ESCAIDE

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology 2014

Stockholm Waterfront Congress Centre
5–7 November 2014
Stockholm, Sweden

ecdc
EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

www.escaide.eu

European Scientific Conference on Applied Infectious Disease Epidemiology

The conference is sponsored by ECDC (European Centre of Disease Prevention and Control) and jointly organised by ECDC, EPIET (European Programme for Intervention Epidemiology), EAN (EPIET Alumni Network), TEPHINET EUROPE (Training Programmes in Epidemiology and Public Health Interventions NETwork)

Table of Contents

Foreword

Welcome to ESCAIDE 2014!

This year has put a sad mark in the history of public health worldwide with the largest ever outbreak of Ebola virus taking place in West Africa. The overwhelming number of cases has raised numerous questions not only on diagnosis, contact tracing and patient care but importantly on anthropological and social issues, and risk management. Thus, the ESCAIDE's session on Public Health Event of the Year 2014 will cover some of these aspects.

Since last year the European Union has a new legislation on serious cross-border health threats. What this means in terms of Europe's ability to combat infectious diseases is covered by this year's Conference as we will hear from both risk assessors and risk managers.

As we continue to see emergence and spread of new microbes, novel approaches to disease surveillance, prevention and control are becoming more pertinent. At the same time, old diseases are unfortunately not yet a closed chapter. Thus, ESCAIDE 2014 will host talks on the new (e.g. next generation surveillance of foodborne diseases) and the old (e.g. tuberculosis, measles and other vaccine-preventable diseases).

Many thanks to you who submitted abstracts. It is your work that builds the core of the Conference irrespective of whether your submission was successful or not. Unfortunately we cannot give visibility to all submitted abstracts but we wish to give you all the appreciation you deserve for your hard work and encourage you to continue to submit your work to ESCAIDE.

As in previous years, we are honoured to have as reviewers leading experts in the field. Their dedication to the quality of the Conference is exceptional and I would like to sincerely thank them on behalf of ESCAIDE's Scientific Committee and all of the event's organisers.

Congratulations to all graduating EPIET and EUPHEM fellows and best wishes for their continued professional development.

I would like to warmly welcome all of you at ESCAIDE 2014, where we can review together the success stories and remaining challenges for infectious disease surveillance in Europe and beyond. In addition to being a scientific conference, ESCAIDE is also a networking and social event. With the expertise and experience that you all are bringing, you will make ESCAIDE 2014 a get-together of outstanding experts, fascinating speakers, experienced colleagues and trusted public health professionals!

Dr Andrea Ammon
Chair, ESCAIDE Scientific Committee

Conference Co-organisers

The European Centre for Disease Prevention and Control (ECDC) is an agency of the European Union whose mission is to identify, assess and communicate current and emerging threats to human health posed by infectious diseases. The core activities of ECDC include surveillance and early warning; collection, evaluation and dissemination of relevant scientific and technical data; provision of scientific opinions and assistance, including training. Regarding training, the aim of the Centre is to support and coordinate training programmes in order to assist Member States and the Commission to have sufficient numbers of trained specialists, in particular in epidemiological surveillance and field investigations; and to have a capability to define health measures to control disease outbreaks. Hence, ECDC is the lead behind the European Programme for Intervention Epidemiology Training (EPIET) and the EU Public Health Microbiology training programme (EUPHEM).

Another key activity of ECDC is the exchange of information, expertise and best practices, for which ESCAIDE is an effective channel.

As the Director of ECDC, I am proud of the continued success of ESCAIDE and glad that ECDC is able to support it. Over the years, ESCAIDE has proven to be a unique, interactive platform for public health professionals to discuss the latest in applied infectious disease epidemiology: from outbreak investigations and surveillance, to novel methodologies, antimicrobial resistance, vaccine effectiveness, prevention programmes and much more. The Conference is an independent forum, welcoming participation and contribution from epidemiologists, microbiologists, public health scientists, and anyone else working in the area of communicable disease prevention and control and keen to share new findings, expertise and ground-breaking ideas. I look forward to discussing these with you at ESCAIDE 2014!

Dr. Marc Sprenger, ECDC Director

EPIET associated programmes and EUPHEM have been working closely with ESCAIDE as the conference initially started as an annual scientific meeting in relation with the fellowships. ESCAIDE is a key mechanism for fellows to integrate with the scientific community working on infectious diseases in Europe through participation in the conference and presentation of their field work. Ebola reminded us this year in the hardest way of the importance of field epidemiology and public health microbiology and we hope that this conference can be an opportunity to emphasize the need to generate evidence for action from the field, by the field and for the field.

Dr. Yvan Hutin & Dr. Aftab Jasir, EPIET & EUPHEM coordination

During the course of their EPIET/FETP/EUPHEM fellowship, fellows build strong networks both within and between the cohorts, fulfilling one of the purposes for which EPIET was originally built. But after those two years? How can fellows maintain such links once their official training programmes are over? This question led to the establishment of the EPIET Alumni Network (EAN) in 2000, which has now expanded to include EU FETP and EUPHEM alumni as well.

The EAN continues to grow each year, aiming always to assist in the maintenance of the network, share and exchange professional experiences, constitute and assure access to a pool of expertise, promote and deliver ongoing training for alumni, provide support to current fellows, and to contribute to both the logistical and scientific organisation of ESCAIDE.

The EAN President sits on the ESCAIDE Scientific Committee, but this is just one of the many activities of the network. The EAN board provides travel grants to our colleagues from low income countries; awards prizes for the best oral and poster presentations; and has also run a highly popular “photo from the field” competition over the past few years. None of these activities would be possible without the dedication of our members, who volunteer their time, ideas, and boundless enthusiasm to ensure that, year on year, these activities are a success.

ESCAIDE provides EAN members with the opportunity to interact with one another. We all know how easy it is to lose touch, despite social networking platforms now available, and ESCAIDE is one highlight in the calendar at which members have the opportunity to catch up face to face. We hold our General Assembly during ESCAIDE, to which all members and current fellows are invited. Decisions affecting the network are made here, including the introduction and voting in of the new board.

We greatly anticipate ESCAIDE from year to year, knowing that it provides us the opportunity to meet new fellows, catch up with old (!) friends, and maintain those strong links between the growing family of field epidemiologists and public health microbiologists to which we belong.

ENJOY!

Naomi Boxall, President of the EPIET Alumni Network (EAN)

In response to the need to develop their public health capabilities and infrastructure, several countries and regions have developed field-based training programmes in applied epidemiology and public health. The main aim of these training programs is to foster the development of field-trained epidemiologists who are competent in the practical application of epidemiologic methods to a wide range of public health problems.

Various models of field-based training programs exist, e.g. the Epidemic Intelligence Service of the U.S. Centers for Disease Control and Prevention, Field Epidemiology Training Programs (FETPs) and field epidemiology and laboratory training programmes (FELTPs). Besides several national FETPs in the European WHO region there are four regional programmes: the European Programme for Intervention Epidemiology Training (EPIET), the European Programme for Public Health Microbiology Training (EUPHEM), the Central Asian and the South Caucasus Programmes.

Regardless of the model, all of them subscribe to the maxim of “training through service.” FETP and FELTP fellows are trained in a set of core competencies that are vital to the practice of public health, while providing a valuable public health service to their countries and regions.

As the result of a global initiative to establish a more formal network of FETPs the “Training Programs in Epidemiology and Public Health Interventions Network” (TEPHINET) was created in 1997, and today consists of 59 FETPs and FELTPs in 85 countries around the world. TEPHINET aims to build a global community of field epidemiologists and laboratorians and to strengthen international public health capacity by supporting the training of field epidemiologists through training and service and networking opportunities.

International scientific conferences are important opportunities for sharing information and achievements among FETP and FELTP fellows, graduates, supervisors and other public health professionals. Overall, these conferences are an opportunity to learn from the experience of others and to acquire new ideas and skills that can be put into action.

As every year TEPHINET has participated in the organization of ESCAIDE and wishes all the participants an inspiring conference with interesting presentations and discussions relevant for your work.

Dr. Katharina Alpers, TEPHINET European Regional Director

Scientific Committee

Andrea Ammon – ECDC, Chair of ESCAIDE Scientific Committee

Andrea is the Deputy to the Director and Head of Resource Management and Coordination Unit at the ECDC. Prior to joining ECDC, Andrea served in several roles at the Robert Koch-Institute, in Berlin, Germany, most recently as Head of Department for Infectious Disease Epidemiology. She has published over 90 peer-reviewed journal articles related to her work.

Johan Giesecke – Karolinska Institute, Sweden

Johan is a Professor of Epidemiology at the Karolinska Institute, Sweden, and the first Chief Scientist at the ECDC, a position he held from 2005 until his recent retirement in September 2014. From a background as an infectious disease clinician, his research interests include: epidemic modelling, HIV/STIs and late sequelae of acute infections. He has published some 150 scientific papers, has written a textbook on infectious disease epidemiology and co-edited another.

Naomi Boxall – President of the EPIET Alumni Network (EAN).

Naomi is a Senior Epidemiologist at Mapi since 2013, having left Public Health England, where she had been for 6 years. From a background that includes a PhD in veterinary epidemiology supported by a biochemistry and genetics undergraduate degree, her research interests now include non-infectious topics to supplement previous experience in gastrointestinal and health-care acquired infections. As president of the EAN board, she represents the vast alumni of EPIET, EU-FETP and (now) EUPHEM on the scientific committee and remains committed to training in field epidemiology.

Aftab Jasir – ECDC/EUPHEM

Aftab is an associate professor, expert public health microbiologist and chief scientific coordinator of European Public Health Microbiology training programme (EUPHEM) at ECDC. In addition to many years professional work as a university teacher and coordinating European projects, Aftab has worked in many public health bodies/organisations (including Lund University hospital, Sweden; HPA, UK and CDC, US). Specialisations include health care associated infections and antibiotic resistance, monitoring and evaluating QA/QC systems, molecular typing, and vaccine and antimicrobial drug development. Aftab is a member of many scientific societies and international advisory boards.

Ines Steffens – ECDC

Ines is the Editor-in-Chief of Eurosurveillance journal. Ines joined ECDC in 2006 as Managing Editor for Eurosurveillance, and between 2007-2011 set up ECDC's Scientific Communication Section. Before Joining ECDC, Ines was Editor-in-Chief for Germany's national epidemiological and public health bulletin, the Epidemiologisches Bulletin at Robert Koch Institute, Berlin, Germany. Ines is a trained internist, with broad clinical experience and expertise in infectious diseases. She holds a masters degree in public health, and has a special interest in communication-related issues.

Howard Needham – ECDC

Howard is the Scientific Liaison Officer at the ECDC. Since 2008, Howard has been coordinator of the ESCAIDE conference and scientific programme under the ESCAIDE Scientific Committee. Howard has a background in biological sciences and has held policy roles in the UK Government and the European Commission in animal health issues and zoonoses, including notably transmissible spongiform encephalopathies and avian influenza. Howard joined the ECDC as the influenza programme coordinator in 2006, and took up his current position in 2008.

Panayotis T. Tassios – University of Athens, Greece (ESCMID representative)

Panayotis is Associate Professor in Molecular Microbiology at the National & Kapodistrian University of Athens, Greece. His research focuses on the molecular typing of bacterial strains and their antimicrobial drug resistance mechanisms, to assist epidemiological investigations and infection control. He is also active in lifelong teaching, on his scientific interests as well as on scientific writing, aided by his experience as Associate Editor of several journals. Panayotis represents the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) on the Scientific Committee.

Mira Kojouharova – NCIPD, Bulgaria (AF Representative)

Mira is the Deputy Director of the National Centre of Infectious and Parasitic Diseases (NCIPD) in Sofia, Bulgaria, and Head of the Epidemiology and Communicable Disease Surveillance Department. Mira holds a professorship, and leads research and teaching in the field of post-graduate education in epidemiology, surveillance and control of communicable diseases and practical work related to the surveillance of communicable diseases in Bulgaria. Mira's research interests are particularly focused on influenza and acute respiratory diseases in adults and children, poliomyelitis and viral hepatitis. Mira is an ECDC Advisory Forum (AF) member, and represents the AF in the ESCAIDE Scientific Committee.

Scientific Committee

Arnold Bosman – ECDC

Arnold is a Public Health Specialist, trained in The Netherlands, focused on providing specialised training in Intervention Epidemiology to public health professionals. He is a member of the EPIET Scientific Conference committee. Currently he is a manager of Public Health Training at ECDC aiming to establish an effective network of training in applied public health (e.g. epidemiology, public health microbiology) in order to strengthen the work force in the EU.

Thea Kølsen Fischer – SSI (NMFP representative)

Thea is a public health virologist heading the Virology Surveillance and Research Unit at the Statens Serum Institut (SSI) and a Professor in Global Health and Inf. Dis. Thea's research has focused on global high-incidence viruses such as influenza, EVs and rotavirus combining epidemiology, molecular profiling and vaccinology. She is specialised in epidemiology and laboratory outbreak management as an EIS Officer at CDC (2003-2005). Thea represents the ECDC National Microbiology Focal points (NMFP) in the ESCAIDE Scientific Committee.

Andreas Jansen – ECDC

Andreas is a medical doctor who worked as an infectious disease clinician and HIV specialist in Germany. From 2005-2006 he was a FETP fellow at the Robert Koch Institute in Berlin, and he joined ECDC in 2009. He is currently the Head of the Scientific Advice Coordination Section at ECDC, responsible for scientific advice procedures and methodologies, and for evidence-based public health.

Yvan J Hutin – ECDC/EPIET

Yvan is the Chief Coordinator of the European Programme for Intervention Epidemiology Training (EPIET). After an MD and a residency in hepato-gastroenterology, he joined the Epidemic Intelligence Service (EIS) of the United States' Centers for Disease Control and Prevention (CDC). As part of his public health career, he worked in Burkina Faso, Uganda and at the World Health Organization in Geneva, India and China. His areas of expertise include epidemiology and prevention of viral hepatitis and Field Epidemiology Training Programmes (FETPs).

Denis Coulombier – ECDC

Denis is a medical doctor, specialist in tropical diseases and in public health. He has an extensive international experience worldwide, including preparing for large sporting events in the field of communicable disease and response, acquired as a surveillance manager in 1996 Olympic Games in Atlanta, as a coordinator of public health surveillance and response in the 1998 FIFA world cup in France and as a WHO advisor for public health surveillance in the 2004 Athens Olympic Games. He joined the Epidemic Intelligence Service of the US Centres for Disease Control and Prevention in 1991 and subsequently worked in the Epidemiology Programme Office of the CDC in health. In 2000, Dr Coulombier was seconded to the World Health Organisation to lead the team in charge of epidemiology capacity strengthening. Since the start-up of the European Centre for Disease Prevention and Control (ECDC) in May 2005 and until March 2011, Dr Coulombier was the head of unit for preparedness and response and since April 2011 he is the head of unit for Surveillance and Response Support. The centre is established in Stockholm, Sweden.

Katharina Alpers – RKI, Germany (TEPHINET representative)

Katharina is the Coordinator for the Postgraduate Training for Applied Epidemiology (PAE), the German Field Epidemiology Training Programme (FETP) and is based at Robert Koch-Institute (RKI) in Berlin. She is currently representing all European FETP in the advisory board of the global FETP network called TEPHINET (Training Programs in Epidemiology and Public Health Interventions Network). Katharina represents TEPHINET in the ESCAIDE Scientific Committee.

Fortunato (Paolo) D'Ancona – ISS, Italy (ETSF representative)

Paolo is a Doctor and Communicable disease epidemiologist at the National Centre for Epidemiology, Surveillance and Health Promotion at the Istituto Superiore di Sanità, Italy. Among several activities, he leads the Italian Network on the surveillance of antimicrobial resistance, and is project leader for the VENICE III project that support vaccine programmes in the EU. Paolo is also training site supervisor for the EPIET programme at Istituto Superiore di Sanità, and is Chair of the EPIET Training Site Forum (ETSF). Paolo represents the ETSF in the ESCAIDE Scientific Committee.

Marc Struelens – ECDC

Marc is the Chief Microbiologist at ECDC. He is former President of the European Society of Clinical Microbiology and Infectious Diseases, and Professor of Medical Microbiology at the Faculty of Medicine of the Université Libre de Bruxelles (ULB) in Belgium. Marc has authored over 200 peer-reviewed articles and 20 book chapters across many disciplines, including molecular epidemiology, control of nosocomial infections, and antimicrobial resistance. He has served as editor of several international scientific journals, been a member of several national and international advisory boards, European Union (EU)-supported research and public health networks, and has served as consultant to the WHO and EU.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2014

Austria

Franz Allerberger
Michael Kunze

Barbados

Angela MC Rose

Belgium

Steven Van Gucht
Silvia Villanueva

Bulgaria

Anna Kurchatova

Canada

Jane Buxton
Lisa Jensen

Finland

Andreas Jacks
Satu Kurkela
Hanna Nohynek

France

Bruno Lina
Marta Valenciano

Germany

Katharina Alpers
Viviane Bremer
Florian Burckhardt
Sandra Dudareva-Vizule
Gerhard Falkenhorst
Christina Frank
Wolfgang Hautmann
Ioannis Karagiannis
Astrid Lewin
Elke Mertens
Matthias Niedrig
Norbert Schwarz
Dagmar Rimek

Greece

Maria Keramarou
Konstantinos Kesanopoulos
Georgia Mandilara
Nikoletta Mavroeidi
Kassiani Mellou
Andreas Mentis
Panayotis Tassios
Loukia Zerva

Hungary

Ivelina Damjanova
Emese Szilágyi

Latvia

Irina Lucenko

Lithuania

Rūta Jankauskienė

Luxembourg

Cinthia Menel Lemos

Malta

Charmaine Gauci
Tanya Melillo

Norway

Ingeborg Aaberge
Preben Aavitsland
Hanne Nøkleby
Line Vold

Sweden

Anders Wallensten
Anders Tegnell
Claes Schalen
Katherina Zakikhany
Birgitta Lesko

Switzerland

Olivier Ronveaux

The Netherlands

Roel A Coutinho
Ellen Stobberingh
Marianne van der Sande

United Kingdom

Naomi Boxall
Paul Crook
Lorraine Doherty
Leticia Franco
Olivier le Polain
Jim McMenamin
Irvine Neil
Christopher J Williams

USA

Peter Gerner-Smidt
Richard Goering

China

Lijie Zhang

Cyprus

Sophia Kyradji

Czech Republic

Jozef Dlhy

Denmark

Thea Kølsen Fischer
Kåre Mølbak

Estonia

Kuulo Kutsar

Iceland

Karl Kristinsson

Ireland

Martin Cormican
Darina O'Flanagan

Italy

Fortunato D'Ancona
Loredana Ingrosso
Domenico Martinelli
Annalisa Pantosti
Giovanni Rezzay
Paola Mastrantonio

Kazakhstan

Simon Ajeilat

Lao People's Democratic Republic

Sabine Dittrich

Poland

Rafał Gierczyński
Magdalena Rosinska
Ewa Sadowy

Portugal

Giraudon Isabelle
Ana Maria Correia
Ricardo Mexia
Raquel Saleao

Romania

Anda Baicus
Maria Damian
Codita Irina
Adriana Pistol
Florin Popovici

Slovakia

Henrieta Hudečková

Spain

Israel Cruz
Zaida Herrador
Mira Kojouharova
Silvia Herrera Leon
Francisco Nogareda

ECDC

Cornelia Adlhoch
Barbara Albiger
Andrea Ammon
Sabrina Bacci
Julien Beaute
Arnold Bosman
Paloma Carrillo-Santisteve
Niklas Danielsson
Helena de Carvalho Gomes
Birgitta de Jong
Irina Dinca
Dragoslav Domanovic
Erika Duffell
Assimoula Economopoulou
Graham Fraser
Johan Giesecke
Jolanta Griskeviciene
Karin Haar
Vahur Hollo
Frantiska Hruba
Yvan Hutin
Josep Jansa
Andreas Jansen
Kari Johansen
Pete Kinross
Saara Kotila
Pierluigi Lopalco
Howard Needham
V. Prikazsky
Emmanuel Robesyn
Polya Rosin
Ettore Severi
Otilia Sfetcu
Gianfranco Spiteri
Ines Steffens
Marc Struelens
Carl Suetens
Edit Szegedi
Lara Tavoschi
Wim Van Bortel
Klaus Weist
Robert Whittaker
Phillip Zucs

Invited Speaker Biographies

Plenary Session A: Key Note Address Close encounters of the “third kind”: pathogens, globalisation and politics

Dr Ilaria Capua,
Istituto Zooprofilattico Sperimentale delle Venezie, Italy

Ilaria Capua, DVM, PhD trained as a veterinarian and has worked ever since graduation as a virologist. She currently sits in Italy’s Parliament since the general elections of February 2013. Until then she was Director of the Division of Comparative Biomedical Sciences at the Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, (Padova, Italy) which hosts the National OIE/FAO Reference Laboratory for Avian Influenza and Newcastle Disease, the OIE Collaborating Center for Diseases at the Human-Animal interface and the FAO Reference Center for Rabies. Her group of 70 staff provides diagnostic assistance at a national and international level and is involved in cutting edge research on influenza viruses and viral zoonoses. Her group collaborates with major research institutes worldwide and has developed international collaborative projects aiming at capitalising on investments for capacity building in developing countries.

She has authored over 200 publications in peer reviewed journals and has published scientific books on Avian Influenza and Newcastle disease and books on careers in science for the general public. She is active in the field of science communication and in promoting female leadership in the scientific arena.

She has been coordinator or partner in several EU funded projects (FP5, FP6, FP7), has coordinated the EFSA FLURISK project, and obtained funding for twinning and trianing/research projects from OIE and FAO.

In 2006, she ignited an international debate on the sharing of genetic information on panzootic H5N1 strains across disciplines. Her advocacy of increased openness was endorsed by OIE, FAO and WHO, and resulted in resolutions towards a greater transparency to achieve improved collaboration between public and animal health in the face of a pandemic threat.

In 2007 Ilaria Capua was among the awardees of the Scientific American 50 award for leadership in science policy, and in 2008 she was included among Seed’s Revolutionary Minds series, for her leadership in promoting sharing of information at an international level. Other international awards include the Penn Vet World Leadership in Animal Health Award in 2011, and the Gordon Memorial Medal in 2012.

In 2014 she was the recipient of the ESCMID Excellence Award for clinical microbiology and infectious diseases.

Plenary Session B: Would Robert Koch still be interested in TB in Europe in 2014?

Dr Kristin Kremer
RIVM, The Netherlands

Dr. Kristin Kremer (PhD) currently coordinates the Bacteriological Serology Diagnostics at the department of Bacteriological and Parasitological Diagnostics of the Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands.

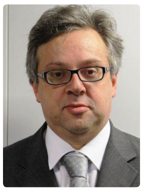
Kristin has over 17 years of experience working at the National Tuberculosis (TB) Reference Laboratory in the Netherlands, which also functioned as a World Health Organization (WHO) Supranational Reference Laboratory. Her fields of expertise include molecular epidemiology of TB, new TB diagnostics and the phylogeny of TB; she has over 140 publications in peer-reviewed journals on these subjects. For three years she worked at the TB and M/XDR-TB Programme of the WHO, Regional Office for Europe in Denmark, where she was responsible for the coordination of the TB laboratory network in the WHO European Region and the organization of drug resistance surveys.

Dr Alistair Story
TB Screening Service Find & Treat, London, UK

Al Story is founder and Clinical Lead of the pan-London Find&Treat Service based out of University College London Hospitals. His core expertise is in tackling communicable diseases among homeless people, drug and alcohol users, prisoners and destitute migrants. His research interests include outreach, integrating point of care diagnostics on the street, case management, the inclusion of service users within MDTs and the use of mobile internet technologies to promote engagement with health services and treatment continuity. He is an original member of the Faculty for Homeless and Inclusion Health and the Pathway Team and lecturer with the Department of Infection and Population Health at University College London.

Invited Speaker Biographies

Plenary Session C:
Cross border threats: approaches to identify and contain multi-state or cross-border outbreaks



Mr Martin Seychell,
European Commission, Health & Consumers Directorate-General

A graduate in chemistry and pharmaceutical technology, Mr. Seychell specialized in Chemical analysis. He has held important positions on several government boards and commissions in Malta, including the Food Safety Commission and the Pesticides Board. Mr Seychell occupied the post of Head of Directorate at the Malta Standards Authority between 2001 and 2006. He has been responsible for the implementation of a number of EU directives in the areas of risk assessment, food safety, chemicals and cosmetic products legislation, and has actively participated in negotiations on major technical proposals such as the new chemicals legislation, REACH, and in screening processes in the areas of free movement of goods, environment and agriculture during the process leading to Malta's accession to the EU. He held the post of Director of Environment in Malta between 2006 and 2011. As Director, he was responsible for a broad range of functions arising from the Maltese Environment Protection Act. He was appointed Deputy Director General for Health and Consumers at the European Commission in March 2011.

Plenary Session D:
Primum non nocere – Why engineer microbes to be more dangerous to humankind

Dr Filippa Lentzos
Kings College London, UK

Dr Filippa Lentzos is a Senior Research Fellow in the Department of Social Science, Health and Medicine at King's College London. Her work focuses on social, political and security aspects of the life sciences, and she is particularly interested in contemporary and historical understandings of the threat of biological weapons, bioterrorism and the strategic use of infection in conflict.

www.filippalentzos.com

Dr Simon Wain-Hobson, Pasteur Institute, France

Simon Wain-Hobson comes from a family of artists and went into science in part to do something different! He obtained his DPhil in biophysics from the University of Oxford. During a post-doc at the Weizmann Institute in Israel he met his French wife and moved to Paris where he switched to human virology, working notably on the AIDS virus HIV, from the earliest hour. Being the first to publish its genetic map his group went on to show that it evolved from a chimpanzee virus. They highlighted with exquisite precision the phenomenal genetic variation and rapid evolution of HIV. After more than 25 years work with the AIDS virus his group found a remarkable connection that allowed them to move into cancer research - cancer genomes harbor tens of thousands of mutations. The Pasteur group showed that humans encode a DNA mutator enzyme, APOBEC3A, which can mutate chromosomal DNA. It is now accepted that this enzyme is a human mutagen on a par with ultraviolet light and cigarette smoke. He is Professor at the Institut Pasteur and has published more than 200 papers. A member of the European Molecular Biology Organization, Academia Europaea, he is Director of the French papillomavirus reference laboratory. He won the André Lwoff prize in 1996 and Athena prize from the French Academy of Sciences in 2007 and is Officier de la Légion d'Honneur. He is presently Board Chair of the Foundation for Vaccine Research in Washington DC. He collects 18C English drinking glasses and publishes on the subject.

Invited Speaker Biographies

Plenary Session E:
Whole genome powered next generation surveillance of foodborne disease

Dr Peter Gerner-Smidt, CDC, Atlanta, USA

Dr. Peter Gerner-Smidt is a Danish MD, ScD with specialty in clinical microbiology. He is the chief of the Enteric Diseases Laboratory Branch in the Division for Foodborne, Waterborne and Environmental Diseases at Centers for Disease Control and Prevention in Atlanta, United States.

Before moving to the United States in 2004, he was the Head of the Danish Reference Centre for Enteric Pathogens and Listeria at Statens Serum Institut in Copenhagen. His research interests are the epidemiology, including subtyping and identification of foodborne, zoonotic and enteric bacterial pathogens. He has co-authored more than 100 papers in peer-reviewed scientific journals, the majority dealing with bacterial taxonomy, identification, epidemiology, and subtyping.

He is leading the effort to implement whole genome sequencing for surveillance of bacterial foodborne infections at CDC and involved in its implementation globally through the Global Microbial Identifier initiative, PulseNet International and the WHO-GFN.

Dr Kathie Grant, Public Health England, UK

Dr Kathie Grant is an internationally recognised expert in foodborne pathogens with 30 years experience in clinical and public health microbiology combined with a strong track record in research. She is head of the Public Health England Gastrointestinal Bacteria Reference Unit at Colindale, London which is the national reference laboratory for a range of foodborne pathogens including Salmonella, E. coli VTEC, Campylobacter, Listeria monocytogenes and Clostridium botulinum. Since joining the laboratory in 2001 she has championed the use of molecular methods which has lead to improvements in the detection and investigation of bacterial foodborne disease within the UK. Her research interests, which include the development of rapid methods for the detection and characterisation of foodborne pathogens, are currently focused on exploiting whole genome sequencing of bacterial pathogens to improve the understanding and control of foodborne disease.

Dr Eva Møller Nielsen, SSI, Denmark

Eva Møller Nielsen, MSc and PhD in microbiology (1992), head of unit of Foodborne Infections, Statens Serum Institut, Denmark. With a background in the veterinary/food section, she moved to public health in 2003 and took the lead of the laboratory-based surveillance of zoonotic and foodborne bacterial infections in Denmark. She is national contact point for Food and Waterborne Diseases of ECDC, European representative in PulseNet International, contractor for ECDC in relation to the TESSy Molecular Surveillance System involving the curation of databases, cluster detection, and organisation of EQA programmes for molecular typing methods for Salmonella, Listeria and VTEC. She has been project leader and participant in several national and European research projects. Her team has played a central role in the international harmonization of typing methods for foodborne bacteria. The last few years, focus has been on implementation of whole genome sequencing to replace conventional typing of bacteria for surveillance and outbreak investigations.

Plenary Session **Abstracts**

This abstract book has been produced using authors supplied copy. Editing has been restricted to some corrections where appropriate. The information in each abstract is the responsibility of the author(s).

Plenary Session **Abstracts**

Plenary Session A 09.00 – 10.30 Wed 5

Plenary Session A: Keynote

Close encounters of the “third kind”: pathogens, globalisation and politics

Presented by:

Dr Iiaria Capua

Affiliation:

DVM, PhD, Member of the Italian Parliament

Abstract

Our globalised environment supports the unprecented spread of pathogens. Human-to-human transmission (close encounters of the “first kind”) with pathogens that are well adapted to the human host causes local and global disease spread. Similarily, pathogen transmission between animals (close encounters of the “second kind”) occur both within and between farms, and is often linked to the trade of commodities, live animals and vector distribution. Close encounters of the “third kind” are those that enable pathogens within the animal reservoir to cross the species barrier and infect humans. Global movement of infected people or animals cause continuous outbreaks of emerging infectious diseases that may be very distant from the index case. This has occurred globally with pandemic viruses such as HIV and influenza (H_1N_1), and to an extent with Ebola and (to date) the MERS coronavirus.

Prompt identification and subsequent management of these outbreaks is essential. Initiatives to support sharing of diagnostic reagents, virus strains and sequences in a timely manner will enable the scientific community to advance its understanding more efficently, but their success is dependant on the willingness of scientists to contribute their tools and data.

Another essential issue is the optimisation of the scientific community to communicate with stakeholders; the development of close encounters of the “first kind” is central to the engagement of the general public in science and health. Scientists also need to to engage with colleagues operating in parallel disciplines (close encounters of the “second kind”) to cross-fertilize and expand their knowledge. Close encounters of the “third kind”concern communication between scientists and politicians and are perhaps the most critical link in the communication chain if operational change is to be achieved in disease management at the global level. This is the the interface where science can be translated into policy initiatives. However, politicians do not base their decisions on the same dataset as health professionals and this causes a misalignment with the priorities of the scientific community. Politicians’ decisions are influenced by newspaper headlines, the interests of their constituencies, citizen’s protests and lobbying by special interest groups. Thus, a disease outbreak with the potential to become a major health issue which is well managed and does not evolve into a troublesome public health event is perceived by the media as a hoax or the result of a conspiracy between scientists and multinational pharma.

Scientists and healthcare workers often achieve great results with the identification and diagnosis of novel pathogens. However media coverage of the potential escape of a virus from a laboratory, the risk of gain of function experiments with H_5N_1 viruses or the latest news questioning the efficacy of Tamiflu, saturate the interest of the political establishment, and above all lead to cuts in funding, shaking the credibility of the scientific community as a whole. This dilutes focus and results in a misdirection of efforts.

It would beneficial for the scientific community to better understand and communicate with the political environment and be proactive in rejecting conspiracy theory or hoax accusations. Doing so would bring added value and would enable the medical research community to improve the outcome of their efforts, with positive consequences for public health as a whole.

Plenary Session B 16.30 – 18.00 Wed 5

Plenary Session B: Would Robert Koch still be interested in TB in Europe in 2014?

Public health relevance of molecular surveillance of tuberculosis in Europe

Presented by:

Dr Kristin Kremer

Affiliations:

Centre for Infectious Diseases Research, Diagnostics and Screening, Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands

Abstract

For a long time after Robert Koch first discovered Mycobacterium tuberculosis it was thought that there were only a few strains of M. tuberculosis. This rapidly changed in the 1990s when molecular typing methods for tuberculosis were developed. Worldwide standardization of these methods identified numerous strains of M. tuberculosis and genotype families resulting from clonal expansion of particular strains. Currently, molecular surveillance is routine practise in many European countries and occasionally genome sequencing is used to study transmission of tuberculosis.

Molecular surveillance of tuberculosis in the Netherlands has contributed significantly to the understanding of the epidemiology of this pathogen in the country. It was useful to detect outbreaks of tuberculosis, but it also disclosed that for many TB cases that were clustered based on DNA-typing, traditional contact tracing could not confirm a link between the cases. Furthermore, laboratory cross-contaminations were identified and it was disclosed that isoniazid resistant strains were as transmissible as drug susceptible strains. Cluster data guided local TB programmes to initiate targeted interventions to prevent further transmission in particular risk groups. Finally, predictors of large clusters were identified and these can be used to determine which measures are needed to control further spread of tuberculosis when a new outbreak is detected.

Molecular surveillance of multidrug-resistant tuberculosis (MDR-TB) in Europe showed that 85% of the international transmission of MDR-TB was caused by a few strains of the Beijing genotype, whereas, only 5% of drug susceptible cases represent this genotype. Research into the genetic and epidemiological background of these strains is ongoing. Quality control is essential while comparing DNA patterns from different countries and next steps should be taken to facilitate cross-border cluster investigations.

Key words: tuberculosis, molecular epidemiology, DNA typing, MDR-TB, transmission

Urban TB

Presented by:

Dr Alistair Story

Affiliation:

TB Screening Service Find & Treat, London, UK

Abstract

Koch's seminal proof of the aetiology of tuberculosis made it possible to regard this captain of all the men of death as avoidable. Old prejudices made way for the real prospect of prevention and cure, with all efforts directed to the containment of contagious consumptives and slaughter of their bacilli. Koch's brilliance displaced prevailing theories on the socio-economic character of tuberculosis and inadvertently obscured the central role of poverty and exclusion in shaping its epidemiology – both then and now.

This Plenary presentation will explore the modern challenges of tuberculosis control in major metropolitan centres and chart the evolution of the Find&Treat service from active case finding through to the development of a successful social determinants model of care. Services working with homeless and vulnerable tuberculosis patients must look beyond microbiological cure and address the social factors that predispose individual to disease and sustain transmission in our communities.

Plenary Session **Abstracts**

Plenary Session C 08.30 – 10.00 Thur 6

Cross-border threats: approaches to identify and contain multi-state or cross-border outbreaks

No abstracts available for this session at time of printing

Plenary Session D 16.40 – 18.10 Thur 6

Primum non nocere – Why engineer microbes to be more dangerous to humankind

People not Pathogens

Presented by:

Dr Simon Wain-Hobson

Affiliation:

Institut Pasteur, Paris

Abstract

Virology is the outsider in biology because of unsurpassed diversity. There are more viruses than cells on the planet. They can switch hosts and pick up genetic material around them. Recently virologists have started to test a pro-active mode of research; is it possible to anticipate the next severe outbreak or even pandemic? To do this requires predicting the next strain. For flu, the experiment is to select avian influenza viruses that are readily transmissible between ferrets, which is considered to reflect this property of human pandemic influenza viruses. One study generated a transmissible virus with a 30x greater case fatality rate compared to Spanish flu. The claims that the information gleaned will help us develop vaccines and drugs that will “nip in the bud” a future pandemic are simply false.

Our track record in predicting human pandemics including influenza, or even outbreaks, is not good. There are ›120 avian virus combinations of the hemagglutinin and neuraminidase, and a multitude of strains for each, such that the options are enormous. On top of which, scientists exaggerate with titles like “H10N8, the next pandemic strain?” – there have only been 3 H10N8 dead end human infections to date. With finite resources, which are glaringly insufficient to solve the Ebola problem, we are going to loose our bearings fast.

From the time of Pasteur and Koch our community has been trying to demolish viruses and bacteria. This pro-active microbiology, termed gain of function research carries with it a biosafety risk, albeit non-zero, but of catastrophic consequences if ever there was an accident. Why engineer such viruses if they can’t deliver robust results? That is the question.

Key words: Avian influenza, gain of function research, non-zero risk, catastrophic consequences

The threat of manufactured disease

Presented by:

Dr Filippa Lentzos

Affiliation:

Department of Social Science, Health and Medicine, King's College London

Abstract

This talk addresses the "Why engineer microbes to be more dangerous to humankind" from the security angle. Bioterrorism, biological weapons and the fear of intentional disease have a long history and are not new thoughts – we knew how to spread disease before we understood the science behind it. I will briefly review some of this early history. I will also address the development of biological weapons in national military programmes of the 20th century, and I will consider what we currently know about terrorists' interest in biological weapons.

I will then turn to consider capability – the other half of the equation in any threat assessment – and I will consider whether advances in the life sciences, and particularly synthetic biology, are altering that equation. Is synthetic biology making it easier for non-experts to manipulate dangerous pathogens and, therefore, making it easier for terrorists to concoct bioweapons? Can non-experts use synthetic biology to design radically new pathogens? Contrary to the dominant narrative permeating scientific and policy discussions, I will argue, firstly, that synthetic biology is not making it easy for anybody to "engineer biology" and, secondly, that even experts have a hard time enhancing disease pathogens. Highlighting the many forms a bioweapon can take, however, I will argue that while there are significant barriers in place to develop complex biological weapons, there are few technical limitations on the crude use of them and the threat of manufactured disease cannot be discounted.

