], applied research [1], workforce capacity [1], capacity-building [1] and emergency operation centre [1]. The median time for support initiation was 16 (IQR 5-30) days. Overall, five assignments were completed, whereas eight were ongoing as of 15-5-2024.

CONCLUSIONS
In its first year of operation, the EUHTF proved to be a new mechanism able to provide rapid support to EU and third countries to strengthen their preparedness and response. The full use of the pools of ECDC Fellows and of External Experts is the next essential step to sharpen the impact the EUHTF can have during crisis and in countries' preparation.

KEYWORDS: European Union, emergency response, preparedness, outbreaks and crises
ABSTRACT ID: 538
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Day 2 – 15.30-16.30

Preparedness

PRESENTER

Eva Maria M. Hodel

ABSTRACT

"Bern, get ready" (BEready), a One Health population-based household cohort for pandemic preparedness: Pilot study about participation and feasibility

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BACKGROUND

The lack of epidemiological data at the start of the COVID-19 pandemic hampered evidence-based decision making in the interest of public health and safety. Early in the pandemic, experts called for cohorts that could provide data about newly emerging infectious diseases in the future. The objective of this study was to test the feasibility of a population-based household cohort for pandemic preparedness with online questionnaires and self-sampling.

METHODS

In 2023, we enrolled households with adults, children and pets in the canton of Bern, Switzerland. After the initial in-person visit, including blood sampling, participants were followed up for 12 months. They took nasal swabs during episodes of respiratory symptoms. At 12 months, they completed online questionnaires and provided a dried blood spot. Enrolment was defined as the number of households enrolled divided by those invited. Using logistic regression, we described the agreement to participate according to demographic and socio-economic variables.

RESULTS

Of 1,338 households invited, 9% agreed to participate. 108 households were enrolled (193 people, 29 cats and 15 dogs). Baseline blood samples were obtained from 95% of participants (184 people, 40 pets). Baseline characteristics were similar between enrolled and invited people. In multivariable analysis, participation was lower in households with 3+ people (adjusted odds ratio, aOR 0.3, 95% confidence interval, CI 0.19–0.46, $p<0.001$) and higher in households with upper secondary or higher education (aOR 2.83, 95%CI 1.15–9.37, $p=0.046$). We did not find associations between participation and age, sex, nationality, household location or income.

CONCLUSIONS

Online questionnaires and self-sampling are feasible methods for household cohort studies on pandemic preparedness. Community engagement could be a way to increase enrolment, especially in larger households and those with lower education.

KEYWORDS: Pandemic Preparedness, One Health, Communicable Diseases, Cohort Studies, Zoonoses
ABSTRACT ID: 130
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POSTER TOUR 15

Day 2 – 15.30-16.30
Preparedness

PRESENTER
Amelie Plymoth

ABSTRACT

The state of the art of professional exchange visits in preparedness in the European Union/European Economic Area

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BACKGROUND

The European Centre for Disease Prevention and Control (ECDC) has designed a professional exchange visit program on preparedness, aiming to provide identified needs for hands-on learning for public health experts from Member States (MS). This program aims to familiarize participants with methods used in other EU/EEA countries, promoting skill development, knowledge exchange and collaboration.

METHODS

In 2024, three professional exchange visits focused on preparedness are arranged, reflecting the MS's prioritization of this area post-COVID pandemic. In 2024, Luxembourg, Portugal, and France host visits, with experts from Belgium, Germany, Ireland, Luxembourg, Malta, The Netherlands, Portugal, Denmark, Estonia, Latvia, and Spain attending for 2-5 days.

RESULTS

Results from training needs assessment and ECDC's National focal points for preparedness response (NFP EPRS) meetings identified gaps in the following areas, around which the program was designed: preparedness and response assessment methodologies and processes, linking assessments to the preparedness cycle, and fostering a culture of assessment among public health experts. Other themes include workforce capacities, resilience planning for healthcare services, and preparing surveillance and public response for mass gatherings, drawing from experiences like the Olympics and festivals.Participants, either NFPs for preparedness and response or by them nominated local experts, identified learning outcomes, designed the agenda, and planed cascading activities. Evaluation data, both quantitative and qualitative, are collected and analysed from these visits, and initial results show the program's benefits of peer-learning across borders. Diverse representation from EU/EEA countries allows rich exchanges, showcasing how countries in relatively equal geographical distribution approach public health challenges within their organizational structures.

CONCLUSIONS

This program contributes significantly to capacity building in European public health, fostering participant networks, and strengthening European cooperation, preparedness, and training in the field.

KEYWORDS: training, curriculum,preparedness,exchange
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POSTER TOUR 15

Day 2 – 15.30-16.30
Preparedness

PRESENTER
Olga Hovardovska

ABSTRACT
Preparedness of European critical infrastructure operators to vector-borne outbreak

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BACKGROUND
The SARS-CoV-2 pandemic has demonstrated the risk of disrupting the operation of Critical Infrastructures (CI) and highlighted the importance of preparedness for infection threats. Vector-borne diseases (VBD) are (re-)emerging threats to Europe and the possibility of outbreaks increases with climate change. Workshops in Slovenia, Italy, and Spain with CI operators were held to identify possible issues in the response and to facilitate preparedness to VBD outbreaks.

METHODS
VBD scenario contained legend, transmission, pathogen, and host characteristics, the clinical course and severity of VBD, epidemiological situation in region and CI institution, and a list of non-pharmaceutical interventions (NPIs). The participants were asked to answer questions that would show their preparedness to tackle a VBD outbreak.

RESULTS
Three national workshops in May 2023 had 63 participants from various CI sectors, like Telecommunications, Healthcare, Water, Transport, Energy, etc. The questions related to the identification of vulnerable workers, the impact on human resources, and the preparedness for the implementation of NPIs were discussed. Actors confirmed that identifying directly vulnerable (due to sociodemographic characteristics) employees is something that can be easily done locally. However, legal regulations complicate identifying indirectly vulnerable (due to health-related risks or household members). Implementation of NPIs is not difficult in case of clear and on-time governmental recommendations and availability of needed equipment in the market. The location of the workplace (indoors or outdoors) and the type of work might impede global strategy development.

CONCLUSIONS
The main gaps in the preparedness of European CI operators for VBD outbreaks are difficulties in the identification of indirectly vulnerable workers; dependence on rapid and clear recommendations from the government and market availability for protective equipment, etc.; and difficulties due to the labor settings.

KEYWORDS: vector-borne disease, outbreak,preparedness
ABSTRACT ID: 648
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POSTER TOUR 15

Day 2 – 15.30-16.30

Preparedness

PRESENTER

Sarah Foulkes

ABSTRACT

Lessons for future pandemic preparedness: The SIREN experience

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BACKGROUND

SIREN is a prospective cohort study in healthcare workers (HCW) across the United Kingdom, established to improve understanding of immunity following SARS-CoV-2 infection and vaccination. The study has evolved with the pandemic and changing public health priorities. Learning from experience delivering pandemic research studies is essential. We aimed to evaluate SIREN delivery to identify and share key lessons for future pandemic preparedness.

METHODS

Process evaluation methodology was used and included both quantitative and qualitative data. Key areas of study design/delivery were described: recruitment, retention and data collection. Focus groups, surveys and SIREN's participant involvement panel (PIP) were used to gain feedback throughout the study.

RESULTS

SIREN initially recruited 44,546 participants who were tested at 135 hospital sites, with 85% cohort retention at 12-months. Testing has continued with successive study extensions, with 5,790 participants testing via postal kits between 01/09/2023 and 31/03/2024, with 96% retention. Changes to testing data capture and testing delivery (from testing at hospitals to postal kits) has minimised data reporting and testing burden on the hospital study teams and participants.Participant focus groups identified barriers to participation, including testing discomfort and study fatigue. From the participant feedback survey, 93% felt that they contributed to the pandemic respond by being in the study and 87% were reassured by receiving their test results. The PIP has been a valuable resource for assessing acceptability to study adaptations, e.g. introducing multiplex testing in Winter 2022/23.

CONCLUSIONS

SIREN has maintained an engaged cohort of HCW and demonstrated agility adapting as the pandemic progressed. Lessons identified about successful recruitment, retention, data infrastructure, testing at scale, and incorporation of qualitative research to ensure interventions are sustainable are invaluable for future pandemic preparedness.

KEYWORDS: COVID-19, SARS-CoV-2, cohort, Lessons learnt, preparedness
ABSTRACT ID: 423
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POSTER TOUR 15

Day 2 – 15.30-16.30

Preparedness

PRESENTER

Douglas Hamilton

ABSTRACT

Food Security Recommendations Following Investigation of an Outbreak Linked to Oyster Consumption

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BACKGROUND
An event attended by 147 people in June 2024 in Ireland resulted in an outbreak of acute gastrointestinal illness affecting 34 individuals. An outbreak investigation was conducted by public health and food safety authorities in Ireland

METHODS
A retrospective cohort study examined associations between food consumption at the event and illness. Oysters consumed at the event were suspected as the source, and oysters harvested from the same production area one week after the event batch were tested for viral and bacterial parameters. A review of potential sewage contamination incidents in the oyster production area was carried out.

RESULTS
Descriptive epidemiology revealed cases experienced a non-severe vomiting/diarrhoeal illness with a short incubation period and duration, clinically suggestive of norovirus. A retrospective cohort study identified a significant association between oyster consumption and gastroenteritis [adjusted OR 9 (95% CI 2.39-34.12, p <0.001)]. No samples were available to confirm a pathogen from human cases or the event batch of oysters. The outbreak was temporally linked to heavy rainfall, sewage overflows, unseasonably high levels of regional norovirus notifications and an emerging genotype (GII.17) in the human population preceding the harvesting of the event batch. Oysters harvested from the same production area one week subsequent to the event batch were recalled as they were found to contain norovirus GII at 407 c/g following depuration.

CONCLUSIONS
We identified oysters contaminated with norovirus as the outbreak source with a moderate degree of certainty. We recommend legislation to set norovirus upper limits in oysters and, secondly, the creation of an early warning system that integrates human norovirus epidemiological data, precipitation data, and sewage overflow data to trigger enhanced food safety controls, including norovirus testing, in bivalve shellfish.

KEYWORDS: Foodborne diseases,gastroenteritis,norovirus,oysters,sewage
ABSTRACT ID: 812
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Day 2 – 15.30-16.30

Disease detection

PRESENTER

Fariya Abdullahi

ABSTRACT

Evaluation of whole genome sequencing versus emm typing for iGAS outbreak management in England

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BACKGROUND

Since April 2010, management of invasive Group A Streptococcus (iGAS) outbreaks in England has used Sanger emm gene typing to evaluate genetic relatedness of epidemiologically linked cases. While emm gene typing is faster, compared to more recent methods its resolution can limit understanding of strain diversity within clusters, identification of transmission routes and appropriate public health action. This study evaluates Whole Genome Sequencing (WGS) and emm typing in iGAS outbreak management to determine if WGS offers benefits for strengthening outbreak response.

METHODS

Emm typing and WGS data from GAS isolates from England submitted to the UKHSA Streptococcus Reference Laboratory between February 2018 and February 2024 were analysed. Interviews with laboratory and bioinformatics personnel (n=7) and a survey for health protection staff (n=8) provided insights into workflows and perspectives on emm typing and WGS data use and utility.

RESULTS

Of 1176 isolates from 183 epidemiologically linked outbreaks, emm typing excluded 198 (17%) unrelated cases from 60 clusters (mean=1.08 per cluster, SD=3.3). WGS excluded an additional 209 (35%) cases from 116 clusters (mean=2.22 per cluster, SD=4.1); a 106% increase in exclusions. Health protection staff acknowledged the enhanced value of WGS for exclusion of unrelated cases and identifying transmission routes but raised concerns regarding turnaround times. Stakeholders highlighted the need for training on interpreting WGS data and standardisation of reporting.

CONCLUSIONS

WGS benefits iGAS outbreak management by enabling exclusion of genetically unrelated cases sharing the same emm type, narrowing the focus of outbreak investigations and potentially conserving resources. However, efforts are needed to standardise reporting and provide stakeholder training to maximize WGS utility. Furthermore, optimising turnaround times and automating analysis is essential for usage of WGS data for timely outbreak management.

KEYWORDS: Streptococcal Infections,Whole Genome Sequencing,Evaluation Study,Public Health Practice,Bacterial Typing Techniques,Outbreak,Streptococcus pyogenes
ABSTRACT ID: 235
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POSTER TOUR 16

Day 2 – 15.30-16.30

Disease detection

PRESENTER
Tom White

ABSTRACT

Use of Large Language Models to Analyse Text Responses in a National HIV Survey

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BACKGROUND

Recent developments in generative AI, specifically the development of Large Language Models (LLMs), have attracted attention as they allow a wider group of users, including epidemiologists, to use LLMs to take on certain resource-intensive analytical tasks. We develop a method for conducting sentiment analysis of open-ended survey questions from a health survey using LLMs.

METHODS

Using Positive Voices 2022, a national survey of people living with HIV as a case study, we used various LLMs to analyse 1,652 responses from an open-ended question on how respondents feel about the statement Undetectable = Untransmissible (U=U). The LLM classified text responses as ‘positive’, ‘negative’, ‘neutral’ or ‘mixed’ based on their sentiment using different model prompting strategies. Model predictions were validated using a manually labelled subset of 400 responses. We tested the likelihood of misclassification based on characteristics of the survey respondents.

RESULTS

The stable-beluga-2-vllm model returned the highest accuracy (f1-score = 0.8925). The most effective combination of classification conditions: using a label set excluding a ‘mixed’ option, providing a few examples within the prompt and requesting the model provide its thought-process. The model slightly overestimated positive sentiment and underestimated negative sentiment. Neutral sentiment was least accurate with 60% (34/56) true neutral responses labelled correctly. Risk of misclassification by the model was not associated with education level, country of origin, ethnicity, age, gender or completion format (paper vs online).

CONCLUSIONS

This preliminary work provides proof-of-concept for using LLMs to perform qualitative analyses of data from health surveys. While our study did not find evidence of bias introduced by the model, we stress the importance of testing LLM outputs for bias. Future analyses will include trialing unprompted LLMs to perform thematic analyses.

KEYWORDS: HIV infections,Sentiment Analysis,Health Surveys,Artificial Intelligence,Validation study
ABSTRACT ID: 640
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POSTER TOUR 16

Day 2 – 15.30-16.30

Disease detection

PRESENTER

Vitor Borges

ABSTRACT

INSaFLU-TELEVIR: an open web-based bioinformatics suite for viral metagenomic detection and routine genomic surveillance

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[12]https://onehealthejp.eu/projects/emerging-threats/jrp-tele-vir

BACKGROUND

Implementation of clinical metagenomics and pathogen genomic surveillance is challenging due to the lack of bioinformatics tools and/or expertise. In order to face this challenge, we have previously developed INSaFLU (https://insaflu.insa.pt/), a free web-based platform for analysis of virus next-generation sequencing data. Here, we considerably expanded its genomic surveillance component and developed a new module (TELEVIR) for metagenomic virus identification.

METHODS

INSaFLU-TELEVIR is compatible with Illumina, Ion Torrent and Oxford Nanopore technologies (ONT) data and is freely available at https://insaflu.insa.pt/ (online tool) and https://github.com/INSaFLU (code). It is mainly written in Python and is available through a Django web framework.

RESULTS

The routine surveillance component was strengthened with new functionalities, including: i) a ONT genome assembly pipeline; ii) automated SARS-CoV-2 lineage classification and Nextclade analysis; iii) Nextstrain phylogeographic analysis [SARS-CoV-2, human and avian influenza, mpox, RSV, and a “generic” build for other viruses]; and, iv) algn2pheno (https://github.com/insapathogenomics/algn2pheno) for screening mutations of interest. Both Illumina and ONT pipelines for consensus generation were benchmarked against commonly used workflows for SARS-CoV-2, yielding similar performance. In parallel, the TELEVIR module for virus detection was developed, after extensive benchmarking of state-of-the-art metagenomics software. TELEVIR allows running several combinations of steps (e.g., with/without host depletion), classification software (e.g., Kraken2, Centrifuge) and databases (e.g., RefSeq viral, Virosaurus), culminating in user- and diagnosis-oriented reports. Finally, to potentiate real-time virus detection during ONT runs, we developed findONTime (https://github.com/INSaFLU/findONTime), a tool aimed at reducing cost and time in metagenomics diagnosis.

CONCLUSIONS

The versatility and functionality of INSaFLU-TELEVIR supplies public and animal health laboratories a free, user-oriented and pan-viral bioinformatics framework that promotes a strengthened and timely viral metagenomic detection and routine genomic surveillance. More information is available at https://doi.org/10.1186/s13073-024-01334-3.

KEYWORDS: genomic surveillance,metagenomics,virus,bioinformatics,public health
ABSTRACT ID: 311
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POSTER TOUR 16

Day 2 – 15.30-16.30
Disease detection

PRESENTER
Mario Martín Sánchez

ABSTRACT

Epidemic Intelligence from Open Sources (EIOS) to detect international public health events – an evaluation in the scope of public health intelligence activities at the Robert Koch Institute, Germany

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BACKGROUND

Epidemic Intelligence from Open Sources (EIOS) is a WHO-led public health intelligence (PHI) initiative and system used for media screening using non-restricted information since 2017. However, its application has rarely been evaluated. On 01.01.2023, the PHI-team at the Robert Koch Institute, Germany, transitioned to using EIOS as primary system to detect international public health events (PH-event). We evaluated the EIOS sensitivity and timeliness to assess its application for detecting international PH-events at the RKI.

METHODS

From 10.07.2023–14.07.2023 and 17.07.2023–21.07.2023, two EIOS-boards (article compilation according to EIOS filter settings of PHI-teams) were screened daily: [1] a PHI-officer screened a “routine EIOS-board” containing selected sources known to the PHI-team pre-EIOS supplemented by non-EIOS sources and [2] an evaluator screened a broader-scoped “evaluation EIOS-board” comprising all medical, scientific, NGO and official EIOS sources. The number and timing of articles screened and selected for reporting were collected per board. We calculated board sensitivity as the proportion of reported PH-events found in EIOS.

RESULTS

1,138 articles from the routine and 35,546 articles from the evaluation board were screened. Twenty international PH-events were reported in daily PHI-reports. Of these, 16 were found in the evaluation board (sensitivity 80%) and 15 in the routine board (sensitivity 75%). The four PH-events not found in EIOS came from restricted sources. PH-events were detected a median of 0.5 days (range 0–2) earlier in the evaluation board compared to the routine board.

CONCLUSIONS

The evaluation board increased the sensitivity and timeliness, but we needed to screen 30 times as many articles. As PHI needs to strike a balance between sensitivity, timeliness and resources, we recommend that PHI teams regularly evaluate their routine activities accordingly, especially when introducing new tools.

KEYWORDS: Public Health Surveillance,Evaluation Studies,Epidemiologic Methods,Epidemics
ABSTRACT ID: 194
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POSTER TOUR 16

Day 2 – 15.30-16.30
Disease detection

PRESENTER
Frederikke Lomholt

ABSTRACT
Evaluation of the newly established automated surveillance system to detect severe acute respiratory infections (SARI) using electronic health records in Denmark, 2022-2023

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BACKGROUND

Denmark is setting up an automated system for routine surveillance of severe acute respiratory infections (SARI) using electronic health records (EHR) and we aimed to evaluate the system's timeliness and its ability to detect changes in COVID-19, influenza and respiratory syncytial virus (RSV) admissions.

METHODS

A SARI case was defined as a hospital admission of at least 12 hours with an ICD-10 code for respiratory disease (J09-J22) or COVID-19 (B34.2, B97.2). We calculated the correlation between the number of weekly SARI cases and weekly admissions with confirmed SARS-CoV-2, influenza virus or RSV from January 2022 through December 2023 using Spearman's Rank Correlation. To analyse the timeliness of data we calculated the proportion of weekly SARI cases identified after 1 and 8 days compared with 29 days and for each delay we plotted the epidemiological curve of weekly SARI cases to compare changes over time.

RESULTS

The correlation coefficient between weekly SARI cases and weekly admissions with confirmed SARS-CoV-2, influenza virus or RSV was 0.95 (95% CI: 0.93-0.97). With an 8-day delay, data were 85%-91% complete compared to data extracted on day 29, whereas data retrieved on day 1 were 41-60% complete. The epidemiological curves further showed that data extracted on day 8 and day 29 identified similar changes in weekly SARI cases, while at several timepoints data on day 1 failed to detect these changes.

CONCLUSIONS

Our national EHR-based SARI surveillance system accurately detected changes in common respiratory viruses, and with a delay of only 8 days, data were almost complete and reliably detecting changes in SARI cases over time. We recommend the use of EHR for SARI surveillance as an alternative to a resource-intensive hospital-based sentinel system.

KEYWORDS: Electronic Health Records,Respiratory Infections,Surveillance Public Health,International Classification of Disease Codes
ABSTRACT ID: 665
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POSTER TOUR 16

Day 2 – 15.30-16.30
Disease detection

PRESENTER

Hannah Höglund-Braun

ABSTRACT

Drafting a manual on standardized work processes for IHR-relevant biological events at the five IHR-designated airports in Germany in the StandAtRisk-project

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BACKGROUND

The International Health Regulations (IHR, 2005) are the key legal framework for prevention and protection against the international spread of disease, establishing legally binding entitlements, responsibilities and recommendations for 196 States Parties. The German government designated five airports (Berlin-Brandenburg, Duesseldorf, Frankfurt, Hamburg, Munich) as IHR points of entry with core capacity requirements. However, health security measures of responsible health authorities in different federal states are neither standardized nor uniformly regulated. Existing heterogeneity with regard to assessment and response to IHR-related biological events does not align with highly standardized processes in international aviation.The StandAtRisk-project aimed at standardization of health protection measures in processes dealing with high consequence infectious diseases (HCID) at the five German IHR-designated airports to develop more harmonized processes to protect against the spread of diseases that could endanger (international) public health.

METHODS

Over the course of two years, ten workshops were conducted with relevant stakeholders from local, state and federal health departments, federal aviation authorities, airport and airline officials, fire and emergency services. All IHR-designated airports were visited. Relevant documentation was gathered, shared, analyzed and specific measures and expertise were compiled using qualitative interviews across different stakeholders.

RESULTS

The results of the workshops were used to define a generic process for dealing with the occurrence of HCID (suspected) cases. Its applicability and robustness were verified using a tabletop exercise including all stakeholders.A standardized process was collaboratively developed, connecting stakeholders at all five IHR-designated airports and defining operational procedures uniformly.

CONCLUSIONS

The standardized processes, presented in a joint online manual, provide guidance for planning and preparing of procedures and measures for IHR-related biological events, not only at IHR-designated airports in Germany.

KEYWORDS: IHR, airports, standardization, HCID
ABSTRACT ID: 97
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POSTER TOUR 16

Day 2 – 15.30-16.30
Disease detection

PRESENTER
Graham Fraser

ABSTRACT

Cluster identification from backwards contact tracing: a key toolbox component for control of pandemic respiratory agents with over-dispersed transmission.

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BACKGROUND
Modelling studies and country reports early in the COVID-19 pandemic indicated substantial value in adding backwards tracing (BCT) to control programmes, due to the over-dispersed character of SARS-CoV2 transmission. Public Health England (PHE) implemented an informatics programme for identification of possible clusters of COVID-19 cases, to assist public health teams with outbreak intelligence and control. This study aimed to describe the programme and evaluate the validity of digital cluster identification.

METHODS
COVID-19 case contact tracing was extended to include questions relating to case activities during the exposure period symptom onset. Cases who reported exposures in the same activities and postcodes within defined time periods were linked as possible clusters; daily intelligence reports were produced for local public health teams. Validity of identified clusters identification was assessed by identification and multiple logistic regression analysis of clusters with two or more cases with indistinguishable genomic analysis.

RESULTS
Over a quarter of a million (269,470) exposure clusters were identified during the study period; clusters were most frequently identified in education (19.8%) shopping (19.4%) and workplace (14,3%) settings. 25% of clusters eligible for analysis were genetically valid. Exposure clusters that included more cases, shorter in duration and including greater numbers of same day events were more likely to indicate genetically valid transmission events.

CONCLUSIONS
Despite its predicted utility in control of an over-dispersed respiratory pathogen, BCT was deployed by few countries in COVID-19 outbreak identification and control. Digital identification of COVID-19 case clusters based on informatics analysis of backwards extended contact tracing interview data proved a valid and efficient method of supporting pandemic outbreak intelligence and control by local [public health teams within a systematic national programme.

KEYWORDS: COVID-19; cluster analysis; contact tracing; pandemics; epidemiology; outbreaks
ABSTRACT ID: 581
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Day 3 – 15.30-16.30

International health and migration

PRESENTER

Ivanna Haman

ABSTRACT

Association of depression and anxiety with traumatic exposures in the pre- and post-migration periods among refugees from Ukraine in Moldova, 2023

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BACKGROUND

Refugees fleeing conflict zones often experience consistent and high levels of post-traumatic mental disorders. There are limited data on the mental health needs of refugees from Ukraine. We assessed the needs of refugees residing in Moldova.

METHODS

We used systematic sampling to select adult refugees from 13 of Moldova's 65 Refugee Accommodation Centers (RACs). We assessed the mental health status, depression (Patient Health Questionnaire-9), anxiety (Generalized Anxiety Disorder-7), and exposure to events/stressors that may lead to trauma (Life Events Checklist for DSM-5). We assessed the association of depression and anxiety with exposure to traumatic events/stressors, in the pre- and post-migration period.

RESULTS

Of the 219 interviewed refugees, the mean age was 47 (range=18-87) years, 161/219 (74%) were women, and Ukrainian 147/219 (67%). Chronic disease was reported by 147/219 (51%).Approximately one-quarter 56/219 (26%) met the criteria for moderate/severe depression, and 47/219 (21%) for moderate/severe Generalized Anxiety Disorder, which was consistent with self-reported post-migration mental health issues among the refugees 58/219 (27%). Of the 56 respondents with depression, 14 (25%) reported seeking medical help for mental health issues, respectively. Pre-migration and post-migration traumatic exposures/stressors were correlated with depression (pre-migration:$r2=0.444$, $p<.001$; post-migration:$r2=0.525$, $p<.001$) and anxiety (pre-migration:$r2=0.412$, $p<.001$; post-migration:$r2=0.447$, $p<.001$).

CONCLUSIONS

The extent of traumatic exposures in the pre-and post-migration periods was significantly associated with depression and anxiety among refugees, the majority of whom were not seeking care for mental health issues. We suggest on-site screening of refugees who self-report mental health issues and arriving refugees for mental health risk factors, referring them for mental health assessments, and investigating the reasons why refugees with mental health issues are not seeking medical help.

KEYWORDS: Mental health,Refugees,depression,Generalized Anxiety Disorder,traumatic events/stressors
ABSTRACT ID: 448

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POSTER TOUR 17

Day 3 – 15.30-16.30

International health and migration

PRESENTER
Saeed Ahmad

ABSTRACT

Assessing Health Disparities and Access: Afghan Refugee Health in Pakistan through Data-Driven Analysis

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BACKGROUND
Pakistan continues to be one of the world's largest refugee-hosting countries with 1.3 million registered refugees, 99 % of which are Afghans. This study evaluates the disparities in health status and healthcare access between Afghan refugees and permanent residents in Pakistan. The assessment employs the Global Reference List 2018 of 100 Core Health Indicators by the World Health Organization as a framework. The primary objective is to utilize population-based cross-sectional analysis to compare health data obtained from Afghan refugees and the resident Pakistani population.

METHODS
A population-based cross-sectional study was conducted using data acquired in 2021, encompassing 960 registered Afghan refugees sourced from the Commissionerate for Afghan Refugees and 20,430 individuals representing the resident Pakistani population, obtained from the Pakistan Bureau of Statistics. Essential health service coverage indicators, focusing on malaria and fundamental healthcare services, aligned with the Global Reference List, served as outcome measures.

RESULTS
The study findings unveiled substantial variations in health and access to healthcare between Afghan refugees and resident populations in Pakistan. Crude ORs demonstrated marked disparities in service coverage indicators related to malaria and essential health services. Age-stratified and sex-stratified ORs exhibited varying degrees of inequalities, signifying distinctive disparities across different demographic segments within the refugee and resident populations.

CONCLUSIONS
Study serves as a critical call to action, highlighting the urgency of addressing health disparities and inequities faced by Afghan refugees residing in Pakistan. The findings underscore the harsh reality of marked differences in health status and access to essential healthcare services between Afghan refugees and the permanent resident population. This study underscores the urgent need to bridge the gaps in healthcare access and address health disparities among Afghan refugees in Pakistan.

KEYWORDS: Migrant health, Afghan refugees,DHIS-2,Pakistan,Afghanistan
ABSTRACT ID: 7
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POSTER TOUR 17

Day 3 –15.30-16.30

International health and migration

PRESENTER

Helena Martínez Alguacil

ABSTRACT

Enhancing public health response to newly arrived migrants: A community intervention in Catalonia

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BACKGROUND

In recent years, Catalonia has experienced an increase in migrants arriving through unsafe routes. The circumstances surrounding migration heighten the risk of infectious diseases and overall health deterioration. Public health interventions are essential to address these challenges. This study describes a community intervention addressed to newly arrived migrants according to the established policy of the Public Health Agency of Catalonia.

METHODS

On February 12, 2024, a group of migrants arrived by small boats in Coma-ruga, Tarragona. Coordination meetings and contextual analyses engaged stakeholders in the initial phase of immigrant reception: Public Health services including Community Health Agents, Primary Care professionals, and the Red Cross. Two interventions were planned and implemented: 1) screening of symptoms related to both infectious and non-communicable diseases, and 2) health education focusing on tuberculosis (TB) awareness and prevention.

RESULTS

A total of 262 migrants, predominantly from Mali (55.7%), Mauritania (22.9%), and Senegal (20.2%) were received. Median age was 23 years, and all were male. Among them, 98 individuals presented symptoms (37.4%), including respiratory (31 cases), dermatological [27], general [19], abdominal [10], and urinary symptoms [8]. This syndromic screening allowed subsequent diagnosis and treatment of 1 case of malaria and 2 cases of schistosomiasis. Additionally, 9 awareness workshops were conducted to enhance active TB surveillance, which resulted in the detection of 4 cases of TB infection.

CONCLUSIONS

Establishing rapid and effective public health interventions for newly arrived migrants is paramount. This intervention tailors health interventions based on the countries of origin of migrants, providing valuable insights and guidance for future scenarios. A coordinated, intersectoral approach involving the Community Health Agents enhances intervention efficacy and incorporates sociocultural perspectives.

KEYWORDS: Community-Based Interventions, Intersectoral Collaboration, Emigrants and Immigrants, Public Health, Tuberculosis, Community Health Workers

ABSTRACT ID: 456

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POSTER TOUR 17

Day 3 – 15.30-16.30

International health and migration

PRESENTER

Anna-Lisa Behnke

ABSTRACT

Piloting recruitment methods for a biobehavioural survey on viral hepatitis in Germany among people born in Türkiye and Romania, HepMig pilot study, May 2023 – March 2024

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BACKGROUND

Data about hepatitis B/C (HBV/HCV) prevalence, behaviour, and healthcare access among foreign-born people in Germany is scarce. We aimed to compare different recruitment methods for biobehavioural surveys to increase participation.

METHODS

After consulting community experts, we piloted the following four methods aiming to recruit 400 adults born in Romania/Türkiye between 05/2023–03/2024: We recruited 1) using posters, flyers, websites, and social media to participate at the local public health authority (LPHA), Frankfurt am Main, 2) inviting people at healthcare/faith-based/cultural/sports institutions and workplaces in Frankfurt (outreach), 3) using websites and social media to participate online, 4) using personal invitation letters to invite Turkish nationals from a previous nation-wide study to participate online. Participants filled in a multilingual questionnaire on socio-demographics, behaviour, and healthcare access, and provided dried blood spots (DBS) for HBV/HCV testing. Online participants were not tested but were asked about their willingness to send a self-collected DBS. We compared numbers of recruited participants per method.

RESULTS

Overall, 44% (175/400) of the targeted number of participants were recruited; 40% were females; 67% were 30–59 years old. 4.6% participated at LPHA, 40% via outreach (37 participants in one church, 28 in one general practice, 5 in one workplace), and 55% online (8 participants after online recruitment, 89 after a personal invitation letter). 34% completed the questionnaire in German, 65% in Romanian or Turkish. 46% of the online participants said they were willing to send a self-collected DBS.

CONCLUSIONS

The recruitment target was not reached despite different approaches. We recommend outreach recruitment, personal invitations, and multilingual study materials. More community involvement is essential to increase participation in surveys among foreign-born people in Germany to estimate HBV/HCV prevalence and improve healthcare access.

KEYWORDS: hepatitis b,hepatitis C,migrants,community participation,health surveys
ABSTRACT ID: 442
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POSTER TOUR 17

Day 3 – 15.30-16.30
International health and migration

PRESENTER
Lena Schneider

ABSTRACT
Spotlight on Corynebacterium (C.) diphtheriae and C. ulcerans: Results of enhanced diphtheria surveillance in Germany, 2017 – 2022

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BACKGROUND
Since 2010, vaccine-preventable diphtheria has been increasing in Germany. We describe the results of an enhanced surveillance to better understand the epidemiology of diphtheria in Germany.

METHODS
Cases notified through statutory surveillance were interviewed retrospectively (01/2017 – 04/2019) and prospectively (05/2019 – 12/2022) by local health authorities using a standardised questionnaire. We descriptively analysed demographic, clinical, epidemiological and microbiological characteristics by Corynebacterium (C.) species.