Plenary Session E 08.30 – 10.00 Fri 7

Whole genome powered next generation surveillance of foodborne disease

Controlled evaluation of whole genome sequencing for surveillance of foodborne infections in the United States

Presented by:

Dr Peter Gerner-Smidt

Affiliation:

Centers for Disease Control & Prevention, Atlanta, GA, USA

Abstract

Whole genome sequencing (WGS) has been used to facilitate investigations of food- and water-borne bacterial outbreaks since 2010 when it was used in conjunction with traditional methods to characterize Vibrio cholerae isolates associated with the cholera outbreak in Haiti.

WGS has been used in parallel with the existing gold standard, pulsed field gel-electrophoresis (PFGE), for laboratory surveillance and investigation of outbreaks of listeriosis since September 2013 in United States. More than 900 clinical isolates and 900 food isolates have been sequenced and analyzed in real-time. WGS was shown to be more discriminatory and provide better resolution than PFGE for outbreak detection and investigation, thereby enabling more efficient focusing of epidemiologic resources. Several outbreaks have been investigated successfully and it has been possible to link sporadic illness to food recalled because of Listeria contamination. Three different approaches have been tested to analyze the WGS data: kmer–analysis is a quick-and-dirty analytical approach that does not provide the same resolution as the high quality single nucleotide polymorphism (hqSNP) and whole genome multi locus sequence typing (wgMLST) approaches. The two latter approaches provide approximately the same resolution but the hqSNP approach does not lead to naming of the profiles and is therefore difficult to communicate unambiguously, whereas the wgMLST approach that builds on detecting allelic variation of the genes in the genome leads to definitive nomenclature and therefore is easy to communicate. Additionally, the gene information that is extracted with wgMLST may be used to predict reference characteristics of the pathogen (species identification, determination of the pathotype, serotyping, virulence characterization, antimicrobial resistance testing).

This observation has led us to begin implementing WGS in the reference characterization of all foodborne pathogens in addition to high discriminatory subtyping for outbreak detection. This way multiple traditional methods will be replaced by a single cost-efficient WGS workflow in the laboratory. WGS is now being implemented in a tiered manner beginning with Listeria, Campylobacter and Shiga toxin-producing E. coli (STEC), followed by Salmonella, Vibrio, and other foodborne bacterial pathogens. In order to succeed, it is critical that the databases and analytical platforms used for surveillance are standardized at the national and international level. Building the analytical platforms is a huge task that can only be achieved through international collaboration. In order to enhance epidemiological investigations it is also essential to create links between the databases containing the epidemiological information and the microbiological databases.

This will lead to a revolution of public health microbiology enhancing not just outbreak investigations but also investigations of the sources of sporadic illness and of the dynamics of foodborne illness.

Evaluation and implementation of WGS for surveillance of foodborne infections in Denmark

Presented by:

Dr Eva Møller Nielsen

Affiliation:

Statens Serum Institut, Copenhagen, Denmark

Abstract

In Denmark, the laboratory-based surveillance of foodborne infections caused by Listeria monocytogenes, Salmonella and Verocytotoxin-producing E. coli (VTEC) is performed by typing of all isolates from patients to detect clusters and link to potential sources. A number of different laboratory techniques such as serotyping, detection of virulence genes and high-discriminatory molecular typing methods are used for this purpose. The availability of new sequencing techniques has allowed for whole-genome-sequencing (WGS) of bacterial isolates to replace this variety of different methods.

It is our goal to implement WGS for surveillance of foodborne pathogens whenever this is feasible scientifically and economically, i.e. useful output and costs comparable to present methods. In 2013, we fully implemented WGS for surveillance of Listeria infections in replacement of PFGE. The past year, we have detected several small clusters with identical isolates or <10 SNP differences. In June-August 2014, a major outbreak of 38 listeriosis cases was detected and the food source was found by the use of WGS. We have used retrospective data for the evaluation of expected variability between epidemiologically linked isolates. For VTEC, our focus has been on extracting the virulence profile and the O:H-serotype. We have promising results for the majority of the relevant serotypes and expect to implement WGS as the routine analysis replacing serotyping, PCR and PFGE. For surveillance of salmonella infections, we perform WGS when clusters are detected based on serotype. Furthermore, WGS compared to MLVA is about to be evaluated for cluster analysis of Salmonella Typhimurium and its monophasic variant.

It is our experience, that WGS can already be used as a routine method for surveillance and outbreak investigations by applying a similar approach for most species. However, there is a need for more tailor-made solutions if backward comparability is wanted.

Keywords: Sequence Analysis, Molecular Typing, Disease Outbreaks, Listeria monocytogenes, Salmonella Infection, Shiga-toxigenic Escherichia coli

Kathie Grant’s abstract was not available at time of printing

Parallel Session **Abstracts**

This abstract book has been produced using authors supplied copy. Editing has been restricted to some corrections where appropriate. The information in each abstract is the responsibility of the author(s).

Parallel Sessions 1 – 3 11.00 – 12.40 Wed 5

Parallel Session 1: Novel methodological approaches for disease investigation, surveillance and control

Application of novel methods to assess the response capacity of front-line laboratories to influenza in the UK, 2013

Amy Mikhail[1], Joanna Ellis[1], Maria Zambon[1]

[1] Public Health England, United Kingdom

Abstract
Since 2005, an external quality assessment (EQA) exercise has been held annually for laboratories participating in the UK influenza molecular testing network. The primary objective is to ensure a robust national response network for influenza virus detection, where diverse real-time PCR assays are employed.

Abstract methods
We developed a novel method, “Qscore”, to evaluate both qualitative and quantitative accuracy in a single index and applied it to the results of the 2013 influenza EQA exercise. The panel, comprising 11 specimens representing diverse influenza A and B viruses was sent by Public Health England to 24 laboratories. Qscores were calculated based on the proportion of correct results, determined via an automated script which evaluated if PCR cycle thresholds (Ct) fell within the expected range for each specimen. Individual laboratory performance was graphically represented by plotting Cts against their deviation from consensus reference values.

Abstract results
21/24 laboratories using 17 different assays for primary typing reported qualitatively correct results for all panel specimens tested; of these 6 laboratories reported quantitative results outside the expected range, yielding Qscores of 73–92%. Difficulties at the haemagglutinin sub-typing level or the influenza A/B typing level were identified; particularly with a swine-origin H3N2 virus. Performance plots facilitated rapid visual identification of laboratories with global deficiencies in sensitivity (false negatives: Ct≥40, n=4) or specificity (false positives: Ct<40, n=2) compared to consensus reference values for each target.

Abstract conclusion
We have demonstrated the application of a novel quality scoring method that facilitates identification of laboratories that may require further technical support and characterises areas of difficulty. This method is applicable to any multi-assay EQA exercises where the primary results are quantitative and allows year-on-year comparisons of individual laboratory performance.

Keywords: External Quality Assurance exercise, UK influenza testing network,quality score, performance, plot response capacity, real-time, polymerase, chain reaction

PRESENTED BY: Amy Mikhail

ESCAIDE REFERENCE NUMBER: 20141989

Interpretations of associations: Assessing the plausibility of results found in a matched case-control study on sporadic human salmonellosis in Lower Saxony, Germany, 2011-2013

Sophie Rettenbacher-Riefler[1], Dagmar Ziehm[1], Lothar Kreienbrock[2], Amely Campe[2], Matthias Pulz[1], Johannes Dreesman[1]

[1] Governmental Institute of Public Health of Lower Saxony, Germany; [2] Department of Biometry, Epidemiology and Information Processing, WHO-Collaboration Centre of Research and Training in Veterinary Public Health, University for Veterinary Medicine, Hannover, Germany

Abstract
In Germany, about 20,000 human salmonella infections (25/100,000 inhabitants) per year are notified, the majority being sporadic cases with an unknown source of infection. To investigate potential risk factors for sporadic human salmonellosis we performed a case-control study among notified cases in Lower Saxony.

Abstract methods
For each case we randomly selected four potential controls matched for age, sex and geographical region from the population register. Data were collected by a self-administered questionnaire and analysed via conditional logistic regression.

Abstract results
Response rates were 60% (425 of 716) in cases and 28 % (800 of 2864) in controls. Analysis of 285 matched pairs revealed significant associations of salmonellosis with raw ground pork consumption (OR 6.0; 95% CI 2.2-20.1), intake of antacids (OR 5.8; 95% CI 1.4-24.5), eating meat at a restaurant (OR 5.7; 95% CI 2.2-14.6) and daily changing or cleaning of dishcloth (OR 2.1; 95% CI 1.2-3.9). Animal contact was significantly negatively associated with salmonellosis (OR 0.5; 95% CI 0.2-1).

Abstract conclusion
Besides corroborating previously identified risk factors, our data show that hygienic behaviour was more frequently reported by cases than controls. Furthermore, our findings suggest a lower risk of illness for people exposed to animals. As positive effects of salmonellae on immune defence have been reported occasionally, our observations appear biologically plausible. However, it seems also likely that case persons overestimated their hygiene behaviour retrospectively. We suggest possibilities how to handle a social desirability bias. Our findings illustrate that a sound interpretation of associations found in case-control studies as risk factors or protective effects also requires knowledge about pathogenesis of an infectious disease.

Keywords: Conditional logistic regression analysis, foodborne zoonosis, “Mett”, causality, pork, etiology

PRESENTED BY: Sophie Rettenbacher-Riefler

ESCAIDE REFERENCE NUMBER: 20141951

Transmission dynamic of MERS-CoV: Multiple imputation approach to estimate the date of onset

Hervé Le Perff[1], Vanina Bousquet[1], Laëtitia Vaillant[1], Sophie Allain-Ioos[1], Thierry Cardoso[1], Magid Herida[1]

[1] Department of the Coordination of Alert and Regional Offices – French National Institute of Public Health, France

Abstract

To understand Middle East Respiratory Syndrome coronavirus (MERS-CoV) outbreak, most of the epidemic curves are plotted using the World Health Organization (WHO) dates of notification (DON) because dates of onset of symptoms (DOS) are often missing. Our objective was to depict the epidemic trends based on the estimated DOS using a multiple imputation (MI) method to get a better picture of the dynamics of transmission.

Abstract methods

We focused on symptomatic and laboratory-confirmed cases notified to WHO between September 2012 and November 2013. Demographics data, symptomatic status, DON and DOS and other auxiliary information were collected when available. When DOS was missing, the delay between DOS and DON was estimated using a MI model; 100 databases were generated and analysed.

Abstract results

WHO notified 163 reported cases with 129 (80%) symptomatic cases, among which 46 (36%) had no DOS. After MI, median delay between DOS and DON was 15days (IC95: 10.8-19.2). MERS-CoV epidemic curve based on DOS suggests that the epidemic starts two weeks (Week 16-2013) before the peak observed in the curve based on DON (Week 18-2013). In addition, this new curve displays a second peak which was not observed in the curve based on DON.

Abstract conclusion

Our estimation shows that the median delay between DOS and DON is longer than the incubation period of the virus and provide new insights of the dynamics of transmission during the first year of MERS-CoV epidemic. When data on the first cases are sparse and this key information is missing, using estimations obtained through MI could provide useful and reliable estimates.

Keywords: MERS-CoV, multiple imputation, dynamic of transmission, date of onset

PRESENTED BY: Hervé Le Perff

ESCAIDE REFERENCE NUMBER: 20142114

Early detection of influenza activity using telephone helpline data

Ricardo Mexia[1], Carlota Louro[2], Baltazar Nunes[1], Teresa Contreiras[1], Carlos Matias[1]

[1] INSA – National Health Institute, Portugal; [2] S24, Portugal

Abstract

The annual influenza season is a recurring time period characterized by the prevalence of outbreaks of influenza. Early detection of these outbreaks is paramount to allocating resources and effective counter measures.

Abstract methods

Using data from the Portuguese health helpline we selected 17 triage algorithms that relate with the influenza case definition used by ECDC. We listed the weekly number of calls for each algorithm and the total number of calls to the counselling line, from week 40 to 20 (seasonal influenza) from 2010-2013. Data was then compared with data from the sentinel system (standard surveillance in Portugal) with up to 5 weeks lag, using a cross correlation function. Correlations above 0,5 were considered of interest. In parallel, the MEM – Moving Epidemic Method was applied to determine a baseline threshold for the beginning of the epidemic period.

Abstract results

We analysed 1.032.724 calls (an average of 10.432 calls each week), and the "cough algorithm" presented the highest correlation (0,83) to data from the sentinel network, with a 3 weeks lag. Using MEM, we were able to detect the beginning of the epidemic period 3 to 5 weeks in advance, comparing to data from the sentinel network.

Abstract conclusion

The baseline provided by the selected algorithms allowed, on average, three weeks of advanced warning for seasonal influenza activity. Using two techniques (cross correlation and MEM) we were able to detect early signs of seasonal influenza activity, specifically with influenza related symptoms, namely coughing.

Keywords: Population surveillance, influenza, baseline, threshold

PRESENTED BY: Ricardo Mexia

ESCAIDE REFERENCE NUMBER: 20142265

Effectiveness of interventions that apply new media to improve vaccine uptake and vaccine coverage: a systematic review

Carlo Signorelli[1], Antonio Ferrari[1], Francesca Spagnoli[1], Sara Visciarelli[1], Andrea Amerio[1], Anna Odone[1]

[1] University of Parma, Italy

Abstract

Vaccine-preventable diseases (VPD) are still a major cause of morbidity and mortality worldwide. In high and middle-income settings, immunization coverage is relatively high. However, in many countries coverage rates are below targets established by international and national boards. Progresses in communication technology might provide useful tools to enhance immunization strategies.

Abstract methods

We conducted a systematic literature review. Studies published from 1999 to September 10th 2013 conducted in countries members of the Organisation for Economic Co-operation and Development were identified by searching Pubmed and Embase, manual searches of references and expert consultation. We focused on interventions that targeted recommended vaccinations for children, adolescents and adults and i) aimed at increasing community demand for immunizations, or ii) were provider-based interventions. The primary outcome was vaccine coverage. Considered secondary outcomes included willingness to receive immunization and perceived helpfulness of the intervention.

Abstract results

Nineteen studies were included in the systematic review. The majority of the studies were conducted in the US (74%, n=14); 68% (n=13) of them were experimental. 11 (58%) reported results on the primary outcome. Retrieved studies explored the role of: text messaging (n.7, 37%), smartphone applications (n.1, 5%), Youtube videos (n.1, 5%), Facebook (n.1, 5%), targeted websites and portals (n.4, 26%), software for every health professional (n.4, 15%), and email communication (n.1, 5%). There is evidence that text messaging, accessing immunization campaign websites, using patient-held web-based portals and computerized reminders increase immunization coverage rates. Insufficient evidence is available on the use of social networks, email communication and smartphone applications.

Abstract conclusion

Although great potential for improving vaccine uptake and coverage by implementing interventions on new media, scant data are available and further research – including cost-effectiveness assessments – is needed.

Keywords: Vaccine preventable diseases; immunization; vaccine coverage; vaccine uptake; new media; social media; communication technology; interventions; systematic review

PRESENTED BY: Anna Odone

ESCAIDE REFERENCE NUMBER: 20142264

Parallel Session 2: Outbreaks (1)

Catering risky food to those at-risk: Salmonella Derby outbreak among the elderly in Berlin, December 2013/January 2014

Christina Frank[1], Dirk Werber[1], Mona Askar[1], Benjamin Bluemel[1], Wolfgang Rabsch[1], Claudia Simon[2], Daniel Sagebiel[2], Claudia Siffczyk[3], Heidi Wichmann-Schauer[4]

[1] Robert Koch Institute, Germany; [2] Berlin State Office for Health and Social Affairs, Infectious Disease Epidemiology and Environmental Health, Germany; [3] Brandenburg State Office of Environment, Health and Consumer Protection, Department of Health, Germany; [4] Federal Institute for Risk Assessment, Germany

Abstract

Hospital case clusters and notification data outbreak alerts indicated increased Salmonella (S.) Derby infections in Berlin and surrounding Brandenburg state in December 2013. Affected were very old patients in hospitals or elder care homes. In one hospital cluster, S. Derby was isolated from a retained sample of raw fermented pork spread ("teewurst") subsequently hypothesized as vehicle of infection.

Abstract methods

Cases had S. Derby/"Group B Salmonella" infections with disease onset 15 November 2013 through 31 January 2014 in Berlin/Brandenburg without travel history. The otherwise rare outbreak strain was typed as phage type 53, with specific PFGE and MLVA types. As cases were deemed unable to provide accurate food histories, epidemiologic investigations focused on case-ascertainment, identifying affected institutions, product tracing and an ecological study, testing associations between teewurst supply and case reporting on the institution level.

Abstract results

Overall 145 cases were ascertained (50% male, median age 76 years, 82% hospitalized, 1 death). In Berlin, 99 cases occurred in 40 institutions (including 21 hospitals), 85% of which had been clearly supplied with teewurst. Supplied hospitals in Berlin were 11 times more likely to report cases, than others (95% CI:3.5-33). All 13 hospitalized patients with available food documentation had been served teewurst 1-3 days pre-illness. S. Derby isolated from teewurst, the stools of 2 butchers producing the teewurst, and patients' stools were microbiologically identical. The outbreak ended shortly after a broad product recall by the teewurst producer on 9 January 2014.

Abstract conclusion

Despite clear recommendations against serving raw fermented meat products in institutional catering for vulnerable populations, the outbreak was likely caused by such a product specifically marketed to hospitals and elder care homes. The recommendation should be re-emphasized and actively communicated.

Keywords: Outbreak, foodborne, infections, salmonella, meat, vulnerable, populations, institutional, catering

PRESENTED BY: Christina Frank

ESCAIDE REFERENCE NUMBER: 20141992

A national outbreak of Salmonella Mikawasima in the UK, 2013: did proton pump inhibitors play a role?

Rachel Freeman[1], Gavin Dabrera[1], C Lane[1], Natalie Adams[2], Lynda Browning[3], Tom Fowler[4], Russell Gorton[4], Tansy Peters[5], Henry Mather[6], Philip Ashton[5], Gauri Godbole[5], Drazenka Tubin-Delic[7], Andre Charlett[1], Ian Fisher[2], Bob Adak[1]

[1] Public Health England, UK; [2] Centre for Infectious Disease Surveillance and Control (CIDSC), Public Health England, UK; [3] Health Protection Scotland (HPS), UK; [4] Field Epidemiology Services, Public Health England, UK; [5] Colindale Reference Microbiology Services, Public Health England (PHE), UK; [6] Scottish Salmonella Shigella and Clostridium difficile Reference Laboratory (SSSCDRL), UK; [7] Food Standards Agency (FSA), UK

Abstract

In November 2013, national public health agencies in England and Scotland identified an increase in laboratory-confirmed Salmonella Mikawasima, an uncommon serovar. Initial results from trawling questionnaires identified a high proportion of cases taking proton pump inhibitors (PPI), although the role of PPI in salmonellosis is still unclear from existing studies. The aim of our study, therefore, was to investigate the association between food and PPI usage with infection.

Abstract methods

An outbreak case was defined as infection in a person aged 18-65 years, who tested positive for S. Mikawasima between 01/10/2013-29/11/2013. We conducted a retrospective case-control study, estimating adjusted odds ratios (aOR) and 95% confidence intervals (CI) using multivariable logistic regression. We compared a case with two controls, frequency-matched by sex and reporting region, selected from staff members working for national public health agencies in regions affected by this outbreak. Data were collected from individuals via telephone interview.

Abstract results

Thirty-nine out of 61 eligible cases and 82 controls were included in the analysis. The median age of study cases was 45 years, 56% were female. One-third of cases were admitted to hospital for their illness and 31% reported taking PPI. Cases were more likely to eat chicken in restaurants (aOR=10.3, 95% CI 2.6-40.4) or from fast-food outlets (aOR=5.0, 95% CI 1.2-21.2), and use PPI (aOR=8.8, 95% CI 2.0-38.3).

Abstract conclusion

Eating chicken outside the home was associated with infection. We confirmed an independent link between PPI and Salmonella infection. We recommend that future epidemiological outbreak studies of salmonellosis should be used to strengthen evidence on the relevance of PPI in Salmonella infection. Biological studies are needed to understand the effect of PPI in the pathogenesis of Salmonella infection.

Keywords: Disease outbreaks, case-control studies, proton pump inhibitors, infection, Salmonella

PRESENTED BY: Rachel Freeman

ESCAIDE REFERENCE NUMBER: 20141994

Salmonella foodborne outbreak following a wedding party: Ust-Kamenogorsk City, East Kazakhstan Region, April 19-20, 2013

Simon Ajeilat, CDC, Kazakhstan

Abstract

On April 20, 2013, 25 individuals were hospitalized with gastroenteritis in Ust-Kamenogorsk City in Eastern Kazakhstan. All attended a wedding party in a cafeteria on April 19. During April 20-24, we conducted an investigation to identify risk factors for the outbreak to prevent future similar occurrences.

Abstract methods

We enrolled in a retrospective cohort study all 190 guests who attended the party. A case-guest was an attendee who had ≥2 episodes/day of diarrhea on April 20-21. Cases (n=37) were identified through surveillance and active case finding. We: 1) interviewed guests regarding foods eaten at the party; 2) collected stool specimens from case-guests and cafeteria staff; 3) inspected the cafeteria. In monovariate analysis, we estimated relative risk (RR) by calculating and comparing attack rates for those who ate and did not eat specific foods. Food items with significant RR were then included in a multivariate logistic regression model.

Abstract results

The disease median incubation period was 24 hours (range, 10-50 hours). Of the 14 food items on the menu, meat-egg salad and vegetable salad, eaten by 81% and 78% of case-patients, respectively, had the highest attack rates (26%, 25%) and the highest RR (2.6, 1.7). In multivariate analysis, only the meat-egg salad was associated with disease (OR=3.9, 95% CI 1.1-7.4). Salmonella enteritidis was isolated from seven case-patients. Through inspection, we identified the simultaneous use of kitchen equipment for raw and ready-to-eat foods; prepared food was kept at room temperature for more than seven hours before serving.

Abstract conclusion

The likely vehicle for disease in this outbreak was the meat-egg salad, probably due to poor handling practices. The cafeteria was temporarily closed; we educated the cafeteria owners to enforce proper food handling practices.

Keywords: Foodborne, outbreak, salmonella enteritidis, Ust-Kamenogorsk, Kazakhstan

PRESENTED BY: Yelena Shevyakova

ESCAIDE REFERENCE NUMBER: 20142002

MLVA-typing of Yersinia enterocolitica identified Christmas pork as the source of an outbreak in Norway, December 2013 to February 2014

Heidi Lange[1], Ragnhild Margit Arnesen[2], Lin Thorstensen Brandal[1], Gro S. Johannessen [3], Pia Paulsen[4], Line Vold[1]

[1] Norwegian Institute of Public Health, Norway; [2] Norwegian Food Safety Authority, Norway; [3] Norwegian Veterinary Institute, Norway; [4] Norwegian Food Safety Authority, Norway

Abstract
On 10 February 2014, the Norwegian Institute of Public Health was notified by the National Reference Laboratory of a cluster of Yersinia enterocolitica serogroup O:9 (Y. enterocolitica O:9) cases sharing a multiple-locus variable number of tandem repeat analysis(MLVA) profile with maximum one locus variation (defined as the outbreak MLVA profile). A Christmas brawn, traditionally processed out of pork lard and head muscles, was the most likely source in a previous Y. enterocolitica O:9 outbreak in Norway in 2006. We investigated the outbreak to identify its source and prevent further cases.

Abstract methods
An outbreak case was an individual with an infection with Y. enterocolitica O:9 with the outbreak MLVA profile, with symptom onset between December 2013 and February 2014, and with no travel history outside Norway within two weeks before onset. Through a trawling questionnaire we gathered information on demographics, symptoms and exposures. Brawn from a suspected local producer was sampled for microbiological investigation. Related human and food isolates were typed by MLVA.

Abstract results
We identified eight outbreak cases (aged 40-68 years), all were interviewed. Six cases lived in Telemark County, five ate Christmas brawn made by a local producer and two cases ate brawn from another brand. The outbreak MLVA profile was detected in one sample of brawn from the local producer.

Abstract conclusion
Descriptive epidemiology and molecular typing of isolates from cases and suspected food identified traditional Christmas brawn as the outbreak source. The product was withdrawn from the market. The occurrence of an earlier outbreak also linked to brawn emphasizes the need for increasing awareness of hygienic measures during pig slaughter in Norway, especially regarding the use of meat taken from the head of the animal.

Keywords: Outbreak, Yersinia enterocolitica, molecular typing, swine, zoonoses

PRESENTED BY: Heidi Lange

ESCAIDE REFERENCE NUMBER: 20142028

Are ready-to-eat salads ready to eat? An outbreak of Salmonella Coeln linked to imported, mixed, pre-washed and bagged salad, Norway, November 2013

Didrik Frimann Vestrheim[2] Heidi Lange[1], Karin Nygård[1], Astrid Louise Wester[1], Marit Lilleby Kvarme[2], Line Vold[1]

[1] Norwegian Institute of Public Health, Norway; [2] Norwegian Food Safety Authority, Norway

Abstract
In November 2013, a nationwide outbreak of Salmonella Coeln was notified by the Norwegian Institute of Public Health. Less than four cases have been notified yearly in the past decade. We investigated the outbreak to identify its source and to recommend preventive measures.

Abstract methods
We defined a case as a person living in Norway with laboratory confirmed S. Coeln, symptom onset October 20th 2013 or later, and no travel history outside Norway in the two preceding weeks. We obtained environmental samples, and retrieved detailed data on purchases of food items by tracking of credit card transactions. The ten first cases were interviewed to identify common exposures using a trawling questionnaire, and the eight sequential cases were included in the case control study. Cases were compared to three controls matched on sex, age and municipality, and calculated matched odds ratios (mOR) with 95 % confidence intervals (CI).

Abstract results
Overall, 25 cases were identified in the period October 20th 2013 and January 4th 2014. Case counts peaked on October 31st 2013, with sporadic cases notified from November 12th 2013. The median age was 40 years (range 2 to 89 years). Information from seven cases and 24 controls was available for analysis. Cases were more likely than controls to have consumed pre-washed and bagged baby leaf salad mix (mOR 20, 95 % CI [2.7-infinity]). Trace-back was used to identify a suspected product and salad ingredient, but we were unable to confirm the suspicion by environmental samples.

Abstract conclusion
Epidemiological investigation suggested that consumption of pre-washed and bagged baby leaf salad mix may have been the cause of the outbreak. A recommendation to wash ready-to-eat salads should be considered to prevent future outbreaks.

Keywords: Outbreak, Salmonella, matched case-control study, lettuce

PRESENTED BY: Didrik Frimann Vestrheim

ESCAIDE REFERENCE NUMBER: 20142062

Parallel Session 3: Vaccine coverage, effectiveness and safety (1)

Evidence of waning immunity against mumps in vaccinated young adults, France 2013

Sabine Vygen[1], Aurélie Fischer[1], Denise Antona[2], Yann Le Strat[2], Patrick Rolland[1], Daniel Levy-Bruhl[3]

[1] French Institute of Public Health Surveillance (InVS), Department of Coordination of Alerts and Regions, Regional office in Aquitaine, France; [2] French Institute of Public Health Surveillance; Department of Infectious Diseases, Unit of vaccine preventable diseases, Saint-Maurice, France; [3] Institut de Veille Sanitare; Vaccine European New Integrated Collaboration Effort (VENICE) Project, France

Abstract

In 2013, clusters of mumps among young adults occurred in France; 72% of the cases had received 2 doses of Mumps-Measles-Rubella (MMR) vaccine. We aimed to determine whether the risk of mumps increases with the number of years since the last dose of MMR vaccination.

Abstract methods

We conducted a multicentre case-control study among clusters of at least two mumps cases (with at least one laboratory confirmed) in universities and military units in France. A case was an individual presenting in 2013 with inflammation of a salivary gland either lasting for ≥2 days or with an epidemiological link to a cluster or with a positive serology and/or PCR. We randomly selected frequency-matched controls, within the clusters, excluding individuals with a history of mumps. We collected clinical and vaccination history data via a web-questionnaire among students and via medical records for soldiers. We calculated odds ratios using logistic regression with fractional polynomial.

Abstract results

We included 85 cases and 321 controls. Mean age of cases and controls were 22 (SD±1.5) and 21 (SD±1.7) years respectively; 59% of cases and 62% of controls were vaccinated twice. Cases were more likely to acquire mumps with increasing time since their second MMR dose (p=0.02). The odds of mumps >10 years after the second dose was 3.97 (95%CI 1.6-9.8) times higher than ≤10 years after the second dose.

Abstract conclusion

Immunity against mumps waned with increasing time since vaccination. Our preliminaryresults contributed to the decision of the French High Council of Public Health to implement the recommendation of a third MMR dose during outbreaks in semi-closed populations for individuals whose second dose dates back >10 years.

Keywords: Mumps, MMR, vaccine effectiveness, waning immunity

PRESENTED BY: Sabine Vygen

ESCAIDE REFERENCE NUMBER: 20141956

Catching the catch-up group – successful HPV vaccination coverage in school-based campaigns, Sweden 2012

Moa Rehn[1], Eva Netterlid[1], Ingrid Uhnoo[1], Sharon Kuhlmann-Berenzon[1], Anders Wallensten[1], Pär Sparèn[2]

[1] Public Health Agency of Sweden, Sweden; [2] Department of Medical Epidemiology and Biostatistics, Karolinska Institute, Sweden

Abstract

The Swedish school-based vaccination programme offers HPV vaccine to girls born ≥1999 in 5-6th grade. In 2012, all counties introduced free-of-charge catch-up vaccination campaigns, targeting girls born 1993-1998. Varying county-level vaccination coverage in the catch-up group by December 2012 suggested that some implementation strategies were more successful. In order to inform future vaccination campaigns we assessed the impact of implementation strategy on catch-up vaccination coverage.

Abstract methods

We conducted a cross-sectional ecological study including all counties (n=21). We surveyed regional health offices about communication strategies and vaccination settings. We estimated coverage of ≥1 dose by 31 December 2012 using data from the voluntary national vaccination registry. We compared counties' catch-up vaccination coverage in terms of communication strategies and vaccination settings, calculating incidence rate ratios (IRR) and 95% confidence intervals (CI) using negative binomial regression.

Abstract results

County level catch-up vaccination coverage varied between 40-82%. All counties offered vaccination through primary healthcare settings, five additionally offered vaccine in some of their schools, and four in all their schools. Counties offering vaccine in all schools had 40% higher catch-up vaccination coverage compared to counties that did not (IRR: 1.4 95% CI: 1.2-1.6). Communication strategies most frequently used were: personal letters (90%), advertisement (76%), oral school-based information (43%) and websites (33%). No single or combined strategy was significantly associated with vaccination coverage after adjusting for vaccination in all schools.

Abstract conclusion

Counties offering HPV vaccination to catch-up groups in all schools were more successful in terms of vaccination coverage. The choice of communication strategy did not explain differences in county level vaccination coverage in our study. Future catch-up vaccination outside the national vaccination program should be implemented primarily within school settings.

Keywords: HPV vaccine; school health services; female adolescents; health communication

PRESENTED BY: Moa Rehn

ESCAIDE REFERENCE NUMBER: 20142026

Assessment of Routine Immunisation Programme-Osun State, South-West, Nigeria, January 2008-December 2012

Rhoda Fadahunsi[1], Olufunmilayo Fawole[1], Oladayo Biya[1], Elizabeth Adedire[1]

[1] Nigeria Field Epidemiology and Laboratory Training Program (NFELTP), Nigeria

Abstract

Immunization is a cost-effective strategy to reduce morbidity and mortality due to the vaccine-preventable diseases. According to National Demographic and Health Survey (NDHS) 2008, the coverage level for third dose of Diphtheria-Pertusis-Tetanus (DPT3) was 66.5% and 65.5% for first dose of Measles-Containing-Vaccine (MCV1) in South-West, Nigeria. We assessed the trend of RI coverage and the performance at the Local Government Area (LGA) level towards meeting the Millennium Development Goal.

Abstract methods

We reviewed RI data from January 2008 to December 2012. We assessed the RI performance using the DPT3 coverage, MCV1-Yellow fever (YF) gap-rate, Bacillus-Calmette-Guerin (BCG)-MCV1 and DPT1-DPT3 drop-out rates. We assessed the completeness and timeliness of reporting, the unimmunized children per year and the proportion of LGAs with coverage levels less than 80%, of the 30 LGAs in Osun State.

Abstract results

The DPT3 coverage in 2008 was 88%, 2009, 81%, 2010, 83%, 2011, 60% and 2012, 74%. Measles coverage in 2008 was 99%, 2009, 85%, 2010, 89%, 2011, 65% and 2012, 81%. In 2012, BCG-MCV1 drop-out rate was 27% and MCV1-YF gap-rate was 24.7%. DPT1-DPT3 drop-out rate was 6% overall and above 10% for seven LGAs in 2012. The proportion of LGAs with measles coverage below 80% was 46.7%(14) in 2008 and 60%(18) in 2012. Timeliness and completeness of reporting for LGAs was more than 90% per year. The proportion of unimmunized children for the state was 12.1% in 2008, 9.8% in 2009, 7.8% in 2010, 33.4% in 2011 and 17.9% in 2012.

Abstract conclusion

The goal of achieving coverage of greater than 80% at the LGA level is not yet attained. Strengthening RI at the LGA level through capacity building and adequate supervision will improve RI performance.

Keywords: Routine-Immunisation, Assessment, DPT coverage, Measles coverage

PRESENTED BY: Rhoda Fadahunsi

ESCAIDE REFERENCE NUMBER: 20142081

National seasonal influenza vaccination in Europe. Overview of surveys conducted by VENICE

Jolita Mereckiene[1], S. Cotter[1], Kari Johansen[2], Svetla Tsolova[2], Pasi Penttinen[2], Pierluigi Lopalco[2], Fortunato D'Ancona[3], Daniel Levy-Bruhl[4], Ole Wichmann[5], Luca Demattè[6], Palle Valentiner-Branth[7], Iwona Stankiewicz[8], Darina O'Flanagan[1]

[1] Health Protection Surveillance Centre, Dublin, Ireland; [2] ECDC, Sweden; [3] Istituto Superiore di Sanità; Vaccine European New Integrated Collaboration Effort (VENICE) Project, Italy; [4] Institut de Veille Sanitare; Vaccine European New Integrated Collaboration Effort (VENICE) Project, France; [5] Robert Koch Institut; Vaccine European New Integrated Collaboration Effort (VENICE) Project, Germany; [6] CINECA Consortium of Universities; Vaccine European New Integrated Collaboration Effort (VENICE) Project, Italy; [7] Statens Serum Institut; Vaccine European New Integrated Collaboration Effort (VENICE) Project, Denmark; [8] National Institute of Public Health – National Institute of Hygiene; Vaccine European New Integrated Collaboration Effort (VENICE) Project, Poland

Abstract

From 2008 VENICE has conducted annual surveys to follow up changes and to identify compliance with the European Commission recommendation to achieve the European Union (EU) goal of 75% vaccination coverage in older age and risk groups by 2014-15.

Abstract methods

In 2013 a survey was undertaken for influenza season 2012-13 across EU/EEA Member States (MS) to determine changes in seasonal influenza vaccination policy and compare vaccination coverage between countries using data obtained from previous surveys. The questionnaire was completed on-line by MS gatekeepers. The questionnaire for United Kingdom was completed separately for England, Northern Ireland, Scotland and Wales.

Abstract results

Of 33 responding countries, all recommend seasonal influenza vaccines to older age groups: 23 countries recommend vaccine for individuals ≥65 years; ten countries have lower age cut-off (ranging from ≥50 to ≥60 years of age). Seven countries recommend vaccination of healthy children. Most countries recommend influenza vaccine for clinical risk groups, pregnant women and health care workers (HCWs). The reported vaccination coverage varied by country and targeted group, ranging from 1.0%- 77.4% (median 45%) for older age groups (n=25); to between 28.0%-80.2% (median 50%) for clinical risk groups (n=9); from 9.5%-45.6% (median 28%) for HCWs (n=13); and from 0.2%- 64.6% (median 16%) for pregnant women (n=10).One third of countries monitor vaccination coverage for the later three groups. Netherlands achieved and United Kingdom almost achvcvvieved the EU goal in older age groups.

Abstract conclusion

VENICE surveys indicate that most countries recommend influenza vaccination for the main risk groups; however few countries have achieved the recommended vaccination coverage. Additional work is needed to improve vaccination coverage across the EU region and lessons learnt in countries with high coverage should be utilized.

Keywords: Influenza, immunisation, vaccination, vaccination coverage, risk groups

PRESENTED BY: Jolita Mereckiene

ESCAIDE REFERENCE NUMBER: 20142101

High vaccine effectiveness and signs of serotype replacement after the introduction of higher valency pneumococcal conjugate vaccines: results of SpIDnet first year

Camelia Savulescu[1], P. Krizova[2], A. Lepoutre[3] ,S. Cotter[4] ,D. Vestrheim[5], A. Sirbu[6], P. Ciruela[7], M. Ordobas[8], M. Guevara[9], E. McDonald[10], E. Morfeldt[11],J. Kozakova[2], C. Levy[12], Jolita Mereckiene[4], B. Winje[5], M. Pana[13],C. Munoz-Almagro[14], L. Garcia[8], J. Castilla[9], G. Edwards[15], B. Henriques[11], L. Pastore Celentano[16], G. Hanquet[1], and SpIDnet group[16]

[1] EpiConcept, France; [2] National Institute of Public Health, Czech Republic; [3] Institut de Veille Sanitaire, France; [4] Health Protection Surveillance Centre, Dublin, Ireland; [5] Norwegian Institute of Public Health, Norway; [6] National Institute of Public Health, Romania; [7] Public Health Agency of Catalonia, Spain; [8] Sub-directorate of Health Promotion and Prevention, Madrid , Spain; [9] Instituto de Salud Pública de Navarra, CIBER Epidemiología y Salud Pública, Spain; [10] Health Protection Scotland (HPS), UK; [11] Public Health Agency, Sweden; [12] ACTIV, France; [13] Cantacuzino Institute, Romania; [14] University Hospital Sant Joan de Deu, Barcelona, Spain; [15] Scottish Haemophilus Legionella Meningococcus and Pneumococcus Reference Laboratory, UK; [16] ECDC, Sweden

Abstract

The ECDC-funded SpIDnet network conducts active population-based surveillance for invasive pneumococcal disease (IPD) in 10 sites from eight countries. Using SpIDnet data, we measured the effectiveness (VE) and impact (VI) of higher valency pneumococcal conjugate vaccines (PCV10/13) on IPD in children <5 years.