RESULTS
Questionnaires were completed for 115/283 (41%) of notified cases caused by C. diphtheriae (n=84, 73%), C. ulcerans (n=30, 26%) and C. silvaticum (n=1, 1%).Of 112 cases with information, 90% presented with cutaneous diphtheria (C. diphtheriae: n=74, C. ulcerans: n=27; including two with respiratory colonisation), 9% with respiratory diphtheria (C. diphtheriae: n=7; C. ulcerans: n=3) and one with cutaneous and respiratory manifestation (C. diphtheriae).Of C. diphtheriae cases, 83% were imported cases among newly-arriving asylum-seekers and migrants observed in 2022. All C. ulcerans infections were acquired locally. C. ulcerans cases were older (median age: 70 vs. 20 years, $p<0.05$, chi2 test), less likely to be male (50% vs. 99%, $p<0.05$, t-test), more likely to have co-morbidities (61% vs. 8%, $p<0.05$, chi2 test) and had more information on vaccination status available (70% vs. 32%, $p<0.05$, chi2 test). Of C. ulcerans cases with vaccination information, 43% reported receiving recommended booster vaccination within the past 10 years.

CONCLUSIONS
In 2017–2022 most diphtheria cases in Germany were cutaneous. Newly-arriving asylum-seekers with skin lesions should routinely be tested for diphtheria infection including respiratory carriage and, if indicated, receive antibiotics and cover wounds to prevent transmission. For older patients, medical providers should emphasise booster vaccination and consider C. ulcerans as differential diagnosis for skin lesions.

KEYWORDS: Transients and Migrants,diphtheria,Corynebacterium,vaccination
ABSTRACT ID: 260
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POSTER TOUR 17

Day 3 – 15.30-16.30

International health and migration

PRESENTER

Laura Anne Paris

ABSTRACT

Infectious diseases and malnutrition in Gaza - August 2024 - approaching 1 year of conflict

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BACKGROUND

As a result of the conflict in Gaza starting on 07/10/2023 health services were critically strained. UNRWA was the major primary healthcare provider, catering to some 1.9 million people across Gaza through its health facilities (HFs). On 28/08/2024, 10 of 26 health centres and 80 shelter medical points were functioning. We aimed to describe trends in infectious diseases and estimate the prevalence of malnutrition in Gaza.

METHODS

UNRWA HFs reported data on consultations of priority infectious diseases, using standardised case definitions, to a clinical database daily. We compared the cumulative incidence between January- August 2024 with the same period in 2023 (pre-conflict) and calculated morbidity proportions for 2024 using total medical consultations as the denominator. Since 07/03/2024, children under 5 attending HFs were screened for malnutrition using mid-upper arm circumference (MUAC). We estimated the prevalence of global acute malnutrition (GAM) defined as MUAC measurement under 125mm.

RESULTS

Compared with January-August 2023, between January and August 2024, acute watery diarrhoea consultations increased 39-fold (451,300 vs 11,562), bloody diarrhoea increased 24-fold (7,470 vs 311), and Hepatitis A cases increased 388-fold (41,891 vs 108), accounting for 5%, 0.1% and 0.3% of total medical consultations during 2024, respectively. By 25 August 2024, the prevalence of GAM was 7.7% (11.8% in 6-23 months age group and 2.6% in 24-59 months age group) among the 66,656 screened children, an 0.8% increase since March 2024.

CONCLUSIONS

The protracted conflict and devastated infrastructure in Gaza has led to a dramatic increase in infectious diseases and malnutrition. We recommend opening of humanitarian corridors, and immediate and sustained international intervention, including a ceasefire to address health needs.

KEYWORDS: Infectious Diseases,Hepatitis A,Malnutrition,Conflict, Diarrhea,Respiratory Illness
ABSTRACT ID: 701

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POSTER TOUR 18

Day 3 – 15.30-16.30

Antimicrobial resistance

PRESENTER

Mark Maguire

ABSTRACT

Characterisation and network analysis of plasmids associated with combined carbapenem and aminoglycoside resistance.

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BACKGROUND

Aminoglycosides are used in the treatment of clinical infections involving Carbapenemase Producing Enterobacterales (CPE). 16S rRNA methyltransferases (RMTs) which are capable of conferring resistance to all aminoglycosides are commonly detected in combination with blaNDM genes. This study aims to assess the relationship between these genes and the mobile genetic elements associated with them.

METHODS

All isolates (n=68) carrying both blaNDM and a 16s methyltransferase gene between 2019 and 2023 were obtained from the Galway Reference Laboratory Service (GRLS). Short-read sequences (PE300) were generated for all isolates and long-read sequences were generated for a subset of isolates (n=29). MOB-recon was used to distinguish plasmid derived contigs from draft assemblies. The distance between plasmids was determined using mash and clusters of related plasmids were identified using network analysis.

RESULTS

Isolates encoding blaNDM-1 were associated with armA (n=31) but also rmtC (n=6) carriage. These genes were co-localised most frequently on incFIB/HI1B (n=12), incM2 (n=10) and incC (n=8) type plasmids which formed clusters in multiple species (range: 2 - 5) and at multiple locations around Ireland. While most plasmids were detected in multiple locations the incM2 plasmids were largely associated with a single hospital. Isolates encoding blaNDM-5 were associated rmtB1 (n=28) carriage. These majority (n=15) were encoded on a diverse range of mosaic incF type plasmids. Two discrete clusters of incM1 (n=3) and incFII (n=4) type plasmids were also detected.

CONCLUSIONS

We demonstrate multiple plasmids capable of conferring resistance to carbapenems and aminoglycosides in multiple species and in multiple locations. The co-dissemination of these genes on highly mobile plasmids poses a significant public health threat.

KEYWORDS: Antimicrobial Resistance,Plasmids,Genomics,Aminoglycosides,Carbapenems
ABSTRACT ID: 576
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POSTER TOUR 18

Day 3 – 15.30-16.30
Antimicrobial resistance

PRESENTER
Patrick Van Schelven

ABSTRACT

Community outbreak with Panton-Valentine Leukocidin-encoding livestock-associated methicillin-resistant Staphylococcus aureus in the Netherlands

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BACKGROUND
Livestock-associated (LA)-MRSA is usually considered less pathogenic and less transmissible between humans, compared to non-LA-MRSA. Here we describe a community outbreak with severe infections of PVL-positive LA-MRSA without livestock contact.

METHODS
MRSA isolates are routinely sent to the RIVM for multiple locus variable-number tandem repeat analysis (MLVA) typing for national surveillance. In the course of the outbreak, PCRs for PVL and LA-MRSA/clonal-complex 0398 were introduced at the regional laboratory, for MRSA isolates with an antibiogram similar to the outbreak strain. Whole genome sequencing (WGS) was performed on all isolates by the RIVM. The municipal health service (MHS) conducted extended source tracing, concentrated around direct skin and/or animal contact of cases.

RESULTS
In November 2023, the first 5 patients with skin lesions with PVL-positive, MLVA type MC0398/MT2306 MRSA were notified by the laboratory to the MHS. Up to May 14th, a total of 25 cases were identified, of which 24 had skin lesions. Disease onset was between September 2023 - February 2024. WGS confirmed a genetic cluster. 22 cases cooperated in source investigation; 18 cases had visited a specific massage centre prior to disease onset. This location was visited by the MHS. One of three employees examined for carriership and 3/16 environmental samples tested positive for the same MRSA type. The massage centre was disinfected thoroughly. The infected employee and all cases were advised eradication therapy.

CONCLUSIONS
This PVL-positive LA-MRSA-strain caused unusually severe skin infections. The outbreak was linked to a massage centre and confirmed human-to-human transmission in the community. These findings suggest changing pathogenicity and transmissibility of LA-MRSA in association with PVL positivity, which emphasizes the need for early detection and rapid source tracing.

KEYWORDS: Methicillin-Resistant Staphylococcus aureus,Disease Outbreaks,Public Health,Netherlands
ABSTRACT ID: 333
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POSTER TOUR 18

Day 3 – 15.30-16.30
Antimicrobial resistance

PRESENTER
Israa Mohammed

ABSTRACT
Nosocomial transmission of methicillin- resistant Staphylococcus aureus (MRSA) between two neonatal and maternity units in Wales

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BACKGROUND
MRSA causes significant morbidity in infants and a financial burden to healthcare. Neonatal units routinely screen for MRSA, including on transfer. Two outbreaks in neonatal (NNU)/maternity units in separate Welsh hospitals were identified in 2022. We describe investigations which integrated laboratory, epidemiological and genomic data.

METHODS
Patient data was extracted from the all-Wales infection prevention case management system, and from Infection Prevention Control (IPC) Teams' case note reviews. Cases were born in hospital A or B, or hospitalised there for >48 hours (hospital-acquired infections), with MRSA detected from clinical or screen specimens from March 2022. MRSA isolates were whole genome sequenced (WGS) at UKHSA Antimicrobial Resistance and Healthcare Associated Infections Reference Unit, using single-nucleotide polymorphisms (SNPs) to assess genetic relatedness.

RESULTS
The hospital A outbreak included 5 cases (4 babies, 1 mother) between March and June 2022. The hospital B outbreak included 11 epidemiologically-linked cases (10 babies, 1 staff) between May 2022 and May 2023. All cases were hospital acquired. All sequenced cases (5 from A, 6 from B), were WGS linked, forming a 5-SNP cluster. The hospital B index case was born in hospital A in May 2022 and transferred to hospital B on that day. Against policy, the baby was not screened until 2 days post-transfer.

CONCLUSIONS
Patient movement and molecular typing data showed MRSA transmission within and between two Welsh hospitals and identified this as a single outbreak. Hospital transfer and failure to comply with screening policy played a role in facilitating transmission across different hospital settings. Enhancing compliance with IPC measures is recommended, including enforcing admission screening for transfers, thorough equipment decontamination, and improving communication between sites for effective isolation.

KEYWORDS: Infection Control; ,Methicillin-Resistant Staphylococcus aureus,Cross Infection,Whole Genome Sequencing
ABSTRACT ID: 208
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POSTER TOUR 18

Day 3 – 15.30-16.30

Antimicrobial resistance

PRESENTER

Svitlana Mandyhra

ABSTRACT

Use of Antimicrobial Sensitivity Testing for Prescribing Antibiotics Among Production Animals in Armenia, Georgia, Moldova, and Ukraine, 2023

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BACKGROUND

In recent years, uncontrolled use of antibiotics in animal husbandry has substantially contributed to increased antimicrobial resistance (AMR). Our study assessed veterinarians' knowledge, attitudes, and practices (KAP) regarding antibiotic prescriptions for production animals (cattle, small ruminants, pigs, and poultry).

METHODS

We conducted a cross-sectional KAP survey among veterinarians who serviced production animals in Armenia, Georgia, Moldova, and Ukraine. Based on the number of production animals, farms, and veterinarians, 79 survey sites were selected. We used a standardized questionnaire to collect data on respondents' demographics, knowledge and attitudes toward AMR, and practices for antibiotic usage.

RESULTS

Of 152 veterinarians, 95% (144/152) reported prescribing antibiotics. Few veterinarians (Armenia: 2/7 [28%]; Moldova: 3/19 [16%]; Georgia: 10/48 [21%]; and Ukraine: 27/70 [39%]) reported conducting antibiotic sensitivity testing (AST) before prescribing antibiotics. The most reported reason for not conducting AST was the lack of a laboratory nearby (81/102; 79%).Penicillins were most prescribed for production animals in Moldova and Ukraine (253/635; 40%) and tetracyclines in Armenia and Georgia (118/293; 40%). Fluoroquinolones were most used for poultry in Moldova and Ukraine (36/80; 45%) and tetracyclines in Georgia (24/40; 60%). Armenia does not use antibiotics in poultry.Reserve group antibiotics such as third-generation cephalosporins and polymyxins were used in Ukraine and Moldova (31/550; 6%), and 44/144 (31%) veterinarians reported prescribing critically important human antibiotics in all countries.

CONCLUSIONS

Low AST use indicates the critical need for accessible laboratory services to promote appropriate antibiotic use. Prescribing reserve and critically important human antibiotics for production animals might contribute to the development and spread of AMR. We suggest reviewing the animal antibiotic use policy as a critical step in identifying an impactful and sustainable pathway for controlling AMR.

KEYWORDS: Antimicrobial resistance (AMR), antibiotics, veterinarians, production animals
ABSTRACT ID: 432
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POSTER TOUR 18

Day 3 – 15.30-16.30

Antimicrobial resistance

PRESENTER

Evangelos Mourkas

ABSTRACT

Proximity to humans is associated with antimicrobial resistant enteric pathogens in wild bird microbiomes

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BACKGROUND

Humans are radically altering global ecology, and one of the most apparent human-induced effects is urbanisation, where high density human habitats disrupt long established ecotones. Changes to these transitional areas between organisms, especially enhanced contact among humans and wild animals, provides new opportunities for the spread of zoonotic pathogens. This poses a serious threat to global public health but little is known about how habitat disruption impacts cross-species pathogen spread.

METHODS

Here we investigated variation in the zoonotic enteric pathogen Campylobacter jejuni. The ubiquity of C. jejuni in wild bird gut microbiomes makes it an ideal organism for understanding how host behaviour and ecology influence pathogen transition and spread. We developed a global geo-spatial analysis pipeline, allowing integration of bird microbiological samples from anywhere in the world with bird distribution data from eBird to calculate the proximity of birds to humans. Then, we analysed 700 C. jejuni isolate genomes from 30 bird species in eight countries using scalable generalised linear model approaches.

RESULTS

Comparing multiple behavioural and ecological traits showed that proximity to human habitation promotes lineage diversity and is associated with antimicrobial resistant (AMR) strains in natural populations. Specifically, wild birds from urban areas harboured up to three times more C. jejuni genotypes and AMR genes.

CONCLUSIONS

This study provides novel methodology and much needed quantitative evidence linking urbanisation to One Health gene pool spread and zoonoses.

KEYWORDS: Campylobacter,Microbial genomics,Antimicrobial resistance,Wild birds,ecology,transmission
ABSTRACT ID: 652
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POSTER TOUR 18

Day 3 – 15.30-16.30

Antimicrobial resistance

PRESENTER

Mihai-Octavian Dan

ABSTRACT

Antimicrobial resistance patterns in Klebsiella pneumoniae strains isolated from a tertiary care hospital in Romania

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BACKGROUND

Antimicrobial resistance stands as a global health challenge, an uprising phenomenon forcing healthcare professionals to constantly improve means of treatment in order to tackle resistant bacteria. Our study aims to assess antimicrobial resistance rates and patterns amongst various Klebsiella pneumoniae isolates, with an emphasis on carbapenemase-producing strains, since this microorganism has often been incriminated as the aetiological factor of severe infections.

METHODS

Between August 2023 and February 2024, 203 non-duplicate Klebsiella pneumoniae strains were isolated from patients admitted to the "Prof. Dr. Matei Bals" National Institute of Infectious Diseases in Bucharest. Bacterial identification was compelled using MALDI-TOF MS Biotyper® (Bruker Daltonik GmbH, Bremen, Germany). Antimicrobial susceptibility testing was performed using MICRONAUT (Bruker Daltonik GmbH, Bremen, Germany), followed by interpretation according to the EUCAST guidelines. Strains presenting MIC to meropenem >0,125 µg/ml were assigned for carbapenemase detection using Resist-3 O.K.N. K-SeT (Coris BioConcept-Belgium).

RESULTS

Sampled strains were isolated from urine (n = 134), lower respiratory tract (n = 29), wounds (n = 25) and blood (n = 15). The screened Klebsiella pneumoniae strains reported high resistance rates to amoxicillin/clavulanic acid (65,02%), followed by trimethoprim/sulfamethoxazole (64,03%), ceftazidime (63,54%), cefepime (60,59%), meropenem (41,87%) and amikacin (36,45%), while the lowest reported resistance rates were to colistin (24,63%). Carbapenemase production was reported among 40,88% of strains (21,68% NDM, 9,63% OXA-48-type, 9,63% KPC, 56,62% OXA+NDM). Amidst carbapenemase-producing strains, 84,93% proved resistant to ceftazidime/avibactam, 90,41% to imipenem/relebactam, 98,63% to ceftolozane/tazobactam and 41,09% to cefiderocol.

CONCLUSIONS

Carbapenemase-producing Klebsiella pneumoniae strains constitute an expansive public health concern due to increasing prevalence and high resistance rates, even against last-resort antimicrobials, thus the development of novel therapeutic strategies is key to improve standards of care.

KEYWORDS: antimicrobial resistance,Klebsiella pneumoniae,carbapenemase,resistance patterns
ABSTRACT ID: 594
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POSTER TOUR 18

Day 3 – 15.30-16.30

Antimicrobial resistance

PRESENTER

Julia Kuhn

ABSTRACT

Antibiotic Resistance in reported Shigella cases in Baden-Wuerttemberg, Germany: A Pilot Study on Resistance Patterns and Phylogenetic Links from March until August 2024

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BACKGROUND

Since 2021, there has been a reported increase in multidrug-resistant (MDR) and extensively drug-resistant (XDR) Shigella infections across Europe. Despite mandatory notification in Germany, increasing use of PCR may reduce the submission of isolates for antibiotic testing. We piloted laboratory surveillance from March until August 2024 to identify antibiotic-resistance patterns in reported Shigella cases.

METHODS

Local health authorities were requested to send stool samples or isolates of Shigella cases to the State Health Laboratory for antibiotic typing (EUCAST) and high-throughput sequencing. The sequenced isolates were compared via RefFinder. We matched the samples to notified cases and conducted descriptive analysis by species, antimicrobial resistance (AMR), sex, and age. MDR was defined as resistance to at least one agent in ≥3 classes of antibiotics and XDR followed CDC-Atlanta definitions.

RESULTS

Of the 57 samples received and 114 Shigella cases notified, we matched 37 (37/114, 32.5%). Shigella was culture-reconfirmed in 21/37 samples (56.8%). Resistance to at least one antibiotic was detected in 20/21 (95.3%) isolates, 13/21 (61.9%) isolates were resistant to the national guideline first-line antibiotics azithromycin and/or cefotaxime, 7/21 (33.3%) were MDR and 4/21 (19.0%) were XDR. 71.4% of MDR cases were male (36-61y, mean 44y). All XDR cases were male (11-60y, mean 58y). Phylogenetic analysis revealed that three (all male, age 37, 57 and 60 years) of 19 sequenced isolates were related to a Dutch cluster from 2023 associated with men who have sex with men.

CONCLUSIONS

Our study indicated that the majority of isolates were resistant to national first-line regime antibiotics, with half classified as MDR or XDR Shigella. We recommend automated antimicrobial resistant notification within mandatory surveillance and regular reporting to improve antibiotic stewardship of Shigella spp.

KEYWORDS: Shigella, MDR, XDR, AMR, Surveillance, Germany
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Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER

Gudrun Witteveen-Freidl

ABSTRACT

Lessons learnt from a One Health stakeholder analysis and systems mapping workshop on avian and swine influenza surveillance in humans in Denmark, August 2023

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BACKGROUND

Avian and swine influenza viruses are ranked among the top ten zoonotic diseases that should be prioritized for coordinated surveillance systems under the One Health approach or fall under cross-border pathogens that threaten the European Union. As part of the European Joint Action UNITED4Surveillance and to strengthen infectious disease preparedness in Denmark, we conducted a stakeholder analysis and systems mapping workshop to map existing and planned surveillance systems for avian and swine influenza virus infections in humans.

METHODS

A modified Mendelow's Matrix was used to identify and classify relevant stakeholders involved in surveillance and management of human zoonotic influenza virus infections. Identified stakeholders, which comprised representatives of public health, animal health and the industry, were invited to participate in a systems mapping workshop.

RESULTS

During the workshop, the stakeholder analysis was refined in plenary and pre-prepared maps of the current surveillance system and planned surveillance pilots were jointly reviewed through moderated discussions. The moderation was based on a joint understanding on how human behavior and bounded rationalities affect system dynamics to allow for a balanced and honest debate across sectors and policies. Identified gaps comprised the absence of or need to update guidelines, improving coordination, concerns regarding technical feasibility, as well as uncertainties regarding personal and economic consequences for persons participating in the surveillance pilots that were assessed to negatively affect compliance.

CONCLUSIONS

On a scale from 1 (very dissatisfied) to 5 (very satisfied), the usefulness of the workshop was evaluated with a median score of 5. Here we showcase how a coordinated approach through stakeholder analysis and systems mapping can help identify gaps in existing and planned surveillance structures and contribute to strengthening One Health collaborations.

KEYWORDS: One Health, zoonoses, influenza, Denmark, humans, animals, systems mapping
ABSTRACT ID: 122
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POSTER TOUR 19

Day 3 – 15.30-16.30
Surveillance of food- and waterborne diseases

PRESENTER
Jasmin S. Kutter

ABSTRACT
Increase of Salmonella enterica serovar Chester cases in Spain, 2023

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BACKGROUND
In August 2023 Germany reported two S.Chester clusters linked to Spain in EpiPulse, affecting seven EU/EAA countries. In parallel, the Spanish Reference Laboratory for salmonellosis detected an increased number of S.Chester cases. Epidemiological investigation failed to identify a common link. We aimed to generate a hypothesis to explain and control the observed increase.

METHODS
We conducted a descriptive analysis of cases, defined as individual diagnosed with S.Chester infection, in Spain between 01.01.2023 and 31.12.2023. We analysed a subset of 45 S.Chester isolates using cgMLST Enterobase scheme (≤7 alleles threshold), which included isolates obtained from humans (n=31) and isolates from food (n=14) that were whole-genome-sequenced and deposited in public repositories by Spanish Regional Public Health laboratories.

RESULTS
We identified 179 cases across Spain, a five-fold increase from 2022; male/female ratio was 1.1, median age was 22 years (range: 0-92 years). cgMLST identified three clusters. Cluster 1 comprised isolates from chicken-derived food (n=14) and human cases (n=14), while clusters 2 and 3 grouped 10 and 2 human isolates respectively. Clusters 1 and 2 were linked to the German cases.

CONCLUSIONS
Chicken-derived food was identified as a likely source of infection but could not explain all cases. Nonetheless, a trace-back investigation to broilers and their origin should be conducted to identify the source of S.Chester contaminated food products. S.Chester is not listed in the EU-regulation for Salmonella serotypes of public health significance. Yet, its continued detection in humans in 2024 suggests potential introduction, colonization, and persistence within specific niches, warranting intensified surveillance and stricter control measures. Whole-genome sequencing and cluster analysis should be integrated into these efforts, particularly where traditional epidemiological links cannot be established.

KEYWORDS: S. Chester, salmonellosis, whole-genome sequencing, cgMLST, cluster analysis
ABSTRACT ID: 362
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POSTER TOUR 19

Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER

Yanshi Yanshi

ABSTRACT

Reptile-Associated Salmonella Enteritidis cases in England following import ban on feeder-mice from an EU importer

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BACKGROUND

A long-standing Reptile-Associated Salmonellosis (RAS) outbreak, first identified in the UK in 2015 through whole genome sequencing, was linked to the feeding of frozen feeder-mice contaminated with Salmonella Enteritidis. Control measures implemented at the implicated production farm and targeted public health messaging failed to result in a notable reduction in disease burden. In February 2022 a ban was imposed on imports of feeder-mice from the farm. We assessed if this ban had an impact on RAS case notifications in England.

METHODS

We analysed the number of cases falling into the 10 Single Nucleotide Polymorphism RAS outbreak cluster reported per month by the UK Health Security Agency reference laboratory in England between 2014-2023. We used an interrupted time-series analysis to assess the change in reporting after the ban was imposed, defining 01/01/2014 to 16/02/2022 and 17/02/2022 to 31/12/2023 as the pre- and post-ban periods respectively.

RESULTS

Overall, 961 cases of RAS were reported during 2014-2023, with 3% cases being notified during the post-ban period. The median cases reported per month reduced from 8 in the pre-ban phase to 4 in the post-ban period. A 4% (95% CI 1%-7%, p=0.003) increase in the number of cases reported per month was seen from 2014 to February 2022. After the ban, cases dropped at the rate of 30% (95% CI 6%-57%, p=0.017) per month, with 9 cases in March 2022 to 1 case in December 2023.

CONCLUSIONS

The feeder-mice ban appeared to have significantly reduced the notification of RAS cases, demonstrating the effectiveness of the import ban, unlike previous control measures. We recommend evaluating control measures to assess efficacy of interventions and support policy decision in similar situations.

KEYWORDS: Reptile-Associated Salmonellosis, Feeder-Mice, Time Series, England
ABSTRACT ID: 596
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POSTER TOUR 19

Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER

Sara Mazzilli

ABSTRACT

National perinatal survey to estimate seroprevalence of Toxoplasma gondii infection among pregnant women in France, 2021

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BACKGROUND

Toxoplasmosis during pregnancy can result in congenital malformations and fetal death. In France, universal antenatal screening and monthly re-testing of seronegative pregnant women has been established since the 1970s. However, decreasing Toxoplasma gondii seroprevalence among pregnant women and lower incidence of congenital toxoplasmosis (2016: 31% and 0.31%, respectively) may challenge the cost-effectiveness of such programs. The aim of this study was to estimate the current seroprevalence among pregnant women participating in the 2021 national perinatal survey (ENP) and determine associated factors.

METHODS

All adult women giving birth in France between 15–21 March 2021 were invited to participate in the ENP. Data collected included demographic information, nationality, socio-economic status, education level, health literacy and Toxoplasma gondii serology. We classified a woman as seropositive if she had IgG antibodies prior to pregnancy or seroconverted during it. Univariable and multivariable regression analyses using a Poisson model with robust error variance were conducted to estimate prevalence ratios (PRs) and identify significant factors associated with seropositivity.

RESULTS

Among the 15,605 participating women, 0.22% seroconverted during pregnancy. The overall seroprevalence was 25.95%. Seropositivity was higher with increasing age (~5% per 5 years), among residents of French overseas territories: Guadeloupe/Saint Martin (PRs:1.07; 95%-CI: 1.03–1.10), La Réunion (PRs:1.10; 95%-CI: 1.08–1.13) and Mayotte (PRs:1.27; 95%-CI: 1.23–1.31), with lower education (PRs:1.22; 95%-CI: 1.04–1.42) and African nationality (PRs:1.11; 95%-CI: 1.02–1.20).

CONCLUSIONS

High seroprevalence for Toxoplasma gondii was found in older women, which may reflect their higher risk of past exposure. The observed geographical differences in seroprevalence may mirror dietary and environmental diversity. Declining overall seroprevalence among pregnant women in France can affect screening effectiveness and warrants a comprehensive review to determine appropriate future prevention strategies.

KEYWORDS: Toxoplasmosis, Seroprevalence, Pregnant Woman, Congenital, France
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POSTER TOUR 19

Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER

Bozena Kocikova

ABSTRACT

The occurrence of hepatitis E virus in human patients from Slovakia

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BACKGROUND

The hepatitis E virus (HEV) is one of the most common cause of acute viral hepatitis worldwide. Eight genotypes have been identified, but most cases in Europe are caused by genotype HEV-3. The main route of transmission is the consumption of undercooked meat and meat products mainly from swine and wild boars. The aim of this study was detection and phylogenetic analysis of HEV among human patients in Slovakia.

METHODS

We analysed blood and stool samples from patients suspected of viral hepatitis E (n=61) from three hospitals in Eastern Slovakia. The majority of the patients were positive for anti-HEV antibodies. All samples were tested by real-time RT-PCR. Positive samples were subsequently analysed by nested RT-PCR and confirmed by sequence analysis.

RESULTS

Overall HEV RNA was detected in samples from 59,02 % (36/61) patients and 26 partial sequences of ORF1 (242 bp) were analysed. All sequences belong to the genotype HEV-3, mostly to subtypes HEV-3e, HEV-3f, HEV-3g (n=22). Only four sequences were different, belonging to subtypes: HEV-3a, HEV-3c and HEV-3m. The nucleotide identity in all analysed samples ranged between 77,3 % to 100 %. Prevalence of HEV RNA was significantly higher in men (77,78 %). All positive patients were older than 40 years and most of them had pre-existing diseases (diabetes mellitus, cancer, obesity, etc.).

CONCLUSIONS

This is the first molecular genetic analysis of HEV among human patients in Slovakia. All cases were caused by genotype HEV-3, mostly by subtypes HEV-3e, HEV-3f and HEV-3g. Important host factors were male sex, age above 40 years and pre-existing diseases. This study was supported by VEGA 1/0220/24.

KEYWORDS: Hepatitis E Virus, Patient, Phylogenetic analysis
ABSTRACT ID: 348
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POSTER TOUR 19

Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER
Sarah Williams

ABSTRACT

Investigation of a significant Cryptosporidium hominis increase across England and Wales, August to September 2023, using a retrospective case-case study revealed associations with travel and swimming

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BACKGROUND

In August 2023, routine surveillance detected unprecedented exceedances in cases of Cryptosporidium hominis in England and Wales (E&W). Increases were also reported in other European countries, with Germany reporting associations with swimming pools and international travel.Whilst C. hominis cases peak seasonally in late summer, the magnitude of increase and widespread distribution of cases was concerning. Early work identified no common exposures, with no changes in surveillance or testing. We conducted further investigations to identify exposures associated with being a case.

METHODS

We compared laboratory confirmed cases of C. hominis with Campylobacter spp. cases using a 1:3 ratio, onset between 14/08/2023 and 30/09/2023. Participants in E&W had completed a routine surveillance questionnaire and had no contact with gastrointestinal symptomatic individuals in the 14 days before their illness.We used a backwards stepwise approach to include exposure variables in a multilevel logistic regression model with random intercepts for geographical region. The final model is presented as adjusted ORs (aOR) and 95% confidence intervals (95%CI).

RESULTS

We included 203/919 cases and 614 controls. Multivariable analysis identified associations with travel to Spain (aOR:6.5, 95%CI:3.5-12.3), swimming pool use (aOR:5.3, 95%CI:2.3-9.3), and for age, children aged 0-4 years had the strongest association of being a case (aOR:3.6, 95%CI:1.5-8.6). We identified associations with swimming in a river and travel to Turkey or France, but these exposures accounted for fewer cases.

CONCLUSIONS

Following the largest recorded increase of C. hominis cases in E&W, we identified several linked exposures suggesting multifactorial causes. To improve existing surveillance and inform public health action, we recommend the development of a standardised questionnaire to enable rapid investigation of future case increases and clear documentation and training to enhance questionnaire completion.

KEYWORDS: Cryptosporidium, United Kingdom, travel, case control study, outbreaks, public health surveillance
ABSTRACT ID: 445
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POSTER TOUR 19

Day 3 – 15.30-16.30

Surveillance of food- and waterborne diseases

PRESENTER

Lucy Findlater

ABSTRACT

The rise in Shiga toxin-producing Escherichia coli (STEC) O26 and the role of farm and nursery settings, England, 2019-2023

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BACKGROUND

Shiga-toxin producing Escherichia coli (STEC) can cause severe gastroenteritis and haemolytic uraemic syndrome (HUS). There has been increasing incidence of STEC O26 in England, with reported outbreaks associated with petting farms and nurseries. To explore potential associations between increasing O26 and farm or nursery attendance, we describe the epidemiology and exposures of STEC cases in England by age over the past five years.

METHODS

We extracted clinical, epidemiological, and microbiological data from national surveillance of laboratory-confirmed STEC cases in England from 2019 to 2023. We conducted descriptive and stratified analysis. Farm or nursery exposure was defined as attendance in the seven days before symptom onset.

RESULTS

There were 7011 STEC cases, increasing from 1112 ^{2019} to 1915 ^{2023}. The age distribution was unchanged (median age 31 years). O26 cases increased from 9.2% of cases in 2019 to 12.2% in 2023. O26 cases had a higher frequency of HUS than non-O26, in those aged 0-4 years (RR 2.76, 95%CI 1.87-4.08) and aged over 5 years (RR 4.25, 95%CI 2.57-7.05). For cases with exposure information (57%, 4026), 14% attended farms ^{459} and 11% nurseries ^{546}, which remained similar over time. Amongst 0-4 year olds, the proportion of cases with O26 was higher in those who did than didn't visit farms (RR 1.50, 95%CI 1.20-1.88) and those who did than didn't attend nursery (RR 1.26, 95%CI 1.03-1.53).

CONCLUSIONS

STEC O26 is an increasing public health issue in England. We provide evidence that O26 is associated with farm or nursery attendance amongst children and associated with severe morbidity in children and adults. Our findings reinforce the need to promptly investigate cases, ascertain exposures to risk settings, and identify and mitigate related outbreaks

KEYWORDS: Shiga-Toxigenic Escherichia coli, Epidemiology, Haemolytic uraemic syndrome, Farms, Nursery schools
ABSTRACT ID: 688
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Orlagh Ingeborg Quinn

ABSTRACT

Shiga toxin–producing Escherichia coli (STEC) O145: H28 outbreak linked to unpasteurised cheese in England and Scotland, 2023

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BACKGROUND

Shiga toxin-producing Escherichia coli (STEC) represents a major public health concern and non-O157 STEC serogroups have been increasingly associated with outbreaks. In November 2023, national gastrointestinal infections surveillance identified a fast-growing outbreak of STEC O145:H28 in England and Scotland. A multidisciplinary investigation was initiated to identify likely infection vehicle(s) and implement control measures.

METHODS

Microbiologically confirmed cases were identified through single-linkage hierarchical clustering based on Single Nucleotide Polymorphisms derived from whole genome sequencing data. Epidemiological investigations identified cases, utilised routine surveillance questionnaires for descriptive analyses and hypothesis generation through a case-case analysis using confirmed non-outbreak cases notified in the same period. Trawling and structured questionnaires were undertaken on exposures of interest. Concurrent food-chain and microbiological investigations were undertaken.