Abstract methods

For PCV13 VE analysis, we compared the vaccination status of IPD cases due to vaccine serotypes with nonPCV13 serotype IPD cases reported from January 2012 to August 2013. We calculated pooled VE as (1-vaccination odds ratio)*100, adjusted for age, sex, underlying conditions and site. For VI analysis, we compared the IPD incidence in the PCV7 period to each year of the subsequent three year PCV10/13 period. After imputing for missing serotypes, we calculated pooled incidence rate ratios (IRR), 95% confidence intervals (CI) and heterogeneity index (I2) using random effect meta-analysis.

Abstract results

The adjusted VE for at least one dose PCV13 was 93.9% (95%CI: 83.9; 97.7) against PCV13 IPD (n=194) and 92.3% (95%CI: 77.8; 97.4) against additional six PCV13non7 IPD serotypes (n=159). The pooled PCV13non7 IPD IRR was 0.80 (95%CI: 0.65; 0.99) for year 1, 0.62 (95%CI: 0.42; 0.80) for year 2 and 0.43 (95%CI: 0.28; 0.66) for year 3. The pooled nonPCV13 IPD IRR was 0.95 (95%CI: 0.64; 1.42), 1.59 (95%CI: 1.06; 2.39) and 1.65 (95%CI: 1.12; 2.44) in year 1, 2, and 3 respectively. The I2 was 25-80%.

Abstract conclusion

Our results indicate a high PCV13 effectiveness. The increase in nonPCV13 incidence counters the decrease in PCV13non7 serotypes, however overall IPD incidence still decreases. Different vaccination schedules and age groups targeted in catch-up campaigns may explain heterogeneity. SpIDnet continuation will enable long-term IPD incidence monitoring after PCV10/13 introduction at a European level.

Keywords: Streptococcus pneumoniae, Pneumococcal Infections, Pneumococcal Vaccines, Vaccine effectiveness, Population Surveillance

PRESENTED BY: Camelia Savulescu

ESCAIDE REFERENCE NUMBER: 20142108

Parallel Sessions 4 – 6 14.00 – 15.00 Wed 5

Parallel Session 4: TB and other respiratory diseases (excluding influenza)

Previously treated tuberculosis: stable proportion and low treatment success, EU/EEA, 2008-2012

Vahur Hollo[1], Csaba Ködmön[1]

[1] ECDC, Sweden

Abstract

A high proportion of tuberculosis (TB) cases previously treated for TB may indicate TB programme underperformance. The aim of this study was to quantify this problem and better characterise those affected to inform targeted TB control efforts.

Abstract methods

We analysed TB routine surveillance data collected in 27 European Union (EU) and 2 European Economic Area (EEA) Member States from 2008 to 2012 and compared new and previously treated cases by time, age, TB site, drug resistance and treatment outcome. Cases with unknown treatment history were excluded from analysis.

Abstract results

Of 379 173 TB cases notified from 2008 to 2012 in 29 countries, treatment history was reported for 300 123 cases (79%) from 24 countries. Of the latter, 44 135 cases (15%, were known to have been previously treated. This proportion remained stable over the last 5 years (mean annual change 0.4%). Among adults (>14 years), median age in previously treated cases was higher (49 years) than in previously untreated cases (46 years)($p<0.005$). Pulmonary TB was diagnosed in 94% of previously treated cases compared to 80% in new cases. MDR-TB was nearly 7 times more prevalent in previously treated cases than in new cases (20% vs. 3%, $p<0.005$). Treatment success (completed or cured) in 2008-2011 was reported for 57% of previously treated cases compared to 79% of new cases.

Abstract conclusion

Previous treatment accounts for a considerable proportion (15%) of TB cases notified in Europe and is not declining. It is clearly associated with a higher prevalence of MDR TB and a worse treatment outcome. To reduce the overall burden of disease, TB programmes should therefore more focus on initial treatment of all categories of patients.

Keywords: Tuberculosis, European Union, surveillance, previous treatment,drug susceptibility

PRESENTED BY: Vahur Hollo

Laboratory-confirmed cases of tuberculosis and drug-resistance in Greece, 2012

Ana Belén Ibarz-Pavón[1],[2], Dimitrios Papaventsis[3], Rania Kalkouni[4], Gerasimos Metaxas[5], Georgia Spala[4], Theano Georgakopoulou[4],Theodoros Gerakis[5], Angelos Pefanis[5], Evangelos Vogiatzakis[3]

[1] European Program for Public Health Microbiology Training (EUPHEM), ECDC, Sweden; [2] National School of Public Health (NSPH), Athens, Greece; [3] Microbiology Laboratory & National Reference Laboratory for Mycobacteria (NRLM), Sotiria Chest Diseases Hospital, Athens, Greece; [4] Hellenic Centre for Disease Control and Prevention (HCDCP), Athens, Greece; [5] Infection Control Committee (ICC), Sotiria Chest Diseases Hospital, Athens, Greece

Abstract

The prevalence of drug-resistant tuberculosis(DR-TB) in Greece remained stable during the past few years despite migration movements from high-prevalence countries. We report information on TB resistance surveillance among newly-diagnosed cases during 2012, since these data were not included in the annual report published by the WHO in 2014 due to untimely submission.

Abstract methods

Laboratory-confirmed TB cases for 2012 were identified in the National Reference Laboratory for Mycobacteria(NRLM) database. Clinical and epidemiological information were obtained from the Hellenic Centre for Disease Control and Prevention(HCDCP) and the Infection Control Committee(ICC). Data were compiled in Excel, and analyzed in Stata12.

Abstract results

We identified 384 laboratory-confirmed cases of TB, of which 67% were male, and 55% were non-Greek. Ages ranged from 17-93yr (Average=44.3;median=37). Pulmonary TB was present in 86% of cases. Sixty-five(17%) DR-TB isolates were identified: thirteen(3.4%) metthe definition of MDR-TB(four resistant to isoniazid and rifampin, and eight resistant to additional first-line drugs), and one met the criteria for XDR-TB. Nine of the 13(69.2%) MDR-TB patients were foreigners. Five out of the 13 cases were notified to the HCDCP, leaving 61.5% of MDR-TB cases unreported. Among non-MDR/XDR resistant isolates, mono-resistance to isoniazid was the most common (19 out of 46 mono-resistant isolates (49.3%)); six poly-resistant isolates were all resistant to isoniazid and at least one additional first-line drug (ethambutol and/or pyrazinamide).

Abstract conclusion

Available data show the proportion of MDR-TB in Greece in 2012(3.4%) was below the European average(4.6%). Under-reporting of MDR-TB cases is high (61.5%). Investigations into this issue are ongoing, and a coordinated effort between NRLM and HCDCP will ensure timely reporting of 2013 data to the WHO. The implementation of a web-based real-time national reporting system is recommended

Keywords: Tuberculosis, drug-resistance, surveillance

PRESENTED BY: Ana Belen Ibarz Pavon

ESCAIDE REFERENCE NUMBER: 20142201

Tuberculosis outbreak investigation using whole genome sequencing, Finland 2012

Pieter Smit[1], Marjo Haanperä[1], Francis Drobniewsky[2], Outi Lyytikäinen[3], Hanna Soini[1]

[1] National Institute for Health and Welfare, Finland; [2] National Mycobacterium Reference Laboratory, Center for Infectious Diseases, Institute for Cell and Molecular Sciences, Barts and the London School of Medicine, UK; [3] Department of Infectious Disease Surveillance and Control, National Institute for Health and Welfare, Helsinki, Finland

Abstract

Since February 2012, a sudden increase in tuberculosis (TB) cases among teenagers and young adults was noticed in Turku, Finland. During a two-year period, 14 outbreak-associated TB cases were detected, 12 of which were culture positive. All 12 isolates had identical spoligotype and MIRU-24 profiles (SIT149 and 594-15), suggesting that the outbreak was clonal. Despite sharing the same genotypic profile, no epidemiological links could be identified for two cases. In order to understand and describe the transmission dynamics at a higher resolution we assessed the usefulness and public health relevance of whole-genome sequencing (WGS) in an on-going outbreak investigation.

Abstract methods

We sequenced the complete genomes of 12 Mycobacterium tuberculosis outbreak isolates and seven historical isolates with the same genotypic profile, using Illumina’s sequencing technology. Epidemiological data was gathered through multiple interviews with cases and contacts.

Abstract results

Two single nucleotide polymorphisms (SNP) were found among the 12 outbreak isolates.The seven historical isolates were genetically distinct from the outbreak, differing with a 15 to 63 SNP difference in their genome.

Abstract conclusion

WGS strongly confirmed that the two cases without epidemiological links were part of the outbreak. It therefore revealed that transmission to casual contacts had occurred, indicating that more cases could be expected. WGS had a public health benefit over traditional TB typing methods in this outbreak situation and can be highly recommended when transmission dynamics need to be assessed at a higher resolution.

Keywords: Tuberculosis, outbreak, whole genome sequencing, genotyping

PRESENTED BY: Pieter Smit

ESCAIDE REFERENCE NUMBER: 20141934

Parallel Session 5: Burden of communicable diseases

Results from the Burden of Communicable Diseases in Europe (BCoDE) study.

Alessandro Cassini[1] ,Edoardo Colzani[1], Alessandro Pini[1], Guido Maringhini[1], Piotr Kramarz[1], Mirjam Kretzschmar[2]

[1] ECDC, Sweden; [2] National Institute for Public Health and the Environment, Bilthoven, The Netherlands

Abstract
The Burden of Communicable Diseases in Europe (BCoDE) is a project led and funded by the European Centre for Disease Prevention and Control (ECDC) and by a European consortium with the purpose of estimating the impact of 32 selected communicable diseases expressed in Disability Adjusted Life Years (DALYs) in the European Union (EU) and EEA/EFTA Member States (MS).

Abstract methods
Literature reviews describing the natural pathway of each disease was performed; the resulting outcome trees included health outcomes and states (severity), transition probabilities, duration of outcomes and case fatality ratios. Disability weights were derived from an ad hoc European study. By default data source for incidence of acute disease was TESSy (age and gender specific, timeframe 2007-2011, all EU/EEA MS included), corrected for under-estimation of notified cases; where necessary alternative methods estimating the true incidence were explored.

Abstract results
Influenza has the highest impact (115 DALY per 100000 general population), followed by hepatitis B (64) and HIV infection (62). Of the total burden 75% is due to Years of Life Lost (YLL) (25% from YLD) and 51% is due to sequelae (49% acute). Diseases with low incidence but high severity have high DALY per case (rabies, listeriosis, vCJD), mostly due to the acute infection (75%). Respiratory tract infections and sexually transmitted diseases account for the highest proportion of burden (almost 70%).

Abstract conclusion
The ranking of diseases according to their impact in DALYs is different from that derived from notification data. The proposed methodology promotes evidence-based approach to population health description, fosters an overview of surveillance data quality and availability, facilitates the communication of complex information to decision makers and provides a tool for planning and prioritisation.

Keywords: Burden of Illness, Health Impact Assessment, BCoDE

PRESENTED BY: Alessandro Cassini

ESCAIDE REFERENCE NUMBER: 20142055

How to estimate the burden of common sequelae due to healthcare-associated neonatal sepsis

Sebastian Haller[1], Alessandro Cassini[2], Muna Abu Sin[1], Tim Eckmanns[1], Thomas Harder[1]

[1] Robert Koch-Institute (RKI), Germany; [2] ECDC, Sweden

Abstract
Calculating the burden of healthcare-associated infections (HAI) involves epidemiological challenges related to the attribution of disability to HAI and to the underlying comorbidity. To date, despite global efforts in the field of summary measures of population health, these challenges have prevented the estimation of HAI burden. We conducted a systematic review, to describe the natural disease pathway (outcome tree), essential basic step to estimate the burden due to healthcare-associated neonatal sepsis.

Abstract methods
Two authors searched independently for systematic reviews in EMBASE, Medline and Cochrane library. Cohort-studies from identified reviews were used for further analysis. Sepsis was defined as detection of bacteria in blood culture. As sequelae we considered: Cerebral palsy (CP), vision impairment (VI), hearing impairment (HI) and death. We performed random-effects meta-analysis of risk differences (RD) and compared these to absolute risks for sequelae among septicaemic neonates.

Abstract results
Our systematic search revealed 207 reviews, of which 4 were eligible for full text evaluation and one fulfilled the inclusion criteria. From this, we extracted 8 cohort-studies (1994-2011) including ≈6000 infants. RD of CP was 8% (95%CI 6-10%), of VI 9% (95%CI 7-11%) and HI 4% (95%CI 2-10%). Absolute risks for these sequelae were ≈two-fold higher than RDs. Mortality data available from one cohort-study: absolute mortality was 38% (RD 14%).

Abstract conclusion
It is crucial to address the background rates of sequelae in a healthcare setting, when estimating the burden of disease – RDs are a suitable tool. Using systematic approaches will increase transparency and reproducibility of burden estimates. We aim to compare the burden of HAIs to other infections to allow an evidence based approach for the description of the impact of infectious diseases in Europe.

Keywords: Sepsis, neonate, burden of disease, systematic review, BCoDE

PRESENTED BY: Sebastian Haller

ESCAIDE REFERENCE NUMBER: 20142134

Preparing for rotavirus vaccine introduction in Norway: how to monitor disease burden and vaccine impact?

Tone Bruun[1], Kirsti Vainio[1], Terese Bekkevold[1], Astrid Rojahn[2], Gunnar Størvold[2], Kirsti Jakobsen[2], Kirsti Egge Haugstad[2], Ketil Størdal[3], Anita Kanestrøm[3], Henrik Døllner[4], Lars Høsøien Skanke[4], Svein Arne Nordbø[4], Ann Marit Gilje[5], Elisebet Haarr[5], Moustafa Gibory[1], Susanne Gjeruldsen Dudman[1], Elmira Flem[1]

[1] Norwegian Institute of Public Health, Norway; [2] Oslo University Hospital Ullevål, Oslo, Norway; [3] Østfold Hospital, Fredrikstad, Norway; [4] St. Olavs University Hospital, Trondheim, Norway; [5] Stavanger University Hospital, Stavanger, Norway

Abstract

Rotavirus vaccination is introduced in the Norwegian childhood immunization program from September 2014. Previous studies demonstrated that rotavirus accounted for over 60% of diarrheal hospitalizations among Norwegian children <5 years of age. Prior to vaccine introduction, we established a surveillance platform to monitor short- and long-term impact of the vaccination program.

Abstract methods

Since January 2014, we initiated active population-based hospital surveillance for rotavirus gastroenteritis in children <5 years of age at four hospitals with a combined catchment population of 31% of Norway. We prospectively survey all children hospitalized for acute gastroenteritis and collect data on demographics and clinical picture. We collect stool samples from enrolled cases and test for rotavirus antigen by an enzyme immunoassay.

Abstract results

Since January through August 2014, we enrolled 249 children <5 years of age. Of these, 167 (67%) had ELISA results available. Rotavirus was detected in 74% of all samples. Detection rates differed between study hospitals from 30% to 83%. Children aged 6-24 months of age accounted for 63.4 % of all confirmed rotavirus cases; 4.1 % of cases were <3 months old. Among rotavirus cases, 72% were classified as severe and 11% as moderate according to the Vesikari severity scale. The mean duration of hospital stay among rotavirus cases was 1.6 (range 0-7) days. No rotavirus-associated deaths were reported.

Abstract conclusion

Preliminary data from active hospital surveillance demonstrate that rotavirus remains to be the most important cause of gastroenteritis in children in Norway. The established surveillance platform will be essential for future monitoring of the impact of rotavirus vaccination.

Keywords: Rotavirus, Gastroenteritis, Rotavirus Vaccines, Children, Epidemiology

PRESENTED BY: Tone Bruun

ESCAIDE REFERENCE NUMBER: 20142198

Parallel Session 6: Emerging and vector-borne diseases

Awareness of Lassa Fever Transmission and Practices in A Semi Urban Community, Oyo state, Southwest Nigeria. February 2014.

Olukemi Olugbade[1], Oluwaseyi Israel[1], Rhoda Fadahunsi[1], Abiodun Ogunniyi[1], Abisola Oladimeji[1], Olufemi Ajumobi[2], A.T Olayinka[3], Ikeoluwapo Ajayi[4]

[1] Nigeria Field Epidemiology Laboratory Training Programme, Asokoro, Abuja, Nigeria; [2] National Malaria Elimination Program. Abuja., Nigeria; [3] Department of Medical Microbiology, Ahmadu Bello University, Zaria; [4] Department Of Epidemiology and Medical Statistics, Faculty of Public Health, University of Ibadan, Ibadan, Oyo state, Nigeria

Abstract

Lassa Fever (LF) is an infectious viral hemorrhagic disease. In endemic areas, LF accounts for about 100,000 – 300,000 cases and 5000 deaths per year. It is transmitted through contact with effluents of Mastomys Natalensis and infected persons. In 2013, outbreaks of LF occurred in 23 of the 36 states in Nigeria with 1,656 cases and 112 deaths. In February 2014, a confirmed case of LF was reported in Saki, Oyo state. We assessed the awareness and evaluated practices identified as risk factors for LF transmission in the area.

Abstract methods

We conducted a cross-sectional survey in February 2014 in Saki, Oyo state. We recruited 107 respondents using a multistage cluster sampling and administered questionnaires to collect data on socio-demographic characteristics, awareness of LF, food handling and waste management practices. We analysed data analysis with Epi Info software.

Abstract results

Mean age was 30.0 ± 10years. There was no significant association between level of education and awareness of LF($p>0.05$). Only 49(46%) had heard of LF, with 23 (50%) having heard from health workers. Overall, 95 (94.1%) had contact with rodents, 76 (76%) trapped rats, 64 (80%) practised open dumping of refuse, 33(34.7%) bush burning, 18(17.8%) roadside drying of food and 15 (15.6%) consumed rats.

Abstract conclusion

Awareness of LF in the study area is generally low. We carried out health education, community sensitization and trained health workers on early case detection of LF. We advocate sustained community health education and adherence of residents to environmental sanitation regulations.

Keywords: Lassa Fever, Awareness, Outbreak, Oyo state

PRESENTED BY: Olukemi Olugbade

ESCAIDE REFERENCE NUMBER: 20142167

Targeted Mass Drug Administration of antimalarials to prevent malaria establishment in Lakonia Greece-transmission period 2013

Maria Tseroni[1], Agoritsa Baka[1], Maria Georgitsou[2], Maria Harvalakou[2], Maria Panoutsakou[2], Ioanna Psinaki[2], Maria Tsoromokou[2], Georgios Karakitsos[2], Chrysovalantis Silvestros[3], Danai Pervanidou[1], Irene Terzaki[1], Anna Vakali[1], Andriani Marka[4], Theano Georgakopoulou[1], Sotirios Tsiodras[5], Athanasios Tsakris[6], Jenny Kremastinou[1],[3], Christos Hadjichristodoulou[4]

[1] Hellenic CDC, Greece; [2] Malwest Project, Greece; [3] KEELPNO, Greece; [4] Medical School, University of Thessaly, Greece; [5] Medical School, University of Athens, Greece; [6] School of Medicine, University of Athens, Greece

Abstract

Malaria reemerged in Greece since 2009 after 35 years, with the detection of locally acquired P. vivax cases. An outbreak in 2011 in Lakonia included 36 local cases, with an additional 10 locally acquired cases in 2012. Public health measures were implemented including Proactive Case Detection (PACD) with fever screening with Reactive ACD in the event of any malaria case, Indoor Residual Spraying (IRS), distribution of Long-lasting insecticide treated Nets (LLINs) and targeted mass antimalarial drug administration (tMDA) to migrants from malaria endemic countries living in the area.

Abstract methods

An empiric antimalarial course of chloroquine and primaquine was selected targeting P. vivax hypnozoites after consultation with an intersectoral working group of experts. tMDA was implemented by 4 field teams(1 health professional and 1 mediator), providing medicines for free under Directly Observed Therapy (DOT). Administration followed mediator obtained informed consent and G6PD testing. Adverse effects were monitored by a structured pharmacovigilance form.

Abstract results

From 22/05- 31/12/2013 a total of 862 migrants from malaria endemic countries completed the course, 41 were lost to follow up and 3 refused treatment, while 17 migrants had G6PD deficiency. Adverse effects were related mostly to chloroquine, with 35.4% reporting at least one 38.7% headache, 37% vertigo/dizziness, 19.3 % abdominal pain. In contrast only 11.5% of persons receiving primaquine reported side effects. One case of haemolytic anemia was detected in a person with a false normal initial G6PD test, later found to have severe enzyme deficiency.

Abstract conclusion

No cases of P. vivax malaria were detected in Evrotas in 2013. tMDA proved a safe public health measure, which in combination with the other interventions contributed to controlling the re-emergence of malaria in this focus in Greece.

Keywords: Malaria, measures, antimalarials, vivax

PRESENTED BY: Agoritsa Baka

ESCAIDE REFERENCE NUMBER: 20142027

Validating serological tests for the diagnosis of Visceral Leishmaniasis in an endemic European country

Mathieu Bangert[1], María Delmans[1], Flores-Chávez[1] ,Pamela Ivonne Llanes-Acevedo[1], Carolina Arcones[1], Carmen Chicharro[1], Emilia García[1], Javier Nieto[1], Israel Cruz[1]

[1] Instituto de Salud Carlos III, Spain

Abstract

Visceral leishmaniasis (VL), the most severe form of leishmaniasis, is increasing within Europe with Mediterranean countries reporting endemic status alongside a worrying northward spread. The most established serological methods for diagnosis are an immunochromatographic test based on recombinant antigen (rk39-ICT) and a direct agglutination test (DAT) based on the whole parasite antigen. To date, no studies using a large set of patients have performed an assessment of both methods within Europe.

Abstract methods

We selected a range of well-characterized serum samples from VL cases including co-infection with HIV, Chagas disease, malaria and other parasitic infections (n=388; years 2010-2014), to test the sensitivity and specificity of rk39-ICT and DAT. A reference immunofluorescence antibody test (IFAT) used in Europe for VL diagnosis was included for comparison.

Abstract results

Our data showed high sensitivity and specificity for the DAT (Sn 92%, CI 80.8-97.8; Sp 98.8%, CI 97-99.7) and rK39-ICT (Sn 78%, CI 64-88.5; Sp 99.7%, CI 98.4-99.9) tests. rk39-ICT had low sensitivity in HIV+ patients (50%, CI 27.2-72.8) but not in HIV– patients (Sn 88.6%, CI 73.3-96.8). The whole antigen DAT techniqueshowed high sensitivity in HIV+ patients (Sn 90.0%, CI 63.3-98.8) and no cross-reaction with Chagas. The IFAT test demonstrated high specificity (Sn 90.0%, CI 78.2-96.7; Sp 95.6%, CI 92.8-97.5) but also cross-reactivity with sera from Chagas disease.

Abstract conclusion

Both serological tests (rK39-ICT and DAT) are adequate for VL diagnosis in the European context. Tests should be chosen according to the epidemiological particularities of each setting. rk39, with high sensitivity in HIV– patients as well as its ease-of-use, makes it suitable for an initial screening method. For VL patients co-infected with HIVor other parasitic infections, the DAT is most suitable.

Keywords: Leishmaniasis, Serology, Validation, Europe

PRESENTED BY: Mathieu Bangert

ESCAIDE REFERENCE NUMBER: 20142070

Parallel Sessions 7 – 9 10.30 – 12.30 Thurs 6

Parallel Session 7: Influenza

Transmission of the first influenza A(H1N1)pdm09 pandemic wave in Australia was driven by undetected infections: pandemic response implications

James Fielding[1], Heath Kelly[1], Kathryn Glass[2], Geoffry Mercer[2]

[1] Victorian Infectious Diseases Reference Laboratory, Australia; [2] The Australian National University, Australia

Abstract

During the first wave of influenza A(H1N1)pdm09 in Victoria, Australia the rapid increase in notified cases and the high proportion with relatively mild symptoms suggested that community transmission was established before cases were identified. This lead to the hypothesis that those with low-level infections were the main drivers of the pandemic. A mathematical model was developed to estimate the relative importance of different levels of disease severity in transmission of the first pandemic wave.

Abstract methods

A deterministic susceptible-infected-recovered model was constructed to describe the first pandemic wave in a population structured by disease severity levels of asymptomatic, low-level symptoms, moderate symptoms and severe symptoms requiring hospitalisation. The model incorporated mixing, infectivity and duration of infectiousness parameters to calculate effective reproduction numbers for each severity level.

Abstract results

With effective reproduction numbers of 1.82 and 1.32 respectively, those with low-level symptoms, and those with asymptomatic infections were responsible for most of the transmission. The effective reproduction numbers for infections resulting in moderate symptoms and hospitalisation were less than one. The same relative effects were observed in sensitivity analyses of parameters in the model.

Abstract conclusion

Transmission of influenza A(H1N1)pdm09 was largely driven by those essentially invisible to the health system. The delay in detection and high proportion of relatively mild infections limited the effectiveness of case-based control measures, such as school closures and antiviral distribution to cases and their contacts. Revision of pandemic plans need to incorporate milder scenarios, with a graded approach to implementation of control measures.

Keywords: Epidemiology, Influenza, Modelling, Pandemic, Transmission

PRESENTED BY: James Fielding

ESCAIDE REFERENCE NUMBER: 20141927

Influenza surveillance in animals: What is our capacity to detect emerging influenza viruses with zoonotic potential?

Sophie Von Dobschuetz[1], Marco DeNardi[2], Kate A Harris[3], Katharina Staerk[4]

[1] Food and Agriculture Organization of the United Nations (FAO), Rome, Italy; [2] Istituto Zooprofilattico Sperimentale delle Venezie, Italy; [3] Animal Health and Veterinary Laboratories Agency (AHVLA), UK; [4] Royal Veterinary College (RVC), UK

Abstract

Influenza A viruses originating from animals can adapt to infect humans following mutation or gene exchange. Identification and characterization of such viruses are therefore prerequisite for pandemic preparedness. Surveillance should be combined with a decision-making process, allowing for appropriate follow-up in case positives are found.

Abstract methods

A cross-sectional survey of national animal influenza surveillance programmes directed at Chief Veterinary Officers from 183 countries was conducted to assess the current capacity to detect influenza viruses with zoonotic potential in animals. The aim was to collect comprehensive and detailed information on influenza surveillance in different animal species, as well as information sharing mechanisms instigated.

Abstract results

Details of 587 animal influenza surveillance system components implemented during the period 2010-2012 were collected for 99 countries. A component is characterized by surveillance type (active, passive), purpose (national or international surveillance system, research), objective (detection, monitoring), influenza targeted (avian, equine, swine, pandemic influenza), and target population (domestic, wild, companion animals).Less than 1% of components analysed were specifically aimed at detecting pandemic influenza viruses in animals and exclusively targeted pigs. This documents the global need for increasing surveillance for potentially zoonotic influenza viruses in relevant animal species.

Abstract conclusion

Recognizing that surveillance in animals is mostly implemented with the objective of safeguarding animal health and international trade, we suggest how existing efforts may be improved and where existing components could be adapted to inform human pandemic risk. Recommendations include (1) integration of several active-representative or risk-based components, (2) targeting subtypes with higher zoonotic risk regardless of their importance for animal production and health, and (3) timely communication of results to the national and international communities, including submission of virus sequences to public databases.

Keywords: Surveillance, pandemics, influenza, zoonotic infectious diseases

PRESENTED BY: Sophie Von Dobschuetz

ESCAIDE REFERENCE NUMBER: 20142063

Pandemic influenza vaccination coverage and severe influenza outcomes during seasons 2009/10 and 2010/11 in five Nordic countries.

Julita Gil Cuesta[1, 2], Hélène Englund[3], Ólafur Gudlaugsson[4], Siri Helene Hauge[5], Outi Lyytikäinen[6], Guðrún Sigmundsdóttir[4], Anders Tegnell[3], Mikko Virtanen[6], Tyra Grove Krause[1]

[1] Statens Serum Institut, Denmark; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden; [3] Public Health Agency of Sweden, Sweden; [4] Centre for Health Security and Communicable Disease Control, Iceland; [5] Norwegian Institute of Public Health, Norway; [6] Department of Infectious Disease Surveillance and Control, National Institute for Health and Welfare, Helsinki, Finland

Abstract

During the 2009/10 influenza A(H1N1)pdm09 pandemic, the Nordic countries Denmark, Sweden, Norway, Finland and Iceland adopted different approaches to pandemic vaccination. In most countries vaccinations began after the epidemic peaked. All countries established surveillance of influenza-associated intensive care unit (ICU) admissions to monitor influenza severity. Our objective was to compare the pandemic vaccination coverage with severe influenza outcomes in 2009/10 and 2010/11 in the Nordic countries.

Abstract methods

We calculated the cumulative pandemic vaccination coverage in season 2009/10 by dividing the number of people vaccinated with the A(H1N1)pdm09 adjuvanted vaccine by the total population per country. We calculated ICU admission rates in seasons 2009/10 and 2010/11 by dividing the number of patients admitted to ICU with laboratory-confirmed A(H1N1)pdm09-infections by 100,000 population.

Abstract results

The vaccination coverage was lower in Denmark (6%) compared to Sweden (60%), Norway (41%), Finland (48%) and Iceland (44%). In 2009/10, the A(H1N1)pdm09 ICU rates (95% CI) were 1.6 (1.4-2.0) in Denmark, 1.2 (1.0-1.4) in Sweden, 3 (2.5-3.5) in Norway, 2.4 (2.0-2.9) in Finland and 5.3 (3.3-8.6) in Iceland. In contrast in 2010/11, Denmark had the highest A(H1N1)pdm09 ICU rate 1.9 (1.5-2.3), compared with 0.6 (0.5-0.8) in Sweden, 0.8 (0.6-1.1) in Norway, 0.9 (0.7-1.2) in Finland and 0.3 (0.0-2.2) in Iceland.

Abstract conclusion

Compared to Denmark, the other four Nordic countries had higher pandemic vaccination coverage and experienced less A(H1N1)pdm09 severe outcomes in season 2010/11. This suggests that the adjuvanted pandemic vaccination may have had an impact on influenza severe outcomes in the season following the pandemic. Surveillance of severe influenza outcomes may be used to monitor the impact of influenza between seasons and support the assessment of different vaccination strategies.

Keywords: Vaccination, Pandemics, Swine-Origin Influenza A H1N1 Virus, Intensive Care Units

PRESENTED BY: Julita Gil Cuesta

ESCAIDE REFERENCE NUMBER: 20142016

Impact of antiviral therapy on severe outcomes among hospitalised patients with confirmed influenza A (H1N1) pdm09 during the 2009-2010 pandemic in the UK

Ana Mateus[1], Jonathan Van-Tam[2], Yadgar Hama-Karim[2], FLUCIN investigators/ Network Collaborators: Colin Armstrong, Stephen J Brett, Barbara Bannister, Joanne E Enstone, Elaine Gadd, Wei Shen Lim, Jim McMenamin, Karl G Nicholson, Peter J Openshaw, Robert C Read, Malcolm G Semple, Bruce L Taylor, UK, Puja Myles[2]

[1] Public Health England, UK; FETP/EPIET Royal Veterinary College, North Mymss, UK; [2] Division of Epidemiology and Public Health, School of Community Health Sciences, University of Nottingham, UK

Abstract

In March 2009, the Department of Health in England established the Influenza Clinical Information Network (FLU-CIN) for the surveillance of hospitalised patients with influenza A (H1N1)pdm09 infection during the pandemic. We assessed impact of antiviral therapy in hospitalised patients with H1N1 infection.

Abstract methods

We investigated the impact of antiviral therapy on (a) proportion of hospitalisations › 48 hours, (b) admission to High Dependency (HDU) or Intensive Care Units (ICU), (c) death and (d) severe outcomes (i.e. admission to HDU, ICU or/and death) between April 2009 and January 2010. Using the FLU-CIN data, we conducted a case-control study nested in a cohort. We examined associations between exposures and outcome through calculating odds ratio (OR) in univariable and multivariable logistic regression models (cut-off p-value: 0.2), adjusted for sex and age. We calculated preventive fraction for patients receiving antiviral therapy.

Abstract results

Fifty-five hospitals provided data from 1,520 patients (Median age: 26 years, range= 0-95, 47.4% male, 54% hospitalisations › 48 hours, 1.1% HDU / ICU admissions and 6.9% deaths (0.5%). Seventy-six percent received antiviral therapy. Compared with others, those who received antiviral therapy within 48 hours of onset (N= 413, 35.6%) were less likely to face prolonged hospitalisation (Adjusted OR= 0.29, 95% CI: 0.16-0.47), had hospitalisation 2.1 days shorter (95% CI: 1.1-3.1) and were less likely to die (Adjusted OR= 0.21, 95% CI: 0.07-0.62). Timely antiviral therapy was associated with a reduction of 79% of deaths.

Abstract conclusion

Early antiviral therapy was associated with improved health outcomes of hospitalised patients with H1N1 infection during the pandemic. Outcomes in H1N1 cases in the community should be monitored and included as part of surveillance systems to better inform antiviral therapy recommendations.

Keywords: Influenza, Human; Antiviral Agents; Influenza A Virus, H1N1 Subtype; Inpatients; Outcome Assessment (Health Care)

PRESENTED BY: Ana Mateus

ESCAIDE REFERENCE NUMBER: 20142154

Contact tracing following influenza exposure on aircraft

Cornelia Adlhoch[1], Katrin Leitmeyer[1]

[1] ECDC, Sweden

Abstract

Air travel has been shown to contribute to the spread of influenza through infected passengers and potentially through in-flight transmission. Contact tracing (CT) can curb chains of transmission, but its role in influenza control is poorly understood.

Abstract methods

A multidisciplinary external expert panel was convened to generate a consensus guidance document on risk assessment related to influenza transmission on aircraft. As a basis for discussion, a systematic literature review was performed using two databases (EMBASE, PubMed) to identify publications on the transmission of influenza virus on aircraft. Independent review of 402 retrieved articles (1970-2014) by two experts yielded 15 articles describing evidence of on-board transmission of influenza viruses. The evidence in these articles was systematically extracted and assessed.

Abstract results

The evidence for on-board transmission of influenza in the reviewed literature was of limited quality. Based on virus characteristics, the expert panel defined three different scenarios for contact tracing:

- Seasonal influenza: no CT recommended.
- Novel influenza virus with pandemic potential OR seasonal influenza virus with increased virulence: based on a situational risk assessment, a timely and comprehensive CT of all passengers should be considered.· Influenza virus with zoonotic potential: based on a situational risk assessment, a restricted CT strategy focusing on close contacts and passengers seated two seats in all directions around the index case should be applied.

Abstract conclusion

There is no universal recommendation to initiate CT after possible on-board exposure to influenza. Decisions on CT should be taken case by case, based on virus characteristics and a situational risk assessment.

Keywords: Risk assessment, influenza virus, aircraft, Europe, contact tracing

PRESENTED BY: Cornelia Adlhoch

ESCAIDE REFERENCE NUMBER: 20142084

Influenza vaccine effectiveness (VE) estimates from the I-MOVE multicentre case-control study in Europe, 2013-14: moderate VE against A(H1N1)pdm09 and low but heterogeneous VE against A(H3N2)

Esther Kissling[1], Marta Valenciano[1], Udo Buchholz[2] ,Amparo Larrauri[3] ,Beatrix Oroszi[4], Coralie Giese[5] , Daniela Pitigoi[6], Ausenda Machado[7], Annicka Reuss[2], Silvia Jiménez Jorge[3], Krisztina Horváth[4], Joan O´Donnell[5], Emilia Lupulescu[6], Raquel Guiomar[7], Alain Moren[1]

[1] EpiConcept, France; [2] Robert Koch Institute, Germany; [3] (National Centre for Epidemiology, Instituto de Salud Carlos III, Spain; [4] Office of the Chief Medical Officer, Hungary; [5] Health Protection Surveillance Centre, Ireland; [6] Cantacuzino Institute, Romania; [7] Instituto Nacional de Saúde Dr Ricardo Jorge, Portugal

Abstract

In I-MOVE's sixth season (Influenza Monitoring Vaccine Effectiveness in Europe), we undertook a multicentre case-control study based on sentinel practitioner surveillance networks in six European Union (EU) countries to measure 2013/14 influenza vaccine effectiveness against medically-attended influenza-like illness (ILI) laboratory-confirmed as influenza. The season was characterised by co-circulation of influenza A(H3N2) and A(H1N1)pdm09 viruses. In the preceding I-MOVE seasons vaccine effectiveness estimates were relatively homogenous among participating countries.

Abstract methods

Practitioners systematically selected ILI patients to swab within eight days of symptom onset. We compared influenza A-positive patients by subtype to influenza-negative patients among those meeting the EU ILI case definition. We conducted country-specific complete case analyses using logistic regression and calculated adjusted vaccine effectiveness (AVE) by subtype, controlling for potential confounders (age, sex, onset month and presence of chronic conditions) where sample size allowed. We calculated heterogeneity between countries using the I2 index and Cochrane's Q-test. We calculated a summary AVE, pooling country-specific AVE estimates using random effects where heterogeneity was found, else using a 1-stage pooling method with country as fixed effect.

Abstract results

We included 3196 ILI patients, among whom there were 532 A(H1N1) pdm09 cases and 622 influenza A(H3N2). Pooled AVE against A(H1N1) pdm09 was 47.5% (95%CI: 16.4-67.0), with no heterogeneity between countries (I2:0.0%, p=0.693). AVE against A(H3N2) was ‹24% for three countries and ›59% for the others (I2=51.5%; p=0.067). Pooled AVE against influenza A(H3N2) was 29.7% (95%CI: -34.4-63.2).

Abstract conclusion

Results suggest overall low to moderate AVE against influenza A(H1N1) pdm09 and A(H3N2), with heterogeneity in AVE by country for A(H3N2), largely unprecedented in I-MOVE. We are further investigating reasons for heterogeneity in the context of geographical differences in virological change, overall and age-specific incidence, and vaccine brands used.

Keywords: Influenza, Influenza vaccine, prevention & control, multicentre studies, case control studies

PRESENTED BY: Esther Kissling

ESCAIDE REFERENCE NUMBER: 20142218

Parallel Session 8: Vaccine-preventable diseases

How many children are unvaccinated in England? Evaluation of a national catch-up MMR campaign in England, April-September 2013

Benedetto Simone[1], Sooria Balasegaram[1], Maya Gobin[2], Charlotte Anderson[2], Andre Charlett[3], Louise Coole[4], Helen Maguire[3], Tom Nichols[3], Chas Rawlings[1], Mary Ramsay[5], Isabel Oliver[3]

[1] Field Epidemiology Services (Victoria), Public Health England, UK; [2] Field Epidemiology Service (Bristol Office), Public Health England, UK; [3] Public Health England, UK; [4] Field Epidemiology Services (Leeds office), Public Health England, UK; [5] Health Protection Services, Immunisation, Hepatitis, and Blood Safety Department, Public Health England, UK

Abstract

In January-March 2013, the number of confirmed measles cases in England increased in 10-16 year-olds. In response, Public Health England launched a national measles-mumps-rubella (MMR) campaign in April-September based on historic coverage data from Child Health Information Systems (CHIS), suggesting ~8% of this age group were unvaccinated. We aimed to estimate coverage at baseline and the proportion of previously unvaccinated children (target) who received MMR by mid-point in the campaign (20/08/2013) to inform further public health action.

Abstract methods

We randomly selected 12/33 London Boroughs and 24/116 local authorities outside of London. In each of these, we randomly sampled 200 children, aged 10-16 years, with no record in CHIS of having been vaccinated at baseline. We validated their CHIS information using GPs' registers at baseline and mid-point. We revised the CHIS estimates using the proportion of unvaccinated children obtained through validation, and derived coverage estimates at baseline and proportion of target population vaccinated at mid-point.

Abstract results

We validated 5,182/6,644 (78%) of the sample records. Estimated coverage at baseline was 94.7% (95% confidence intervals, CI: 93.5-96.0%), lower in London (86.9%, 95%CI: 83.0-90.9%) than outside London (96.1%, 95%CI 95.5-96.8%). The campaign reached 10.8% (95%CI: 7.0-14.6%) of target population, lower in London (7.1%, 95%CI: 4.9-9.3) than outside London (11.4%, 95%CI: 7.0-15.9%). Coverage increased by 0.6% up to 95.3% (95% CI: 94.1-96.4%), around 210,000 children remaining unvaccinated at mid-point.

Abstract conclusion

Estimated MMR coverage was higher than routinely reported. Mid-point coverage reached the 95% campaign objective. However, <11% of the target was reached and coverage remains low in London. No further national campaigns are needed but targeted local vaccination activities should be considered. Further work is needed to identify factors associated with non-vaccination.

Keywords: Measles-Mumps-Rubella Vaccine; England; Vaccination; Health campaigns; Evaluation

PRESENTED BY: Benedetto Simone

ESCAIDE REFERENCE NUMBER: 20141967

Estimating the impact of meningococcal group C conjugate vaccine on hospitalization for invasive disease in Italy, 2001-2011

Domenico Martinelli[1], Vanessa Cozza[2, 3], Maria Giovanna Cappelli[4], Rosa Prato [1, 3]

[1] Department of Medical and Surgical Sciences, University of Foggia, Foggia, Italy; [2] Sector of Hygiene, Department of Medical and Surgical Sciences, University of Foggia, Foggia, Italy; [3] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden; [4] Department of Biomedical Sciences and Human Oncology, University of Bari, Bari, Italy

Abstract

Since several European countries have introduced serogroup C conjugate (MenC) vaccine in their routine immunization schedules at the beginning of 2000s, a decrease in the burden of invasive disease caused by Neisseria meningitidis (IMD) has been observed. In Italy, MenC was nationally recommended in 2006 and progressively introduced in all regions; in 2012, it was included in the list of essential health interventions and actively offered, free of charge, to all new-borns and adolescents. We estimated the impact of MenC national immunization programme comparing hospitalization data for IMD in pre- and post-vaccination era.

Abstract methods

We analysed national hospital discharge records for IMD (ICD-9CM: 320.xx, inpatient admissions) from 2001 to 2011 and calculated hospitalization rates. To assess differences between pre- and MenC vaccination era, we computed Hospitalization Risk Ratios (HRRs) with 95%CIs using Poisson regression models. We stratified the analysis by age.

Abstract results

In pre-vaccination era (2001-2005), an average of 389 hospitalizations/year were registered, with the highest rates in infants and children 0-4 years of age (4.6 x100,000) and in adolescents 10-17 years old (2,9 x100,000). In MenC vaccine era (2006-2011), the average number of hospitalizations was 271/year (hospitalization rate 0-4 years: 2.7 x100,000; 10-17 years: 0.8 x100,000). Between pre- and MenC vaccine era, HRR was 0.67 (95CI%: 0.57-0.79), with significant reductions both in children (HRR: 0.57, 95CI%: 0.38-0.86) and adolescents (HRR: 0.6, 95CI%: 0.45-0.87).

Abstract conclusion

In Italy, MenC universal routine vaccination is showing a large impact on IMD morbidity,especially in young children and in adolescents. Our results suggest that improving MenC vaccination coverage can further decrease IMD burden, most of which could be now prevented by the introduction of multicomponent meningococcal serogroup B vaccine.

Keywords: Vaccine impact; serogroup C conjugate vaccine; hospitalization

PRESENTED BY: Domenico Martinelli

ESCAIDE REFERENCE NUMBER: 20142008

Immunization coverage assessment and drop-out rates for different vaccines among children in rural Atakumosa, Southwestern Nigeria

Elizabeth Adedire[1], Ikeoluwapo Ajayi[2], Olufunmilayo Fawole[3], Olufemi Ajumobi[4], Patrick Nguku[3], Gabrielle Ponggesee[3]

[1] LAUTECH Teaching Hospital, Nigeria; [2] Department Of Epidemiology and Medical Statistics, Faculty of Public Health, University of Ibadan, Ibadan, Oyo state, Nigeria; [3] Nigeria Field Epidemiology and Laboratory Training Program (NFELTP), Nigeria; [4] National Malaria Elimination Program. Abuja, Nigeria

Abstract

Routine immunization (RI) has contributed immensely to significant reduction in mortality from vaccine preventable diseases (VPD) among children. To achieve maximal protection against vaccine-preventable diseases, a child should receive all immunizations within recommended intervals. The Nigerian Demographic and Health Survey, 2008 showed that 57.8% of children had received all recommended vaccines in Osun State far below WHO target of 80%. We conducted this study to determine RI coverage and drop-out rate (DOR) for RI vaccines in Atakumosa.

Abstract methods

Acommunity based cross-sectional survey of750children aged 12-23 months selected from 30 clusters in rural Atakumosa, using WHO Expanded program of Immunization (EPI) cluster sampling technique. We collected data on socio-demographic characteristics and history of vaccination using semi-structured questionnaire, vaccination cards were also reviewed. We computed the vaccination card retention (VCR) rate and calculated coverage rates for each vaccine antigen. We defined DOR as proportional difference between the consecutive vaccines. DOR for BCG-Measles and DPT1-DPT3 were calculated using Microsoft excel 2007 and Epi info version 7.

Abstract results

Mean age of children was 17.2 (±4) months. VCR rate was 63.0%. BCG had highest coverage rate of 54.8%, DPT1 (54.0%), OPV1 (52.0%), DPT2 (50.0%) and DPT3 (47.3%). The lowest coverage was observed for Measles (42.8%). DOR for BCG-Measles and DPT1-DPT3 was 21.8% and 12.4%, respectively. Children who were delivered in a health facility, (AOR=1.8, 95% CI = 1.2-2.7) were more likely to complete recommended vaccination.

Abstract conclusion

Vaccine coverage in these rural areas remained low and DOR were relatively high. There is need to improve on the completion of vaccinations. Further research to explore factors hindering completion of RI in this LGA is recommended.

Keywords: Vaccines, coverage rate, drop-out, rural, nigeria

PRESENTED BY: Elizabeth Adedire

ESCAIDE REFERENCE NUMBER: 20142012

Invasive pneumococcal disease (IPD) and effect of pneumococcal conjugate vaccines in Ireland in 2008-2013

Jolita Mereckiene[1], Margaret Fitzgerald[1], S. Cotter[1], Mary Corcoran[2], Hilary Humphreys[3] , Imelda Vickers[2], Robert Cunney[1, 2], Stephen Murchan[1], Darina O'Flanagan[1]

[1] Health Protection Surveillance Centre, Ireland; [2] Epidemiology and Molecular Biology Unit, Children's University Hospital, Temple Street, Ireland; [3] Education and Research Centre, Royal College of Surgeons in Ireland and Beaumont Hospital, Ireland

Abstract

Since 2008 enhanced surveillance of invasive pneumococcal disease (IPD) is undertaken on children and adolescents ‹15 yearsin Ireland. At national level data are collated in the Computerised Infectious Disease Reporting system. Since 2007 the National Pneumococcal Typing Laboratory offers a typing service to laboratories for all invasive S. pneumoniae isolates submitted. In 2008 pneumococcal conjugate vaccine (PCV7) was introduced for infants at 2, 6 and 12 months of age. A catch-up campaign was also implemented for children ‹2 years of age. In 2010 PCV13 replaced PCV7.

Abstract methods

We described IPD surveillance data for 2008-2013 in order to evaluate effect of PCV7 and PCV13 vaccines in Ireland. We calculated confidence intervals (CI) for proportions.

Abstract results

The incidence of confirmed IPD in 2013 (7.6/100,000;95%CI:6.9-8.4) declined by 20% compared with 2008 (9.5/100,000;95%CI:8.6-10.5). There has been a decline in IPD in all age groups due to PCV7 serotypes. The greatest effect has been in children ‹2 years of age; the incidence declined by 98% (28.0/100,000;95%CI:19.7-38.7 in 2008 versus 0.7/100 000;95%CI:0.03-3.4 in 2013). The decline due to the additional six PCV13 serotypes was 72% (7.4/100 000;95%CI:3.4-14.1 in 2008 versus 2.1/100 000;95%CI:0.4-6.0 in 2013) in this age group. The incidence of IPD due to non-PCV13 serotypes increased in some age groups. The predominant serotypes were 7F and 19A in overall population and 7F and 22F in children ‹2 years of age in 2013.Three vaccine failures due to serotype 19A were reported in 2013.

Abstract conclusion

PCV has a significant effect in reducing overall incidence of IPD in total population and in children ‹2 years of age indicating indirect immunity effect. Enhanced surveillance should continue to monitor future effect of PCV and IPD serotype distribution.

Keywords: Invasive pneumococcal disease, incidence, surveillance, pneumococcal vaccines.

PRESENTED BY: Jolita Mereckiene

ESCAIDE REFERENCE NUMBER: 20142091

Introduction of a national herpes zoster (shingles) vaccination programme in Scotland – monitoring the impact on neuropathic pain

Heather Murdoch[1], Kevin Pollock[1], John Love[1], Mag McFadden[2], Claire Cameron[1], Jim McMenamin[1], Guy McGivern[2]

[1] Health Protection Scotland (HPS), UK; [2] NHS National Services Scotland, UK

Abstract

Herpes zoster or shingles is characterised by a painful vesicular skin rash and incidence rises with increasing age. The main complication of shingles is post-herpetic neuralgia (PHN), a long-lasting neuropathic pain after rash has resolved. Patients have reported pain ranging from moderate to severe and debilitating effects on mood, mobility, sleep and overall quality of life. In Scotland, approximately 7,000 people aged 70 years and above develop shingles each year. Of these, between 700 -1,400 develop PHN. In September 2013 the first national herpes zoster (Shingles) Immunisation campaign was launched using Zostavax® vaccine. In Scotland, the vaccine is available from general practice (GP) surgeries to non-immunocompromised adults aged 70 years with a catch-up programme offered to 79 year olds. Treating PHN effectively, with tolerable side effects is a major clinical challenge with options including analgesics, anti-depressants, anticonvulsants and opioid pain medications e.g. morphine and topical treatments.

Abstract methods

Health Protection Scotland (HPS) established a system of population based surveillance to monitor the impact of the programme. People suffering from herpes zoster will usually consult their general practitioner (GP) and an aggregated data set is available from all the GP practices in Scotland. This has been supplemented by secondary care surveillance, prescribing data and numbers attending pain clinics.

Abstract results

Analysis of the first year of the programme will be presented including the impact on GP consultations, presentations of severe disease and on prescribing data, the latter which provides a proxy measurement of the impact of the vaccine.

Abstract conclusion

With the introduction of this vaccine comes a unique epidemiological opportunity to monitor the impact on the incidence of shingles and on occurrence of zoster related neuropathic pain.

Keywords: Herpes Zoster Vaccine, Neuralgia

PRESENTED BY: Heather Murdoch

ESCAIDE REFERENCE NUMBER: 20142226

Epidemiological pattern of mumps epidemic waves, associated hospitalizations and complications. Spain, 1998-2013

Noemi Lopez-Perea[1], Josefa Masa Calles[1], Fernando de Ory[2], María de Viarce Torres de Mier[1], María Victoria Martínez de Aragón[1]

[1] National Center for Epidemiology, Carlos III Health Institute. Ciber Epidemiología y Salud Pública (CIBERESP), Spain; [2] National Center for Microbiology, Carlos III Health Institute, Spain

Abstract

Mumps vaccine (Jeryl-Lynn-strain) was introduced in Spain in 1981 at 15months-aged. In 1995, second dose was introduced at 11 years-aged, and changed to 3-6 years-aged in 1999. During 1992-1999, Rubini-strain was administered in many regions and withdrawn due to low effectiveness. Despite high vaccination coverage (>95% since 1999), epidemics continued to appear.We aimed at characterizingthe 3 epidemic mumps-waves during 1998-2013, identifying changes in susceptible population related, and give recommendations to the national vaccination programme.

Abstract methods

Cases were obtained from the National Surveillance Network and hospitalizations from the national registry of hospitalizations (up to 2011, last year available). We defined 3 periods according to the epidemic waves (P1:1998-2003; P2:2004-2009; P3:2010-2013). We calculated period incidence rates (IR), hospitalization rates (HR) and complications rates among hospitalized cases (CR), by age-group.

Abstract results

In the study period, 88,208 cases were notified, 1,624 (1.8%) were hospitalized of which 624 had complications (34%). In P1, the most affected group was 1-4 years (IR=71.7 cases/100,000 population); in P2 was 15-19 (IR=33.0) and in P3, 15-19 (IR=53.9). The highest HR in P1 occurred at 15-19 years (HR=5.9 hospitalizations/million), in P2 at 20-24 (HR=3.9) and in P3, 15-19 (HR=1.1). The most affected group by complications was 15-24 years (CR=3.5 hospitalizations/million). Only in P1, CR in 5-9 age-group was similar to 15-19 (5.1 vs 5.9).

Abstract conclusion

Throughout the 3 waves, incidence shifted from kids to teenagers, according to the history of vaccination in Spain. Cohorts born during years of low vaccination coverage, vaccinated with Rubini-strain, or with only one dose were the most affected population. In addition to maintaining high vaccination coverage, in case of outbreaks, vaccination to the mentioned cohorts should be considered.

Keywords: Mumps, Epidemiological Surveillance, Vaccination, Inmunization Programs

PRESENTED BY: Noemi Lopez-Perea

ESCAIDE REFERENCE NUMBER: 20142259

Parallel Session 9: Outbreaks (2)

Investigation of a National Outbreak of Verotoxigenic E. coli (VTEC) in Ireland, 2013

Anne Carroll[1], Patricia Garvey[1], Paul McKeown[1], Eleanor McNamara[2]

[1] Health Protection Surveillance Centre, Dublin, Ireland; [2] VTEC Reference Laboratory, HSE, Dublin, Ireland;

Abstract

Ireland has the highest incidence of VTEC in Europe (12/100000 in 2012). In August 2013 the VTEC Reference Laboratory, Dublin (VTEC-RL) alerted the Health Protection Surveillance Centre (HPSC) of a number of VTEC O157 isolates from all over Ireland with one of two closely related PFGE patterns. One of these patterns had not been previously observed in Ireland. A multidisciplinary Outbreak Team was convened to investigate.

Abstract methods

We defined a confirmed case as: A person with VTEC O157 vtx2 with PFGE profile A) IE-O157-029 or B) IE-O157-271 with a date of onset of symptoms on or after August 1st 2013. Probable cases were VTEC O157 vtx2, but awaiting PFGE analysis. Trawling questionnaires were undertaken on cases and epidemiological, microbiological and environmental data collated.

Abstract results

Between August 2013 and December 2013, 51 cases of VTEC O157 belonging to one of the two outbreak PFGE profiles were reported. Cases were observed in 7/8 Irish Health Regions. When data from cases associated with PFGE profiles A and B were analysed, significant differences in the two groups were observed with respect to date of onset (profile A Median week 37 profile B median week 40, $p=0.013$), geographical distribution (profile A predominantly south, profile B predominantly west, $p=0.008$) and age group (Profile A median 22 years, profile B median 50 years $p=0.042$). The outbreak was declared over in March 2014 without a source being defined.

Abstract conclusion

Two national VTEC outbreaks were running concurrently in Ireland. These outbreaks would not have been detected and investigated without PFGE profiling. It is recommended that all VTEC isolates are referred to VTEC-RL for PFGE.

Keywords: VTEC, Outbreak, PFGE

PRESENTED BY: Anne Carroll

ESCAIDE REFERENCE NUMBER: 20142174

A Legionnaires' disease outbreak associated with cooling towers in Warstein, Germany, August 2013

Anna Maisa[1], Ansgar Brockmann[2], Frank Renken[2], Christian Lück[3], Stefan Pleischl[4], Martin Exner[4], Inka Daniels-Haardt[1], Annette Jurke[1]

[1] Department of Infectiology and Hygiene, NRW Centre for Health, Münster, Germany; [2] Public Health Department, Soest, Germany; [3] Institute for Medical Microbiology and Hygiene, National Consulting Laboratory for Legionella, University of Technology, Dresden, Germany; [4] Institute for Hygiene and Public Health, University of Bonn, Bonn, Germany

Abstract

Legionnaires' disease (LD) results mainly from inhalation of aerosols containing the bacterium Legionella pneumophila, which may cause atypical severe pneumonia. Between the 1st of August and 6th of September an unusual cluster of patients with LD of unknown etiology in Warstein, North Rhine-Westphalia, Germany was notified to the public health authorities.

Abstract methods

Laboratory investigation was performed according to requirements of European case definition. A questionnaire had been used to narrow down possible sources of infection. Cases and controls were matched for age-group and sex.Odds ratio (OR), 95% confidence interval (CI) and p-values were calculated by logistic regression. Values of p.

Abstract results

The outbreak accounted for 78 laboratory-confirmed cases including one death. Legionella pneumophila, serogroup 1, subtype Knoxville, sequence type 345, could be identified as the epidemic strain. Cases were 19 to 94 years old, 64% were males. The case fatality rate was 1.28%, 91% of cases were hospitalised, 17% of those needed intensive care. In the univariable analysis cases were almost five times more likely to smoke than controls (OR 4.869; 95% CI 2.378-9.967; $p<0.0001$). Furthermore cases were three times more likely to live in a 2 km distance around one source including the town centre and parts of the surrounding than controls (OR 3.443; 95% CI 1.261-9.559; $p<0.016$).

Abstract conclusion

This is the largest outbreak in Germany of LD to date, which was caused due to a series of uncommon events most probably by more than one source involving industrial cooling towers. Quick epidemiological assessment, source tracing and closure, rapid testing and early treatment are necessary to limit morbidity and mortality. Maintenance of cooling towers must be reliable to prevent such LD-outbreaks in future.

Keywords: Outbreak; pneumonia; Legionnaires' disease; infection control; water microbiology

PRESENTED BY: Annette Jurke

ESCAIDE REFERENCE NUMBER: 20142216

Norovirus outbreak after corporate birthday party buffet associated with asymptomatic catering staff in Bavaria, Germany, December 2013

Nadine Zeitlmann[1, 2, 3], Annette Heissenhuber[3], Stefan Guenther[4], Nikolaus Ackermann[3], Marina Hoehne[5], Wolfgang Hautmann[3]

[1] Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [3] Bavarian Health and Food Safety Authority, Oberschleissheim, Germany; [4] Health Authority Weilheim-Schongau, Weilheim, Germany; [5] Department for Infectious Diseases, Robert Koch Institute, Berlin, Germany

Abstract

On 16/12/2013 a local health authority informed us of a gastroenteritis outbreak among guests of a birthday party buffet on 13/12/2013 catered by a local butcher. We initiated an outbreak investigation to identify possible vehicles and modes of transmission.

Abstract methods

On 19/12/2013 we distributed postal questionnaires to 89 party guests asking about symptoms and consumed food. We defined cases as guests reporting diarrhoea or vomiting between 10 and 60 hours after start of the buffet. Stool specimens from cases, catering staff, and samples from left-over food items from buffet and catering shop, all taken 16-17/12/2013, were tested for norovirus. Isolates were submitted for molecular typing. We calculated overall and food-specific attack rates (AR) and risk ratios (RR) using univariable analyses. Food safety officers inspected the catering company.

Abstract results

Seventy-eight guests responded (88%). All had eaten from the buffet. Thirty cases (ARoverall: 38%) occurred, of which 83% with disease onset 15/12/2013. All cases had consumed raw cabbage salad (ARcabbage: 45%), 29 cases also roasted pork (ARpork: 41%, RR: 2.5, 95%-CI: 0.41-15), the only food-items home-made by the caterers. Caterers reported gastrointestinal symptoms in the week before, but stated to be asymptomatic at time of food preparation. Norovirus was detected in 3/3 specimens of guests and in 9/11 of the caterers. No food sample tested positive. Molecular analyses revealed identical norovirus sequences from two cases and two caterers of the recombinant genotype GII.14/II.P7 never detected before in Germany.

Abstract conclusion

Our results suggest cabbage salad contaminated during preparation by asymptomatic caterers as the most likely vehicle for this norovirus outbreak. Food-handlers need to pay increased attention to hygiene also after recovery of gastroenteric symptoms due to the prolonged shedding of norovirus.

Keywords: Norovirus, foodborne diseases, food handling, gastroenteritis

PRESENTED BY: Nadine Zeitlmann

ESCAIDE REFERENCE NUMBER: 20142159

Outbreak of Yersinia pseudotuberculosis O1 infection in Southern Finland associated with raw milk consumption, February-April, 2014

Triin Pärn[1], Sari Huusko[2], Jukka Ollgren[2], Saara Salmenlinna[2], Saija Hallanvuo[3], Annika Pihlajasaari[4], Seija Heikkinen[5], Ruska Rimhanen[2]

[1] Finnish National Institute for Health and Welfare, Finland; [2] Department of Infectious Diseases Surveillance and Control, National Institute for Health and Welfare (THL), Finland; [3] Finnish Food Safety Authority Evira, Research and Laboratory Department, Food and Feed Microbiology Unit, Helsinki, Finland; [4] Finnish Food Safety Authority Evira, Control Department, Food Hygiene Unit, Helsinki, Finland; [5] The City of Porvoo, Environmental Health Department, Porvoo, Finland

Abstract

In April 2014, a municipal authority from Southern Finland reported a Yersinia pseudotuberculosis (Yp) outbreak to the National Institute for Health and Welfare. We investigated the outbreak to identify its source.

Abstract methods

Clinical laboratories in Finland must report Yp infections identified by stool culture or antibodies in serum to the National Infectious Disease Registry (NIDR). We defined a case as a person notified for Yp infection during February-April 2014 and matched them with controls chosen among their healthy family members. Information on raw milk consumption (suggested as source of the infection in trawling interviews) and exposures associated with previous Yp outbreaks was collected by using a web-based questionnaire and analysed by family-matched exact logistic regression. The Food Safety Authority conducted a trace-back to identify the source farm. Reference laboratories typed Yp isolates from patients, raw milk, and milk filter originating from case's home and suspected farm by serotyping, pulsed field gel electrophoresis (PFGE) and multiple-locus variable-number of tandem repeats analysis (MLVA).

Abstract results

We identified 54 Yp infections from NIDR. Preliminarily, 22 families out of 48 participated (family response: 46%). 24 of 66 respondents met the case definition (median age: 12 years, 58% males). Compared with controls, cases were more likely to have consumed raw milk from one producer (median unbiased estimate of OR=15, p-value 0.002). Isolates from milk and milk filter had identical serotype (O1), PFGE and MLVA profiles to isolates typed from eight patients.

Abstract conclusion

Contaminated raw milk originating from one farm in Southern Finland was the likely source of this outbreak. We recommended heating raw milk before consumption. The farm discontinued commercial production of raw milk until the municipal authority will accept its new control plan.

Keywords: Yersinia pseudotuberculosis, disease outbreaks, raw milk, Finland

PRESENTED BY: Triin Pärn

ESCAIDE REFERENCE NUMBER: 20142233

Parallel Sessions 10 – 12 13.30 – 15.10 Thurs 6

Parallel Session 10: Outbreaks (3)

Sub-clinical pertussis infection in teenage children as a vehicle for transmission; seroepidemiology of recent infection during a school outbreak, UK 2012

Amy Mikhail[1], Sonia Ribeiro[1], David Litt[1], Nick Andrews[1], Gayatri Amirthalingam[1], Philip Monk[1], Norman K. Fry[1]

[1] Public Health England, UK

Abstract
There has been a marked resurgence of pertussis across the UK since 2011, with a notable increase in incidence amongst older children. In March 2012, a cluster of 7 cases from an English boarding school was reported, triggering an investigation and school-wide vaccination campaign. We conducted a seroprevalence survey to determine the extent of this outbreak.

Abstract methods
Data on the presence of clinical symptoms compatible with pertussis infection (persistent cough >2 weeks) were collected from 842 students aged 10–19 years (65% of school population). Seroprevalence for each year of age was determined by assessing oral fluid specimens from 327 students for evidence of recent pertussis infection (defined as anti-pertussis toxin IgG levels >70 arbitrary units) by in-house ELISA.

Abstract results
135 students met our clinical case definition, of which of which 29/55 tested had serological evidence of recent pertussis infection. 54 asymptomatic students were also seropositive (geometric mean titre: 146AU). The earliest cough onset date for a seropositive student was in September 2011. Seroprevalence increased with age and was highest amongst 18–19 year-olds (P=0.015) who had not received a preschool booster vaccination. Students were 3 times more likely to be seropositive if they had a cough (Risk Ratio 95%CI: 1.93–3.88) and had higher anti-pertussis toxin IgG titres (geometric mean 71 vs. 29AU, P=0.0001). There was no significant association between titre and time since cough onset.

Abstract conclusion
This investigation uncovered evidence of widespread transmission at the school, which began 5 months earlier than the first reported cluster and included a high proportion of asymptomatic infections. These findings highlight the importance of early identification and the need for a rapid response to outbreaks in closed settings.

Keywords: Whooping cough, Bordetella, pertussis, seroepidemiologic studies, oral fluids, asymptomatic infections, enzyme-linked, immunosorbent assay

PRESENTED BY: Amy Mikhail

ESCAIDE REFERENCE NUMBER: 20141988

An outbreak of acute gastroenteritis associated with group A Rotavirus in a residential long-term care facility in Slovenia, April 2013

Maja Subelj[1, 2], Veronika Ucakar[1], Irena Klavs[1]

[1] National Institute of Public Health of Slovenia, Ljubljana,Slovenia; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden

Abstract
From January 2008 to April 2014, sixteen Rotavirus outbreaks in long-term care facilities (LTCFs) were reported in Slovenia. In 2013, an outbreak of acute gastroenteritis in LTCF was reported to the Institute of Public Health of Ljubljana. Our objective was to describe the outbreak, identify factors associated with infection, and recommend control measures.

Abstract methods
We defined a probable case as a resident of the LTCF with acute diarrhoea and at least one of the following symptoms: fever, vomiting, nausea, fatigue, headache, and abdominal pain between April 11 and 23, 2013; confirmed cases had enzyme immunoassay-confirmed Rotavirus infection. We described cases and compared their exposures with those of controls, selected randomly from residents at a 2:1 control:case ratio. We calculated adjusted odds ratios (aORs) and 95% confidence intervals (CIs) in a multivariable logistic regression model. We obtained stool specimens and tested for enteric pathogens with enzyme immunoassay.

Abstract results
The attack rate among residents was 14.7%. Twenty-eight (84.8%) of the affected residents were females. The age ranged from 71 to 95 years (median 85.5 years). In addition to acute diarrhoea, the most common symptoms were fatigue (54.1%) and nausea (45.9%). The median duration of gastroenteritis was three days (range 1-13 days). Two patients provided stool samples; Rotavirus group A was detected in one. Having more than two comorbidities (aOR=4.7; 95% CI: 1.14-19.0), and being ambulant (aOR=12.3; 95% CI: 1.14-133) were significantly associated with infection.

Abstract conclusion
During the outbreak, we advised residents to avoid group activities until two days after cessation of symptoms. Those with comorbidities were alerted to their increased risk and advised to retain in their premises during the outbreak.

Keywords: Rotavirus; gastroenteritis; outbreak; case-control study; Slovenia

PRESENTED BY: Maja Subelj

ESCAIDE REFERENCE NUMBER: 20141960

Cluster of diarrhea following typhoon Haiyan, Philippines, November-December 2013: A four-hour investigation

Michael Edelstein[1, 2], Boyd Cerro[3], John O'Brien[4], Altaf Musani[5]

[1] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [2] Public Health Agency of Sweden, Solna, Sweden; [3] Regional Epidemiology Surveillance Unit, Department of Health Region VIII, Palo, Philippines; [4] Catholic Relief Services, Baltimore, United States; [5] World Health Organization, Philippines

Abstract

On 14 December 2013, a health centre in Leyte Province, Philippines, reported five febrile diarrhea cases from one remote village; more villagers had allegedly become sick since typhoon Haiyan (8 November). On 19 December, the Philippine Army airlifted us in the village to identify the source, treat symptomatic individuals and implement control measures.

Abstract methods

Epidemiologists, water/sanitation specialists, clinicians and logisticians prepared questionnaires, analysis plans and supplies (medication, water purification tablets) in advance. Upon 10h00 arrival, we enumerated and interviewed villagers, collected rectal swabs from symptomatic individuals, inspected and tested water sources for pathogens. We described cases (villagers with ≥ 3 loose stools/day after 8 November) by time and person and compared cases with controls in terms of exposures through odds ratios (OR) and 95% confidence intervals (95%CI).

Abstract results

Among 350 individuals in 56 households, we identified 35 cases (median age: 2, range 0-49; median symptom duration: 2.5 days, range 1-30) and one death. 3 cases had bloody diarrhea. Cases started occurring on 9 November, peaked on 11 November, decreased, and peaked again on 12 December, with 7 symptomatic when we visited. Compared with 9 controls, 17 cases were less likely to use soap (OR 0.09, 95% CI 0.01-0 .79). The typhoon destroyed the main water pipe, forcing all villagers to use a spring located underneath latrines and grazing areas. No pathogens were isolated from rectal swabs. Water specimens grew E.coli>100 MPN/100ml.

Abstract conclusion

A contaminated spring likely caused this post-disaster cluster, which may have been further propagated by poor hygiene. We treated symptomatic cases, distributed water containers and purification solution to all households, and departed at 14h00. Following our recommendations, the pipe was repaired. No further cases were reported.

Keywords: Disease outbreak; Philippines; disaster; Escherichia coli

PRESENTED BY: Michael Edelstein

ESCAIDE REFERENCE NUMBER: 20141975

A prolonged outbreak of Salmonella Infantis associated with pork products in central Germany, April to October 2013

Sabine Schroeder[1, 2], Manuela Harries[2, 3, 4], Rita Prager[5], Wolfgang Rabsch[5], Dagmar Rimek[1]

[1] Thuringian State Authority for Consumer Protection, Bad Langensalza, Germany; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [3] Governmental Institute of Public Health of Lower Saxony, Hannover, Germany; [4] Postgraduate Training for Applied Epidemiology (PAE, German Field Epidemiology Training Programme), Robert Koch Institute, Berlin, Germany; [5] Robert Koch Institute, Wernigerode, Germany

Abstract

An increase of salmonellosis cases in central Germany, caused by Salmonella Infantis, was observed in May 2013. We investigated to identify vehicles of infection.

Abstract methods

We analysed surveillance data and conducted trawling interviews, a case-control study, and food trace back. Cases were defined as persons residing in central Germany with laboratory-confirmed infection with the outbreak strain and onset of disease after 16/04/2013. We described cases by demography, onset of disease, and place of infection. For each case aged above 17 years, we recruited one control from the cases' neighbourhood by random digit dialling and compared exposures using odds ratios (OR) and 95% confidence intervals (CI). Isolates of human, animal, food, and environmental origin were characterized by serotyping, phage-typing, and pulsed-field-gel-electrophoresis.

Abstract results

We identified 267 cases between 16/04/2013 and 26/10/2013 in four federal central German states (Thuringia: 186, Lower Saxony: 44, Saxony-Anhalt: 31, Hesse: 6) with a median age of 56 (0-93) years; 146 (55%) were males. Eighty-seven (32%) were hospitalized; one person died. Thirty-six (67%) of 54 cases and 25 (45%) of 56 controls had eaten minced meat from local butcher shops (OR=2.5; 95% CI: 1.1-5.8). Cases were more likely to have eaten minced pork several times a week than controls (OR=6.0; 95% CI: 1.0-34.4). The outbreak strain was Salmonella Infantis phage-type 29 XbaI27, isolated from raw pork products from different butcheries, from a slaughterhouse, and pigs at one farm.

Abstract conclusion

One of the largest Salmonella outbreaks in Germany within the last 10 years was associated with consumption of pork. Insufficient hygiene measures in the slaughterhouse were the most probable cause of the ongoing transmission. Improvement of the process control during slaughter was recommended to prevent further outbreaks.

Keywords: Outbreak, salmonella, case-control study, pork, Germany

PRESENTED BY: Sabine Schroeder

ESCAIDE REFERENCE NUMBER: 20141983

Outbreak of Salmonella Goldcoast associated with whelks: a novel vehicle of infection, England, 2013

Thomas Inns[1], Gillian Beasley[2], Giri Shankar[2]

[1] Public Health England, UK; [2] Anglia and Essex Public Health England Centre, Public Health England, UK;

Abstract

We observed an increase in laboratory-confirmed cases of Salmonella enterica serotype Goldcoast in England during September 2013. From laboratory-based surveillance data we expected one case; 17 were recorded. In response, we undertook a national investigation to identify the source of infection and implement control measures to prevent further cases.

Abstract methods

Through a telephone-based trawling questionnaire we generated the hypothesis of whelk (sea snail) consumption being associated with infection; we tested this in a case-control study.Cases, defined as persons resident in England with Salmonella Goldcoast infection between 1 June and 31 December 2013, were compared to controls recruited through a geographically-based systematic digit dialling process. We used logistic regression to quantify associations (adjusted Odds Ratios (aOR) with 95% Confidence Interval (95%CI)) between exposures and illness. Food trace-back and environmental investigations were undertaken by environmental health officers and the Food Standards Agency.

Abstract results

Forty three cases (67% male, median age 65 years), residing throughout the country, were identified; 26 reported whelk consumption and 21 ate whelks supplied by Factory X. Twenty cases and 27 controls were included in the analytic study. Cases were more likely than controls to eat whelks (aOR=109, 95% CI =7.7-1539); 16/20 cases were exposed. Two cooked whelk samples and six environmental samples from Factory X tested positive for Salmonella Goldcoast.

Abstract conclusion

We present epidemiological, environmental, microbiological and food trace-back results, which all support the conclusion that this outbreak was associated with consumption of whelks processed by Factory X. Whelks from Factory X were recalled and control measures were implemented. We recommend that suppliers of cooked whelks ensure proper heat treatment of whelks and cleaning of equipment to ensure no contamination from raw to cooked products.

Keywords: Disease outbreaks; Salmonella: Case-control studies

PRESENTED BY: Thomas Inns

ESCAIDE REFERENCE NUMBER: 20141985

The perils of gourmet eating: outbreak of gastroenteritis due to enteric viruses at a high-end London restaurant, January 2014

Amy Mikhail[1], Alan Hunter[1], Alistair Blake[1], Laura Pomeroy[1], Benedetto Simone[2], Piers Mook[2], Paul Crook[1], Kirsty Hewitt[1], Nollaig Hallihan[3], Philip Goodchild[3], Derren Ready[1], David James Allen[1], Bob Adak[1], Tom Nichols[1], Yimmy Chow[1], Sarah Anderson[1]

[1] Public Health England, UK; [2] Field Epidemiology Services (Victoria), Public Health England, UK; [3] Westminster City Council, UK

Abstract

In January 2014, Public Health England was notified of 64 clusters of gastroenteritis cases amongst diners at a gourmet restaurant in London, owned by a chef known for their experimental cooking methods. Here we describe the investigation of this outbreak.

Abstract methods

We conducted a case control study by interviewing affected diners using questionnaires delivered online or via telephone. Cases were defined as diners who became unwell with at least two of diarrhoea, vomiting, nausea or stomach cramps within 72 hours of eating at the restaurant and co-diners who remained well after their meal were recruited as controls. Stool specimens from recently symptomatic cases and food samples from the restaurant were screened for common bacterial and viral causes of gastroenteritis. Information on staff illness and food preparation methods was also collected. We calculated odds ratios for exposures to different menu items, common ingredients and exposure to potentially infectious food handlers. Multi-variable analysis was conducted using logistic regression.

Abstract results

In total, 104 diners and 19 staff met our case definition. Cases had a median onset of 31 hours after eating and median illness duration of 2 days. Norovirus genogroup I (n=8), II (n=11) and sapovirus (n=6) were detected in stool specimens from 13/24 cases screened. Cockles were found to be highly contaminated with multiple genotypes of norovirus genogroups I, II and sapovirus. Cases were seven times more likely to have eaten dishes containing cockles (adjusted OR 6.93; 95%CI 1.68 – 28.49) than controls.