RESULTS

Of 36 confirmed cases, with symptom-onset between 25/07-23/12/2023; 54% were female, median age of 36 years (range 2-81 years). Overall, 65% cases reported bloody diarrhoea, 58% were hospitalised, and one developed Haemolytic Uraemic Syndrome and died. The case-case analysis identified domestic travel (OR=27, 95%CI 7-13, $p<0.001$), although travel was to and from different destinations. Further investigation identified unpasteurised cheese served by one train operator as the vehicle in 16/17 cases; an additional case had purchased the product from the implicated farm shop. The product was recalled on 24/12/2023. The outbreak strain was detected in two faecal samples collected from the environment at the source farm but not in the cheese, in which another STEC serotype (O109) was identified.

CONCLUSIONS

Although unpasteurised cheese is a risk factor for STEC infection, the source was detected through the unusual association with domestic travel, precipitating timely implementation of control measures. We recommend clearer labelling of products that pose a risk to public health.

KEYWORDS: Shiga toxin–producing Escherichia coli,gastrointestinal infections,foodborne illness,surveillance,outbreak,epidemiology
ABSTRACT ID: 655
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Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Ioana Bujila

ABSTRACT

Outbreak of the novel Cryptosporidium parvum subtype IIyA11 linked to mixed kale salad from salad bars in Sweden, December 2023

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BACKGROUND

In December 2023, notifications of cryptosporidiosis cases increased in Sweden. Molecular typing detected a novel subtype, Cryptosporidium parvum IIyA11. Initial trawling questionnaires identified salad bars in supermarkets and leafy green vegetables as potential sources. In January 2024, we initiated a national outbreak investigation to identify the source and support public health actions.

METHODS

We conducted a case-control study including cases defined as domestic laboratory confirmed cryptosporidiosis with symptom onset 15/12/2023-01/01/2024. Controls were recruited from a national random pool and frequency matched by age group, sex and county. We used an online questionnaire with inquiries about salads, vegetables, and salad bar consumption in supermarkets. We calculated adjusted odds ratios (aOR) with 95% confidence intervals (95%CI) using multivariable logistic regressions.

RESULTS

We identified 60 cases; median age of 44 years (range 16-81), 73% women. The case-control study included 38 cases and 368 controls. Compared to controls (8%), cases (85%) were more likely to have consumed items from salad bars in supermarkets (aOR 58; 95%CI: 22-186). In regards to food items from salad bars, cases (62%) were more likely to have consumed mixed kale salad compared to controls (32%) (aOR 3.6; 95%CI: 1.2-12). Trace-back investigations identified kale producers from Sweden, Belgium and Spain, but no particular grower was identified and no food samples were available.

CONCLUSIONS

Mixed kale salad from salad bars in supermarkets was the most likely source of infection. The detection of a novel subtype underscores the importance of adequate typing methods in surveillance and outbreak detection. It is important to understand how the contamination of kale and other leafy vegetables occurs in order to prevent future outbreaks and apply adequate preventive measures.

KEYWORDS: Epidemiology, Infectious Disease Outbreaks, Cryptosporidium, Molecular typing
ABSTRACT ID: 153
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Florian Burckhardt

ABSTRACT

Listeria monocytogenes outbreak linked to artisanal blackened olives in Baden-Wuerttemberg, Germany 2023

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BACKGROUND
In December 2020 whole genome sequencing of the National Reference Laboratory detected a cluster of previously unrelated Listeriosis cases of cgMLST-type 5498 (“pi8”). First cases were notified in December 2020 and clustered in southern Germany. We investigated the outbreak to identify the source and stop it.

METHODS
We defined cases as culture or PCR positive and having cgMLST5498 with disease onset from December 2020. Cases were interviewed with the structured Listeriosis-questionnaire of the Federal Health Agency about food consumption during the exposure period. Answers were shared with the State laboratory for food control (CVUAS-S) to inform enhanced environmental sampling.

RESULTS
Of the 20 pi8-cases, five were pregnancy related, nine were from Baden-Wuerttemberg and eight from neighbouring States. Median age was 58 years (range: 0-93), 13 were female and seven male. Two cases died, however of reasons other than Listeriosis. Ten of 13 cases interviewed mentioned having eaten blackened pickled olives during their incubation periods. In September 2023, CVUA-S sequenced a pi8-Listeria submitted by a voluntary self-monitoring artisanal pickle manufacturer. The spike of an industrial tin opener for blackened olives was identified as reservoir. The German food monitoring program reported in 2022 that among olives tested, only blackened had Listeria.

CONCLUSIONS
Voluntary self-monitoring and sequencing of all bacterial food samples led to the rapid attribution of blackened olives as outbreak vehicle for the Germany wide pi8-Listeriosis outbreak. Regular sampling and daily disinfection of the tin opener were ordered. After October 2023, no new cases were notified. Non-pasteurised, blackened olives should be considered as risk factors for Listeriosis and not eaten during pregnancy. Treating green olives with ferrous gluconate for blackening might enhance growth or invasive capabilities of Listeria.

KEYWORDS: listeriosis,blackened olives,Germany,pregnancy
ABSTRACT ID: 510
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Mahmut Akdag

ABSTRACT

Enteropathogenic E. coli gastroenteritis outbreak in Agri Province, Turkiye, March 2023

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BACKGROUND

On 29 March 2023, an early warning alert was received from acute gastroenteritis (AGE) syndromic surveillance system (n=957) in Agri Province, Turkiye. We investigated the outbreak to identify the source, risk factors and recommend control and prevention measures.

METHODS

A probable case was defined as a person admitted to Agri Province hospital with symptoms of nausea or vomiting or diarrhoea between 28 March-5 April 2023. We conducted 1:1 unmatched case control study to compare 114 probable cases and their asymptomatic neighbourhood controls calculating crude and adjusted Odds Ratio (OR) with 95% confidence interval (CI). We evaluated stool samples (n=5) via Polymerase Chain Reaction and culture and water samples (n=23) for residual chlorine, chemicals and microbiological parameters.

RESULTS

The crude attack rate was 1.6%. Common symptoms included diarrhoea (89.8%), nausea (78.6%), abdominal pain (76.5%) and vomiting (81.6%). Consumption of tap water (OR=3.3, 95%CI:1.6-6.5), and bottled water (OR=0.4, 95%CI:0.2-0.7) were associated with illness. After controlling for bottled water, consumption of tap water (ORadj:3.5, 95% CI:1.1-11.2) was significantly associated with the illness. The water samples tested positive for Enterococcus spp., Coliform bacteria, Escherichia coli. Enteropathogenic E. coli (EPEC) was isolated from two stool samples. Environmental investigation revealed that there were low levels of free chlorine prior to the outbreak, and both primary chlorination devices and water network were found to be damaged.

CONCLUSIONS

The primary water source contamination originating as a result of the damaged water network and chlorination devices was identified as the root cause for the outbreak. Super-chlorination was implemented after chlorination devices were repaired. We recommended maintaining spare chlorination devices, regular monitoring of free chlorine levels and quality enhancement of water pipes to mitigate future incidents.

KEYWORDS: EPEC, Gastroenteritis,Outbreaks,Waterborne diseases,Case-control studies
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Emomali Kurbonov

ABSTRACT

Brucellosis outbreak in northwestern Tajikistan in 2023: a matched case-control study

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BACKGROUND

A sharp increase in brucellosis incidence was observed in northwestern Tajikistan (from 1.0/100,000 people in 2022 to 32,7/100,000 by May 2023). Most cases, 82% (84/103), were from the same village (population=10,712). We investigated to identify risk factors and mitigate disease.

METHODS

Using a case-control design, we conducted face-to-face interviews and collected blood from May-July 2023. Cases were the first person in a household diagnosed with brucellosis in February-June 2023. Two controls were selected for each case (neighbors from different households matched by age and sex). Controls testing positive were excluded (13%). We conducted conditional multivariable logistic regression to assess association with brucellosis.

RESULTS

Of 84 cases, 57 (58%) met inclusion criteria. Of which, 68% were 15-44 years old and 44% were male. Common symptoms were joint pain (95%), fever (84%), weakness (72%), and night sweats (65%). All cases and 94% of controls (n=114) had unvaccinated livestock (mostly cattle, sheep or goats). A greater proportion of cases than controls had consumed homemade kaymak (clotted cream from unpasteurized milk) (89% vs 36%), home-produced meat (98% vs 82%) or neighborhood-produced milk (81% vs 61%); or engaged in animal slaughter (42% vs 11%) or animal grooming (32% vs 10%). Brucellosis was associated with consumption of homemade kaymak (adjusted odds ratio [AOR]=60.6, confidence interval [CI]=4.2-873.0, p=0.003), homemade meat (AOR=55.1, CI=1.2-2,549.0, p=0.040), neighborhood milk (AOR=8.6, CI=1.6-47.9, p=0.014), animal slaughter (AOR=50.9, CI=2.8-919.0, p=0.008) or animal grooming (AOR=15.6, CI=1.1-234.0, p=0.047).

CONCLUSIONS

Contact with unvaccinated livestock or consumption of their products was a key contributor to this outbreak. Cases were likely higher than reported. Following our investigation, an education and vaccination was carried out and no more brucellosis cases were reported after August 2023.

KEYWORDS: Disease Outbreaks, Brucellosis, Animals, Case-Control Studies, Milk,Tajikistan
ABSTRACT ID: 431
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Gethin Jones

ABSTRACT

A large Cryptosporidium parvum outbreak associated with a lamb-feeding event at a working farm in South Wales, March-April 2024: a retrospective cohort study

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BACKGROUND

During March and April 2024, 59 laboratory-confirmed Cryptosporidium cases linked to a working farm offering a lamb-feeding experience were notified to Public Health Wales. Environmental investigations highlighted multiple risk factors and microbiological investigations genetically linked lambs to outbreak cases. A retrospective cohort study was conducted to identify high-risk activities at the farm to tailor interventions.

METHODS

Exposure information including participation in various farm activities was collected via an online survey distributed to those booking the lamb-feeding experience. Cases were defined as any individual reporting gastrointestinal symptoms within 3-14 days of attendance. A multivariable logistic regression model was determined by forward stepwise inclusion of variables (p-value<0.2) considering goodness-of-fit (Akaike information criterion) to give adjusted odds ratios (aOR) and 95% confidence intervals (95%CI).

RESULTS

Of the 540 eligible responses, we identified 168 cases. Cases were mostly female (79%), with a median age of 31 years (range 1-80 years). Cases were less likely to have thoroughly washed their hands (aOR 0.5, 95%CI: 0.2-1.0), and more likely to have had visible faeces on their person (aOR 3.6, 95%CI: 2.1-6.2), or kissed/had face-contact with lambs (aOR 2.4, 95%CI: 1.2-4.8). The highest odds were among children aged <9 years (aOR 4.5, 95%CI: 2.0-10.0).

CONCLUSIONS

This Cryptosporidium outbreak represents the largest associated with a farm-setting in Wales. This study supports environmental and microbiological investigations that lambs were the source of the outbreak. We provide evidence that close-contact at lamb-feeding events presents an increased likelihood of illness, suggesting farms should limit animal contact at these events and revisions to established codes of practice may be necessary. Enhancing risk awareness among farmers/visitors is needed, particularly regarding children, alongside ensuring availability of adequate sanitisation facilities.

KEYWORDS: Cryptosporidium,Zoonoses,Farm,Cohort study,Lamb-feeding
ABSTRACT ID: 734
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POSTER TOUR 20

Day 3 – 15.30-16.30

Food- and waterborne disease outbreaks

PRESENTER

Fanny Chereau

ABSTRACT

Cross-border outbreak of Yersinia enterocolitica bioserotype 2/O: 9 infections linked to unpasteurized goat milk cheese produced in France, 2024

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BACKGROUND

Yersiniosis is the third cause of bacterial foodborne zoonosis in the European Union, but outbreaks are rare. In France, Yersinia enterocolitica (YE) bioserotype 4/O:3 is most frequent (87%), followed by 2/O:9 (11%). Whole genome sequencing (WGS) of YE was implemented in 2018 for routine surveillance. In March 2024, the notification of a YE 2/O:9 genomic cluster led to an outbreak investigation, to identify the source and implement control measures.

METHODS

We collected information on clinical aspects, food consumption and environmental exposures of WGS-confirmed cases, using trawling questionnaire and iterative interviewing. We traced back suspected foods using loyalty cards. Food and environmental strains isolated from suspected sources were characterized and their genome sequenced.

RESULTS

As of August 27, 2024, 174 cases (median age 50, 56 % women) were identified with isolation dates between January 27 and August 12, 2024. We interviewed 67 cases: 31 confirmed consumption of an unpasteurized goat's milk cheese wrapped in chestnut leaves. Traceback investigations identified a unique cheese factory. YE 2/O:9 strains were detected in cheese at the factory and in the environment at a milk producer. WGS confirmed that clinical, food and environmental isolates belonged to the same cluster. An Epipulse alert identified 7 additional cases in Belgium (5 cases), Norway and Luxembourg. Implementation of control measures in July 2024 included withdrawals from the market. The cheese was distributed in 22 countries.

CONCLUSIONS

This is the first documented outbreak of YE bioserotype 2/O:9 linked to raw goat's milk cheese. In France, grazing farm animals were identified as a reservoir for YE bioserotype 2/O:9. YE must be considered as a biological risk associated with unpasteurized milk products consumption and included in microbiological controls at production.

KEYWORDS: Cross-border,yersinia enterocolitica,outbreak,unpasteurized milk
ABSTRACT ID: 719
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POSTER TOUR 21

Day 3 – 15.30-16.30

Hepatitis and vaccination efforts

PRESENTER

Ana Paula Finatto Canabarro

ABSTRACT

Chronic hepatitis B infections in the European Union/European Economic Area countries: estimates of prevalence using the UNAIDS Workbook Method

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BACKGROUND

Up-to-date estimates of chronic hepatitis B (CHB) prevalence in key and general populations are essential for informing hepatitis B policies and monitoring the progress towards the Sustainable Development Goals targets. Models to estimate CHB prevalence often do not include key populations. This study aimed to estimate the CHB prevalence in the European Union/European Economic Area (EU/EEA), overall, by country and by key population group.

METHODS

The Robert Koch-Institut's adapted UNAIDS workbook was utilised to estimate the CHB prevalence for 2022 at national-level for each EU/EEA country and, within each country, for the key populations men who have sex with men (MSM), people who inject drugs (PWID), and migrants. The adapted workbook combines data on population size and CHB prevalence for each population group, collected from scientific sources and validated through communication with ECDC's national focal points.

RESULTS

National CHB estimate prevalences ranged from 0.3% (0.2%–0.4%) to 3.1% (2.8%–3.3%). CHB estimates among migrant populations varied from 0.8% (0.5%–1.0%) to 10.5% (9.3%–11.9%), among PWID from 0.0% to 8.7% (uncertainties could not be calculated), and among MSM from 0.0% (0.0%–0.0%) to 10.5% (10.2%–10.8%). The CHB prevalence estimate for the EU/EEA region was 0.7% (0.5% - 0.9%), with 3,202,000 (2,392,000–4,131,000) individuals living with CHB in 2022.

CONCLUSIONS

The workbook estimates suggest that the CHB burden is still high in the EU/EEA region, although varying importantly between countries and within countries' population groups. Although the workbook method has significant limitations, such as not addressing the overlap of populations, it can serve an alternative for obtaining CHB estimates for EU/EEA countries.

KEYWORDS: Hepatitis B,Human viral hepatitis,Prevalence,Epidemiological method
ABSTRACT ID: 41
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POSTER TOUR 21

Day 3 – 15.30-16.30

Hepatitis and vaccination efforts

PRESENTER

Celia O'Hare

ABSTRACT

National investigation and response to a cluster of acute hepatitis B cases in Ireland 2023-24 – implications for Ireland's new national sexual health strategy

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BACKGROUND

Risk factors for hepatitis B virus (HBV) infection include sexual contact and injecting drug use. We describe the cluster investigation and control measures following detection of five cases of acute HBV infection in the same geographical region over six months.

METHODS

A national Public Health led Incident Management Team (IMT) had representation from sexual health, hepatology, infectious disease, addiction and primary care services, and gay, bisexual and other men-who-have-sex-with-men (gbMSM) non-governmental organisations. Epidemiological review of national trends, detailed re-interviews, enhanced surveillance, contact tracing, and HBV genotyping were undertaken. Communications to clinicians and at-risk groups were developed

RESULTS

The cluster differed from acute HBV cases over the prior 5 years: younger, closely geographically linked, with a higher proportion gbMSM and non-injecting drug users. Anonymous sexual contacts limited contact tracing, however two sequenced cases had HBV genotype F1 – a comparatively rare genotype in Ireland. Control measures included vaccination of contacts, communication with clinicians and a co-created targeted health promotion campaign - including messaging on social and hook-up sites, and an information video featuring a prominent community leader and HIV activist. IMT response was limited by poor data availability on HBV vaccination coverage in gbMSM; and although vaccination of identified close contacts was funded, universal free vaccination in primary care for all at-risk groups is not.