Abstract conclusion

We conclude that inadequately cooked contaminated cockles were the primary vehicle driving this outbreak, supplemented by possible cross-contamination. Adequate cooking temperatures (>70°C) are strongly recommended, particularly for shellfish which are vulnerable to contamination by sewage outflows.

Keywords: Gastroenteritis, experimental cooking, norovirus, sapovirus Cerastoderma edule (cockles), Contaminated shellfish

PRESENTED BY: Amy Mikhail

ESCAIDE REFERENCE NUMBER: 20141987

Parallel Session 11: HIV and sexually-transmitted infections

Molecular epidemiology suggests ongoing transmission of hepatitis B virus in rural parts of the Netherlands, 2009-2013

Loes Soetens[1], Birgit van Benthem[1], Anouk Urbanus[1], Jeroen Cremer[1], Kim Benschop[1], Ariene Rietveld[2], Susan Hahné

[1] RIVM, The Netherlands; [2] Municipal Health Service Hart voor Brabant, The Netherlands; [3] National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands

Abstract

Since the introduction (2002) of the hepatitis B vaccination programme targeted at high-risk groups, the reported acute hepatitis B incidence in the Netherlands declined and reached its nadir in 2013. Yet, recent regional signals about increased number of hepatitis B cases raised the question how hepatitis B incidence was distributed over the country. In this study, regional differences in hepatitis B epidemiology were investigated using epidemiological and molecular typing data.

Abstract methods

Acute hepatitis B virus (HBV) infections, reported between 2009-2013, were included. Fragments of S and C gene were amplified and sequenced (part of the surveillance since 2004). Regional differences in incidence were studied by geographical mapping of cases and cluster analysis. Regional differences in transmission were studied by constructing regional maximum parsimony trees based on the S or C gene to measure genetic clustering of cases.

Abstract results

In 431 (50.2%) of the 858 notified cases (2009-2013), the S and/or C gene of the virus could be sequenced. Most infections were acquired through sexual contact, by both heterosexual (n=322) and homosexual (n=242) sexual contact. Geographical mapping of notified cases revealed that incidences in rural border areas of the Netherlands were highest. Geographic cluster analysis identified two significant clusters (p.

Abstract conclusion

This study showed that regional differences in HBV epidemiology were present in the Netherlands. Rural border regions showed higher incidences and more ongoing transmission than the inland areas. Further preventive measures, such as outreach-vaccination, should focus more on these regions.

Keywords: Hepatitis B; Molecular epidemiology; Geographic mapping; Cluster analysis; Surveillance

PRESENTED BY: Loes Soetens

ESCAIDE REFERENCE NUMBER: 20142069

Epidemiology and antimicrobial resistance of gonorrhea in Finland, 2007-2013

Triin Pärn[1], Jukka Ollgren[2], Jari Jalava[2], Eija Hiltunen-Back[2], Eveliina Tarkka[3], Outi Lyytikäinen[2]

[1] Finnish National Institute for Health and Welfare, Finland; [2] Department of Infectious Diseases Surveillance and Control, National Institute for Health and Welfare (THL), Finland; [3] Clinical Bacteriology Unit, Helsinki University Central Hospital, Finland

Abstract

Several European countries have observed an increase in gonorrhea infections and globally emerging antimicrobial resistance to third-generation cephalosporins is complicating treatment. We analyzed Finnish surveillance data and antimicrobial resistance of gonorrhea from 2007-2013 in order to provide recommendations for prevention and treatment.

Abstract methods

Laboratories notify positive gonorrhea findings and physicians cases to the National Infectious Diseases Registry. Physicians' notifications include data on country of infection and route of transmission. Data on antimicrobial resistance by age groups is reported to a separate system (since 2008). We evaluated trends by age, sex and residence using Poisson regression and calculated proportions of gonorrhea isolates resistant to antimicrobials.

Abstract results

During 2007-2013, a total of 1749 cases were reported: 75% were males, 22% among men having sex with men (MSM) and 35% acquired abroad, with no significant change in proportions over time. Men accounted for 86% of travel-related infections. The incidence increased from 3.6/100,000 population in 2007 to 4.9/100,000 in 2013 ($p<0.001$). The increase occurred among both genders, persons aged 20-29 years and residents of Helsinki ($p<0.001$). During 2008-2013, 777 isolates were tested for antimicrobial susceptibility. Ciprofloxacin resistance increased from 55% in 2008 to 62% in 2013; 7 (1%) isolates showed intermediate resistance to ceftriaxone.

Abstract conclusion

Despite the increasing trend, the overall rate of gonorrhea in Finland remained low. Prevention measures should be targeted to young adults in metropolitan area, male international travelers and MSM. Cephalosporin resistance has not yet been detected, allowing it to continue as first-line treatment.

Keywords: Gonorrhoea, antimicrobial resistance, surveillance system

PRESENTED BY: Triin Pärn

ESCAIDE REFERENCE NUMBER: 20141974

Was there any impact of the ECDC Guidance on Chlamydia control in Europe five years after publication?

Otilia Sfetcu[1], Bethan Davies[2] Helen Ward[2], Minttu Rönn[2], Ingrid van den Broek[3], Jan van Bergen[4], Susana Barragan[1], Caroline Daamen[1], Nicola Low[5], Andrew Amato[1]

[1] European Centre for Disease Prevention and Control (ECDC), Sweden; [2] Infectious Diseases Epidemiology, School of Public Health, Imperial College London, UK; [3] Unit of Epidemiology and Surveillance, RIVM/Centre for Infectious Disease Control Netherlands, The Netherlands; [4] RIVM/Centre for Infectious Disease Control, University of Amsterdam, and STI AIDS Netherlands, The Netherlands; [5] Institute of Social and Preventive Medicine (ISPM), University of Bern, Switzerland

Abstract

In 2007, a survey of chlamydia control activities documented wide variation between European Union/European Economic Area (EU/EEA) countries. In 2009, the European Centre for Disease Prevention and Control (ECDC) published Chlamydia control in Europe Guidance, aiming to support the policy making process in Member States. Five years after publication, ECDC evaluated the guidance's impact on policy and explored the need for revision.

Abstract methods

ECDC surveys in 2007 and 2012 described national chlamydia prevention and control activities. Questions in the 2012 survey investigated awareness and specific use of guidance. The guidance audience was defined by: Google Analytics statistics on guidance webpage visits (2011-2014) and keyword searches for citations in the published literature (ISI Web of Knowledge, PubMed, Google Scholar and Researchgate). An expert focus group reviewed the results and identified areas for guidance revision.

Abstract results

Fewer countries reported no organised activities in 2012 compared to 2007 (20% (6/28) versus 45% (11/27)). Combinations of case management, partner notification and opportunistic testing were reported by 46% (13/28) in 2012, up from 22% (6/27) in 2007. In 2012, 92% (24/26) countries stated they were aware of the guidance; 44% (11/25) used the guidance for: writing new policy/strategy (n=5), raising awareness for chlamydia (n=4), improving surveillance (n=4), obtaining funding (n=2) or reviewing existing control frameworks (n=2). There were less than 200 guidance webpage visits and 40 peer-review publications cited the guidance.

Abstract conclusion

Chlamydia control activities strengthened in EU/EEA Member States and the ECDC guidance reportedly influenced for policy changes in some countries. To better inform policy decision processes, guidance revision is planned by ECDC; priority areas for scientific advice include primary prevention, partner notification, opportunistic testing and testing in pregnancy.

Keywords: Chlamydia, policy, evaluation, prevention and control, ECDC

PRESENTED BY: Otilia Sfetcu

ESCAIDE REFERENCE NUMBER: 20142202

Communicating better with MSM – better prevention of HIV/AIDS/STIs and hepatitis

Irina Dinca[1], Piotr Wysocki[2], Matthias Wentzlaff-Eggebert[3], Dirk Sander[3], Andrew Amato[1]

[1] ECDC, Sweden; [2] National AIDS Centre Poland, Poland; [3] Deutsche AIDS-Hilfe e.V., Germany

Abstract

The recent HIV/AIDS trend in the EU is relatively stable, however there are still groups more affected - men who have sex with men (MSM). Other diseases transmitted via sexual intercourse, e.g. STIs and hepatitis affect MSM disproportionally. There is a need to design and implement more effective targeted communication activities to reduce risk behaviours and contribute to improving this situation.

Abstract methods

ECDC launched a project to develop guidance on communication strategy and key messages around MSM and HIV/AIDS/STI and hepatitis prevention. The steps involved: rapid desk review of research and grey literature, expert and stakeholder/key informants consultation and then an intensive iterative consultation process reviewing the guidance as it develops. A wide range of stakeholders were involved, including experts from non-governmental organizations (NGOs).

Abstract results

The communication strategy proposes principles, rationales, components and pathways to developing communication programs tailored to local needs. Not posing as a "magic bullet", the document proposes a flexible structure and elements to take into account when designing a communication strategy, providing with a practical "menu" from which strategists can pick and choose the elements most appropriate to a given context. The key message part is structured in three layers, according to their complexity: a) "blunt and direct" messages – basic information; b) "detailed and explanatory" messages – to support informed decision making; c) "nuanced and holistic" messages – provide relevant details. Examples are used throughout to illustrate various types of messages and highlight good practice. A step-by-step guide is also included.

Abstract conclusion

This type of hands-on document, produced through an intensive participatory approach, can be of great assistance in the countries in designing, implementing and evaluating communication activities in the area mentioned above.

Keywords: MSM, communication, key messages, guidance, HIV/AIDS/STIs, hepatitis.

PRESENTED BY: Irina Dinca

ESCAIDE REFERENCE NUMBER: 20142250

Surveillance in the time of austerity; Portuguese HIV/AIDS Surveillance achieves a 30% improvement in efficiency after LEAN inspired changes to processing.

Tara Shivaji[1], Helena Cortes[2], Martins Antonio Diniz[1], Paulo J. Nogueira[3], Paula Vasconcelos[1], Andreia Silva[1]

[1] Directorate General of Health, Portugal; [2] National Institute of Health, Ricardo Jorge, Lisbon Portugal; [3] Directorate of Analysis and Information, Directorate-General of Health; Preventive Medicine Institute, Medical Faculty of Lisbon, Portugal

Abstract

In 2013, following reminders about statutory notification of HIV/AIDS, Portuguese clinicians notified all cases, irrespective of previous notification. At the same time, hospitals introduced electronic records that automatically generated paper notification reports. No supplemental resources were available to process the 10-fold increase in notifications. The ensuing backlog caused delays in providing timely information for HIV program planning and evaluation. We investigated whether management principles from the automobile industry (LEAN) could improve data management efficiency.

Abstract methods

Efficiency was defined as the time spent processing the paper report into electronic surveillance information. We used value stream mapping to understand the process and employed focus groups to identify areas for improvement (LEAN methodology). We recorded the time taken to complete this process for randomly selected batches of reports and calculated the average time per report.

Abstract results

When consulted, stakeholders expressed the need for information about recent HIV/AIDS diagnoses. We prioritized processing cases diagnosed between 2011-2013. We reduced data-entry errors and transcribing time by inserting drop-down menus and automatic variable calculators. We implemented auto-search during data entry to prevent duplication. We redesigned the data entry mask to match the paper report. Before intervention, processing time was 9 minutes and 28 seconds (95%CI 8:53-10:58) per report. Two months post-intervention, this was 6 minutes and 34 seconds (95% CI 6:25-6:43), reducing the time to process the remaining backlog (10,000 reports) by 54 days.

Abstract conclusion

Applying LEAN techniques to HIV/AIDS surveillance in Portugal enabled delivery of crucial information to national and international HIV stakeholders through a 30% reduction in data processing time and optimization of data quality. Public health practitioners should consider LEAN techniques to improve data quality and efficiency of surveillance systems.

Keywords: HIV Acquired Immunodeficiency, Syndrome, Surveillance, Quality Improvement, Total Quality Management

PRESENTED BY: Tara Shivaji

ESCAIDE REFERENCE NUMBER: 20142197

Parallel Session 12: Zoonoses

Rapid information to the public helps to contain Trichinellosis outbreak: early post-exposure prophylaxis limits infection after exposure to contaminated raw meat products, Germany, 2013

Susanne Barbara Schink[1], Mirko Faber[1], Anne Mayer-Scholl[2], Christoph Ziesch[3], Ralph Schönfelder[4], Heidi Wichmann-Schauer[2], Karsten Nöckler[2], Klaus Stark[1]

[1] Robert Koch Institute, Germany; [2] Federal Institute for Risk Assessment, Germany; [3] Public Health Department, Görlitz Administrative District, Germany; [4] Food Safety and Veterinary Authority, Görlitz Administrative District, Germany

Abstract

Raw meat products are enjoyed as delicacies in some parts of Europe. Food safety authorities alerted that Trichinella-infested meat had entered the food chain in Germany in March 2013. Mobile vendors sold ≥300 raw wild boar sausages within 5 days. Public health authorities issued guidelines including post-exposure prophylaxis (PEP) by mebendazole on this low prevalence disease usually associated with exposure abroad. We examined the timing and effectiveness of PEP in this outbreak and inquired about the first news source.

Abstract methods

From March to December 2013, we interviewed all persons who reported to local public health offices on amount consumed, symptoms, post-exposure medication, news medium and prior disease-specific knowledge. Serum samples were tested by an in-house Trichinella-specific ELISA. We defined cases as persons presenting with myalgia and/or periorbital swelling post exposure and Trichinella-specific IgM and IgG antibodies. We investigated factors determining PEP failure. Relative risks (RR) and 95% confidence intervals (CI) were calculated using exact Poisson regression.

Abstract results

Eighty-two persons were interviewed and tested. Antibodies were detected in 21/82 (26%) participants, 14/21 (67%) met the case definition. Mebendazole was taken by 48 persons; 20 (48%) started within 0-5 days, 14 (33%) within 6-10 days and 8 (19%) ≥11 days. Cases more likely occurred among those starting PEP within 6-10 days (4/14, 29%), compared to starting within 0-5 days (0/20, 0%); (RR=8.5, 95%CI 1.1-∞). Respondents received information first through newspapers (40%), radio (22%) and word-of-mouth (9%).

Abstract conclusion

PEP appears to be more effective in preventing infection when given early, preferably ≤5 days. Given the low prevalence and high unfamiliarity with Trichinellosis among physicians and patients, we recommend that public health professionals fast-track PEP and communicate information broadly through various media.

Keywords: Trichinellosis, food-borne disease, zoonosis, post-exposure prophylaxis, communication.

PRESENTED BY: Susanne Barbara Schink

ESCAIDE REFERENCE NUMBER: 20142061

Nationwide registry-based analysis of Q fever incidence and pregnancy outcome during an outbreak in The Netherlands

Marit M.A. de Lange[1], Chantal W.P.M. Hukkelhoven[2], Janna M. Munster[3], Peter M. Schneeberger[4], Wim van der Hoek[5]

[1] National Institute for Public Health and the Environment, The Netherlands; [2] The Netherlands Perinatal Registry, The Netherlands; [3] University Medical Centre Groningen, The Netherlands; [4] Jeroen Bosch Hospital, The Netherlands; [5] Department for Respiratory Infections, Centre for Infectious Diseases, Epidemiology and Surveillance. National Institute for Public Health and the Environment (RIVM), The Netherlands

Abstract

Studies on Q fever and serious obstetric complications show inconsistent results. Therefore, during the Dutch Q fever epidemic in 2008-2010, pregnant women were not routinely screened for antibodies against Coxiella burnetii. The aim of this study was to assess whether Q fever affected areas had higher rates of adverse pregnancy outcome than areas not affected by Q fever, in order to evaluate the policy of not implementing large-scale screening.

Abstract methods

In this nationwide population-based retrospective cohort study (N=369,372), we performed a multivariate multilevel analysis to investigate whether residing in a Q fever area in 2008-2010 was associated with adverse pregnancy outcome (composite measure of preterm delivery, baby small for gestational age, and perinatal mortality). In addition, we estimated the population attributable fraction (PAF).

Abstract results

During the Q fever epidemic years, there was a non-significant association between residing in a Q fever affected area and adverse pregnancy outcome (adjusted OR: 1.03, [95% CI: 0.99 - 1.08]). The PAF for this non-significant relationship was 0.34% (95% CI: -0.13% - 0.81%).

Abstract conclusion

This ecological study found no association between residing in a Q fever affected area and adverse pregnancy outcome. Early detection of infection would require mass screening of pregnant women and this seems not justified considering the results of the present study and uncertainties about efficacy and adverse effects of antibiotic treatment.

Keywords: Q fever, Coxiella burnetii, Humans, Pregnancy complications, Netherlands

PRESENTED BY: Marit M.A. de Lange

ESCAIDE REFERENCE NUMBER: 20142066

Shiga toxin-producing Escherichia coli in faeces of Swedish children: evaluation of a PCR screening regimen with repeated weekly samplings

Andreas Matussek[1], Ing-Marie Einemo[1], Anna Jogenfors[1], Sven Löfdahl[2], Sture Löfgren[1]

[1] Jönköping County Council, Sweden; [2] Public Health Agency of Sweden, Sweden

Abstract

We investigated the prevalence of Shiga toxin-producing Escherichia coli (STEC) and Shiga toxin (Stx) types in children with diarrhoea. We correlated the four most common serotypes with clinical symptoms, duration of stx in faeces and characteristics of strains. We also evaluated the PCR screening regimen and origin of infection.

Abstract methods

All routine diarrhoeal samples from patients below ten years of age (n=10342) from 1 May 2003 through April 2013 in the County of Jönköping, Sweden, were included. Patients were divided in one group where analyses of STEC was requested (n=2366) and one screening group (n=7976). The presence of stx in faecal samples was determined by PCR and patients positive for stx were sampled weekly.

Abstract results

A total of 191 patients were included and in 88 cases STEC isolation and serotyping was successful. The prevalence was 1.8 % and 1.5 % in the requested group and in the screened group, respectively (p=0.5) and we detected no difference between the groups regarding severity of symptoms. Patients with stx2 were more often hospitalized ($p<0.0001$), had bloody diarrhoea ($p<0.0001$) and haemolytic uremic syndrome (HUS) (p=0.04). No difference in the duration of stx in faeces was seen between serotypes, stx type and eaeA presence. In Sweden stx2 was more commonly detected than in patients infected abroad ($p<0.0001$).

Abstract conclusion

We show comparable prevalence and disease severity between the patient groups. A high diversity of serotypes, of which also non-O157 serotypes caused severe disease, was found. These findings underline the need for improved regimens for STEC detection and physician awareness. Furthermore, no correlation between duration of stx in faeces and serotype, stx types, eaeA, age and gender was found.

Keywords: STEC, Shiga toxin, serotype, PCR, screening

PRESENTED BY: Andreas Matussek

ESCAIDE REFERENCE NUMBER: 20142109

Large cohort study shows gradual improvement of long-term health status of Q-fever patients over a 24-month period

Joris van Loenhout[1], Jeannine Hautvast[1], Jan Vercoulen[1], Reinier Akkermans[1], Clementine Wijkmans[2], Koos van der Velden[1], John Paget[1]

[1] Radboud University Medical Center, The Netherlands; [2] GGD Hart voor Brabant, The Netherlands

Abstract

Between 2007-2011, Q-fever notifications in the Netherlands increased dramatically and reached a cumulative total of 4107 cases, making it the largest documented outbreak in the world. Studies show that the long-term health status of many Q-fever patients is impaired, but so far only small groups of patients over a limited period have been studied. We therefore aimed to assess the health status of Q-fever patients over a 24-month period and to identify factors associated with health status.

Abstract methods

In a cohort study, laboratory-confirmed Q-fever patients participated at several time points after onset of illness (3, 6, 9, 12, 18, 24 months). Scores on twelve subdomains from two health status instruments were calculated for each time point to determine progression and compare these scores to reference groups.

Abstract results

The study included 336 Q-fever patients. Despite a significant linear improvement over time in nine of the twelve health status subdomains, patients generally had low health status scores at 24 months. For example, the proportion of patients with severe fatigue improved from 73·0% at three months to 60·0% at twelve months and 37·0% at twenty-four months, but this was still high compared to a healthy reference group (2·5%). For the three most severely affected subdomains -'Fatigue', 'General Quality of Life' and 'Role Physical'- the baseline characteristics significantly associated with a long-term reduced health status were being female, being a young adult and having pre-existing health problems.

Abstract conclusion

These findings show that many Q-fever patients suffer from a reduced health status long after the acute phase of their illness, which health care workers need to acknowledge and support in their contact with these patients.

Keywords: Q-fever, Coxiella burnetii, health status, quality of life

PRESENTED BY: Jeannine Hautvast

ESCAIDE REFERENCE NUMBER: 20142243

Outbreak of psittacosis cases related to food preparation, Aquitaine, France, May 2013

Laure Meurice[1], Véronique Servas[1], Isabelle Chossat[2], Karine Laroucau[3], Hélène Royer[4], Bertille De Barbeyrac[5], Sabine Vygen[1], Véronique Vaillant[1], Patrick Rolland[1]

[1] French Institute of Public Health Surveillance (InVS), Department of Coordination of Alerts and Regions, Regional office in Aquitaine, France; [2] Hospital in Villeneuve sur Lot, France; 3 National reference laboratory of avian Chlamydiae , France; [4] Regional Health Department Lot-et-Garonne, Aquitaine, France; [5] University of Bordeaux, National reference centre for Chlamydiae, France

Abstract

In May 2013, a hospital in Aquitaine region reported hospitalization of 4 patients presenting acute respiratory illness in the temporal context of the emergence of the Middle East Respiratory Syndrome Coronavirus (MersCoV). First investigations revealed a common exposure to poultry. Initial suspicion of MersCoV or avian influenza virus A(H7N9) were discarded and psittacosis was diagnosed. We aimed to describe the outbreak, to identify the source of contamination and implement control measures.

Abstract methods

We initiated active case finding by contacting patients and doctors who had notified the initial cases. We conducted a descriptive study using a standardized questionnaire. A possible case was a participant of the poultry preparation for the two wedding meals, presenting fever and one other flu-like symptom after the 14th of May 2013. Case confirmation was via positive PCR for Chlamydia psittaci of rhino-pharyngeal swabs or sputum. Veterinary investigations were undertaken with visits to the farming site. Cloacal swabs from chickens were taken and analyzed by PCR.

Abstract results

Four possible and 4 confirmed cases of psittacosis were identified among 15 women who had eviscerated about one hundred chickens (attack rate 53%) in the farm. All cases had flu-like symptoms, 4 cases presented a pneumopathy. Among 5 cases who had sputum smears done before initiating antibiotic treatment, 4 PCRs were positive for Chlamydia psittaci genotype E/B. Veterinary investigations revealed non conformities at the farm. Poultry samples were positive for Chlamydia psittaci genotype E/B.

Abstract conclusion

Outbreaks of psittacosis are rare. Transmission in the described event occurred via unprotected manipulation of infected poultry. Individual protection (masks, gloves), when in contact to poultry faeces, is essential to prevent such episodes. Infected poultry was eliminated and the farm was temporarily closed.

Keywords: Psittacosis, zoonose, emerging viruses

PRESENTED BY: Sabine Vygen

ESCAIDE REFERENCE NUMBER: 20142031

Parallel Sessions 13 – 15 10.30 – 12.10 Fri 7

Parallel Session 13: Food and waterborne diseases

Risk factors for sporadic cryptosporidiosis cases in the Netherlands, a mid-term analysis of an ongoing case-control study

Laura Nic Lochlainn[1, 2], Jussi Sane[1], Jeroen Roelfsema[1], Titia Kortbeek[1], Wilfred Van Pelt[1], Barbara Schimmer[1]

[1] National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden

Abstract

In 2012, an increase in cryptosporidiosis occurred in the Netherlands, but no single source was identified. Studies on risk factors for cryptosporidiosis are few. In 2013, we began a two-year population-based case-control study to identify risk factors for sporadic disease.

Abstract methods

We defined a cryptosporidiosis case as occurrence of gastrointestinal illness within two weeks of laboratory confirmation (microscopy or PCR). Cryptosporidium speciation was performed by RT-PCR. Cases were recruited by GPs. Five controls were selected per case from the population register and frequency matched on age. A questionnaire was posted to cases and controls. We excluded travel-related cases from the risk factor analysis and calculated adjusted odds ratios (aOR) using logistic regression.

Abstract results

In the first year of the study, we obtained speciation data for 136 cases; 119 were C. parvum (88%) and 17 were C. hominis. We included 192 cases (response 52%; 61% female; median age 24 years (range 1-95)) and 587 controls (response 32%; 56% female; median age 21 years (range 0.5-84)). Cases were more likely than controls to swim in rivers or lakes (aOR 4.9; 95% CI:2.0-12), to be exposed to cattle (aOR 3.8; 95% CI:2.0-7.0), to eat barbequed foods (aOR 3.8; 95%CI:2.4-6.1) and to have household members with diarrhoeal illness (aOR 1.8; 95%CI:1.1-3.0). Cases were less likely to play in a sandbox compared to controls (aOR 0.4; 95% CI:0.2-0.7).

Abstract conclusion

This study identified C. parvum as the predominant species. We found exposure to cattle, swimming in rivers or lakes, diarrhoeal illness among household members and consuming barbeque as possible risk factors for cryptosporidiosis. Information about potential risks of Cryptosporidium exposure during outdoor recreational activities and improvements in hand-hygiene within households could prevent future infections.

Keywords: Cryptosporidiosis, Case-control, Sporadic, Risk factors, the Netherlands

PRESENTED BY: Laura Nic Lochlainn

ESCAIDE REFERENCE NUMBER: 20142076

The role of unchlorinated drinking water in transmission of opportunistic pathogenic nontuberculous mycobacteria to patients in the Netherlands

Paul van der Wielen[1], Marijan Uytewaal-Aarts[1], Bart Wullings[1], Kim van Eck[2], Jakko van Ingen[2]

[1] KWR Watercycle Research Institute, The Netherlands; [2] Radboud University Nijmegen Medical Centre, The Netherlands

Abstract

Certain nontuberculous mycobacteria (NTM) species are opportunistic pathogens and can cause severe infections in immunocompromised persons. In many western countries drinking water has been identified as a transmission route of some of these pathogenic NTM. In the Netherlands, NTM infection is mainly caused by M. avium, M. kansasii, M. xenopi and M. malmoense. A study was conducted to investigate the presence of these and other NTM species in drinking water in the Netherlands.

Abstract methods

Drinking water samples were obtained from the tap directly and/or after flushing at 10 locations from 10 distribution systems that receive drinking water produced from groundwater or surface water. Subsequently, DNA was isolated from these samples and the presence of the four pathogenic NTM species was determined with newly developed species-specific qPCR methods. In addition, NTM-species in drinking water were determined using next generation sequencing methods targeting the hsp65 gene.

Abstract results

Results demonstrated that NTM were present in all analysed drinking water samples, but M. avium, M. xenopi and M. malmoense were never detected. M. kansasii was detected in a very small number of samples, but gene copy numbers were low. The sequence analysis of the hsp65 gene revealed that most sequences belonged to not yet cultivated NTM species, that are probably not involved in disease. A low number of sequences were related to described NTM species, but these species are not or sporadically involved in disease in the Netherlands.

Abstract conclusion

Overall, we conclude from our study that unchlorinated drinking water in the Netherland does not seem to be an important transmission route of pathogenic NTM in the Netherlands.

Keywords: Nontuberculous mycobacteria, Drinking water, Transmission, Mycobacterium avium, Mycobacterium kansasii, Mycobacterium malmoense

PRESENTED BY: Paul van der Wielen

ESCAIDE REFERENCE NUMBER: 20142145

Double jeopardy - A case-control study of risk factors for sporadic non-pregnancy associated listeriosis in Germany, 2012-2013

Karina Preussel[1], Patrick Schmich[1], Klaus Stark[1], Dirk Werber[1]

[1] Robert Koch Institute (RKI), Germany

Abstract

Non-pregnancy associated (N-PA) listeriosis is a rare but severe foodborne disease with a high case-fatality rate (8%). It is caused by infection with Listeria monocytogenes, which is notifiable in Germany. Incidence has increased in recent years, but risk factors for sporadic N-PA listeriosis in Germany have not yet been investigated. We aimed at identifying underlying conditions and foods associated with N-PA listeriosis.

Abstract methods

We conducted a prospective case-control study in Germany, March 2012- December 2013, including sporadic N-PA patients legally notified with Listeria monocytogenes infection and age-frequency (<66y, 66-75y, >75y) matched control persons identified from a nationwide random telephone sample. A standard questionnaire covered sociodemographic characteristics, underlying diseases, therapies and >60 items of food consumed and purchased. After univariable screening, we conducted multivariable logistic regression analysis, adjusting for age categories and host factors identified as part of the minimally sufficient adjustment set using causal diagram theory.

Abstract results

Overall, 109 cases and 1,990 controls were analyzed. Majority of cases (72%) had underlying conditions or took therapies that were immuno-compromising compared to 32% of controls (c2 test, $p<0.001$). In multivariable analysis, adjusting for age-category, 46 cases (44%) were strongly associated with current or recent immunosuppressive therapy (OR 9.4, 95%CI 5.3–16.4) and 29 (28%) with chronic disease (OR 2.9, 95%CI 1.5 – 5.4), compared to controls. Furthermore, consumption of cold frankfurters (sausages, OR 2.6; 95%CI 1.6-4.2), packaged cheese (OR 1.9; 95%CI 1.2-3.1) and sliced cheese (OR 2.1; 95%CI 1.3-3.5) was associated with N-PA listeriosis – each with a population attributable fraction of approximately 25%.

Abstract conclusion

Recommendations to prevent N-PA listeriosis in Germany should target immuno-compromised persons and include foods identified in this study, all sharing long refrigerator shelf-lives.

Keywords: Listeriosis, foodborne diseases, case-control studies, risk factors, prevention, immunosuppression

PRESENTED BY: Karina Preußel

ESCAIDE REFERENCE NUMBER: 20142177

Risk of hepatitis A decreased among Dutch travellers to most endemic regions,2003-2011

Jussi Sane[1, 2], Rita de Sousa[1], [3], Wilfred Van Pelt[3], Linda Verhoef[1], Mariska Petrignani, Marion Koopmans[5]

[1] National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [3] European Programme for Public Health Microbiology Training (EUPHEM), ECDC, Stockholm, Sweden; [4] Public Health Service Rotterdam-Rijnmond, The Netherlands; [5] Erasmus Medical Centre, Rotterdam, The Netherlands

Abstract

Hepatitis A remains a threat among unvaccinated European travellers visiting endemic areas. We estimated the risk of hepatitis A among Dutch travellers to direct public health actions.

Abstract methods

We counted 2003-2011 travel-related hepatitis A cases notified in Dutch surveillance (including information on probable country of infection, by WHO endemicity classification). We estimated the number of travellers from an annual holiday survey, based on a random sample of a predefined population responding to questions related to travel. We calculated attack rates (AR) per 100,000 travellers with 95% confidence intervals (CI). We assessed trends over three-year intervals using chi-square.

Abstract results

Of the 2,094 cases notified in 2003-2011, 931 (44%) were imported (Median age:17, range 1-83;55% males). The proportion of travel-related cases was stable (45% in 2003-2005, 48% in 2006-2008, 40% in 2009-2011). Morocco (n=272,29%), Turkey (n=98,11%) and Egypt (n=87,9%) accounted for the largest proportion of travel-related cases. Returnees from Morocco faced the highest AR (61.4 per 100,000 travellers), followed by India (13.3), Brazil (7.1) and Egypt (4.6). In terms of regions, ARs among returnees from high or intermediate endemic regions declined from 7.5 per 100,000 travellers (95% CI 6.7-8.4) in 2003-2005 to 3.5 (95% CI 3.0-4.0) in 2009-2011 ($p<0.01$).

Abstract conclusion

While attack rates of hepatitis A decreased in the last ten years among Dutch travellers to endemic regions in the world, travel still accounts for 40% of hepatitis A cases. Routine risk monitoring using these methods must continue. Barriers to the immunisation of travellers must be identified and addressed.

Keywords: Hepatitis A, traveller, risk, attack rate, The Netherlands

PRESENTED BY: Jussi Sane

ESCAIDE REFERENCE NUMBER: 20142058

Risk factors for hepatitis A among children under five years-of-age in Bishkek City, Kyrgyzstan, October 1-December 31, 2012

Simon Ajeilat[1], Elnura Duishenali[2], Nurila Altymysheva[3]

[1] CDC, Kazakhstan; [2] Central Asial FELTP-Naryn oblast AIDS Center, Ministry of Health in Kyrgyz Republic, Kyrgyzstan; [3] Central Asia FELTP-Department of Disease Prevention and Expertise, Ministry of Health in Kyrgyz Republic, Kyrgyzstan

Abstract

During Jan–Sep 2012, authorities in Bishkek city, Kyrgyzstan, reported 291 children <5 years-of-age with hepatitis A (HA); 145 were hospitalized and two died. During the same period of 2011, only 81 children had HA. To identify risk factors for HA and recommend appropriate control measures, we conducted a population-based case-control study among city children <5 years-of-age diagnosed during October–December 2012.

Abstract methods

Case-children (n=201) had acute-onset of jaundice with positive HA IgM or elevated liver enzymes, and negative tests for other viral hepatitis markers. We enrolled case-children as ascertained through surveillance; all were from different families. Control-children were without history of jaundice and randomly selected from the under-five census lists (n=186). We interviewed parents regarding food habits, water sources, and observed household sanitary conditions. Study exposures were measured within two months of interviews. We used logistic regression to assess HA-risk factor associations.

Abstract results

Of the 201 case-children's families, 165 (82%) reported having water outages, and 32 (16%) had another family member with HA during the two months prior to interviews. In multivariate analysis, risk factors for HA were: having another family member with HA (OR=17.3, 95% CI 4.3-69.2), interrupted water supply (OR 11.7, 95% CI=5.8-23.4). Having a washstand in the household was protective (OR=0.1, 95% CI=0.04-0.37). None of the study children were vaccinated against HA.

Abstract conclusion

Some children were infected due to unsafe water during outages, other children were infected in families with previous HA cases and with poor sanitary conditions. City residents should be advised to boil water from uncertain sources during outages and to observe good sanitary practices at home. A consideration of inclusion of HA vaccine into the national vaccination strategy is warranted.

Keywords: Hepatitis A, Bishkek, Kyrgyzstan, case-control risk factors

PRESENTED BY: Aizat Kulzhabaeva

ESCAIDE REFERENCE NUMBER: 20142000

Parallel Session 14: Surveillance (1)

The use of syndromic surveillance to monitor the incidence of arthropod bites requiring healthcare in England

Sophie Newitt[1], Alex Elliot[2], Roger Morbey[2], Gillian Smith[2], Hayley Durnall[3], Maaike Pietzsch[4], Jolyon Medlock[4], Steve Leach[4]

[1] Field Epidemiology Service, West Midlands and; Field Epidemiology Training Programme, Public Health; England, UK; [2] Real-time Syndromic Surveillance Team, Public Health England, UK; [3] RCGP Research and Surveillance Centre, UK; [4] Public Health England, UK

Abstract

The predicted increase in temperature arising from climate change may result in changes to the numbers of arthropods in the UK but there is currently no surveillance system in place to monitor arthropod bites. This project examined the potential utility of existing syndromic surveillance systems to monitor the incidence of arthropod bites in England.

Abstract methods

This retrospective observational study utilised arthropod bites requiring healthcare from six national syndromic surveillance systems to calculate and describe baseline incidence between 2000 and 2013 by sex, age and geographical region. The relationship between bites and temperature was examined using negative binomial regression with a time series component. Incidence rate ratios (IRR) and 95% confidence intervals were calculated.

Abstract results

In England, we estimated during summer months (weeks 20–40) arthropod bites contributed a weekly median of 3507 GP consultations, 750 to 908 calls to telephone health helplines, 675 emergency department attendances and 1,285 GP out-of-hours attendances. In all systems, incidence was highest during summer months compared to the rest of the year; IRRs ranged between systems from 2.03 (95%CI 1.18–3.49) to 6.07 (95%CI 5.51–6.69) and in persons aged 45-64 years compared to 0-4 years, IRRs ranged from 1.57 (95%CI 1.46–1.69) to 7.25 (95%CI 6.96–7.54). No geographical patterns or trends over time were observed. Arthropod bites in all systems were positively associated with temperature, IRRs ranged from 1.09 (95%CI 1.08–1.11) to 1.24 (95%CI 1.23–1.25).

Abstract conclusion

Syndromic surveillance systems have been used to establish and describe baseline incidence for arthropod bites requiring healthcare in England. These can now be monitored routinely to assess the impact of climate change and provide early warning of changes in the burden of disease.

Keywords: Syndromic surveillance, arthropod, climate change, incidence

PRESENTED BY: Sophie Newitt

ESCAIDE REFERENCE NUMBER: 20141952

Evaluation of Austrian Measles Surveillance, 2009-2013

Yung-Ching Lin[1], *Franz Allerberger*[1], *Peter Kreidl*[2], *Daniela Schmid*[1]

[1] Austrian Agency for Health and Food Safety, Vienna, Austria; [2] Ministry of Health, Vienna, Austria

Abstract

WHO developed key surveillance performance indicators to monitor progress toward measles elimination by 2015. Since 2009, Austrian public health authorities enter case-based data, reported by physicians and laboratories, into a national electronic reporting system (ERS). We evaluated data completeness and reporting timeliness of measles surveillance as per CDC guidelines and assessed three WHO key performance indicators to identify areas for improvement.

Abstract methods

We analysed the 415 measles case-records in the 2009–2013 ERS-database. For each year, we calculated completeness of vaccination status records as the proportion of case-records with complete vaccination status among all case-records, and case-reporting timeliness as the proportion of case-records reported ≤1 day since diagnosis. Performance indicators assessed were: proportion of case-records with available laboratory results, number of cases discarded as non-measles using laboratory criteria/100,000 population, and the proportion of outbreaks investigated for virus genotype/total number of outbreaks.

Abstract results

Between 2009–2013, 60%, 43%, 73%, 70%, and 64% of case-records included vaccination status, and 33%, 59%, 67%, 50%, and 75% of cases were notified within a day, respectively (WHO target: ≥80%). Laboratory confirmation was available in 57%, 81%, 88%, 69%, and 92% of records (target: ≥80%) and rate of discarded cases was 0.01, 0.01, 0, 0, and 0/100,000 population (target: ≥2/100,000). The proportion of outbreaks investigated for genotype was 67% (2/3), 29% (2/7), 50% (9/18), 0% (0/3) and 78% (7/9) (target: ≥80%).

Abstract conclusion

Despite improving measles surveillance performance since 2009, none of the indicators met WHO targets sustainably. We recommend knowledge/attitude/practice surveys among healthcare providers, public health authorities, and measles laboratories to help identify causes for under-performance.

Keywords: Measles, surveillance, evaluation, disease elimination, Austria

PRESENTED BY: Yung-Ching Lin

ESCAIDE REFERENCE NUMBER: 20141978

CIDARS: A nationwide web-based automated outbreak early warning system in China

Zhongjie Li[1], *Shengjie Lai*[1], *Honglong Zhang*[1], *Hongjie Yu*[1], *Yajia Lan*[2] , *Weizhong Yang* [1]

[1] Division of Infectious Diseases, Key Laboratory of Surveillance and Early-warning on Infectious Disease, Chinese Center for Disease Control and Prevention, Beijing, China. lizj@chinacdc.cn; [2] Key Laboratory of Surveillance and Early-warning on Infectious Disease, Chinese Center for Disease Control and Prevention, Beijing, China

Abstract

How to timely detect the outbreaks is one of the major challenges for outbreak response. In China, one nationwide outbreak early warning system, China Infectious Disease Automated-alert and Response System (CIDARS), was developed, which automatically conducted the aberration detection on the large volume of surveillance data. Three aberration detection methods, including fixed value method, moving percentile method and EARS-C3 (one CUSUM method), were adopted for the 32 notifiable infectious diseases. The aberration signals were distributed to the local epidemiologists via cell phone, and the response output for each signal was reported.

CIDARS has been routinely used by more than 3,000 public health departments and 16,400 epidemiological staffs at different levels. From 2011 to 2013, 960,831 signals were generated nationwide, with the median time of signal response was 1.0 hour. After signal initial verification and field investigation by local epidemiologists, CIDARS detected 2,490 outbreaks on 17 diseases. We further take hand, foot and mouth disease, one of the leading disease in China, as example to evaluate the performance on preventing outbreak from spreading. We found that CIDARS detected 573 outbreaks (sensitivity: 92.7%), with a mean time to detection of 2.1 days and specificity of 95.0%. Following the implementation of CIDARS, mean size of outbreaks decreased from 19.4 to 15.8 cases per outbreak, and mean interval between outbreak onset and initial report decreased by 1 day.

Our study indicated that the application of CIDARS could contribute to enhance the timeliness of outbreak early detection and rapid response, so as to prevent the outbreak spreading. In the future, CIDARS should further improve the surveillance data quality, optimize detection algorithms, and explore reasonable evaluation methods.

Key words: Infectious disease, System, Outbreak detection, Rapid response e

PRESENTED BY: Zhongjie Li

ESCAIDE REFERENCE NUMBER: 20141997

The impact of new national guidance for public health management of enteric fever in England

Katherine Russell[1], Jamie Lopez Bernal[2], Sarah Addiman[3], Delphine Grynszpan[4], Joanne Freedman[1], Sooria Balasegaram[5]

[1] Centre for Infectious Disease Surveillance and Control, Public Health England, UK; [2] Department of Health Services Research and Policy, London School of Hygiene and Tropical Medicine, UK; [3] North East and North Central London Health Protection Team, Public Health England, UK; [4] North West London Health Protection Team, Public Health England, UK; [5] Field Epidemiology Services, Public Health England, UK

Abstract

In February 2012, new guidance by the Typhoid and Paratyphoid working group was issued in England for the public health management of enteric fever. The guidance reduced the timing and number of clearance samples and the exclusion criteria. This evaluation focussed on the effectiveness in preventing secondary transmission through a review of cases reported in the first year.

Abstract methods

We included cases reported throughout England (February 2012 - January 2013). We performed a qualitative analysis of cases not linked to recent travel. We performed a quantitative analysis of confirmed cases reported in London; looking at the number of clearance samples, periods of exclusion, and adherence to the new guidance. Finally we undertook a user survey with national stakeholders.

Abstract results

349 cases of enteric fever were reported in the 12 months after the new guidance was issued. 20 (6%) were not related to travel to endemic areas; 7 were classified as chronic carriers, 2 were secondary transmission from household members and 11 had no source identified. 92 cases were reported in London, with 12 (13%) requiring clearance samples and exclusion from work or school. For these cases, there were 98 fewer clearance samples required and the mean number of days excluded decreased by 32 days compared to the old guidance. Close contacts requiring screening reduced from 265 to 154. 39 responses were received from the survey, expressing overall satisfaction with the new guidance.

Abstract conclusion

This evaluation indicates that the new guidance has reduced the number of clearance samples taken and days of exclusion, and thus increased compliance to the guidelines. There was no observed increase in secondary transmission of enteric fever within England.

Keywords: Enteric fever; Typhoid fever; Paratyphoid fever; Salmonella

PRESENTED BY: Katherine Russell

ESCAIDE REFERENCE NUMBER: 20142049

Mobile-based disease surveillance from formal and informal health care providers in resource-limited settings. Experience from Madhya Pradesh, India

Vishal Diwan[1], Deepak Agnihotri[1], Vijay Mahadik[1], Anette Hulth[2]

[1] R.D.Gardi Medical College, Ujjain, India; [2] Department of Public Health Sciences, Karolinska Institutet, Sweden

Abstract

Infectious disease surveillance is a challenge for a country like India. Surveillance data are collected from governmental and private qualified facilities but not from informal health care providers; the latter constituting almost half of the health care sector. This study describes a real-time mobile-based syndromic surveillance system and its application in a resource-limited setting, collecting data from formal and informal health care providers.

Abstract methods

This cross-sectional study was conducted in year 2013 in two districts of Madhya Pradesh, India, including three formal and six informal health providers. Research assistants were posted in the clinics during working hours and submitted in real-time patient information and disease symptoms to a central server using mobile phones. The patients' place of residence was geocoded.

Abstract results

Information on 20,424 patients was collected in the mobile-based system. 48% presented with fever, 38% with body ache, 37% with headache, 21% with vomiting, 22% with runny nose, 21 % with abdominal pain and 9% with loose motion. During the same time period, the government disease surveillance program reported around 22,000 fever cases in one of the study district, highlighting a huge underreport in their data. Additionally, we found that patients from more than 600 villages visited the health care providers included in our study.

Abstract conclusion

The study demonstrated that the designated mobile-based system can be used for diseases surveillance from formal and informal providers in resource-limited settings. Real-time collection increases timely reporting of disease data for better outbreak management. Cooperation from providers, data quality and internet connectivity need further investigations.

Keywords: Surveillance, India, informal health care providers, Mobile Applications

PRESENTED BY: Vishal Diwan

ESCAIDE REFERENCE NUMBER: 20142138

Parallel Session 15: Vaccine coverage, effectiveness and safety (2)

Moderate to high seasonal influenza vaccine effectiveness in Ireland: a test-negative case-control study, I-MOVE project, 2013-2014

Coralie Giese[1], Lisa Domegan[1], Darina O'Flanagan[1], Joan O´Donnell[1], Derval Igoe[2], Claire Collins[3], Michael Joyce[3], Suzie Coughlan[4], Allison Waters[4], Joanne Moran[4]

[1] Health Protection Surveillance Centre, Ireland; [2] HSE, Ireland; [3] Irish College of General Practitioners, Dublin, Ireland; [4] National Virus Reference Laboratory, University College, Dublin, Ireland

Abstract

As part of the Influenza Monitoring Vaccine Effectiveness in Europe (I-MOVE), we undertook a test-negative case-control study to estimate 2013/14 influenza vaccine effectiveness (VE) in Ireland.

Abstract methods

Sentinel general practitioners swabbed influenza-like illness (ILI) patients within seven days of symptom onset using systematic sampling. We compared laboratory confirmed influenza cases with influenza laboratory-negative patients among those meeting the EU ILI case definition, in terms of influenza vaccination status. We considered patients as vaccinated if the interval between receiving a dose of vaccine and symptom onset was ›14 days. We used logistic regression to calculate influenza VE and 95% confidence intervals (95%CI), adjusting for potential confounders (age, presence of at least one underlying medical condition, smoking, sex and month of symptom onset).

Abstract results

We included 103 cases and 70 controls in the analysis. Crude VE was 66% (95%CI 7 to 88) overall, 60% (95%CI -29 to 89) against influenza A(H3) and 68% (95%CI -25 to 94) against influenza A(H1)pdm09. Adjusted VE against all influenza subtypes was 72% (95%CI 10 to 91). Among target groups for vaccination (N=46), crude VE was 31% (95%CI -167 to 82) overall, 19% (95%CI -295 to 84) against influenza A(H3) and 35% (95%CI -308 to 91) against influenza A(H1)pdm09.

Abstract conclusion

Results suggest moderate to high protection from 2013/14 trivalent influenza vaccines against laboratory-confirmed influenza in Ireland. VE against influenza A(H3) was low among target groups for vaccination. Efforts to improve influenza vaccines should continue to better protect those at risk of severe illness or complications.

Keywords: Influenza, influenza vaccine, vaccine effectiveness, case control studies

PRESENTED BY: Coralie Giese

ESCAIDE REFERENCE NUMBER: 20142119

Intussusception in Sicily: hospitalization trends before the introduction of rotavirus vaccination, 2003-2012

Roberto Furnari[1], Sebastiano Addario Pollina[2], Mario Cuccia[3]

[1] University of Catania, Italy; [2] Dipartimento Attività Sanitarie e Osservatorio Epidemiologico, Palermo, Sicily, Italy; [3] Dipartimento di Prevenzione, Servizio Epidemiologia e Prevenzione, ASP Catania, Sicily, Italy

Abstract

In 2013 the rotavirus monovalent vaccine RIX4414 was introduced in the Sicilian immunization schedule (two doses from the 9th to the 24th week). Post licensure monitoring still reports a small increased risk for intussusception in vaccinees. This study aims to assess intussusception trends among Sicilian infants by the analysis of hospitalization discharges (HDs) from 2003 to 2012 (49,130 average newborns per year).

Abstract methods

We performed a retrospective cross-sectional study from 2003 to 2012, extracting all the intussusception cases registered on the regional HD database that occurred in infants ‹1 year of age. Case definition: hospitalization associated with the ICD9-CM code 560.0 (Intussusception). The cases were distributed by week of age and gender. A Rate Ratio (RR) was estimated for gender. Census data were used to estimate Incidence Rate (IR). We estimated the expected intussusceptions per year in the vaccination time window, identifying all cases that occurred in 9 - 28 week old infants.

Abstract results

We observed a total of 144 cases. The average number per year was 14.4 cases. Average IR per year: 29.3 per 105, range: 17.6 (2004); 37.4 (2005). From 2003 to 2012 no particular trend appeared. The intussusception risk was greater in male infants (RR: 1.79; 95% CI: 1.69–1.87). In the time window we observed 71 cases. Average per year: 6.9 cases, range: 3 (2009, 2011, 2012), 11 (2003, 2010).

Abstract conclusion

The incidence rate for intussusception in Sicilian infants is comparable to those estimated in countries (Canada, UK, USA) that have already introduced rotavirus vaccination. In Sicily we also need to implement an active post-marketing surveillance system to register any shifting in intussusception number with respect to the pre-vaccination era.

Keywords: Rotavirus vaccines, intussusception, immunization schedule, hospitalization, retrospective studies

PRESENTED BY: Roberto Furnari

ESCAIDE REFERENCE NUMBER: 20142153

A mumps outbreak among adolescents highly vaccinated with two doses, Klatovy, Czech Republic, 2011

Anna Kubatova[1], P. Pazdiora[1], Y. Hutin[2], Kostas Danis[2], H. Šebestova[3], V. Prikazsky[4]

[1] Regional Public Health Authority, Pilsen, Czech Republic; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden; [3] National Institute of Public Health, Prague, Czech Republic; [4] European Centre for Disease Prevention and Control, Stockholm, Sweden

Abstract

Czech Republic introduced mumps vaccination in 1987 (Jeryl Lynn and derived RIT4385 strain) at 15 months with a second dose at 21-25 months. After 22 years of low incidence, we investigated an outbreak in 2011 to understand the determinants of re-emergence.

Abstract methods

We defined cases clinically (National guidelines). Local epidemiologists reported cases using physicians' records that included data on age, sex, vaccination status and laboratory confirmation. We analysed surveillance data and estimated vaccination coverage from the routine annual surveys. We compared reported laboratory-confirmed cases with controls randomly selected among the same primary care physicians' registers, frequency-matched for age and clinical practice, to calculate vaccine effectiveness (1- matched odds ratio).

Abstract results

443 cases were reported in 2011 (56% males; median age: 17 years, range 3-72; 37% serologically confirmed; 81.3% vaccinated once and 81.0% vaccinated twice). The highest attack rate (4,318/100,000) was among 15-19 year-olds, who accounted for 45.1% of cases (coverage in the population: 99.0% for one dose, 97.0% for two doses). Among the 125 confirmed cases, none had received one dose and 119 (95.2%) had received two doses while among the 647 controls, 6 had received one dose and 640 (98.9%) two doses (two-dose vaccine effectiveness: 96%, 95%CI: 72%-100%).

Abstract conclusion

Young adults of the Klatovy district faced an outbreak of mumps despite long standing high two-dose coverage. Precise estimates of vaccine effectiveness were difficult to generate and some vaccine failure cannot be excluded. Future studies exploring the factors associated with vaccine failure may help understanding the mechanisms of such outbreaks in order to identify who could potentially benefit from a third dose of vaccine.

Keywords: Mumps, surveillance, vaccination coverage, vaccine effectiveness

PRESENTED BY: Anna Kubatova

ESCAIDE REFERENCE NUMBER: 20142203

High effectiveness and impact of universal Rotavirus vaccination in Finland 4 years after its introduction into National Immunisation Program (NIP)

Hélène Bricout[1], Matti Uhari[2], Marjo Renko[2], Maria Hemming[3], Marjo Salminen[3], Timo Vesikari[3], Laurence Torcel Pagnon[1], François Simondon[1]

[1] Sanofi Pasteur MSD, Epidemiology Department, France; [2] University of Oulu, Department of Pediatrics, Finland; [3] University of Tampere, Vaccine Research Center, Finland

Abstract

Finland introduced universal rotavirus (RV) vaccination (RotaTeq® at 2, 3 and 5 months) in September 2009. The coverage soon reached that of other NIP vaccination (›95%).

Abstract methods

A prospective hospital based study was conducted in Tampere and Oulu University hospitals from December 2009 to August 2013. RotaTeq® vaccine effectiveness was estimated by a test-negative case control analysis in NIP age eligible children (over 6 months): cases were defined as RV acute gastroenteritis (RV AGE) with an EIA+ and RT-PCR+ stool specimen and controls were RV negative AGE. ICD-10 discharge codes were also retrospectively collected from September 2001 to August 2013. RV-AGE and all-cause AGE incidences were estimated before vaccination (2001-2006) and post-NIP period (2009-2013) to estimate the vaccination program impact.

Abstract results

Of 134 AGE episodes, 17 were RV-AGE cases and 117 were controls. RotaTeq® VE for fully vaccinated children was 94.4% (95%CI: 79.8;98.4), p. The reduction of the RV-AGE hospitalization incidences in the target age group (6-47 months) was 86.5% (95%CI: 82.2;89.7) and of all-cause AGE 71.3% (95%CI: 68.5;73.8). In the children non eligible for NIP (4-15 years), no significant reduction in RV-AGE hospitalizations was observed.

Abstract conclusion

RotaTeq® showed high VE to prevent RV-AGE hospitalizations over 4 years. A low number of cases in the context of high VE and coverage allowed estimating precise VE only after 4 years. A strong impact of RotaTeq® vaccination program was also confirmed with reduction of RV-AGE and all cause hospitalization in age eligible children. The reduction of GE hospitalizations non coded specifically as rotavirus suggested that testing and coding practices may underestimate the true rate of RV hospitalizations.

Keywords: Rotavirus, vaccine, effectiveness, impact

PRESENTED BY: Hélène Bricout

ESCAIDE REFERENCE NUMBER: 20142238

Maternal pertussis vaccination is effective in preventing pertussis in infants: a case-control study in England and Wales, 2012- 2013

Gavin Dabrera[1], Gayatri Amirthalingam[1], Nick Andrews[1], Norman K. Fry[1], Sonia Ribeiro[1], Helen Campbell[2], Edna Kara[2], Mary Ramsay[3]

[1] Public Health England, UK; [2] Immunisation, Hepatitis and Blood Safety Department, Centre for Infectious Disease Surveillance and Control, Public Health England, UK; [3] Health Protection Services, Immunisation, Hepatitis, and Blood Safety department, Public Health England, UK

Abstract

Pertussis outbreaks have occurred in several countries worldwide, despite high vaccine coverage. Since 2011, there has been a national pertussis outbreak in England and Wales (E&W) with increased numbers of infant deaths. From October 2012, pregnant women were offered one dose of acellular pertussis vaccine between 28-38 weeks' gestation, as a temporary outbreak response. The aim of this was to protect infants through trans-placental antibody transfer, prior to primary immunisations starting at eight weeks of age. As this intervention had not been used previously, our objective was to estimate the vaccine effectiveness (VE) of maternal vaccination in preventing laboratory-confirmed pertussis infection in infants.

Abstract methods

We used a case-control study design. Cases were included if they were aged less than 8 weeks at onset, resident in E&W, notified between 2012-2013 and culture/PCR confirmed by the national reference laboratory. Family doctors of each case in E&W were requested to identify two controls; these were healthy infants born consecutively after the case and registered in the same practice. Family doctors provided information on maternal pertussis vaccination for both cases and controls. We calculated VE as 1-OR (odds ratio for association between maternal vaccination and pertussis infection) and adjusted for sex, geographical region and birth period using logistic regression.

Abstract results

Data were available for 58 cases and 55 controls. Mothers of 10(17%) cases and 39(71%) controls received pertussis vaccine. The unadjusted VE was 91% (95% confidence interval: 77-97%). VE adjusted for sex, geographical region and birth period was 93% (81-97%).

Abstract conclusion

Maternal pertussis vaccination is effective in preventing pertussis infection in infants aged under 8 weeks during a national outbreak and should be considered in other countries experiencing pertussis outbreaks.

Keywords: Pertussis, pregnancy, vaccination, infants

PRESENTED BY: Gavin Dabrera

ESCAIDE REFERENCE NUMBER: 20141944

Parallel Sessions 16 – 18 13.10 – 14.50 Fri 7

Parallel Session 16: Epidemiology and microbiology driving public health policy

Decreased prevalence of carried Streptococcus pneumoniae and genetic shifts of non-vaccine serotypes after changing the 7 pneumococcal conjugate vaccine to the 13-valent vaccine in Norway

Anneke Steens[1], Ingeborg Aaberge[1], Dominique Caugant[1], Didrik Vestrheim[1]

[1] Norwegian Institute of Public Health, Norway

Abstract

Pneumococcal carriage studies in children provide information on circulating serotypes and insight in mechanisms behind bacterial-population dynamics, which are useful for monitoring post-vaccination changes. In 2011, the 13-valent pneumococcal conjugate vaccine (PCV13) replaced the 7-valent vaccine which was used since 2006 for childhood immunisation in Norway. We assessed vaccine-induced changes in prevalence and serotype and genetic diversity of isolates carried by children younger than 6 years.

Abstract methods

A cross-sectional study collecting questionnaire data and nasopharyngeal swabs was performed in autumn 2013 among children attending day-care centres (DCC) in and near Oslo. Serotyping and multilocus sequence typing was performed on all isolates. Results were compared to similar studies performed in 2006 (610 swabs, 538 isolates) and 2008 (600 swabs, 562 isolates). The diversity of serotypes and sequence types (ST) was defined by Simpson's diversity index (D).

Abstract results

We obtained 583 isolates from 874 children. The carriage prevalence decreased from 78/100 children [95%CI 73-82] in 2006 and 80/100 [76-84] in 2008 to 62/100 [58-66]. PCV13-serotypes accounted for 7% of isolates in 2013 [n=65]. The prevalence of nonPCV13-serotypes increased from 2006 (33/100 [26-39]) to 2008 (57/100 [51-62]), and remained at that level in 2013 (56/100 [52-60]). Among nonPCV13-serotypes with increased prevalence, 22F, 21 and 31 increased by clonal expansion, while 23B and 23A increased by expansion, introduction of existing and novel clones and by possible capsule switch. The serotype and genetic diversity slightly decreased in 2013 (lower D, fewer ST covering 50% of isolates).

Abstract conclusion

Switching to PCV13 has decreased carriage of vaccine-serotypes, without coinciding increase in non-vaccine-types. A shift among circulating nonPCV13-serotypes was caused by clonal expansion and introduction of clones. Capsule switch rarely occurred.

Keywords: Pneumococcal conjugate vaccine, carriage, childhood vaccination programme, MLST

PRESENTED BY: Anneke Steens

ESCAIDE REFERENCE NUMBER: 20142128

Decision-rules for regional recommendation of vaccination against Tick Borne Encephalitis in Sweden

Malin Kark[1], Lisa Brouwers[1]

[1] Public Health Agency of Sweden, Sweden

Abstract

Tick Borne Encephalitis (TBE) is a notifiable disease that causes major disease burden. National decision-rules could help our 21 councils in deciding on annual information strategies regarding vaccination recommendations. An international or national consensus on such decision-rules is missing. Our intention was to identify practical decision-rules that could be used by the local infectious disease control agencies.

Abstract methods

We designed rules based on annual change in number of cases and only on cases during a single year. The rules were applied on cases per county in years 1986-2012. The "increase rule" alarmed when there was a positive change in number of cases during two consecutive years. The "case rule", based on number of cases, identified "risk area" when there were at least 5 cases over a 5 year period or at least 2 cases in a single year and "high risk area" if there were more than 25 cases over a 5 year period. To avoid irrelevant alarms, small increases, the "incidence condition" was added; incidence must be higher than 1 per 100 000 people for the rule to signal.

Abstract results

In 7 out of 21 counties the "increase rule" signalled one or more years. Stockholm County was classified as a "high risk area" during the whole period. The "increase rule" signals earlier than the "case rule" in almost all counties.

Abstract conclusion

We suggest that vaccination against TBE is recommended in a county, if either the "increase rule" or the "case rule" for "high risk area" signals, or if any rule have signalled at least once during the period 1986-2012. When "risk area" is signalled for, an assessment at the local situation is recommended.

Keywords: Decision-rules, Incidence, Risk area, Sweden, TBE, Vaccination

PRESENTED BY: Malin Kark

ESCAIDE REFERENCE NUMBER: 20142215

Epidemiological impact and cost-effectiveness of vaccination against meningococcal B disease in France

Heloise Lecocq[1], Isabelle Parent du Chatelet[2], Muhamed-Kheir Taha[3], Daniel Levy-Bruhl[2], Benoit Dervaux[1]

[1] EA 2674, Lille University School of Medicine, France; [2] French Institute for Public Health Surveillance (InVS), Saint-Maurice, France [3] National Reference Center for Meningococci, Pasteur Institute, France

Abstract

In France, the incidence of serogroup B invasive meningococcal disease varied between 0.6 and 0.8 /100 000 in the last 10 years. A study on the impact and cost-effectiveness of different vaccination strategies based on the newly licensed Bexsero® vaccine was performed as part of the decision-making process regarding its potential inclusion in the vaccination schedule.

Abstract methods

We used the model developed by De Wals et al. for meningococcal C to which we added a multiple cohorts Markovian component. Herd immunity was reproduced in sensitivity analysis. Data on safety and immunogenicity from the licencing dossier were used. Three main population targets were evaluated for vaccination: infants at 3, 5, 6 and 13 months, toddlers at 13, 15 and 27 months and adolescents at 15 years. Three vaccine prices were considered: 20, 40 and 60 € per dose. Costs and health outcomes (Quality Adjusted Life Years gained) were discounted at 4% (base-case).

Abstract results

In the base-case analysis, for an 80% vaccination coverage for all doses, the proportion of avoided cases at equilibrium remained below 30% irrespective of the scenario considered. Even for a cost of 20€ per dose, the incremental cost-effectiveness ratio (ICER) varied between 274 000 and 845 000 €/QALY gained. In the sensitivity analyses, including herd immunity and a 20 % increase in incidence, the reduction in incidence reached 64,4 % and the ICER decreased to 77 500 €/QALY.

Abstract conclusion

Those results contributed to the French High council for Public Health recommendation in October 2013, in disfavour of the routine vaccination of infants and/or adolescents with Bexsero®, in the absence of data on effectiveness of the vaccine on carriage.

Keywords: Meningococcal B vaccine, cost-effectiveness, vaccination strategy, modelling

PRESENTED BY: Isabelle Parent du Chatelet

ESCAIDE REFERENCE NUMBER: 20142117

Evaluating implementation of polio vaccination and stool screening among Syrian asylum seekers, Germany, 2013/2014

Nadine Zeitlmann[1,2,3], Maja George[4], Katrin Neubauer[4]. Gerhard Falkenhorst[4]

[1] Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany; [2] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Control and Prevention (ECDC), Stockholm, Sweden; [3] Bavarian Health and Food Safety Authority, Oberschleissheim, Germany; [4] Robert Koch Institute, Berlin, Germany

Abstract

Following the polio outbreak in Syria, on 01/11/2013 RKI recommended vaccinating incompletely vaccinated residents and staff of asylum seeker reception centres (RC) and stool screening in a target group of Syrian asylum seekers aged <3 years. We evaluated implementation in the first three months (01/112013-31/01/2014) to identify bottlenecks and improve future recommendations.

Abstract methods

We e-mailed a questionnaire to health managers of the RC in Germany asking for the number of incoming asylum seekers, stool testing practices, vaccination efforts and implementation obstacles in the study period. They self-rated the implementation of the recommendations and suggested improvements.

Abstract results

Twenty RC responded. Daily occupancy ranged from 150 to 1900 asylum seekers, who stayed for 2.5 to 330 days at the RC. By 15/11/2013, 16 RC had implemented vaccination. All RC offered vaccination for the target group, 5 additionally for other residents and staff. Nineteen RC screened stools, but only 3 managed to screen all targeted. Staff shortage and asylum seekers' unknown vaccination status were the most frequently named obstacles to vaccination, reported by 11 and 7 RC, respectively. Regarding stool screening, 10 RC reported language barriers and 8 considerable logistical challenges. Nine RC had a pre-existing standing order for vaccination and/or stool screening. Three RC self-rated their implementation as "very good'', 8 as "good" and 9, especially those hosting >=600 asylum seekers, "less good''. Five RC requested information material in more languages.

Abstract conclusion

German RC vaccinated against polio and screened stools of Syrian asylum seekers to a varying extent. Addressing reported staff shortages and RC's difficulties with obtaining residents' vaccination status and provision of multilingual information material may improve the implementation of future recommendations.

Keywords: polio, Syria, surveillance, vaccination, refugees, Germany

PRESENTED BY: Nadine Zeitlmann

ESCAIDE REFERENCE NUMBER: 20142162

Notifiable disease or not: a tool to help public health policy makers decide

Ewout Fanoy[1], Paul Bijkerk[2],Katina Kardamanidis[2], Simone van der Plas[2], Margreet te Wierik[2], Mirjam Kretzschmar[2], George Haringhuizen[2], Hans van Vliet[2], Marianne van der Sande[4]

[1] GGD region of Utrecht, The Netherlands; [2] National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands; [3] Public Health Service, GGD region Utrecht, Zeist, The Netherlands; [4] RIVM/CIb, The Netherlands

Abstract

Public health policy makers may need to consider whether to make a disease notifiable in case of unusual events. In the Netherlands, there are criteria for notifiable diseases, but no specific guidelines to support the decision making process. We therefore developed a tool to guide decisions towards whether or not an infectious disease should be made notifiable.

Abstract methods

The tool was built using criteria for notifiable diseases from the Dutch Public Health Act, ECDC and WHO notifications, and legal and practical considerations. Criteria were merged and classified by effectiveness (prevalence and severity of disease, possibility of source and contact tracing, derivate risks for vaccination policy, international consequences), feasibility (workload, possibility of diagnosis) and necessity (subsidiarity, privacy) of notification. We trialed the tool for hepatitis E, dengue and Middle East Respiratory Syndrome coronavirus (MERS-CoV), for which advise on notifiable status was recently requested by the Dutch Ministry of Health.

Abstract results

Using the tool, hepatitis E was not found to be eligible for notification as the burden of the disease is unknown, the route of transmission remains unclear and therefore source-tracing is unlikely to be effective. For dengue fever, notification in the Dutch Caribbean could be supported, as this would strengthen current control measures. MERS-CoV should be notifiable, considering the reported high case fatality rate and need for implementing preventive measures following an imported case.

Abstract conclusion

The tool stimulated a transparent, reproducible and structured decision making process and helped users identify issues that need clarification. We recommend its use by public health policy makers.

Keywords: Disease notification, mandatory reporting, guideline

PRESENTED BY: Ewout Fanoy

ESCAIDE REFERENCE NUMBER: 20142043

Parallel Session 17: Surveillance (2)

Public Health Monitoring of the XX Commonwealth Games, Glasgow 2014

Alex Sanchez-Vivar[1], Kostas Danis[2], Marion Muehlen[3], Jim McMenamin[1]

[1] Health Protection Scotland, UK; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden; [3] ECDC, Sweden

Abstract
Mass gatherings can potentially present public health risks for visitors and local populations. From 23/07/2014 to 03/08/2014, Glasgow (Scotland) will host the 2014 Commonwealth Games, with ≈6,500 athletes and officials from 71 participating nations. Health Protection Scotland (HPS) is implementing surveillance and building the capacity to identify and respond to potential public health threats during the Games.

Abstract methods
We reviewed experience from previous mass gathering events, and consulted stakeholders on what systems are necessary to provide real-time health-related information. Based on those, we enhanced existing surveillance schemes, developed new event-based syndromic and rumour surveillance systems. The Commonwealth Surveillance Team (CoST) will coordinate all surveillance schemes during the Games.

Abstract results
During the enhanced surveillance period (from30/06/2014 and six weeks onwards), existing systems will move from weekly to daily reporting, with CoST monitoring daily: influenza-like-illness, acute respiratory infections, vomiting, diarrhoea and gastrointestinal infections in the community; accident and emergency attendances from sentinel hospitals across Glasgow; calls received by the Scottish nurse-led telephone helpline; and all-cause mortality. Event-based surveillance will be newly established for: syndrome-based over-the-counter medicines sales; attendance to the Athletes' Village polyclinic; and social media information (twitter monitoring). Together with the European Centre for Disease Prevention and Control, HPS will monitor international infectious disease threats with potential to impact health. Situation reports will be published daily.

Abstract conclusion
Enhanced and event-based surveillance systems for the Games will allow monitoring health threats on a daily basis, ensuring that no relevant events are missed. The introduction of novel surveillance schemes and fine-tuning existing ones will be the Game's legacy for Scotland, as well as its contribution to best practice in planning future mass gathering surveillance.

Keywords: Surveillance; mass gathering; syndromic surveillance; events-based surveillance; enhanced surveillance

PRESENTED BY: Alex Sanchez-Vivar

ESCAIDE REFERENCE NUMBER: 20142193

Establishment of Active Disease Surveillance in Eight Reporting Hospitals in Tacloban City and Other health Facilities in Areas Affected by Typhoon Haiyan Philippines, 2013

Ruth Alma Ramos[1], Vikki Carr De Los Reyes[1], Ma Nemia Sucaldito[2], Enrique Tayag[1]

[1] FETP-Philippines, Philippines; [2] Department of Health Philippines, Philippines

Abstract
On November 8, 2013, typhoon Haiyan led to the displacement of thousands of people and severe damage to infrastructures. There was incomplete data as to the state and the existence of a surveillance system in health facilities. Hence the urgent need to establish active disease surveillance to determine early potential disease outbreaks and monitor trends and priority health needs.

Abstract methods
A developmental study was done. Eight hospitals in Tacloban City and other health facilities in Leyte and Samar Provinces were randomly chosen as surveillance sites. Acute watery diarrhea, leptospirosis, tetanus and dengue were identified as the diseases with outbreak potential. A standard case definition was established for each disease. Standard reporting forms were collected daily by FETP fellows and suspect cases admitted in the hospitals were interviewed using a standard questionnaire by identified disease surveillance officer. Data collected were encoded, analyzed, interpreted and disseminated to the Secretary of Health and other national and local decision makers.

Abstract results
A total of 279 acute watery diarrhea cases, 14 cases of Leptospirosis, 15 cases of Tetanus and 6 cases of Dengue were identified. There was one Leptospirosis (CFR=8%) and 4 Tetanus (CFR=27%) deaths. Increasing number of acute watery diarrhea was noted in Kananga, Leyte and an immediate outbreak investigation was conducted by FETP fellows. 54 suspect measles cases were reported from Biliran and Tacloban City.

Abstract conclusion
The devastating effect of typhoon Haiyan on health services has led to the lack of reliable data and information system in Eastern Visayas in terms of prevention and response. Active disease surveillance post-disaster is recommended to identify diseases with outbreak potential so immediate control measures could be instituted.

Keywords: Active disease surveillance; outbreaks; control measures, reliable data

PRESENTED BY: Ruth Alma Ramos

ESCAIDE REFERENCE NUMBER: 20142194

Implementing a syndromic surveillance system in Kefalonia island, Greece, after destructive earthquakes, February-March 2014. Results and evaluation of the surveillance system.

Chrysovalantis Silvestros[1], Eleni Triantafillou[2], George Rigakos[2], Eleni Papoutsidou[2], Katerina Tsekou[2], Anastasios Konstantopoulos[2], Spyridoula Karadima[2], Theodora Nikolopoulou[2], Spyros Likiardopoulos[3], Gerasimos Pantelios[3], Georgios Kouris[3], Georgios Christodoulakis[4], Kassiani Mellou[2],Theano Georgakopoulou[2], Christos Hadjichristodoulou[5], Yannis Tselentis[6]

[1] KEELPNO, Greece; [2] Hellenic Center of Disease Control and Prevention (HCDCP), Greece; [3] General Hospital of Argostoliou, Kefalonia, Greece; [4] General Hospital of Lixouriou, Kefalonia, Greece; [5] Medical School, University of Thessaly, Greece; [6] University of Crete, Regional Laboratory of Public Health, Greece; [7] Laboratory of Clinical Bacteriology, Parasitology, Zoonoses, and Geographical Medicine (WHO Collaborating Center), Medical School, Heraklion, Crete, Greece

Abstract

Kefalonia, Greece (population 35,801), was struck by two earthquakes in early 2014. We implemented a syndromic surveillance system for early detection and control of outbreaks, which have occurred after similar events elsewhere.

Abstract methods

We asked clinicians in several sites to report cases of 4 syndromes (gastroenteritis, bloody diarrhea, fever of unknown origin and acute respiratory infection) in island residents (permanent and temporary), using a standard daily reporting form (including zero returns, actively sought by telephone where absent), from 7 February to 31 March. The reporting sites were a ship that hosted homeless people, the emergency departments of the two public general hospitals and the island's healthcare center. A signal/cluster was defined as more than two cases by syndrome and reporting site that exceeded the expected number (mean for the previous 3 days plus 2 standard deviations). We evaluated the timeliness (interval between examination and notification), internal completeness (percentage of missing information) and validity of the system (percentage of confirmed outbreaks within all signals).

Abstract results

Reporting lasted 53 days (hospitals) and 22 days (ship). 113 (24% zero) notifications were received passively (76%). In total, 306 syndrome cases were reported; 141 fever, 93 respiratory infection, 71 gastroenteritis and one bloody diarrhea cases. The lag from examination to reporting was 0-6 days (median 1 day); completeness was 90% on patient's information -symptoms, residency area, date of onset. After investigation our surveillance system led to one true signal (out of 16).

Abstract conclusion

The outbreak detected was not identified by any of the other surveillance system. This cluster of 22 gastroenteritis cases resulted to the recall of 180 meals that had already been distributed but not consumed and a larger outbreak was prevented.

Keywords: Public health surveillance; syndrome; earthquakes; disease outbreak; Kefalonia; island

PRESENTED BY: Chrysovalantis Silvestros

ESCAIDE REFERENCE NUMBER: 20141926

Etiology of Influenza-Like Illnesses in Reunion Island, general practitioners sentinel network, 2011 and 2012

Elise Brottet[1], Marie-Christine Jaffar-Bandjee[2], Laurent Filleul[1]

[1] French institute for public health surveillance, France; [2] CHU Réunion, Reunion, France

Abstract

Influenza surveillance in Reunion Island is based on a sentinel network of general practitioners (GP) who report the weekly number of consultations for influenza-like illness (ILI) and perform sample of nasal swabs. Swabs are sent to the university hospital laboratory to test for influenza viruses and for type identification. Surveillance reports show that a large proportion of ILI is influenza negative. The aim of this study was to describe the etiology of ILI in a sample of patients from the sentinel network.

Abstract methods

We randomly selected 250 swabs kept in the laboratory and collected in 2011-2012 from ILI patients (fever≥38°C and cough). We performed multiplex RT- PCR for 18 viruses and 4 bacteria, described the results and compared them with ILI activity.

Abstract results

Laboratory results were available for 222 samples. We detected respiratory pathogens in 169/222 (76%) samples. Rhinovirus was the most commonly detected virus (23.4%), followed by Influenza A (21.2%), Influenza B (12.6%), Coronavirus (4.9%) and Human Metapneumovirus (3.6%). Co-infections were detected in 9 swabs, including 6 with influenza. Human Metapneumovirus, Respiratory Syncytial Virus A and B and Coronavirus NL63 were detected only in summer, whereas Parainfluenza viruses were detected in winter. Comparing laboratory results with GP surveillance data, we identified a peak of ILI activity that corresponded to Parainfluenza circulation. Other increases in ILI activity corresponded to influenza circulation.