CONCLUSIONS

No epidemiological link between the cases was identified, however a common source of infection was plausible in two sequenced cases. Increased community and clinician awareness, together with community-led promotion of vaccination may prevent future outbreaks. National policy issues regarding vaccination coverage data and equity of vaccine reimbursement persist and must be key considerations in the development of Ireland's new national sexual health strategy.

KEYWORDS: hepatitis b,vaccines,sexual health,health equity,Sexual and Gender Minorities
ABSTRACT ID: 617
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POSTER TOUR 21

Day 3 – 15.30-16.30
Hepatitis and vaccination efforts

PRESENTER
Klara Röbl

ABSTRACT
Assessment of mother-to-child-transmission of hepatitis B in Germany based on routine surveillance data, 2019–2023

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BACKGROUND
Germany aims to eliminate hepatitis B (HepB). Monitoring mother-to-child-transmission (MTCT) is important, but estimates of HepB-MTCT in Germany are missing. We used routine surveillance data to calculate HepB-MTCT-incidence in Germany to clarify further prevention needs and the usability of routine data for HepB-MTCT-monitoring.

METHODS
We included notified HepB-cases among children aged <=10 years born in Germany or with unknown country of birth between 2019–2023. Probable MTCT-cases were defined as children born in Germany with reported perinatal transmission or positive maternal HepB-serostatus. Possible MTCT-cases were defined as children missing any of the aforementioned information. We calculated proportions, incidences and median age together with inter-quartile-ranges (IQR) of probable and possible HepB-MTCT-cases and compared their age distributions using the Mann-Whitney-U-test.

RESULTS
In total 78 HepB-cases were included; 18 (23%) were categorized as probable, and 53 (68%) as possible MTCT-cases. Seven (9%) cases did not fulfil any MTCT-case definition. For possible MTCT-cases, information was missing on country of birth (n=10; 19%), transmission route (n=10; 19%) or both (n=33; 62%). The mean incidence of probable MTCT-cases was 0.05/100.000 compared to 0.15/100.000 for possible and probable MTCT-cases together. Probable MTCT-cases were younger than possible MTCT-cases (median: 0 (IQR 0–2) vs. 3 (IQR 0–7) years, p-value: <0.01).

CONCLUSIONS
Missing information leads to uncertainty in calculations of HepB-MTCT-incidence that use routine surveillance data. Older possible MTCT-cases suggest other infection sources or late detection and reporting among them. Nevertheless, cases with probable perinatal transmission in Germany highlight the need to intensify efforts to achieve HepB-MTCT-elimination. This includes intensified surveillance of HepB-MTCT-cases to obtain a precise estimate of MTCT-incidence and to assess coverage of both HepB-screening during pregnancy and neonates' post-exposure-prophylaxis.

KEYWORDS: Hepatitis B, Germany, Mother-to-Child-Transmission, Surveillance
ABSTRACT ID: 142
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POSTER TOUR 21

Day 3 – 15.30-16.30

Hepatitis and vaccination efforts

PRESENTER

Sameera Lyons

ABSTRACT

Eliminating mother to child transmission of hepatitis B virus (HBV): monitoring outcomes for infants born to mothers living with hepatitis B infection in England, 2014-2023

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BACKGROUND

Pregnant women in England are screened for HBV, HIV and syphilis with infants born to HBV positive women offered vaccination at birth and immunoglobulin if indicated. Since 2014 a dried blood spot (DBS) test for hepatitis B surface antigen (HBsAg) has been offered to these infants at 12 months to determine if mother to child transmission (MTCT) has occurred.

METHODS

Data from antenatal screening services was linked to DBS samples received at the Blood Borne Virus Unit in UKHSA. Outcome data for infants born to mothers with HBV was analysed using virological and demographic data including mother's country of birth (CoB), deprivation and e-antigen (HBeAg) status.

RESULTS

Antenatal screening and birth dose coverage is routinely >99% and >98% respectively. Since 2014, 10,348 DBS samples have been received with 17 infants (0.16%) testing positive for HBsAg. DBS uptake is varied and in 2021-2022 69.2% of eligible infants were tested by the service. Rates of MTCT have decreased from 0.92% in 2014/2015 to no reported events in 2022/2023. Of positive infants, all were born to HBeAg positive women. Where mother's CoB was known (76.5%) all were born outside the UK; mainly in East/Southeast Asia and Eastern Europe. Half of these women lived in the 20% most deprived neighbourhoods of England. Amongst positive infants, 82.4% had birth vaccine, 7 had HBIG (the rest are unknown). HBsAg mutations linked to vaccine escape were also detected.

CONCLUSIONS

DBS testing has been vital in demonstrating the effectiveness of the selective programme in England with MTCT rates consistently below WHO elimination targets. However, transmissions do occur, often amongst deprived populations and ethnic minorities highlighting populations where screening, vaccination and antiviral treatment could be improved.

KEYWORDS: mother-to-child transmission,elimination,hepatitis B virus,outcomes
ABSTRACT ID: 542
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POSTER TOUR 21

Day 3 – 15.30-16.30

Hepatitis and vaccination efforts

PRESENTER

Joana Cardoso

ABSTRACT

Effect of risk management and communication in vaccination during a hepatitis A outbreak in Portugal

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BACKGROUND

Portugal faces a hepatitis A outbreak, surging since mid-January 2024, mainly affecting men who have sex with men (MSM). In response, besides contact-tracing, the Portuguese Directorate-General of Health launched a risk communication campaign targeting health care professionals and at-risk individuals thorough diverse channels, such as social media platforms and dating apps (Grindr), to increase awareness and promote vaccination. We intend to evaluate the impact of this intervention on the number of vaccines administered to the general population, as well as men aged 20-49, identified as the highest-risk group for hepatitis A.

METHODS

We conducted a retrospective study analysing national records of hepatitis A vaccines administered from January 1, 2023, to April 18, 2024. We used Poisson Regression to assess the impact of the intervention by comparing the incidence rate ratio (IRR) of vaccines administered during the campaign (weeks 11-16, 2024) to a baseline period (week 1 2023 - week 10, 2024).

RESULTS

Weekly median number of vaccines administered during campaign was 1846.5 and 1303.5 in the baseline period. Poisson regression analysis indicated that the intervention significantly increased vaccination counts, with an overall IRR of 1.4 (95% CI = 1.39-1.44, p<0.001), suggesting a 41% increase in vaccines administered due to the intervention. Among men aged 20-49 years, the IRR was 1.6 (95% CI = 1.54-1.67, p<0.001), indicating a 60% increase in vaccination counts for this subgroup.

CONCLUSIONS

These findings suggest that public health measures including risk communication were effective in promoting vaccination during the hepatitis A outbreak, particularly among men aged 20-49. Effective risk communication is essential for promoting cooperation, compliance with prevention measures and, ultimately, controlling the outbreak. Future campaigns should consider diverse communication channels to increase impact.

KEYWORDS: Hepatitis A; Disease Outbreaks; Vaccination; Risk Communication Campaigns; Intervention Studies
ABSTRACT ID: 588
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POSTER TOUR 21

Day 3 – 15.30-16.30
Hepatitis and vaccination efforts

PRESENTER
Jebril Gebril

ABSTRACT
Seroprevalence of HIV, Hepatitis B, and C infections among pregnant women in Libya, 2023-2024

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BACKGROUND
Globally, hepatitis B virus (HBV), hepatitis C virus (HCV), and HIV are major health threats. In Libya, data on these infections among pregnant women are scarce. This cross-sectional study aimed to estimate the prevalence and identify risk factors of infectious diseases among pregnant women to establish evidence-based preventive policiesGlobally, hepatitis B virus (HBV), hepatitis C virus (HCV), and HIV are major health threats. In Libya, data on these infections among pregnant women are scarce. This cross-sectional study aimed to estimate the prevalence and identify risk of infectious diseases among pregnant women to establish evidence-based preventive policies.

METHODS
A simple random sample of pregnant women was selected from three randomly chosen antenatal clinics (one public and two private). Between January 2023 and January 2024, we interviewed participants face-to-face to collect information on sociodemographic characteristics and risk exposure histories. All participants were tested for HBV, HCV, and HIV. We estimated prevalence with 95% confidence intervals (95%CI) and calculated prevalence ratios (PR) using log-binomial regression.

RESULTS
Of the 975 participants, 0.8% (95% CI=0.04%-1.6%) tested positive for HBV, 0.2% for HCV (95% CI=0.0%-0.7%), and 0.6% for HIV (95% CI=0.02%-1.3%). There were no mixed infections. Of all participants, 7.6% reported a history of sharing personal tools such as needles and syringes, but all tested negative. However, 16% had a history of sexually transmitted infections (STIs) (PR=1.05, 95% CI=0.23-4.93), and 8.2% reported having a blood transfusion (PR=0.74, 95% CI=0.10-5.64).

CONCLUSIONS
The estimated HIV, HBV, and HCV prevalence was low compared with global epidemiological data. We recommend enhancing screening procedures for those infections among pregnant women and continuing to promote community awareness of STIs, to reduce the adverse impacts of these diseases on public health.

KEYWORDS: Seroprevalence, HBV, HCV, HIV, pregnant women, Libya
ABSTRACT ID: 680
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POSTER TOUR 21

Day 3 – 15.30-16.30

Hepatitis and vaccination efforts

PRESENTER

Eve Matthews

ABSTRACT

Investigation of a cluster of adult acute hepatitis of unknown aetiology in Greater Manchester, January-July 2024

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BACKGROUND

Acute hepatitis of unknown aetiology (AHUA) is an acute liver injury where common causes (e.g., hepatitis viruses A-E) are ruled out. In England, AHUA is not routinely notified, and no surveillance exists in adults.In February 2024, a localised cluster of AHUA cases admitted to one hospital was notified to UKHSA. We aimed to identify common exposures.

METHODS

Cases were individuals with AHUA with serum transaminase >500IU/L, admitted to hospital in North West England, with a sample date on or after 01/01/2024. We conducted stimulated passive case finding through hepatologists in Greater Manchester and surrounding hospitals in neighbouring counties; enhanced surveillance continued in Manchester until July. We implemented a comprehensive trawling questionnaire and performed descriptive analysis. A local NHS Trust conducted laboratory investigations.

RESULTS

We identified 11 cases of AHUA between February and July. Despite wider case finding, case residences clustered in a localised geography (81% within 2km of another case, all within 30km). Cases were all adults (median 48; range 24-81 years) and 73% were female. Cases experienced moderate illness with variable symptoms, minimal or no coagulopathy, and markedly raised AST/ALT (up to 7060IU/L). No cases died. Autoimmune and common infectious causes were ruled out.Ten trawling questionnaires were completed. No links or unusual common exposures were identified.

CONCLUSIONS

Despite thorough investigations following guidance, this cluster, notably among adults, remains unexplained. Cases may have been sporadic or linked to an unrecognised factor. As AHUA is not routinely notified, we lacked readily available baseline data to substantiate outbreak existence. We recommend exploring analysis of alternative indicators (e.g., ICD-10 codes) in existing datasets to generate baselines to support verification of AHUA outbreaks and describe AHUA in North West England.

KEYWORDS: Hepatitis ,Surveillance,Outbreak investigation,England
ABSTRACT ID: 802
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POSTER TOUR 22

Day 3 – 15.30-16.30
Modelling

PRESENTER
Sasikiran Kandula

ABSTRACT

Estimating excess mortality in the Nordics between 2020-23 using a multi-model approach

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BACKGROUND
Excess mortality is a more comprehensive measure of Covid-19 burden than cause-specific mortality. However, estimates based on a single model insufficiently account for the different sources of uncertainty. Similarly, while national-level estimates are useful, geographically and demographically stratified estimates are necessary to uncover the heterogeneous impact of the pandemic.

METHODS
In this study, using monthly all-cause mortality over twelve years in four Nordic countries -- Denmark, Finland, Norway and Sweden -- stratified by age, sex and subregion, we built three distinct models (timeseries, generalized additive, spatial random effects) to forecast mortality expected during the pandemic years (2020-2023). Model averaging improved over forecast skill of the individual models under temporal cross-validation and maintained good interval coverage even at long forecast horizons.

RESULTS
Sweden had an excess mortality of 69 per 100,000 population (95% prediction interval (PI): 44-95) in 2020 and no statistically significant excess (observed all-cause deaths within 95% PI of expected deaths) in 2021-2023. Denmark had excess mortality in 2021 (40; 95% PI: 3-76) and 2022 (72; 95% PI: 26-114), Norway in 2022 (86; 95% PI: 45-124) and likely in 2023 (46; 95% PI: 0-90), and Finland during 2021 (61; 95% PI:34-89), 2022 (158; 95% PI: 127-188) and 2023 (116; 95% PI: 83-148). The elderly (70+ years) contributed nearly all the excess deaths in these countries, while women had lower median excess mortality than men. Excess mortality rates in capital regions were lower than the respective national rates.

CONCLUSIONS
Our results indicate considerable differential impact of the pandemic among (and within) Nordic countries. Our estimates can support further analyses on associations between excess mortality and Covid-attributed deaths, socioeconomic characteristics, and type/timing of response measures, to inform pandemic preparedness.

KEYWORDS: COVID-19,Excess Mortality,Statistical models,model verification,combination models
ABSTRACT ID: 117
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POSTER TOUR 22

Day 3 – 15.30-16.30

Modelling

PRESENTER

Hailin Feng

ABSTRACT

Modelling West Nile virus (WNV) seroprevalence and infection burden in Europe

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BACKGROUND

West Nile Virus (WNV) is one of the most recent emerging mosquito-borne pathogens in Europe where each year hundreds of human cases are recorded. This study aims to investigate spatiotemporal heterogeneities in both infection risk and reporting rates at the European scale.

METHODS

We conducted a systematic literature review in Embase and MEDLINE to extract all eligible studies assessing the overall or age-stratified WNV seroprevalence (proportion of population exposed to WNV) following the PRISMA guidelines. A catalytic model was then fitted to the extracted age-stratified seroprevalence data to estimate the constant-in-time force of infection (FOI), which is the average annual per capita risk of infection for susceptible individuals. We then evaluated the reporting rate of WNV by matching the recorded case data with the number of infections inferred from the seroprevalence estimates.

RESULTS

We identified 18 age-stratified seroprevalence datasets among 109 extracted eligible studies conducted between 1958 and 2021 in 23 countries. Our analysis identified hotspots of WNV infection including Ionian Islands, Greece (mean FOI: 0.019, 95% credible interval (CrI) [0.0042, 0.052]) and Satu Mare, Romania (mean FOI: 0.0027, 95% CrI [0.0017, 0.039]). The average age-group specific reporting rate varied from 0.0011% in age-group 60-69 to 0.28% among 80+ years old.

CONCLUSIONS

To the best of our knowledge, this is the first effort at collating published human WNV seroprevalence data in Europe. Overall, we observed large spatial variability in both the WNV infection risk and in the proportion of infections reported to surveillance. Our findings can help strengthen WNV surveillance and provide opportunities to investigate the drivers of the large heterogeneities in WNV infection burden across Europe.

KEYWORDS: West Nile virus, seroprevalence, human, Europe, Disease transmission, Surveillance, mathematical model
ABSTRACT ID: 114

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POSTER TOUR 22

Day 3 – 15.30-16.30

Modelling

PRESENTER

Jim Duggan

ABSTRACT

Forecasting Seasonal Influenza Hospitalisations in Ireland using a Population SLIR Transmission Model with Hamiltonian Monte Carlo (HMC)

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BACKGROUND

Seasonal influenza places a significant burden on the healthcare system, placing demands on admissions, hospital beds, and intensive care unit resources. The rationale for the study was to augment existing time-series planning methods in order to assess the feasibility of deploying a hybrid deterministic (SLIR) and statistical inference (HMC) model and embed these within Ireland's Health Protection Surveillance Centre's winter planning process.

METHODS

A Susceptible-Latent-Infectious-Recovered (SLIR) deterministic model was deployed to simulate disease progression and resulting hospitalisations. The model assumptions included: fixed demographics, a constant contact rate, a single influenza A virus subtype circulating, a fixed number of vaccinations, and that hospitalisations occur in the same week as infections. Hamiltonian Monte Carlo, a novel statistical inference technique, generated case projections and parameter estimates of: the weekly average contact rate, the hospitalisation fraction, and the seasonal influenza reproduction number.

RESULTS

An analytics pipeline was implemented, with hospitalisation data for laboratory confirmed influenza extracted from the Irish notifiable disease surveillance system, and forecasts generated using Stella, R and stan (HMC). Outputs included case projections and parameter inference. Scenarios were run for three vaccine effectiveness levels [0.2, 0.4, 0.6]. The SLIR model performed well to project the inflection points and peaks. Sample results from week 5 ^{2024}, assuming vaccine effectiveness of 40% were: mean effective contacts/week 4.67 [4.52-4.81]; mean hospitalisation fraction 0.0024 [0.0016-0.0037]; and a mean reproduction number of 1.34 [1.29-1.37].