Abstract conclusion

A screening of respiratory pathogens responsible for ILI has been realized for the first time in Reunion Island. During the influenza surveillance period, more than 50% of ILI patients tested negative for influenza. The etiology remained unknown for only 24% of samples. In the future, detailed clinical data should be collected to compare symptoms between pathogens.

Keywords: Influenza, Respiratory Tract Infections, Etiology, Sentinel surveillance, Reunion Island

PRESENTED BY: Elise Brottet

ESCAIDE REFERENCE NUMBER: 20141932

Prevalence of hepatitis E virus infection among blood donors resident in Apennines mountains, central Italy

Claudia Lucarelli[1], Enea Spada[1], Paola Chionne[1], Elisabetta Madonna[1], Cinzia Marcantonio[1], Patrizio Pezzotti[2], Roberto Bruni[1], Luigi Dell'Orso[3], Katia Ragone[3], Carla Tomei[4], Anna Rita Ciccaglione[1]

[1] Istituto Superiore di Sanità, Italy; [2] National AIDS Unit - Italian National Institute of Health, Rome, Italy; [3] Servizio di Immunoematologia e Trasfusionale Ospedale, Italy; [4] Centro Raccolta Sangue Comitato Regionale CRI Abruzzo, L'Aquila, Italy

Abstract

Hepatitis E virus (HEV) is emerging as an under-diagnosed disease in industrialized countries, with many sub-clinical infections. In Italy, HEV diagnostic test is not routinely performed and previous seroprevalence studies suggested a prevalence from 1% to 6%. We estimated the prevalence of hepatitis E antibodies and evaluated potential exposures in blood donors from l'Aquila province, in central Italy.

Abstract methods

In February-March 2014, we carried out a cross-sectional study among blood donors attending the blood transfusion unit in L'Aquila. We analyzed sera for anti HEV IgG by ELISA and interviewed donors to collect information on possible exposure. We performed univariate and multivariable analysis, estimating prevalence rate ratios (PRR) by binomial regression.

Abstract results

Amongst the 313 blood donors (median age: 48 years, 19.5% of females) 153 (48.9%, 95% CI: 43-54) were IgG-positive. Seroprevalence increased with age (35.2%, 45.1%, 50.0% and 61.3% in donors aged <35, 35-44, 45-54 and 65+ years old, respectively; p=0.19). Men had higher prevalence than women (51.2 vs. 39.3%, p=0.24). Seroprevalence was higher among those who cultivated a kitchen garden (53 vs. 41.6%, p=0.17) and those who ate raw dried pork liver sausages (54.9 vs. 23.3%, p<0.01). Multiple binomial regression showed that eating raw dried pork liver sausage was associated with past and present infection (APRR=2.35, 95% CI: 1.4-4.1).

Abstract conclusion

Prevalence of anti-HEV IgG was high among blood donors of all age groups in this area. Consumption of raw dried pork liver sausages may represent a particular source of HEV infection. We recommended to implement test for HEV in patients with suspected hepatitis The high prevalence detected prompts further studies about incidence of the disease at national level, HEV infectivity and transmissibility by blood products.

Keywords: Hepatitis E, blood donors, seroepidemiological studies, cross-sectional studies

PRESENTED BY: Claudia Lucarelli

ESCAIDE REFERENCE NUMBER: 20142112

Parallel Session 18: Measles

The transcontinental spread of measles from the Netherlands to Canada and the United States in 2013/2014: The well-travelled D8 measles genotype

Laura Nic Lochlainn[1, 2], Lindsey Sherrard[3], Theresa St. Jean[4], Monika Naus[5], Jill Fediurek[6], Charla DeBolt[7], Rob van Binnendijk[1], Helma Ruijs[1], Susan Hahné[1]

[1] National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands; [2] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [3] Public Health Agency of Canada, Ottawa, Canada; [4] Alberta Health Services, Edmonton, Alberta, Canada; [5] British Columbia Centre for Disease Control, Vancouver, Canada; [6] Public Health Ontario, Toronto, Canada; [7] Washington State Department of Health, Shoreline, Washington, USA

Abstract

In North America, religious Dutch communities share historical and cultural links with the Netherlands. In 2013/2014, a large measles outbreak in the Netherlands posed a risk to Canada, who eliminated measles in 1998. The Dutch outbreak was predominantly among orthodox-reformed Protestants with low vaccination. We aimed to describe measles importations from the Netherlands to Canada in 2013/2014, to highlight the risk of measles spread in unvaccinated groups.

Abstract methods

Public health authorities in Canada investigated measles importations from the Netherlands and subsequent outbreaks. Laboratory confirmation included genotyping.

Abstract results

Between August 2013 to March 2014, Canada identified four imported cases among unvaccinated travellers from the Netherlands with links to orthodox-reformed Protestant communities. The D8 genotype (MVs/Taunton.GBR/27.12) associated with the Dutch outbreak was confirmed in all cases. Single importations into Ontario (August 2013) and British Columbia (November 2013) did not result in onward transmission. In October 2013, Alberta reported 41 cases following a single importation. All cases belonged to the same religious Dutch community. In March 2014, British Columbia declared an outbreak with over 400 cases. The outbreak spread rapidly in a low vaccination school-setting and subsequently to six US residents, including a case with ties to the index school. Of all cases, greater than 95% belonged to the same religious community.

Abstract conclusion

Measles importations from the Netherlands into Canada resulted in two local outbreaks and subsequent spread to the US. The outbreaks occurred among religious Dutch communities with low vaccination, highlighting the susceptibility of these groups. Continued targeted communication regarding measles activity to unvaccinated groups will allow informed decisions about vaccination and other preventive measures, such as refraining from travel.

Keywords: Measles, travellers, unvaccinated, The Netherlands, Canada, United States

PRESENTED BY: Laura Nic Lochlainn

ESCAIDE REFERENCE NUMBER: 20142089

Cross-border health threat: a measles outbreak on a cruise ship, western Mediterranean sea, 2014

Tommi Kärki[1, 2, 3, 4], Antonietta Filia[3, 4], Antonino Bella[3, 4], Martina Del Manso[3, 4], Maria Cristina Rota[3, 4], Fortunato D'Ancona[3, 4], Peter Kreidl[5], Tarik Derrough[2], Ettore Severi[2], Simone Lanini[6], Maria Rosaria Capobianchi[6], Fabio Magurano[3, 7], Loredana Nicoletti[3, 7], Loredana Vellucci[8], Maria Grazia Pompa[8], Silvia Declich[3, 4]

[1] European Programme for Intervention Epidemiology Training (EPIET), Stockholm, Sweden; [2] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; [3] Istituto Superiore di Sanità (ISS), Rome, Italy; [4] National Centre for Epidemiology Surveillance and Health Promotion (CNESPS), Rome, Italy; [5] Ministry of Health, Vienna, Austria; [6] National Institute for Infectious Diseases (INMI) "Lazzaro Spallanzani" Rome, Italy; [7] Department of Infectious, Parasitic and Immune-mediated Diseases, Rome, Italy; [8] Ministry of Health, Directorate General for Prevention, Rome, Italy

Abstract

On 26/02/2014, a cruising company reported a cluster of suspected measles cases among the crew aboard their ship. Symptomatic crew members were disembarked in Italy. The Italian Ministry of Health coordinated investigations to assess the extent of the outbreak and control activities to prevent further transmission.

Abstract methods

Cases in the crew were assessed at the port. ECDC sent an international case-finding alert to ascertain further cases in passengers. The company provided data on persons aboard, including the crew's self-reported immunization status. We obtained information on probable (fever and rash) and confirmed (probable with positive PCR and/or IgM antibody) cases, aboard the ship after 1/1/2014 or linked to another case aboard, from the Italian surveillance system and the Austrian Ministry of Health, and calculated attack rates (AR).

Abstract results

There were 42 cases, 34/42 (80%) confirmed, with onset between 20/2/2014 and 28/3/2014. Most cases (73%, 22/42) occurred among the crew (22/968, AR 2.3%). Seven cases occurred among passengers (N≈3300 per week), one among other workers aboard, 12 among contacts on mainland. The median age of cases was 26 (range 1-42) years. Vaccination status was known for 29 cases: 25 were unvaccinated, 3 incompletely vaccinated, one fully vaccinated (n=8, n=2, n=1 among the crew, respectively). Of the crew, 15% (142/968) reported previous vaccination and 11% (108/968) a history of measles.

Abstract conclusion

Lack of immunity among the crew led to a measles outbreak aboard the cruise ship and on mainland. Cruise ships, with both passengers and crew coming from countries where measles may be circulating, are potential settings for disease transmission. We recommend verifying vaccination status and providing appropriate vaccinations to the crew. Also, cruise ship passengers should be properly immunized.

Keywords: Measles, outbreak, naval medicine, vaccination

PRESENTED BY: Tommi Kärki

ESCAIDE REFERENCE NUMBER: 20141920

Measles Elimination in Portugal: data from 2004 to 2013

Liliana Gomes[1], Catia Sousa Pinto[2], Teresa Fernandes[3], Paulo J. Nogueira[4]

[1] ACeS Loures-Odivelas, Division of Epidemiology and Vigilance, Directorate-General of Health, Portugal; [2] Division of Epidemiology and Vigilance, Directorate-General of Health, Portugal; [3] Directorate of Disease Prevention and Health Promotion, Directorate-General of Health, Portugal; [4] Directorate of Analysis and Information, Directorate-General of Health; Preventive Medicine Institute, Medical Faculty of Lisbon, Portugal

Abstract

Despite being a vaccine-preventable disease, measles' outbreaks continue to happen in Europe, mainly due to insufficient vaccination coverage. Portugal, however, is among the EU/EEA countries with the highest measles vaccination coverage (>95% for 2 doses at least since 2006) and the lowest notification rates for the disease (<1/million at least since 2004). Our aim was to characterize measles incidence and indicators of measles elimination in Portugal, from 2004 to 2013.

Abstract methods

Measles cases within Portugal's National Mandatory Notification Diseases Surveillance System between 1st January 2004 and 31st December 2013 were analyzed. The case definition used (possible, probable and confirmed) was based on the EU case definitions of 2002 and 2008.

Abstract results

From January 2004 to December 2013, 52 possible measles cases were notified in Portugal, 23 were classified as confirmed, 1 as probable, 4 as possible, and 24 were discarded cases. Of the 24 confirmed and probable cases, 12 (50%) were imported and 12 (50%) were secondary cases (including 5 in migrants and 3 in healthcare professionals). Imported cases originated from Europe (7 cases), Africa (4 cases) and Asia (1 case). Except for 2009 and 2012, the majority of these cases were not vaccinated against measles.

Abstract conclusion

Portugal has low incidence of measles due to high vaccination coverage of the population and all primary cases are imported. Non-vaccinated migrants and healthcare professionals are high-risk populations, therefore it is recommended to develop targeted measures to increase vaccination coverage in these groups, according to the national guidelines.

Keywords: Measles, Disease Elimination, Surveillance, Portugal, Epidemiology, Vaccination.

PRESENTED BY: Liliana Gomes

ESCAIDE REFERENCE NUMBER: 20142262

Measles Outbreak in Olorunda Local Government-Osun State, Nigeria, January-April, 2013

Rhoda Fadahunsi[1], Olufunmilayo[1], Oladayo Biya[1], Elizabeth Adedire[1], Taoheed Alabi[2]

[1] Nigeria Field Epidemiology Laboratory Training Programme, Asokoro, Abuja, Nigeria; [2] Olorunda Local Government, Osun State, Nigeria

Abstract

Measles epidemic usually occurs during the dry season from November to May.It has its greatest incidence in children below 2 years of age in the developing countries. A suspected outbreak of measles was reported in Olorunda Local Government Area (LGA). We investigated to describe the outbreak, confirm the aetiologic agent, and profer measures to prevent future occurrence.

Abstract methods

Case definition of measles was given as any person with fever and maculopapular (non-vesicular) generalized rash and cough, coryza or conjunctivitis (red eyes) or any person in whom a clinician suspects measles from January to April 2013 residing in Olorunda LGA. We obtained line-list of cases and did a descriptive analysis of the outbreak. We collected data on vaccination status, age, date of onset of rash, outcome of infection and others. We calculated attack rate (AR) and CFR. Eighteen blood samples were collected and sent to the laboratory for confirmation.

Abstract results

Of the 64 cases, 68.8%(44/64) were under five years, of these, 56.8%(25/44) were below two years. Age-specific AR was 134/100,000 population for below five years, 15/100,000 population for five years and above. CFR was 3.1%. The two deaths were aged below two years, one had zero dose of measles vaccine and the other unknown. Sabo ward was the most affected of 11 wards (31.3%). Proportion of the unvaccinated was 50.0% (32/64) with 59.4%(19/32) below 5years. Eight of the 18 blood samples were measles IgM positive.

Abstract conclusion

The high proportion of the unvaccinated could have resulted in increased accumulation of susceptibles leading to the outbreak. Thus intervention targeting the unimmunized that are below 5years will reduce the number of susceptibles and outbreak occurrence.

Keywords: Measles outbreak, Surveillance, Attack rate, Unvaccinated

PRESENTED BY: Rhoda Fadahunsi

ESCAIDE REFERENCE NUMBER: 20142077

2013 Outbreak of Measles in a Non-Immunizing Population in Alberta, Canada: How Preparedness Planning Assisted in Containing Transmission to Ten Households

Tanis Kershaw[1], Vivien Suttorp[2], Kimberley Simmonds[3], Theresa St. Jean[4]

[1] Public Health Agency of Canada, Canada; [2] South Zone - Alberta Health Services, Canada; [3] Alberta Health, Canada; [4] Alberta Health Services, Edmonton, Alberta, Canada

Abstract

The first outbreak of measles in Alberta since 2000 was declared on October 18, 2013 as a result of a case reported in a non-immunized teenager returning from the Netherlands. The case belonged to a community where immunization is generally not accepted; therefore, risk of spread was high. The local Medical Officer of Health had identified the potential for an outbreak among this population and preparedness planning with the community had begun in August, 2013. We report the details of the outbreak to demonstrate how planning assisted in containing transmission.

Abstract methods

Descriptive epidemiology on cases and social networking analysis on cases and household contacts was completed. Public health measures implemented to control the outbreak, developed during preparedness planning, included: mass immunization clinics, a mobile measles assessment team (MMAT), and a measles assessment centre (MAC).

Abstract results

A total of 42 confirmed cases were identified between October 16th and November 25th. The majority of cases were male (52.4%) and the average age was 12 (range <1 to 24 years). Six complications were reported, resulting in one hospitalization and no deaths. All cases were unimmunized and were located among five neighbouring communities. All but two cases were epidemiologically linked within ten households. The MMAT was mobilized 84 times and 167 individuals were assessed in the MAC. A total of 1,302 individuals were immunized at eight mass clinics.

Abstract conclusion

Preparedness planning and the public health measures implemented during the outbreak were essential in containing transmission to ten households. Exploring strategies for controlling spread of an outbreak in a non-immunizing population is important. In this outbreak, working with the community during preparedness planning led to a collaborative effort to minimize transmission.

Keywords: Measles, Disease Outbreaks, Immunization, Communicable Disease Control, Public Health, Canada

PRESENTED BY: Vivien Suttorp

ESCAIDE REFERENCE NUMBER: 20142105

Poster **Abstracts**

This abstract book has been produced using authors supplied copy. Editing has been restricted to some corrections where appropriate. The information in each abstract is the responsibility of the author(s).

Poster **Abstracts** – Poster Session A

Poster Session A 15.10 – 16.10 Wed 5

Antimicrobial Resistance (1)

Treatment and Antibiotic Resistance in Gonococcal Infections In Galicia (Spain)

Maria-Jesús Purrinos-Hermida[1],Isabel Losada Castillo[2], M.I. Santiago-Pérez[2], Grupo de Trabajo SOGAMIC[3]

[1] Spanish Field Epidemiology Training Program; [2] Servicio de Epidemiología (dirección xeral de Innovación e Xestión de Saúde Pública Spain); [3] Sociedad Gallega de Microbiología, Spain

Abstract

Multiple antibiotic resistance has become a serious problem in gonococcal infections nowdays and the ECDC has presented a control plan for this problem. Two of its pillars are: a) adequate treatment of cases and contacts (ceftriaxone with azithromycin, or exceptionally cefixime instead of ceftriaxone); and b) culture and antibiogram. The objective of this study is to ascertain treatments used (antibiotic type), sampling and culture frequency and antibiotic resistance in Galicia

Abstract methods

We checked the clinical records of declared cases, both suspected and confirmed (cultured or ADN), in Galicia during 2012 and 2013. The following variables, among others, were recorded: first treatment (antibiotic), diagnostic technique used and antibiogram results (sensitive, partial sensitivity and resistance)

Abstract results

244 cases were detected (71% confirmed) and 233 clinical records were reviewed. Of these, in 187 cases a record of the first treatment used was available, 146 (62%) had a positive culture and 129 an antibiogram. The treatment prescribed followed ECDC recommendations (with ceftriaxone) only in 3% of cases, up to 10% if cefixime was included as valid. 44% of first treatments included azithromycin, 30% quinolones and 20% doxycycline, alone or combined. Proportion of sensitive strains was low for tetracyclines (18%) and quinolones (40%) and larger for azithromycin (85%). All studied strains were sensitive to ceftriaxone and cefixime

Abstract conclusion

We observed an important disagreement between the treatment actually used and ECDC recommendations which requires immediate remedial action. We observed a high proportion of cases in which culture was performed. We did not observe any negative changes in sensitivity to ceftriaxona or cefixima

Keywords: Gonorrhoea, Threat, Resistant

PRESENTED BY: Maria-Jesús Purrinos-Hermida

ESCAIDE REFERENCE NUMBER: 20141921

Vancomycin-resistant enterococci with vanA gene in hospital infection unit patients and local environmental reservoirs

Veronika Oravcova[1], Matus Mihalcin[2], Lucie Pospisilova[1], [3], Ivan Literak[1]

[1] University of Veterinary and Pharmaceutical Sciences Brno, Czech Republic; [2] Clinic of Infectious Diseases, University Hospital, Masaryk University, Brno, Czech Republic; [3] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology

Abstract

We studied epidemiology of colonization with vancomycin-resistant enterococci (VRE) of patients treated for Clostridium difficile infection at the Department of Infectious Diseases, University Hospital Brno, Czech Republic.

Abstract methods

From June to October 2013 we collected 49 fecal samples from hospitalized patients (some patients were sampled repeatedly), 11 fecal samples from staff, and 23 smears from hospital settings. Samples were cultured for VRE on Slanetz-Bartley agar with vancomycin (32 mg/l). Suspected colonies were selected, identified, tested for antibiotic susceptibility and resistance and virulence genes. Furthermore, VRE isolates were typed by pulsed-field gel electrophoresis and multi-locus sequence typing (MLST).

Abstract results

VRE with vanA gene were found in 26 (72%) of 36 tested patients. Some patients were colonized by more isolates, hence we obtained 40 vanA-carrying VRE. Five of the not VRE-colonized patients, when admitted to hospital, became colonized during hospitalization. We didn't find VRE colonization of hospital personnel, but we found VRE in hospital settings including room after disinfection. VRE belonged to Enterococcus faecium (35 isolates), E. faecalis (4) and E. raffinosus (1). All isolates were multi-resistant, resistances were encoded by ermB, aac(3')-IIIa, aac(6')-Ie-aph(2'')-Ia, tet(M) and tet(L) genes. Virulence of 31 (89%) E. faecium isolates was encoded by esp and/or hyl gene, E. faecalis carried gelE, cylA and asa1 virulence genes. Based on MLST analysis, all E. faecium isolates belonged to high-risk clonal complex 17, represented as ST17, ST18, ST19, ST262 and new ST884. E. faecalis isolates belonged to ST6 and ST536.

Abstract conclusion

Despite of low frequency of VRE infections in Czech hospitals, we found common VRE colonization of patients treated for Clostridium difficile infections.This study was funded by project CEITEC (CZ.1.05/1.1.00/02.0068) and IGA VFU (17/2014/FVHE).

Keywords: Humans, antibiotic resistance, glycopeptides, Enterococcus sp., Clostridium difficile

PRESENTED BY: Veronika Oravcova

ESCAIDE REFERENCE NUMBER: 20142064

Comparative analysis of IncX plasmids harbouring resistance genes to clinically relevant antibiotics in Enterobacteriaceae

Hana Dobiasova[1], Jiri Vojtech[1], Monika Dolejska[1]

[1] University of Veterinary and Pharmaceutical Sciences Brno, Czech Republic

Abstract

IncX plasmids are nowadays recognized as a diverse group of plasmids associated with the most relevant resistance genes – plasmid-mediated quinolone resistance, extended spectrum beta-lactamase and carbapenemase genes. The aim of the study was to compare IncX plasmids from non-related Enterobacteriaceae isolates from various sources.

Abstract methods

IncX1-X4 plasmids were screened in a collection of 1800 Enterobacteriaceae isolates resistant to cefotaxime or with reduced susceptibility to ciprofloxacin originating from animals, environment and humans from Europe, North and South America, Africa, Australia using PCR. Relevant antibiotic resistance genes were tested using PCR and sequencing. Relatedness of isolates was determined using pulsed-field gel electrophoresis (PFGE). Conjugation and transformation experiments were performed. IncX plasmids' sizes were determined by S1-nuclease and PFGE. Relatedness of IncX plasmids was assessed using restriction analysis and hybridization targeting taxC gene and relevant resistance genes.

Abstract results

A total of 189 Enterobacteriaceae isolates (10,5 %, n = 1800) resistant to cefotaxime or with reduced susceptibility to ciprofloxacin harboured at least one IncX subgroup including 8 isolates harbouring 2-3 distinct IncX subgroups. IncX1 subgroup was the most prevalent (107 isolates), followed by IncX2 (47), IncX4 (28) and IncX3 (16). IncX1-X4 plasmids (30-70 kb) carried predominantly qnrS1 (78 isolates) separately, or accompanied by blaTEM-1 on IncX1-X2 or tet(A) on IncX2 plasmids. Based on restriction analysis and hybridization, highly related IncX plasmids were found in isolates from different sources and origin.

Abstract conclusion

IncX plasmids were shown to be important vectors of plasmid-mediated quinolone resistance genes in Enterobacteriaceae of animal, environmental and human origin all over the world and their further spreading might poses a risk for public health. The study was funded by CEITEC (CZ.1.05/1.1.00/02.0068), IGA VFU Brno (13/2014/FVHE), IGA MZ (NT14398).

Keywords: Plasmids, Enterobacteriaceae, Quinolones, Drug Resistance, Microbial

PRESENTED BY: Hana Dobiasova

ESCAIDE REFERENCE NUMBER: 20142072

Carbapenemases in bacteria from wildlife: IMP-4-producing Enterobacteriaceae from Silver Gulls in Australia

Monika Dolejska[1], Martina Masarikova[1], Hana Dobiasova[1], Martin Havlicek[2], Nicholas Carlile[3] ,David Priddel[3], Alois Cizek[1],Ivan Literak[1]

[1] University of Veterinary and Pharmaceutical Sciences Brno, Czech Republic; [2] Small Animal Specialist Hospital, Australia; [3] Office of Environment and Heritage, Australia

Abstract

The spread of carbapenemase-producing enterobacteria (CPE) is causing an unprecedented public health crisis. The aim of the present study was to assess the occurrence of CPE in Silver Gulls (Chroicocephalus novaehollandiae) from three nesting colonies in Australia (Five Islands, Glebe, Montague Island).

Abstract methods

A total of 504 cloacal samples were taken from young gulls using a sterile cotton swab in 2012. The samples were cultivated on CHROMagar KPC and subsequently on MacConkey agar with meropenem (0,125 mg/L) and ZnSO4 (100 mg/L). Isolates were identified using MALDI-TOF and tested for carbapenemase genes (blaIMP, blaVIM, blaNDM, blaKPC, blaOXA-48) by PCR and sequencing. Clonality of E. coli isolates was determined by pulsed-field gel electrophoresis (PFGE).

Abstract results

Eighty (16%) Enterobacteriaceae isolates of various species (Escherichia coli, E. fergusoni, Klebsiella pneumoniae, Proteus mirabilis, P. vulgaris, P. penneri, Enterobacter cloacae, E. aerogenes, Citrobacter freundii, C. brakii, Kluyvera georgiana) with reduced susceptibility to carbapenems were obtained from a total of 504 cloacal samples. All the isolates originated from gulls in Five Islands (40%, nsample=200) and carried blaIMP-4 gene. More than one bacterial species/genotype per cloacal sample was identified in 34 (43%, nIMP-4=80) samples. IMP-4-positive isolates of E. coli with identical PFGE profiles from different birds were found. Non-related isolates with different macrorestriction profiles were also identified showing the role of horizontal transfer of the blaIMP-4 gene.

Abstract conclusion

The results demonstrate high level of environmental contamination by carbapenemase-producing bacteria in one location in eastern coast of Australia. Close contact of gulls with sources of clinically important multiresistant Enterobacteriaceae in urban and suburban areas can contribute to the further dissemination of these bacteria in the environment.Funded by 'CEITEC' CZ.1.05/1.1.00/02.0068.

Keywords: Charadriiformes, Enterobacteriaceae, Carbapenemase, Australia

PRESENTED BY: Hana Dobiasova

ESCAIDE REFERENCE NUMBER: 20142080

Salmonella enterica diarizonae (50:z52:z35) carrying IBC-1 type extended-spectrum beta-lactamase (ESBL) isolated from a child, Greece 2013

Kyriaki Tryfinopoulou[1], Georgia Mandilara[2], Panagiota Giakkoupi[1], [3], [4], Alkiviadis Vatopoulos[5]

[1] Central Public Health Laboratory, Greece; [2] National Reference Centre for Salmonella, Shigella, VTEC, Greece; [3] Antimicrobial Resistance and HAI Laboratory; [4] HCDCP-Vari, Attica-Greece; [5] National School of Public Health, Greece

Abstract

Emerging resistance to extended-spectrum cephalosporins (ESCs) in Salmonella spp. is a substantial public health concern. Herein we present a ESCs- resistant clinical Salmonella enterica diarizonae isolateofthe extremely rare antigenic type 50:z52:z35 from Greece.

Abstract methods

Three Salmonella spp isolates (isolated in April, May and June 2013) from a hospitalized paediatric oncologic patient, were sent to the National Reference Centre for Salmonella (NRCS) for further testing. Serotype was determined using the slide agglutination method, according to Kauffmann-White-Le Minor scheme. Antimicrobial susceptibility testing and phenotypic test for the detection of ESBLs were performed using the disk diffusion method and the double-disk synergy tests (DDST) respectively. Conjugation experiments were carried out in broth cultures using E.coli 1R716 Str R as recipient. PCR and subsequent DNA sequencing of the PCR products were applied for the detection of the respective bla genes.

Abstract results

All three isolates were serotyped as S. enterica diarizonae, of the very rare antigenic type 50:z52:z35. The clinical isolates were found resistant to penicillins, aminiglycosides, trimethorpim, tetracycline and ceftazidime and cefotaxime. β- lactam resistance was transferred at a high conjugation frequency rate per donor cell. Double-disk synergy tests in the clinical isolates and the transconjugants appeared positive. PCR and sequencing revealed the presence of blaIBC-1.

Abstract conclusion

For the first time in Greece, Salmonella isolates of the very rare antigenic type S. enterica diarizonae (50:z52:z35) were found resistant to third-generation cephalosporins due to the production of blaIBC. The fact that they were recovered from a paediatric immunocompromised patient with history of repeated hospital admissions emphasizes the role of the hospital environment's selection pressure and the need for continuous monitoring of the ESC resistance in Salmonella spp.

Keywords: Salmonella spp., extended – spectrum cephalosporins, blaIBC-1

PRESENTED BY: Kyriaki Tryfinopoulou

ESCAIDE REFERENCE NUMBER: 20142229

A laboratory assessment of the epidemiology of Multi-Drug Resistance amongst epidemic strains of Vibrio cholera from southern Ghana-2013

George Khumalo Kuma[1], Japheth A Opintan[2], Samuel Sackey[3], Anthony Dongdem[1], [4], Donne Ameme[3], Kofi Nyarko[3], Harry Asmah[5], Lawrence Henry Ofosu-Appiah[1], [4], Lorreta Antwi[1], [4], Christian Badu Adabor[5]

[1] Ghana Health Service, Ghana; [2] University of Ghana Medical School, Ghana; [3] University of Ghana School of Public Health, Ghana; [4] National Public Health Reference Laboratory, Ghana; [5] School of Allied Health Sciences, University of Ghana

Abstract

Antimicrobial resistance has been widely reported in several microbial organisms. There has been no comprehensive surveillance on Multi-Drug-Resistance (MDR) amongst Vibrio cholera isolates in Ghana to determine prescription patterns. This study assessed prevalence and epidemiological distribution of MDR Vibrio isolates and sought to determine the molecular basis of their resistance.

Abstract methods

A total of 300 archived Vibrio isolates from 2010-2012 obtained from three southern regions of Ghana, Greater Accra(GAR),Central and Volta regions were retyped and screened for antibiotic susceptibilities using Kirby Bauer method. We reviewed records of 98 selected isolates that were MDR and analysed them by distribution and screened for Integron Class 1 and 2 resistant gene markers using conventional PCR techniques.

Abstract results

All 300 isolates were Vibrio cholera O1, Ogawa with 98(32.7%) being MDR. Amongst the MDRs, highest levels of resistance were observed in Erythromycin: 98(100.0%) and Trimethroprim: 97(99.0%), and least in Azithromycin, 0(0%), Ciprofloxacin 1(1.0%), Doxycycline 27(27.6%) and Tetracycline 29(29.6%). Only 65 (66.3%) of the MDRs were correctly linked to their records in the laboratory logbooks. Of the identified records, 41/65(63.1%) and 24/65(36.9%) were isolated from males and females respectively, mean age 25.8years ± 13.3.(Range:2-65). Most of the MDR isolates were from Agegroup ≥15 years, 53 /65(81.5%) with majority from the GAR, 60/65(92.3%). None of the isolates haboured the Integron Class 1 and 2 genes.

Abstract conclusion

This study reveals high prevalence of MDR Vibrio cholera lacking integron genes from Southern Ghana. Azithromycin and ciprofloxacin appears to be most appropriate for treatment of cholera. Study brings to fore lapses and the urgent need for accurate labeling and records keeping in typical laboratory settings for comprehensive surveillance data analysis. This need has been discussed with laboratory personnel.

Keywords: Surveillance, Epidemiology, Ghana, Vibrio cholera, Multi Drug Resistance, Integron gene.

PRESENTED BY: George Khumalo Kuma

ESCAIDE REFERENCE NUMBER: 20142163

Healthcare associated infections (1)

Are early deaths following bloodstream infections preventable?

Keiju Kontula[1], Kirsi Skogberg[1], Jukka Ollgren[2], Asko Järvinen[1], Outi Lyytikäinen[2]

[1] Helsinki University Hospital; [2] Department of Infectious Diseases Surveillance and Control, National Institute for Health and Welfare (THL), Finland

Abstract

One third of deaths caused by bloodstream infections (BSI) have previously been shown to occur within two first days after the onset. The aim of our study was to analyze patients' characteristics and causative pathogens of BSIs leading to early deaths in order to explore possibilities for prevention.

Abstract methods

Patients with BSI in Helsinki and Uusimaa region (population, 1.5 million) in 2007 were identified from the National Infectious Disease Register (n=2172) and data on deaths within 2 days after the first positive blood culture from the Population Information System (n=76). Patient records were reviewed by one investigator.

Abstract results

The mean age of the patients was 73 years (range, 34-103) and 51% were females. Of the BSIs, 55% were community-acquired (CA-BSI) and 45% healthcare-associated (HA-BSI). Rapidly fatal underlying conditions were more common in HA-BSIs vs. CA-BSIs (38% vs. 19%, $p=0.06$). The most common pathogens in CA-BSIs were Streptococcus pneumonia (29%) and Eschericia coli (24%), and in HA-BSIs Pseudomonas aeruginosa (24%) and Staphylococcus aureus (18%). In both groups, respiratory tract (50%) and abdomen (17%) were the most common foci. Empiric antimicrobial treatment was more often appropriate in CA-BSIs vs. HA-BSIs (81% vs. 41%, $p<0.001$). Treatment delay was longer in CA-BSIs assessed by the proportion of patients with antimicrobial treatment within 3 days after symptom onset (68% vs. 96%, $p=0.06$). Patients with non-optimal care (ineffective or delayed antimicrobial treatment) tended to be associated with overweight and excessive alcohol use.

Abstract conclusion

BSI patients dying early often have severe comorbidities and other risk factors. Our results emphasize the importance of prompt initiation of appropriate antimicrobials. S. pneumonia and S. aureus were common pathogens, highlighting the role of pneumococcal and influenza vaccination in prevention.

Keywords: Bloodstream infection, outcome, healthcare-associated, community-acquired

PRESENTED BY: Keiju Kontula

ESCAIDE REFERENCE NUMBER: 20142207

Examining the rate of invasive Candida infection in UK critical care units using multi-level modelling: a prospective cohort study

Lynsey Patterson[1], Ronan McMullan[2], Lourda Geoghegan[1], David Harrison[3]

[1] Public Health Agency (NI); [2] Belfast Health and Social Care Trust, United Kingdom; [3] Intensive Care National Audit and Research Centre, United Kingdom

Abstract

Rates of invasive Candida infection (ICI) vary between countries but this has not been modeled in previous analyses of ICI risk factors. In the UK, a large prospective multicentre study in critical care units was used to examine known risk factors for ICI and quantify variation between units.

Abstract methods

During July 2009-March 2011, 96 UK critical care units were included. Cases were non-neutropenic individuals aged 18 years and over who developed ICI after ICU admission. The main outcome was the rate of ICI per 10,000 ICU bed days and known risk factors and unit level factors were included in a multi-level logistic regression model.

Abstract results

There were 225 cases of ICI (4.02/1000 admissions and 6.84/10,000 bed days) and a threefold variation in ICI rates across 13 UK regions. Approximately 4% of the variation in rates per 10,000 bed days can be attributed to unit level factors. Known factors independently associated with an increased risk of ICI included abdominal surgery (adjusted incidence rate ratio (AIRR) 1.97 95% CI 1.45, 2.67), parenteral nutrition (AIRR 1.89 95% CI 1.32, 2.70), fungal colonisation (AIRR 2.21 95% CI 1.29, 3.79) and indwelling devices (central venous catheters and drains). Patients with ICI also had a higher risk of death in the unit (AIRR 2.11 95% CI 1.56, 2.83).

Abstract conclusion

A marginal 4% of the variation in ICI rates can be attributed to unit level factors having adjusted for individual, unit and regional level covariates. The analysis is the first to quantify the variation in ICI rates attributable to unit level factors and provides further evidence for known risk factors for ICI.

Keywords: Candidemia, critical care, Multilevel Analysis, risk factors

PRESENTED BY: Lynsey Patterson

ESCAIDE REFERENCE NUMBER: 20142212

A large-scale outbreak of viral keratoconjunctivitis related to healthcare-associated transmission in Canada

Julio Soto[1], Mihaela Gheorghe[2], Manon Gingras[3], Hélène Chouinard[3], Julie Lafrenière[3], Suzie Bernier[3], Claudette Viens[3], François Desbiens[3]

[1] Institut national de santé publique du Québec, Montreal (Qc), Canada; [2] Canadian Field Epidemiology Program, Public Health Agency of Canada, Canada; [3] Agence de la santé et des services socioaux de la Côte-Nord, Baie-Comeau (QC), Canada

Abstract

Worldwide, viral keratoconjunctivits (VKC) is a leading cause of common eye infections, occurring in various health-care settings and in the community. We report the largest documented VKC outbreak in Canada, which occurred in a small town in Northern Quebec. The main objective of this investigation was to characterize the outbreak.

Abstract methods

A descriptive study was conducted using medical records of patients who were diagnosed with VKC between December 1st, 2013 and March 1st, 2014. A case definition was adapted from clinical criteria for VKC. A sample of cases was tested for viral culture, Adenovirus-specific DNA, and Adenovirus PCR typing. Chi-square tests were conducted to examine differences between nosocomial and community-acquired cases.

Abstract results

In total, 1,437 cases (overall incidence rate of 34.0 per 1,000 inhabitants) were reported over the course of five months. Medical records were reviewed for 939 cases. Up to 238 (25.4%) cases were nosocomial (hospital being the only source of exposure), while 701 (74.7%) were community-acquired. Severe disease was significantly higher among nosocomial compared with community-acquired cases; 25.4% and 9.2%, respectively ($p<0.001$). Among respondents, the majority of cases, 63.8% (n=81), had previously consulted the ophthalmology clinic within three weeks of their VKC episode. The outbreak began with three clusters of VKC associated with the ophtamology clinic, followed by rapid transmission to other hospital services and finally into the community. Adenovirus serotype 8 was identified through laboratory testing.

Abstract conclusion

This study suggests that clusters of VKC nosocomial cases contributed to the spread of the infection into the community. It highlights the importance of infection control procedures for medical personnel, including disinfection of commonly used instruments, cohorting, and early reporting of suspected VKC cases, particularly in ophthalmology clinics.

Keywords: Keratoconjunctivitis, Adenoviridae, disease outbreaks, cross infection, community-acquired infections

PRESENTED BY: Mihaela Gheorghe

ESCAIDE REFERENCE NUMBER: 20142221

Outbreak of Infections by *Acinetobacter Baumanii* in a Critical Care Unit

Isidra Tenza-Iglesias[1], EJ Silva-Contreras[1], José L. Carretero-Ares[1], P. García-Shimizu[1], A. Gimeno Gascon[1], JC. Rodriguez[1], C. Escriva-Pons[1], M. Fuster-Pérez[1], José Sánchez Payá[1]

[1] Hospital General Universitario de Alicante, Spain

Abstract

Although in recent years nosocomial infections by multiresistant germs, a growing problem, have become endemic, outbreaks can occur at any time. Our objective is to describe an outbreak of nosocomial infection-colonization bycarbapenem-resistant *Acinetobacter baumannii* (CRAB) in a critical care unit (CCU).