CONCLUSIONS

The combined SLIR/HMC model outputs were successfully communicated to national leads for health service planning, with weekly parameter estimates, along with a 2-4 week forecast window for hospitalised cases generated. Future work will involve: enhanced automation of the forecasting process analytics pipeline, and adding age-cohorts to the model.

KEYWORDS: Public Health; Modelling; Influenza; Mathematical computing; Ireland
ABSTRACT ID: 52
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POSTER TOUR 22

Day 3 – 15.30-16.30

Modelling

PRESENTER

Nicolò Gozzi

ABSTRACT

Introducing RespiCast: the first European respiratory diseases forecasting hub

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BACKGROUND

Over the past years, collaborative modelling hubs emerged as an innovative tool to forecast and project the dynamics of several infectious diseases, including ebola, influenza, dengue, and COVID-19. Here we introduce RespiCast, the first European Respiratory Diseases Forecasting Hub.

METHODS

RespiCast builds upon the experience of the European COVID-19 Forecasting Hub, developed by the European Center for Disease Prevention and Control in response to the emergency to provide short-terms forecasts on cases, deaths, and hospitalizations linked to COVID-19. RespiCast extends these targets introducing influenza-like-illness (ILI) and acute respiratory infections (ARI) incidence. More in detail, over the 2023/24 winter season, modelling teams worldwide were invited to submit each week probabilistic forecasts on these targets in order to characterise the short term evolution of respiratory infections in Europe. Submitted forecasts were then combined into an ensemble forecast (representing the hub consensus) and evaluated in real time against a baseline model using several performance metrics.

RESULTS

Over 18 forecasting rounds, 7 modelling teams representing 5 countries contributed to RespiCast with a total of 15 models and 340k forecasting points. As of April 10, 2024, the ensemble model features better forecasting performance with respect to the baseline in ~80% of countries for both targets. Nonetheless, we find that model performance depends on several factors, including data availability and quality, country-specific effects, the evaluation metric considered, and the ensemble definition.

CONCLUSIONS

In conclusion, RespiCast marks a step toward strengthening European preparedness to public health crises by integrating epidemic modelling outcomes with actionable policy insights. Indeed, it can be used for anticipating surges in public health demands during winter months, tracking short-term trajectory of respiratory diseases across Europe, and facilitating cross-country comparisons.

KEYWORDS: Public Health, Europe, Forecasting, Epidemics
ABSTRACT ID: 141
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POSTER TOUR 22

Day 3 – 15.30-16.30

Modelling

PRESENTER

Laurene Peckeu-Abboud

ABSTRACT

Integrating epidemiological modelling into the evidence-based methodology used in health-policy assessment. The example of the updated French vaccination strategy against invasive meningococcal diseas

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BACKGROUND

The French National Immunization Technical Advisory Group provides recommendations to the Ministry of Health by systematically gathering, reviewing, and evaluating available scientific evidence within the local French epidemiological and social context. This evidence–based methodology often lacks quantifiable projections to assist in decision making. In this example, we assessed if children younger than one year, adolescents and young adults in France need to be vaccinated for meningococcal (Men) serogroups ACWY and B.

METHODS

We conducted our standard assessment including literature review and epidemiological and safety data analyses. But we commissioned a compartmental dynamical transmission model estimating numbers of averted cases and numbers of needed to vaccinate for various MenACWY and MenB immunisation scenarios, which we hypothesized would inform decision making.

RESULTS

Drawing from epidemiological and microbiological surveillance data, vaccine characteristics, vaccine effectiveness studies, pharmacovigilance data, and modelling outcomes identifying a most effective strategy for reducing MenW IMD cases and assessing modest impact of MenB adolescent vaccination, the French vaccine strategy against invasive meningococcal disease (IMD) was updated as follows: mandatory MenACWY and MenB vaccination for children < 1 year and recommended MenACWY, but not MenB, vaccination for adolescents and young adults aged 11-14 years, with a catch-up campaign for 15-24 years.

CONCLUSIONS

The mathematical modelling strengthened the conclusions reached from the standard assessment by providing quantification of vaccine impact, despite uncertainties on modelling assumptions. This informed the decisions regarding the IMD vaccine strategies. We therefore recommend systematically integrating modelled evidence into the decision-making process when health-policy questions amenable to modelling. We also encourage peer-reviewed publications to highlight the benefits of these methods and ensure high quality assessment standards as recommended by the WHO IVIR-AC subgroup.

KEYWORDS: epidemiological modelling ,evidence-based methodology ,health-policy assessment,invasive meningococcal disease
ABSTRACT ID: 420
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POSTER TOUR 22

Day 3 – 15.30-16.30

Modelling

PRESENTER

Nataliia Halushko

ABSTRACT

Factors of hepatitis C transmission in Ukraine: the impact of dental interventions

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BACKGROUND

In Ukraine, the availability of specific hepatitis C treatment has significantly improved, but substantial changes in the epidemic process have not been observed. In this context, exploring other approaches to combat hepatitis C, particularly those focused on interrupting the virus's transmission mechanism, is crucial. Our research aimed to identify the most significant factors of hepatitis C transmission.

METHODS

We conducted a correlation-regression analysis using Stata15. The dependent variable (y): incidence of viral hepatitis C. Independent variables: number of visits to dentists (x1), dental prosthetics (x2), and hospitalizations in surgical (x3) and dental (x4) departments. Number of observations of dependent and independent variables 25 (equal to the number of administrative-territorial units in the country). We calculated regression coefficients (β) for each independent variable and the intercept (β0). Model adequacy was assessed using the adjusted coefficient of determination ($adjR^2$) and tests: Shapiro-Wilk (normality of residuals), Breusch-Pagan (heteroskedasticity), Breusch-Godfrey (autocorrelation), and Variance Inflation Factor (VIF, for detection multicollinearity). The statistical significance of the coefficients and hypothesis testing were conducted using the p-value.To improve the model, logarithmic transformations of the independent variables were performed. Statistically insignificant variables were excluded.

RESULTS

The obtained regression model is as follows: $y = 7.57 \ln(x1) + 4.18 \ln(x4) - 117.37$The variable ln(x1) was significant (β1=7.57, p=0.008), the variable ln (x4) was also significant (β4=4.18, p=0.02). The model explains nearly 66% of the variation in the dependent variable (adjR-squared=0.6561) and indicates no multicollinearity (VIF=1.35), is homoscedastic (p=0.2078), has normally distributed residuals (p=0.28243), and no autocorrelation (p=0.3495).

CONCLUSIONS

The primary predictors of acute hepatitis C incidence in Ukraine are dental interventions, highlighting the need for further investigation into the specifics of pathogen transmission during procedures.

KEYWORDS: Hepatitis C, dental interventions, pathogen transmission, risk factors,Healthcare associated infections
ABSTRACT ID: 814
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POSTER TOUR 23

Day 3 – 15.30-16.30

Surveillance of respiratory diseases

PRESENTER

Irene Bianconi

ABSTRACT

Tracking seasonal influenza trends in South Tyrol during season 2022-2023 using genomic surveillance data

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BACKGROUND

Influenza seasons are characterized by a complex interplay of co-circulating strains with high spatial and temporal heterogeneity among regions. We combined epidemiological, virological and genomic surveillance data to provide a comprehensive analysis of influenza subtypes circulating in the South Tyrol region (Italy), leveraging phylogenetic and phylodynamic approaches.

METHODS

Clinical samples were collected from hospital patients exhibiting influenza-like symptoms between 2022 and 2023. Molecular diagnostics were employed to track the prevalence of different strains. Whole genome sequencing was conducted, and hemagglutinin (HA) gene sequences were used for detailed phylogenetic analysis. A Birth-Death Skyline model was applied to estimate strain-specific effective reproduction numbers (Re) and attack rates.

RESULTS

Out of 4891 samples tested, 862 resulted positive for influenza; of these, 224 genomes were sequenced. Phylogenetic analysis of HA gene revealed A(H3N2) strains predominantly clustering in clade 3C.2a1b.2a.2b, followed by 3C.2a1b.2a.1b. A(H1N1pdm09) strains predominantly clustered in clade 6B.1A.5a.2a. Exclusive circulation of B(Victoria) subtype strains aligned with the global trend, falling within clade V1A.3a.2. A(H3N2) predominantly circulating at the beginning of the season was gradually replaced by B(Victoria) in January. A low incidence of A(H1N1pdm09) was identified throughout the season. The effective reproduction number was estimated to be 1.16-1.35 (95%CI) for A(H3N2), 1.06-1.34 for A(H1N1pdm09), and 1.02-1.29 for B(Victoria).. 95%CI of attack rates were 6.3%-33.5% for A(H3N2), 0.6%-5.0% for A(H1N1pdm09) and 0.8%-6.5% for B(Victoria).

CONCLUSIONS

Our study confirms the added value of integrating routine epidemiological and virological data with genomic surveillance to characterize the influenza transmission dynamics. The analysis of these data can inform vaccine strain selection processes and provide quantitative estimation of subtype-specific reproduction numbers and attack rates.

KEYWORDS: Influenza, genomic surveillance, reproduction number, phylogenetic, phylodynamic, hemagglutinin gene
ABSTRACT ID: 559
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POSTER TOUR 23

Day 3 – 15.30-16.30
Surveillance of respiratory diseases

PRESENTER

Alejandra González-Sánchez

ABSTRACT

Genomic evolution of human respiratory syncytial virus during a decade (2013–2023) in Barcelona: bridging the path to monoclonal antibody surveillance

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BACKGROUND

New prophylaxis strategies against human respiratory syncytial virus (HRSV) are starting to be used, targeting different populations. This supposes the first time HRSV faces an external selective pressure, which might drive its natural evolution.

METHODS

Respiratory specimens from patients with RTI suspicion at Hospital Universitari Vall d'Hebron (Barcelona, Spain) were collected from October/2013 to May/2023. Whole-genome sequencing was performed with Illumina in randomly-selected samples. Phylogenetic analyses were performed with BEAST v1.10.4. Signals of selection and evolutionary pressures were inferred by population dynamics and evolutionary analyses. Mutations in major surface proteins were genetic and structurally characterised, emphasizing those within antigenic epitopes.

RESULTS

Among 139,625 samples, 5.3% were HRSV-positive, with a higher prevalence observed in the paediatric population (9.3%). Pandemic-related shifts in seasonal patterns returned to normal in 2022–2023. A total of 198 (6.6%) whole-genome sequences were obtained for HRSV-A, belonging to A.D, A.D.1, A.D.2.1, A.D.2.2, A.D.2.2.1, A.D.3, A.D.3.1, A.D.5 and A.D.5.2 lineages (within GA2.3.5 G-clade), while 167 (4.3%) were sequenced for HRSV-B, belonging to B.D, B.D.1.1, B.D.4, B.D.4.1, B.D.4.1.1, B.D.E.1, B.D.E.2 and B.D.E.3 (within GB5.0.2, GB5.0.3, GB5.0.4a and GB5.0.5a G-clades). HRSV-B exhibited a higher evolution rate (7.5e-4 vs 5.2e-4). Post-SARS-CoV-2 pandemic, both subtypes showed increased evolutionary rates and decreased effective population size initially, followed by a sharp increase. Analyses indicated negative selective pressure on HRSV. Mutations in antigenic epitopes (M274I and S276N in palivizumab-targeted site II, and K65R, N201S, L204I, I206M, Q209R/K, and S211N/G in nirsevimab-targeted site Ø) were identified.

CONCLUSIONS

In the context of the large-scale use of nirsevimab in 2023–2024 season, and the future use of other mAb and vaccines, continuous epidemiological and genomic surveillance is crucial, especially to monitor the emergence of potential resistance-related mutations.

KEYWORDS: human respiratory syncytial virus,surveillance,whole genome sequencing,monoclonal antibodies,evolution
ABSTRACT ID: 623
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POSTER TOUR 23

Day 3 – 15.30-16.30

Surveillance of respiratory diseases

PRESENTER

Jonilda Sulo

ABSTRACT

Usefulness of Syndromic Surveillance in Real-Time Influenza Monitoring, Albania, 2019-2022

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BACKGROUND

In 1999 the Albanian Institute of Public Health launched the ALERT syndromic surveillance system (SSS) as an early warning mechanism for communicable diseases. The system aggregates weekly data from 400 healthcare centers, categorizing cases by syndromes and age groups. This study aimed to estimate the system's capabilities in predicting the occurrence of influenza season, especially in areas with limited laboratory capacity.

METHODS

We used syndromic surveillance records from 2019-2022. We utilized trend analysis and Pearson correlation to explore relationships between Upper and Lower Respiratory Infections (ULRI) data and lab-confirmed influenza cases. Lag analysis was employed to identify any time discrepancy between increased ULRI cases and influenza seasons. We estimated the ALERT system's performance by calculating sensitivity (SE) and positive predictive value (PPV)

RESULTS

Between 2019 and 2022, approximately 2 million ULRI cases and 1,231 confirmed influenza cases were recorded. Mean annual numbers were 493,910.2 (SD: 1,362.7) and 307.7 (SD: 17.3) for ULRI and influenza-positive cases, respectively. We found a good correlation between ULRI cases and confirmed influenza cases (r=0.79; 95% CI: 0.72-0.82), with 0.73% (95% CI: 0.64-0.80) of percentage of positivity. Lag analysis showed the strongest correlation between ULRI data and influenza-confirmed cases at zero weeks lag, indicating real-time concordance. The sensitivity and PPV of the ULRI surveillance for influenza detection were 78.7% (95% CI: 62.2-89.3) and 81.2% (95% CI: 64.6-91.1), respectively

CONCLUSIONS

The ALERT SSS is effective for real-time influenza detection, with high sensitivity and positive predictive value. Its strong correlation with confirmed cases underscores its value in monitoring flu trends. To refine its predictive accuracy for influenza trends, predictive modelling techniques, such as machine learning models, should be incorporated to improve foresight capabilities and operational efficiency.

KEYWORDS: syndromic surveillance, influenza, trend analyses, sensitivity, positive predictive value
ABSTRACT ID: 244
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Day 3 – 15.30-16.30

Surveillance of respiratory diseases

PRESENTER

Maja Mrzel

ABSTRACT

Implementation of the moving epidemic method for RSV season detection and timely public health response in the post-COVID era, Slovenia, 2015-2024

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BACKGROUND

In the post-COVID era, the previous fixed 7% of positive tests threshold to define the beginning of RSV season in Slovenia became invalid, as increased use of multiplex-PCR for respiratory viruses increased numbers of positive tests and lowered positivity rate. We implemented the moving epidemic method (MEM) to improve timely public health response for the 2024/2025 season.

METHODS

We collected data from accredited laboratories (n=9-14 (2015-2024)). Using the MEM, we modelled weekly RSV data (numbers (first model) and percentages of positive tests (second model)) from 25/5/2015 to 5/5/2024, excluding season 2020/2021. We used the fixed criterium method with optimized parameter to estimate the start of the season, arithmetic mean with 95% confidence interval (CI) upper limit to estimate thresholds, and geometric mean with 40%, 90%, and 97.5% CI upper limits to estimate intensity levels. The goodness of fit of the models was evaluated using a sequential validation procedure and measured with the Youden's index (YI=(sensitivity + specificity – 1)*100).

RESULTS

The first model estimated the start of the 2024/2025 season in week 52 and the second model in week 51. The seasonal threshold was estimated at 45 positive tests or 5% of positive tests per week. Intensity levels ranged from low (46-126 positive tests; 6-14%) to very high (>274; >21%). Sensitivity, specificity, and YI were 97%, 90% and 87% for number of positive tests per week, and 94%, 92% and 86% for percentage of positive tests per week, respectively.

CONCLUSIONS

Based on the high goodness of fit of the models, we recommend MEM implementation for the 2024/2025 season and continuous monitoring of RSV data to ensure timely preventive strategies, planning of public health interventions and hospital preparedness.

KEYWORDS: Moving epidemic method, Respiratory syncytial virus, Seasonality, Surveillance, Slovenia
ABSTRACT ID: 156

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Day 3 – 15.30-16.30
Surveillance of respiratory diseases

PRESENTER
Manuela Harries

ABSTRACT

Change of influenza burden between Corona pre-pandemic and pandemic times from 2014 to 2023: Analysis based on FLUNET data in Europe

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BACKGROUND

This work quantifies the impact of the COVID-19 pandemic and associated non-pharmaceutical interventions (NPIs) on influenza activity in European countries from 2014 to 2023.

METHODS

The data spanned nine flu seasons and were collected from 33 sentinel (physicians/laboratories/hospitals) and 34 non-sentinel (e.g. schools, primary care facilities) sources from European countries, and were statistically analyzed using paired t-tests and correlation analysis.

RESULTS

In the 2019-2020 influenza season, positive cases decreased by 25% (95% CI: -4.82 - 45.71, p = 0.09) compared to reference seasons (2014-2019), while the begin and intensity of influenza waves remained unchanged. The 2020-2021 season witnessed a significant decline in positive influenza cases, with a 0.41% (95% CI: 0.29-0.58, p < 0.001) of the reference values recorded. In the 2021-2022 season, where NPIs were still in place, positive influenza cases remained at one-third of reference values and had an inverse relationship with the extent of NPIs. The season's onset was delayed by around five weeks, and the time of maximal positivity by three weeks, indicating a significant impact of ongoing NPIs. The season of 2022-2023 began five weeks earlier than usual. Although mean positive numbers increased by 42% (95% CI: 03.01 - 96.61, p = 0.033), season positivity, and maximal positivity largely remained the same.

CONCLUSIONS

Our quantitative analysis of influenza dynamics during the COVID-19 pandemic underscores the effectiveness of NPIs in reducing influenza cases during the 2021-2022 season. However, the remarkable resurgence of influenza in 2020-2021 was transient. Preliminary findings of a systematic review (CRD42022360015) suggest a significant decline in absolute influenza case numbers. Further research is needed to understand how they relate to the SARS-CoV-2 seasonality.

KEYWORDS: surveillance, influenza season, Europe, COVID-19 intervention measures, (non-) sentinel
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Surveillance of respiratory diseases

PRESENTER

Julia Mutevelli

ABSTRACT

Post-pandemic rebound of Group A streptococcal infections in children in Germany, 2017 to 2024

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BACKGROUND

Group A Streptococcus (GAS) infections are responsible for kindergarten and school absenteeism, while invasive GAS (iGAS) infections cause significant disease burden among children. After reduced GAS and iGAS incidences during the COVID-19 pandemic, infections increased sharply in Germany during the post-pandemic period. We aimed to investigate a possible rebound-effect of GAS infections among children in Germany after the pandemic.

METHODS

We analysed routine diagnostic data on GAS infections in children under 15 years from a voluntary laboratory-based surveillance system covering about one third of healthcare facilities in Germany. Isolates from nasopharyngeal swabs were defined as non-invasive GAS infections. We used Poisson and negative binomial regression to estimate the expected isolate counts and their relative change with 95% confidence intervals (CI) in the pandemic (03/2020 – 12/2022) and post-pandemic period (01/2023 – 03/2024) relative to pre-pandemic years (01/2017 – 02/2020).

RESULTS

Non-invasive GAS infections in children decreased by 78% (95%CI: 74%–82%) during the COVID-19 pandemic compared to pre-pandemic years, corresponding to 43000 fewer isolates than expected (–300 isolates/week). This was followed by a 42% increase (95%CI: 8%–86%) during the post-pandemic period compared to pre-pandemic years, corresponding to 12000 more isolates than expected (+225 isolates/week).

CONCLUSIONS

Our findings suggest a rebound-effect of GAS infections in children following the COVID-19 pandemic. Potential reasons include increased susceptibility and risk of secondary bacterial infections enhanced by high co-circulation of influenza and respiratory syncytial virus following the relaxation of public health and social measures. Our results indicate that, while an interim prevention of GAS infections is possible, further research and continuous surveillance of GAS is necessary to establish long-lasting prevention strategies.

KEYWORDS: Streptococcus pyogenes, Group A streptococcus, pediatric infections, COVID-19
ABSTRACT ID: 191
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Surveillance of respiratory diseases

PRESENTER
Kaisa Jaakkola

ABSTRACT

Post-COVID-19 outbreak of Parvovirus B19 affecting pregnant women - A retrospective study of laboratory-confirmed human Parvovirus B19 congenital cases 2016-2024 in the Lyon Metropolitan area.

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BACKGROUND

Human parvovirus B19(B19V) is a widespread virus causing childhood disease but also congenital infections that occasionally lead to severe fetal complications or loss. Recently, an interruption of 3-4 year epidemic cycle, together with post-COVID-19 increase in B19V infections have been reported by some countries, and a nationwide alert was launched in France in April 2024. Our objective was to evaluate whether there is an increase in congenital B19V infections in the Lyon Metropolitan area.

METHODS

We conducted a retrospective study of women tested for B19V at Hospices Civils de Lyon 01.01.2016–19.04.2024. Amniotic fluid PCR samples positive for B19V were classified as congenital cases. We calculated the positive proportions with confidence intervals (95%CI, the Wilson method) and compared the different periods (Fisher's exact test). Immunity was serologically assessed, and women tested negative for anti-B19V IgG categorized as susceptible.

RESULTS

We identified 12 congenital cases, 4 predating 05/2023 and 8 from the past 12 months(05/2023-04/2024). The positive proportion of B19V in amniotic fluid samples was significantly higher over the past 12 months (25.0%; 95%CI:13.3-42.1 vs 3.7%; 95%CI:1.5-9.2, $p<0.001$).Serological assessment of women aged 14-45 years(n=4545, mean age 31.1) indicated an increase in the susceptible population in 2021(30.0%) to 2022(34.0%), with decrease and return to pre-pandemic levels in early 2023(28.0%). Differences in immunity were not statistically significant.

CONCLUSIONS

Our results suggest an ongoing parvovirus B19 outbreak with an unusually high number of congenital infections. Notifying healthcare workers and pregnant women of B19V risks is recommended.Our study is limited by the absence of systematic sampling and screening criteria for B19V. Syndromic surveillance of congenital cases, and incorporation of genomic data would support early detection of B19V outbreaks and tracking prevalent strains.

KEYWORDS: Human parvovirus B19,Infectious disease outbreaks,Pregnancy,Congenital infections
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Day 3 – 15.30-16.30

Surveillance of vaccine-preventable diseases

PRESENTER

Hester de Melker

ABSTRACT

Invasive meningococcal disease serogroup B: spatiotemporal cluster identification using finetype data, The Netherlands, 2005-2023

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BACKGROUND

In the Netherlands, ~90% of invasive meningococcal disease (IMD) cases are due to serogroup B. Currently, IMD-B cluster identification is mainly based on epidemiological investigations. PorA and FetA finetype is routinely obtained through DNA-sequencing but not systematically used for cluster identification. We aimed to assess whether systematic spatiotemporal analysis using finetype could lead to cluster identification.

METHODS

We extracted national surveillance data for laboratory-confirmed IMD-B cases between 01/01/2005 and 31/12/2023. We included cases with complete finetype data. For each finetype occurring at least twice within two years, we aggregated data by week and municipality (n=342). We calculated an expected baseline using generalized linear models for each finetype, including a temporal trend. To identify time-space clusters, we calculated Poisson scan-statistics comparing observed to expected counts through Monte Carlo hypothesis testing.

RESULTS

We observed 1,729 IMD-B cases in the 992-week study period of which 1,642 (95%) had complete finetype and municipality data. There were 453 distinct finetypes; 308 (68%) occurred once and 28 (6%) occurred twice but with an interval longer than two years. Of the remaining 117 (26%) finetypes with potential clustering (1,278 cases; 78% of cases), 72 (62%) caused between 2-5 cases. Preliminary results of the ten most prevalent finetypes identified 11 clusters ($p < 0.05$) among nine finetypes, with finetypes indicating distinct spatial clustering.

CONCLUSIONS

Meningococcal B isolates causing IMD were highly diverse as indicated by a wide range of finetypes, but we could identify spatiotemporal clusters using routinely-generated data. We recommend comparing our results with epidemiologically identified clusters and whole-genome sequencing data of IMD-B isolates to determine whether to incorporate spatiotemporal scanning by finetype in routine surveillance and cluster detection.

KEYWORDS: Meningococcal infections,Cluster Analysis,Spatio-Temporal Analysis,DNA Sequencing
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Surveillance of vaccine-preventable diseases

PRESENTER

Marta Soler Soneira

ABSTRACT

Uneven geographical distribution of invasive meningococcal disease in Spain, 1996-2022

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BACKGROUND

In Spain vaccination against invasive meningococcal disease (IMD) exists since 2000 (serogroup C) and 2019 (serogroup A, W, Y), respectively and vaccination coverage of IMD in infants is high in all regions. However, the epidemiology of IMD differs geographically. Our aim was to assess the consistency of differences using two information systems to promote studies that analyze causes and develop tailored public health measures.

METHODS

We obtained IMD confirmed cases from the Spanish National Surveillance System and National hospitalization registry during 1996-2022. The population denominators were obtained from the National Statistics Institute. For both information sources, we calculated crude incidence (IR) per 100,000 population, for different years, and indirectly standardized incidence (SIR) by region as a ratio of observed and expected cases (derived from national age-sex-specific population rates). We compared IRs of both systems with proportion tests (α=5%).

RESULTS

Between 1996-2022, 15,231 confirmed cases were reported in 19 Spanish regions, with national IR ranging from 3.68 cases/100,000 ^{1997} to 0.14 cases/100,000 ^{2022}. The highest IR in all regions was observed in infants (IR 23.6, 95%CI: 22.7-24.5) and for serogroup B IMD (IR 0.94, 95%CI: 0.92-0.96). IMD by serogroup W and Y increased between 2015–2019 and accounted for 3.5% of all cases. The SIR in six northern regions consistently exceeded 1.0, with "Pais Vasco" region having the highest 25-year SIR (2.56, 95%CI:2.46-2.68). National and regional SIRs from both information systems were similar (p>0.05).

CONCLUSIONS

A decline of IMD incidence over the last 25 years was observed in Spain, resulting from nation-wide vaccination programs. Northern regions had a higher risk of IMD. To apply targeted measures, factors explaining this regional pattern need to be further investigated.

KEYWORDS: Invasive Meningocococcal disease, Neisseria meningitidis, invasive, Immunization Programs, Spain
ABSTRACT ID: 502
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Surveillance of vaccine-preventable diseases

PRESENTER
Joshua Menadue

ABSTRACT

Investigation the largest wave of pertussis since 2016 in Wales, UK

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BACKGROUND
Whooping cough is a notifiable disease in Wales, with cases typically peaking every three to four years. During 2023/24, cases have been reported in greater numbers than in previous seasons. Pertussis can be fatal in infants, however the maternal vaccination program in Wales has been successful thus far in averting mortality in infants. We describe the latest increase, comparing to previous years to help inform public health response.

METHODS
All notifications were extracted from the national case and incident management system between Week 1 2013 to Week 19 2024. We defined an epidemiological year as ISO Week 27 to Week 26. We compared notifications up to Week 19 of the 2023/24 season to previous years. Notified cases were summarised by sex, age group and geographical region, using chi-square to test for differences in distributions between years.

RESULTS
There were significant differences in distribution of cases by age in 2023/24 compared to six of the previous eight seasons. The proportion of notifications in the 10-19 years age group increased to 24.5% compared to the 2022/23 season (5.9%), whilst the proportion in the most at-risk group (less than a year old) decreased from 18.8% to 4.5%. The largest increase by geographical region was seen in North Wales (14.7% to 25.1%).

CONCLUSIONS
The age and geographic distribution appear to be different to previous seasons, particularly in the proportion of infant notifications. However continued surveillance and vaccination uptake monitoring is essential to protect this vulnerable group. These results informed the public health response, particularly around vaccination messaging. Next steps include a post-season evaluation of pertussis surveillance, using clinical notifications and laboratory data to inform a robust surveillance plan for future seasons.

KEYWORDS: Whooping Cough,Wales,Incidence,Infants,Vaccination
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Surveillance of vaccine-preventable diseases

PRESENTER

Mareike Wollenweber

ABSTRACT

Seroprevalence of varicella zoster virus IgG-antibodies in newborns and children up to 2 years of age in Lower Saxony and Bremen, Germany 2003-2023

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BACKGROUND

In Germany, a two-dose vaccination scheme against varicella zoster virus (VZV) has been recommended for all children and adolescents (11 months up to 17 years) since 2004. Newborns are protected by maternal antibodies, however, data on the duration is limited, due to challenges in recruiting sufficient numbers of young children for seroprevalence studies. MERIN (Meningitis and Encephalitis Registry in Lower Saxony and Bremen) offers differential diagnostic clarification of hospitalized meningitis or encephalitis patients. In this context, serological parameters such as immunoglobulin (Ig) G-antibodies against vaccine preventable diseases (e.g., VZV) are determined. We used MERIN data collected between 2003–2023 to assess VZV-IgG-antibody status in newborns and young children, thus overcoming recruitment challenges and deducing Public Health recommendations.

METHODS

We calculated VZV seroprevalences from MERIN data and applied piecewise linear regression to investigate monthly changes in seroprevalence over the first two years of life.

RESULTS

Data on VZV-IgG-antibody-status were available for 2,181 children younger than two years old, of which 52% (n=1,142) were seropositive. Newborns had a seroprevalence of 94%. The levels declined monthly by 15% to a minimum of 1% at 7 months. Between months 6–10, seropositivity remained below 6%, then increased by 5% each month up to 88% at the age of 2 years.

CONCLUSIONS

We observed a rapid decline in maternal VZV-IgG-antibodies over the first 7 months of life and identified gaps in immunity. Approximately 95% of children aged 6 to 10 months were unprotected. Our findings suggest raising awareness towards vulnerable life periods and potential exposures, such as travelling, childcare, and early childhood education facilities. Results may further support decision-making in outbreaks and should be considered for adapting the starting point for VZV vaccination.

KEYWORDS: seroprevalence, varicella zoster virus,chickenpox,vaccination,maternal antibodies
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POSTER TOUR 24

Day 3 – 15.30-16.30

Surveillance of vaccine-preventable diseases

PRESENTER

Dritan Bejko

ABSTRACT

Pertussis outbreak centered among immunized adolescents in Luxembourg, 2024

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BACKGROUND

Despite an estimated vaccination coverage exceeding 90% among children, pertussis cases increased in the first four months of 2024 in Luxembourg. The pertussis vaccination schedule foresees doses administered at 2, 4, and 11 months of age, along with boosters at 5-6 years and 15-20 years of age. We conducted a descriptive analysis of this outbreak to facilitate targeted interventions and strengthen control measures against pertussis.

METHODS

In accordance with the law on mandatory reporting of infectious diseases, laboratories declared cases of pertussis and provided socio-demographic and contact information. Cases were contacted for vaccination status and school attendance. Descriptive analysis was performed using SPSS 28.0.

RESULTS

In contrast to 18 cases reported for the whole year of 2023, 548 cases were notified between January 1st and May 6th 2024 with a peak in mid-March. The median age was 14 years and the highest proportion of cases (61.5%) was observed in 10-15 year olds. 285(52.0%) cases were students at secondary and 103(18.8%) at primary schools with 18 schools registering more than 5 cases. Only 5(0.9%) cases were <1 year, and 6(1.1%) were >65 years old. Six cases required hospitalization, including a 4-month-old infant, a 22-month-old infant, and an 95 years old individual. There were no recorded fatalities. Most cases 446(80.8%) had documented vaccination records with a median time since last dose of 7 years.

CONCLUSIONS

We report an outbreak of pertussis mainly affecting immunized adolescents who had received their last booster dose 7 years ago, indicating waning immunity. Adjusting the vaccination schedule to administer booster doses at 11-12 years instead of 15-20 years could be a measure to reduce transmission of pertussis in school settings.

KEYWORDS: Pertussis, Adolescent, Vaccination, Disease Outbreaks, Schools
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POSTER TOUR 24

Day 3 – 15.30-16.30

Surveillance of vaccine-preventable diseases

PRESENTER

Juan Juaneda

ABSTRACT

Mpox vaccination and outreach in the Valencian Community, Spain: response to PHEIC and coverage of high-risk groups

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BACKGROUND

On 14 August, the World Health Organization (WHO) declared a public health emergency of international concern (PHEIC) in response to the spread of mpox in neighbouring countries of the Democratic Republic of Congo. In line with WHO and ECDC recommendations, a targeted vaccination programme was implemented to reduce the risk of local transmission.

METHODS

The vaccination strategy was scaled up from 3 to 27 vaccination sites, including 3 sexually transmitted infection units and 24 preventive medicine departments. Referral pathways were established at all levels of care to ensure access. Active recruitment targeted individuals on HIV pre-exposure prophylaxis (PrEP), and electronic nudges (text messages) were sent to unvaccinated or incompletely vaccinated individuals, highlighting the risk of mpox and the expanded vaccination sites.

RESULTS

By 22 September, 1,431 doses had been administered in 2024, with 98.1% administered as pre-exposure and 1.9% as post-exposure prophylaxis. Of those receiving PrEP (n=2,305), 763 (33.1%) received at least one dose before PHEIC (28.9% two doses, 4.2% one dose). After the PHEIC declaration at week 34, the number of weekly doses increased by a factor of 4.6. On 28 August 2024, 1,614 target persons remained unvaccinated or incompletely vaccinated. After text message reminders, 192 were vaccinated within 14 days and 316 by 23 September. Final PrEP coverage was 49.9% with at least one dose and 33.5% with two doses.

CONCLUSIONS

Targeted vaccination efforts in the Valencian Community increased coverage among high-risk populations. The expansion of sites, the establishment of referral pathways and the use of text message reminders were effective in improving vaccination rates. Weekly evaluations will continue, and additional electronic nudges for those receiving PrEP will be considered if uptake slows.

KEYWORDS: Mpox (monkeypox),Immunization Programs,Vaccination Coverage,Text Messaging,
Public Health Infrastructure
ABSTRACT ID: 786

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