Abstract methods

In December 2013, the Healthcare-Associated Infections Surveillance System detected a temporospatial clustering of cases of CRAB in seven beds of a CCU, free of these infections in the previous six months. Convenient infection control measures and recommendations (contact precautions for these patients, standard precautions in the remaining, use of alcohol-based hand rub solution, group of patients, checklist of cleaning procedures, environmental microbiological controls, smear controls) were implemented. In each case, a sheet of epidemiological surveillance is filled (admission date, age, sex, intrinsic and extrinsic risk factors, infection criteria, infection location, discharge reason). Epidemic curve is described.

Abstract results

There were 12 nosocomial CRAB infections-colonizations (10 infections, 2 colonizations), distributed as follows: week 48-2013 (1), 49-2013 (1), 50-2013 (2), 51-2013 (2), 52-2013 (3); 1-2014 (1), 2-2014 (0), 3-2014 (1), 4-2014 (1), 5-11-2014 (0). All isolated strains had the same antibiotype pattern; the genotipic study was concordant in the seven samples studied.

Abstract conclusion

Temporospatial occurrence of cases suggests that the most likely mechanism of transmission was the direct/indirect cross-transmission via hands of personnel. Surveillance system has allowed detecting cases; thus, early implementation of recommendations to control infections has shown effectiveness. Prevention strategies for this health problem have two fundamental pillars: appropriate degree of compliance with the recommendations on standard precautions (mainly, hand hygiene) and policies of appropriate use of antimicrobials, to reduce the population of susceptible patients to the maximum.

Keywords: Healthcare associated infections, Outbreaks, Antimicrobial resistance, Surveillance

PRESENTED BY: José Sánchez Payá

ESCAIDE REFERENCE NUMBER: 20142223

Hospital-acquired Clostridium difficile infection in a Hematology center from Cluj-Napoca, Romania, 2013

Delia Mihaela Herghea[1], Anca Bojan[1], [2], Letitia Blag[1], Adeline Honciuc[1]

[1] Oncology Institute "I.Chiricuta" Cluj Napoca, Romania; [2] University of Medicine and Pharmacy "Iuliu Hatieganu" Cluj Napoca, Romania

Abstract
To evaluate the incidence of hospital-acquired Clostridium difficile infection (HA-CDI) in patients with hematologic malignancies.

Abstract methods
Retrospective analysis of HA-CDI in patients admitted to the Hematology Department of the Oncology Institute "I. Chiricuta" from Cluj-Napoca, Romania, between January and December 2013. HA-CDI was considered if diagnosis of CDI was made more than 48 hours after admission. Proportion and incidence of HA-CDI were calculated.

Abstract results
Of the 2072 patients admitted to the Hematology unit during the study period, 52 (2.51%) had HA-CDI. The annual incidence of HA-CDI was 3.03/1000 patient-days. Incidence decreased from 4.22/1000 patients-days in the January-March quarter to 1.84/1000 patients days in the October-December quarter. The peak values were in January and in June 2013 (5.01 /1000 patient-days and 4.81/1000 patient –days respectively). Mean age of the patients was 57.6±14.3 years (21-84). The most cases of CDI occurred in patients with lymphoma (30.8%), acute leukemia (28.8%) and chronic leukemia (11.5%). Mean time between admission and CDI onset was 13.4±10.3 days (3-48). Recurrence occurred in 11.5% of the patients after metronidazole or vancomycin treatment. Mean hospital stay was 21.2±11.4 days (5-64).

Abstract conclusion
Patients receiving chemotherapy are at increased risk for Clostridium. difficile infection. Surveillance and further studies are required to assess the epidemiology of HA-CDI in patients with hematologic malignancies.

Keywords: Clostridium difficile infection, hematologic malignancies

PRESENTED BY: Delia Mihaela Herghea

ESCAIDE REFERENCE NUMBER: 20142237

Problems Associated with whe use of Antimicrobials: Evolution of Clostridium Difficile Infections in the Period 2011-2013

E. Javier Silva-Contreras[1], M. El Attabi[1], A. Sánchez-Bautista[1], E. Mérino-Lucas[1], JC. Rodriguez[1], G. Riera[1], C. García-González[1], C. Escriva-Pons[1], José Sánchez Payá[1]

[1] Hospital General Universitario de Alicante, Spain

Abstract
Clostridium difficile infections (CDI) have increased over the past few years, largely by the use of antibiotics. Assessing the effectiveness of strategies for prevention and control of these infections is required. The objective is to describe the evolution of the incidence of nosocomial CDI within a third level hospital during the 2011-2013 period.

Abstract methods
Starting surveillance of all patients admitted with diarrhea and CDI microbiologically confirmed (antigen positive [Ag +] and toxin positive or negative [Tox +/-]). A case is considered nosocomial when: patient has started an episode of diarrhea after the first 48 hours of admission, or the symptoms occur during the first 48 hours before admission and the patient has been discharged from the hospital in the previous four weeks. The frequency measurement used is the Incidence Rate (IR) per 10,000 days of stay; for comparison of IR (2012 vs 2011 and 2013 vs 2011), risk ratio (RR) is used, with 95% confidence interval (95%CI).

Abstract results
Incidence of CDI in 2011 was 2.09 per 1044 days of stay; in 2012 was 2.55, RR=1.22 (0.82–1.82); in 2013 was 2.90, RR=1.39 (0.94–2.05). The incidence of CDI (Ag +, Tox +) was 0.84 in 2011, 0.60 in 2012, RR=0.72 (0.35-1.49), and 0.93 in 2013, RR=1.11 (0.58–2.14). The incidence of CDI (Ag +, Tox -) was 1,26 in 2011, 1,95 in 2012, RR=1,55 (0.95-2.54), and 1.97 in 2013, RR=1.56 (0.96-2.57).

Abstract conclusion
There was an increase, although not statistically significant, in incidence of CDI. To reduce the risk of acquiring CDI, programs optimizing antimicrobial use are a strategic element to improve the use of antimicrobials.

Keywords: Healthcare Associated Infections, Surveillance, Clostridium difficile, Antibiotics

PRESENTED BY: José Sánchez Payá

ESCAIDE REFERENCE NUMBER: 20142241

TB & other respiratory diseases (excluding influenza)

Investigation of an Outbreak of Multidrug-resistant Tuberculosis in a Workplace Setting.

Chantal Migone[1], Margaret O'Sullivan[1, 2, 3], Tim Jackson[1, 2, 3], Anne Sheahan[1, 2, 3]

[1] HSE, Ireland; [2] Department of Public Health Ireland; [3] St Finbarr's Hospital, Douglas Road, Cork, Ireland

Abstract

In December 2012, a case of sputum-positive Pulmonary Tuberculosis (TB) in a factory worker was notified to Public Health. Sputum Culture and Sensitivity revealed MDR-TB. Contact tracing identified two further cases of sputum negative Pulmonary TB in workers. Contact tracing was extended to wider workplace contacts. 477 contacts were screened.

Abstract methods

Household and close work contacts were screened with Tuberculin Skin Test (TST) in accordance with National Guidelines. The decision was made to screen wider contacts with Interferon Gamma Release Assay (IGRA). Some close contacts, tested initially with TST, also had IGRA testing, following risk assessment.

Abstract results

The overwhelming majority of contacts were born outside Ireland. Most had been vaccinated with BCG. Rates of Latent TB Infection (LTBI) were high in both household contacts 55% (n=9) and workplace contacts 42% (n=107). Two cases of active TB were found which were treated as MDR-TB. In extended workplace contacts, LTBI rates were lower at 11.2%. (n=361). Rates of LTBI in non-Irish born contacts were double that of Irish born contacts.

Abstract conclusion

High rates of LTBI in household and close work contacts were considered to be due to exposure to MDR-TB in the index case. For wider contacts, rates of LTBI were lower. Background exposure to TB in countries of high TB endemicity was a likely factor. The confounding effects of BCG on TST results could not be excluded. Therefore two different management strategies were used for contacts with LTBI; household and close work contacts were managed as MDR-TB contacts, while wider contacts who were not irish-born were managed as having LTBI due to exposure to TB in their country of origin. No further cases of TB were identified in contacts.

Keywords: Contact-tracing, Latent tuberculosis (LTBI), tuberculosis Multidrug-resistant (MDR-TB), Interferon gamma Release Assays (IGRA)

PRESENTED BY: Chantal Migone

ESCAIDE REFERENCE NUMBER: 20142118

Final results of QuantiFERON-TB Gold In-Tube screening for latent tuberculosis in a cohort of patients with HIV infection.

Monica Sañé Schepisi[1], Mario Pasquale Parracino[1], Alessia Mammone[1], Rita Bellagamba[1], Carmela Pinnetti[1], Stefania Cicalini[1], Alessandro Sampaolesi[1], Adriana Ammassari[1], Delia Goletti[1], Enrico Girardi[1]

[1] Italian National Institute for Infectious Diseases, IRCSS L. Spallanzani, Epidemiology Dept, Italy

Abstract

Tuberculosis (TB) preventive therapy in people living with HIV is strongly recommended. IGRAs can be used instead of tuberculin skin test to identify HIV-1-infected individuals who could benefit from latent TB infection (LTBI) treatment. After the initiation of highly active anti-retroviral therapy (HAART), repeat testing for LTBI is recommended for HIV-infected persons previously known to have negative results, as immune system recovery could restore the ability to react to IGRAs.

Abstract methods

We analysed variation over time among people with HIV infection screened for LTBI by QFT-GIT. 193 individuals first screened in 2006-2011 were tested again in 2013-2014 period. Patients with suspected active TB and those diagnosed with TB within 1 month of QFT testing were excluded.

Abstract results

At initial visit average CD4+ cell count was 325.1 cell/µl. QFT-GIT was positive in 14 cases (7,3%) and indeterminate in 13 cases (6,7%); positivity was associated with being born in high TB incidence country and with higher CD4+ cell count. All patients started HAART and average CD4+ cell count increased to 523.4 cell/µl. At follow-up, 4/14 (28,6%) initially QFT-IT positive patients reverted to negative; all those resulted indeterminate converted to negative and among 166 initially negative, 4 (2.4%) converted to positive. No association between CD4 count variation and QFT-IT conversion to positive or reversion to negative was found.

Abstract conclusion

Severe immunosuppression had an impact of QFT results. No association between CD4+ cell count variation and QFT-IT conversion to positive or reversion to negative was found. Our data do not offer support to the recommendation to repeat LTBI screening in persons with HIV after HAART related immune reconstitution in a low TB incidence country.

Keywords: HIV infection, tuberculosis, latent tuberculosis infection, IGRA

PRESENTED BY: Monica Sañé Schepisi

ESCAIDE REFERENCE NUMBER: 20142242

Molecular surveillance pilot on multi-drug resistant tuberculosis in the EU/EEA

Csaba Ködmön[1], Karin Johansson[1], Ivo Van Walle[1]

[1] ECDC, Sweden

Abstract

Molecular epidemiology allows identification of recent transmission and associated risk factors, detection of non-conventional transmission contexts, and TB control programme impact measurement. From January 2013 to May 2014, ECDC and 12 EU/EEA Member States piloted molecular surveillance of MDR-TB through the TESSy – Molecular Surveillance System (TESSy-MSS) and evaluated the system in May 2014.

Abstract methods

MDR-TB molecular typing data collected at European level were analysed. Data input, processing and output as well as user survey data provided by 12 laboratories and 25 National Focal Points were analysed.

Abstract results

From the MDR-TB Project database 1810 typing profiles (years 2003-2011) from 23 EU/EEA Member States were transferred and 499 (3% linked to surveillance data) typing profiles were uploaded by 12 Member States (years 2012- 2013) during the pilot period. The typing coverage in 2012 was 21.4% (304 of 1421 notified cases). The median reporting delay for strains isolated in 2012-2013 was 271 days (48-438). Nineteen of 39 survey participants found TESSy-MSS useful for MDR TB molecular surveillance and 28 out of 38 supported the continuation of molecular typing data collection, but only 2 out of 11 found the system user-friendly.

Abstract conclusion

The system has proved its usefulness in collecting molecular typing data for MDR-TB and shown potential in detecting cross-border molecular clusters. In order to improve its potential and public health value TESSy-MSS should be more user-friendly and provide more complex analysis features. In addition, the reporting timeliness, data completeness, typing coverage and data linkage to epidemiological data should be improved.

Keywords: Tuberculosis, European Union, molecular surveillance, MDR TB

PRESENTED BY: Csaba Ködmön

ESCAIDE REFERENCE NUMBER: 20142042

The effectiveness of convalescent plasma for the treatment of severe acute respiratory infections of viral aetiology such as Middle East Respiratory Syndrome coronavirus: a systematic review and exploratory meta-analysis

Maria Saavedra-Campos[1], John Mair-Jenkins[2], Kenneth Baillie[3], Paul Cleary[1], Fu-Meng Khaw[2], Wei Shen Lim[4], Sophia Makki[1], Kevin D. Rooney[5], Jonathan S. Nguyen-Van-Tam[6], Charles R. Beck[6]

[1] Public Health England, UK; [2] East Midlands Centre, Public Health England, Nottingham, UK; [3] The Roslin Institute, University of Edinburgh, Edinburgh, UK; [4] Respiratory Medicine, Nottingham University Hospitals NHS Trust, Nottingham, UK; [5] The Institute of Care and Practice Improvement, University of the West of Scotland, Hamilton, UK; [6] Division of Epidemiology and Public Health, University of Nottingham, Nottingham, UK

Abstract

Middle East Respiratory Syndrome coronavirus (MERS-CoV) is an emerging respiratory infection with a case-fatality exceeding 40%. Current approaches to clinical management centre on supportive care. We conducted a systematic review to evaluate the effectiveness of convalescent plasma for treatment of severe acute respiratory infections of viral aetiology.

Abstract methods

We conducted a systematic review following the PRISMA statement. The primary method of analysis was narrative synthesis. We searched healthcare databases and sources of grey literature in July 2013; reviewers working in duplicate sifted records against eligibility criteria, extracted data and assessed bias, using a standardized form. We undertook exploratory post hoc meta-analyses to pool study estimates using a random effects model and assessed statistical heterogeneity using I2 test.

Abstract results

We identified 32 eligible studies (6 case studies, 20 case-series, 2 comparison studies, 1 prospective cohort and 3 systematic reviews) of SARS-CoV and severe influenza, involving 1,327 patients and with an overall low quality. We found that mortality associated with convalescent plasma therapy consistently decreased between 7% to 23% for SARS-CoV patients and between 18% to 70% for severe influenza cases, especially if given early after symptom onset. The odds of a fatal outcome, across all viral aetiologies, decreased with plasma therapy, compared with placebo or no therapy (pooled OR 0.25; 95%CI 0.14-0.45; $p < 0.001$; I2 0%; 8 studies). No serious adverse events or complications due to therapy were documented.

Abstract conclusion

Convalescent plasma therapy may have reduced mortality and appeared safe. However, this is based on predominately low quality, uncontrolled studies. This therapy may be effective in the treatment of MERS-CoV infections and should be evaluated further in the context of a clinical trial or other formal evaluation.

Keywords: MERS coronavirus, convalescent plasma, systematic review, meta-analysis

PRESENTED BY: Maria Saavedra-Campos

ESCAIDE REFERENCE NUMBER: 20141935

Far away from the guideline: Diagnostic and preventive treatment of children who had contact to persons with tuberculosis infections. A survey in Lower Saxony, Germany, 2007-2012

Martina Scharlach[1]

[1] Governmental Institute of Public Health of Lower Saxony, Germany

Abstract

After contact to a person with tuberculosis (TB), diagnostic and preventive drug treatment (PT) should – in contrast to adults – be applied immediately to children under the age of five, who are at higher risk to develop active TB. A previous study among contact persons of all ages however revealed that PT is often refused. In the present study we assessed diagnostic and PT in small children.

Abstract methods

We collected data from children up to 5 years of age that were investigated during routine contact tracing between 2007-2012, by local public health departments (LPHD) in Lower Saxony. Applied diagnostics (according to the national recommendations on TB control: tuberculin skin test, interferon-gamma release assay, radiographic test), duration of PT treatment and possible reasons for refusal of PT were analysed descriptively.

Abstract results

From a total of 276 children, 89 (32 %) cases underwent appropriate diagnostics. Radiography was performed in 92 children (33 %) only. Preventive treatment was given to 56 (20 %) children and refused for 215 (78 %) children. Most common reasons for refusal of PT were a supposed minimum risk for developing active TB because of rare contact (43 cases, 20 %) and rejection by parents (42 cases, 20 %).

Abstract conclusion

Although national recommendations recommend a clear investigation schedule, adequate diagnostics and PT after contact to persons with TB infection are rarely performed in children. We recommend increasing awareness for exposed children and focussing primarily on close contacts. Better information of parents might increase the number of children that receive PT and at the same time reduce excessive testing after rare contact. Our information flyer “Tuberculosis in children” was distributed to LPHD in six languages.

Keywords: Tuberculosis, latent tuberculosis infection, contact tracing, preventive therapy

PRESENTED BY: Martina Scharlach

ESCAIDE REFERENCE NUMBER: 20141950

Predictors of delay in initiation of treatment among newly-diagnosed pulmonary tuberculosis patients in Karaganda City, Kazakhstan, 2012-2013

Simon Ajeilat[1], *Sholpan Suleimen*[2]

[1] CDC, Kazakhstan; [2] U.S. CDC, Central Asia Office

Abstract

Treatment delay of pulmonary tuberculosis (PTB) can lead to advanced destructive disease forms and more infection transmissions to others. In 2011, 1,122 new tuberculosis patients were identified in Karaganda (notification rate 83/100,000) and 516 (46%) of them had destructive forms. This cross-sectional study aims to estimate the prevalence of treatment delay (TD) and its determinants among newly diagnosed PTB patients in Karaganda city.

Abstract methods

We enrolled all newly diagnosed active PTB patients aged ≥17 and identified in Karaganda TB registry during 2012-2013 (n=245). We defined TD as ≥30 days between onset of cough and treatment initiation. Through personal interviews, we collected information on patients’ demographics, socio-economic, and behavioral factors. Clinical data were obtained from medical records, and healthcare facility characteristics from facility records. We used logistic regression to assess associations between the study factors and TD.

Abstract results

93 (38%) patients had TD. The least delay, 18% (4/22), was among those who owned a car. The highest TD was among smokers (45%; 39/86) and women (46%; 40/87). In multivariate logistic regression, women were more likely to delay (OR=2.3, 95% CI=1.3-4.3), as were current smokers (OR=1.8, 95% CI=0.9-3.4), while patients who owned a car were less likely to delay (OR=0.3, 95% CI=0.1-0.9). Characteristics of healthcare facilities were not predictors of delay.

Abstract conclusion

The lower odds of delay among car owners might be attributed to a higher socio-economic status, while smokers are more likely to delay as they probably attribute cough to the habit of smoking. As delay is generally high in the study population, we recommend that health authorities distribute appropriate messages through appropriate channels to people with cough lasting more than two weeks to attend for timely TB evaluation.

Keywords: Tuberculosis, treatment delay, determinants, Kazakhstan

PRESENTED BY: Sholpan Suleimen & Lyazzat Sekerbayeva

ESCAIDE REFERENCE NUMBER: 20141999

Public Health microbiology and molecular epidemiology

Detection of diphtheria toxin gene-bearing and non-toxin gene-bearing Corynebacterium diphtheriae and Corynebacterium ulcerans/Corynebacterium pseudotuberculosis using a quadruplex Rotor-Gene Q PCR assay

Aruni De Zoysa[1], Norman K Fry[1], Androulla Efstratiou[1], Timothy Harrison[1]

[1] Public Health England, Centre for Infections, RVPBRU, Colindale, UK

Abstract

Background. Detection of toxigenicity is the most important test for the microbiological confirmation of a clinical diagnosis of diphtheria. Routineidentification and characterization of pathogenic corynebacteria is undertaken by phenotypic methods and demonstration of toxin production by the Elek test. We report the development of a Rotor-Gene qPCR assay for the detection of tox bearing and non-tox bearing C. diphtheriae, C. ulcerans/C. pseudotuberculosis in DNA extracts from cultures. The PCR targets the rpoB gene and the A-subunit of the toxin gene. Green fluorescent protein DNA is used as an Internal Process Control to check for PCR inhibitors.

Abstract methods

Methods. Sensitivity, specificity and reproducibility were determined according to recommended guidelines. To determine specificity 87 non-target strains (13 genera, 48 species) were used. Fifity-one clinical isolates of toxigenic and non-toxigenic C. diphtheriae and C. ulcerans,confirmed by phenotypic tests, were chosen blindly and tested. The assay was run in parallel with phenotypic testing of presumptive C. diphtheriae/ C.ulcerans/ C. pseudotuberculosis strains submitted to the Reference Unit.

Abstract results

Results. Specificity was 100%. Four isolates which were Elek -ve were found to be tox gene +ve by PCR. These possess the tox gene but do not express diphtheria toxin. Therefore, tox gene +ve strains should be tested by the Elek test to confirm toxin expression. Empirical LOD for the target genes was 0.5 genome copies/ reaction; PCR efficiency was 89-91.6%; and 100% correlation was seen with the phenotypic results.

Abstract conclusion

Conclusions. The qPCR is 100% specific for detection of pathogenic corynebacteria. The method is rapid, sensitive, specific and reproducible and could be an excellent tool for use in other European laboratories. To date the assay has shown 100% agreement with phenotypic results.

Keywords: Corynebacterium, qPCR, Diphtheria, Toxin gene

PRESENTED BY: Aruni De Zoysa

ESCAIDE REFERENCE NUMBER: 20142082

Human Papillomavirus (HPV) and Chlamydia trachomatis (Ct) infections in undocumented immigrant women in Milan (Northern Italy)

Ester Fasoli[1], Elena Rosanna Frati[1], Marianna Martinelli[1], Silvia Bianchi[1], Daniela Colzani[1], Luciana Carnelli[2], Franca Fossati-Bellani[2], Pierfranco Olivani[3], Elisabetta Tanzi[1]

[1] University of Milan, Department of Biomedical Sciences for Health, Italy; [2] Lega italiana della Lotta contro i Tumori (LILT), section of Milan, Italy; [3] Naga Onlus, Italy

Abstract

HPV and Ct diffusion data in immigrant women are incomplete and appropriate strategies must be directed specifically to these patients. This study aimed to evaluate the molecular epidemiology of HPV and Ct infections among undocumented migrant women living in Milan not involved in cervical cytology screening program in the formal healthcare system. Molecular assays were performed in urine samples.

Abstract methods

537/757 women (median age 36 years; range 18-65 years), who visited Naga Onlus Centre in Milan between June 2012 and December 2013, were enrolled. Informed consent was obtained by all participants. HPV and Ct DNA were detected by PCR amplification of ORF L1 and of 150bp segment of cryptic plasmid, respectively. All HPV DNA positive samples were subjected to viral typing using a restriction fragment length polymorphism (RFLP) assay. Positive women were subsequently called to perform a Pap-test and/or antibiotic treatment.

Abstract results

Most of the women enrolled came from Latin-America (43.4%) and East-Europe (30.7%). 22.5% were immigrants from less than one year. The prevalence of HPV infection was 24.2%, 66.1% of which were sustained by HR-clade genotypes. The prevalence of Ct infection was 7.8%; 3.2% of women were HPV/Ct co-infected. 38.5% of HPV positive women have undergone Pap-test.

Abstract conclusion

These data indicate that screening by urine testing is highly accepted from undocumented immigrant women and highlight the need to plan and monitor HPV and Ct surveillance strategies, particularly in countries like Italy with current high migration rate. The urine sampling seems to increase screening uptake among women at increased risk for cervical cancer or reproductive tract infections.

Keywords: Human Papillomavirus, Chlamydia trachomatis, immigrant women, urine samples

PRESENTED BY: Ester Fasoli

ESCAIDE REFERENCE NUMBER: 20142088

Development of a Directory of Microbiology Laboratory Services (EULabServe) to support laboratory based surveillance and preparedness in the EU

Amanda Ozin[1], Katrin Leitmeyer[1]

[1] ECDC, Sweden

Abstract

Not all countries have the full capacity to perform specialised testing required for pathogen detection/characterisation and molecular surveillance of infectious diseases. In order to fulfil EU obligations on cross-border health threats they rely on international collaborations. Knowledge about current practices of accessing laboratory services is the basis for deciding on the need for, and the requirements of, an EU laboratory directory of microbiological testing services (EULabServe).

Abstract methods

An extensive consultation process among the 31 European Centre of Disease Control and Prevention (ECDC) National Microbiology Focal Points (NMFP) involved bi-annual meetings (2008-2013) and a structured survey. Within the process, NMFPs were provided with information collected through bi-lateral interviews (22 experts/15 countries) and an on-line survey (140 experts/31 countries). Experts from the EU communicable disease network structures were selected to reflect the differences in public health microbiology systems and capacities. The subsequently developed prototype web-based directory has been first tested with experts in rare and (re)emerging pathogens.

Abstract results

Consensus agreement was reached supporting the development of a simple, easy to maintain tool that allows information sharing on specialized microbiological laboratory services within the EU. Highest priority was given for rare and (re)emerging pathogens. Testing of EULabServe confirmed readiness for use across EU communicable disease networks. Basic-level information on reference services provided and contacts will be openly available, moderated by the ECDC, and annually updated.

Abstract conclusion

According to the identified needs, ECDC has prepared and tested the first generic, EU-wide open service directory for public health microbiology laboratory services. This tool is expected to help countries to easily identify collaborating partners for surveillance and epidemic preparedness and to find cost-effective solutions in complying with their legal requirements.

Keywords: Public Health, Microbiology, Preparedness, European Union

PRESENTED BY: Ozin-Hofsaess

ESCAIDE REFERENCE NUMBER: 20142050

Factors Influencing Infant Feeding Choices By Mothers Attending Prevention of Mother To Child Transmission of HIV Clinics in Oyo State, Nigeria

Aishat Usman[1], Olufunmilayo Fawole[2], Magbagbeola Dairo[3]

[1] NFELTP, Nigeria; [2] Nigeria Field Epidemiology and Laboratory Training Program, Nigeria; [3] University of Ibadan, Nigeria

Abstract

In sub-Saharan Africa, Mother-to-child transmission (MTCT) of HIV is responsible for about 90% of HIV infections in children, and about half of these pediatric infections are thought to have been acquired through breastfeeding. This study determines factors influencing infant feeding choices of mothers enrolled in Prevention of Mother to Child Transmission (PMTCT) of HIV clinics in Oyo State.

Abstract methods

Cross-sectional survey of 600 HIV-positive women delivered of live babies. In a two-stage sampling procedure, 600 women were chosen by systematic random sampling from six out of ten PMTCT clinics. Semi-structured interviewer administered questionnaire was used to obtain data on socio-demographics, infant feeding choice, disclosure of HIV status, antenatal care visits, influence of family on these choices. Data was analyzed using Epi-info version7. Four Focus Group Discussions (FGDs) were conducted with the aid of FGD guide and analyzed using thematic approach.

Abstract results

Mothers (86%) aged 31 ± 5.7years, 61% had disclosed their HIV status to their spouses and 93% were earning ≤ ₦29,000 monthly. Infant feeding choices were EBF (61%), ERF (26%) and MF (13%). Predictors of ERF were desire to reduce the risk of transmission of HIV [AOR = 2.5, (1.0-11.3)] and disclosure of HIV status to spouses [AOR = 5.0, (3.8-23.0)]. Predictors of EBF were infant feeding counseling [AOR = 2.7, (1.6-6.9)] and fear of stigmatization [AOR = 7. 2, (2.1-23.6)]. Predictors of MF neighbors' advice [AOR = 4.6, (1.6-24.4)] and infant illnesses [AOR = 6.8, (4.0 -35.1)]. FGDs revealed pressure from family members as the major reason for Mixed Feeding practice.

Abstract conclusion

Mixed Feeding is still prevalent due to family pressure. Family members' education on safer infantfeeding practices in the context of HIV should be implemented.

Keywords: Mother-to-child transmission, Infant feeding choice, HIV

PRESENTED BY: Aishat Usman

ESCAIDE REFERENCE NUMBER: 20141943

Detection of Carbapenem, Cephalosporin, and Quinolone Resistance coding genes in E. coli isolated from hospital waste water : a matter of concern

Salesh Chandran[1], Vishal Diwan[2], A.J Tamhankar[3], Biljo Joseph[4], Senia Rosales Klintz[3], Sathish Mundayoor[5], Cecilia Stålsby Lundborg[3], Ragini Macaden[1]

[1] St John's Research Institute, Bangalore, India; [2] R.D. Gardi Medical College, India; [3] Global Health/IHCAR, Department of Public Health Sciences, Karolinska Institutet, Sweden; [4] Departments of Biotechnology, Christ University, Bangalore, India; [5] Mycobacterial Research Group, Department of Molecular Microbiology, Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India

Abstract

Emergence and dissemination of antibiotic resistant bacteria is a serious public health problem worldwide. Extensive use of antibiotics in hospital settings is known to contribute to this problem. The resistant bacteria can spread to the community via aquatic systems from the hospital wastewater.

Abstract methods

This study was done to detect the presence of Escherichia coli resistant to cephalosporins, carbapenems and quinolones in hospital waste-water. Waste-waters from a rural (H1) and an urban (H2) hospital were tested. Genes coding for chromosomal and plasmid- mediated resistance and phylogenetic grouping was detected by Multiplex Polymerase chain reaction (PCR) and for genetic relatedness by rep-PCR.

Abstract results

Out of 190 (H1=94; H2=96) E. coli examined, 44% were resistant to both cephalosporins and quinolones and 3% to imipenem. ESBLs were detected phenotypically in 96% of the isolates, the gene blaCTX-M coding for 87% and blaTEM for 63%. Quinolone-resistance was due to mutations in gyrA and parC genes in 97% and plasmid- coded aac-(6')-Ib-cr in 89% of isolates. Only in one carbapenem resistant E. coli, NDM-1 was detected. Nearly 67% of the isolates belonged to phylogenetic group B2. Rep-PCR showed considerable diversity of genotypes among the isolates.A molecular microbiology survey of hospital waste water showed contamination with diverse E.coli strains of broad resistance profile with genetic determinants to major therapeutic classes of antimicrobial agents. No comparison was made with domestic wastewater from the same region.

Abstract conclusion

Presence of cephalosporin and quinolone resistant E. coli in hospital wastewater is a matter of concern and stresses the need to place an efficient water treatment plants in health care settings that can minimize the number of bacteria released into the environment.

Keywords: hospital waste water, multidrug resistant E. coli, cephalosporin resistance, quinolones resistance, carbapenem resistance.

PRESENTED BY: Salesh Chandran

ESCAIDE REFERENCE NUMBER: 20142165

International External Quality Assessment (EQA) for molecular detection of Lassa virus (LASV) performed in 2013 reveals the need to optimize diagnostic protocols.

Sergejs Nikisins[1], [2], Toni Rieger[3], Pranav Patel[1], Stephan Günther[3], Matthias Niedrig[1]

[1] Robert Koch Institute, Centre for Biological Threats and Special Pathogens, Berlin, Germany; [2] European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm; [3] Bernhard Nocht Institute for Tropical Medicine, Germany

Abstract

LASV is one of the most prominent imported virus cussing viral hemorrhagic fevers (VHF) within Europe and North America hence there are international demands for standardized methods for rapid and accurate diagnosis. RT-PCR is the method of choice for early detection of virus RNA in blood. EQA was therefore, established by the ENIVD network and distributed amongst 28 international laboratories involved in VHF diagnostics.

Abstract methods

A proficiency panel of 16 samples comprising thirteen inactivated and stable LASV was prepared: Josiah strains (7), Liberian strains (4), Nigerian CSF strain and AV strain. Samples containing Lymphocytic Choriomeningitis virus (LCMV) and two negatives were also included. Results were classified as: "optimal" when all results were correct; "acceptable" 1 to 2 incorrect results and "need for improvement" with >2 incorrect results. Sensitivity for detecting LASV was also determined. Results for the LCMV sample were scored separately to evaluate ability to distinguish LCMV from LASV.

Abstract results

The response rate was 86%; 24 laboratories from 17 countries (13 Europe, 1 Africa, 1 Asia, 2 America). Optimal results were reported by 54.2% (n = 13); acceptable 16.7% (n = 4); need for improvement 29.1% (n = 7). 54.2% (n = 13) achieved 100% sensitivity; 12.5% (n = 3) achieved 92% sensitivity and the remainder 58-83%. Five laboratories could not distinguish LCMV from LASV, reporting false positive LASV for the LCMV sample.

Abstract conclusion

Laboratory testing is essential to confirm clinical diagnosis, as LASV is not easily distinguished from other febrile diseases. Regular EQA monitors laboratory performance and this study highlighted that most participants were able to correctly detect LASV, however, a small number should urgently review and optimize their LASV detection protocols.

Keywords: LASV, External Quality Assurance, sensitivity, Molecular detection

PRESENTED BY: Sergejs Nikisins

ESCAIDE REFERENCE NUMBER: 20141942

Burden of communicable diseases

Incidence of herpes zoster and related complications – a population-based cohort study in Sweden

Karin Sundström[1], Karin Söderberg Löfdahl[2], Jonas Hällgren[3], Caroline Weibull[3], Tomas Bergström[4], Pär Sparèn[3], Lisen Arnheim Dahlström[3]

[1] Bernhard Nocht Institute for Tropical Medicine, Germany; [2] Dept of Laboratory Medicine, Karolinska University Hospital Huddinge, Sweden; [3] Karolinska Institutet, Sweden; [4] Gothenburg University, Sweden

Abstract
The purpose of this study was to estimate incidence of herpes zoster (HZ), and rates of complications from herpes zoster before introducing zoster vaccination in Sweden.

Abstract methods
A register-based retrospective cohort study conducted in Västra Götaland County (1.5 million population) in Sweden. The 2008-2010 data of patients with HZ and related complications were extracted from several databases of primary health care clinics and hospitals by using the HZ ICD-10 Codes and the unique ID number of patients. Incidence rates of HZ and related complications (e.g post herpetic neuralgia PHN)/1000 person year were calculated and stratified by age and sex.

Abstract results
There were 13269 new HZ cases during the study period. The incidence of herpes zoster in both genders, when taking into account all ICD-10 codes used for herpes zoster diagnosis (B02), was 3.25 (95% CI: 3.16-3.34) per 1000 person years in 2010. The incidence was consistently higher in women than in men. In 2010 the incidence in women was 3.90 (95% CI: 3.76-4.04) per 1000 person years compared to 2.59 (95% CI: 2.48-2.71) in men. The incidence gradually increased with age and was highest in men and women over 80 years of age (9.2 per 1000 person years, 95% CI: 8.8-9.6) during 2008-2010. There were 278 new PHN cases during 2008-2010, with an incidence ranging from 1.4 cases per 100 000 person years (95% CI: 1.0-1.9) in the 0-49 years age group, to 41.1 (95% CI: 33.5-49.9) in individuals above age 80.

Abstract conclusion
We find incidence rates of herpes zoster similar to those previously reported in other parts of the world. Age is the major risk factor.

Keywords: Herpes zoster, incidence, varicella zoster virus, cohort studies

PRESENTED BY: Lisen Arnheim Dahlström

ESCAIDE REFERENCE NUMBER: 20141948

The characterization of hepatitis C infections from 1995 to 2013 in Finland

Elisa Huovinen[1], Maarit Sillanpää[1], Mikko Virtanen[1], Salla Toikkanen[1], Heljä-marja Surcel[1], Henrikki Brummer-Korvenkontio[1], Kirsi Liitsola[1], Mika Salminen[1], Markku Kuusi[1], Ilkka Julkunen[1]

[1] National Institute for Health and Welfare, Finland

Abstract
Hepatitis C is the most common hepatitis virus in Finland. So far, there is no information how much we have a hepatitis C-infected people in Finland, and what are the implications that HCV-infection has caused to them.

Abstract methods
In Finland all diagnosed hepatitis C infections have been reported to National Disease Register starting at 1995 and we have characterized HCV-infected persons who were reported to NIDR with personal identification code.

Abstract results
The total number of HCV-diagnosed patients still alive at the end of 2013 is 18 195, corresponding to 0.3 % prevalence. Majority of the new HCV-diagnoses are detected in young adults between 20 to 30 years old. Two thirds of HCV-diagnosed persons are male. There is large geographical variation of HCV-prevalence in Finland. From HCV-diagnosed persons 17% have died by the end of year 2013. The HCV-infected persons have higher mortality compared to the general Finnish population (SMR 9.4 95% CI 9.0-9.8). The most common causes of death are related to external causes and liver diseases. The most common route of HCV-transmission in Finland is the use of intravenous drugs. Prevalence of HCV-Ab could be as high as 75% in users of intravenous drugs. In pregnant women the prevalence was 0.19% in 1985, compared to 0.64% in 2010.On the contrary the prevalence in blood donors has been low during last years (0.010% and lower). The most common HCV-genotype is 3a.

Abstract conclusion
Hepatitis C infections are diagnosed at young age in Finland and the consequences of the disease have therefore time to develop. Although HCV-patients die quite young, the burden of disease is still remarkable.

Keywords: Hepatitis C, Finland, prevalence, incidence, mortality

PRESENTED BY: Elisa Huovinen

ESCAIDE REFERENCE NUMBER: 20141972

Burden of non-typhoid Salmonella and Campylobacter, metropolitan France, 2008-2012

Dieter van Cauteren[1], Véronique Vaillant[1], Cécile Sommen[1], Lisa King[1], Nathalie Jourdan-Da Silva[1], François-Xavier Weill[2], Simon Le Hello[2], Francis Mégraud Henriette de Valk[1], Jean Claude Desenclos[1]

[1] French Institute of Public Health Surveillance (InVS), France; [2] National reference Centre of Salmonella, Pasteur Institute, France; [3] National reference Centre of Campylobacter and Helicobacter, France

Abstract

Disease burden estimates are important for setting priorities for surveillance, research, prevention and control strategies. We estimated the community incidence, number of hospitalisations and deaths for non-typhoid Salmonella and Campylobacter infections in metropolitan France.

Abstract methods

For both infections we used data from national laboratory surveillance, hospital discharge, health insurance, and vital statistics complemented by specific surveys to assess the frequency of care seeking for gastro-enteritis, describe laboratory practices and completeness of case reporting. We used Monte Carlo simulations taking into account uncertainty of parameters derived from the above data sources to produce national estimate of the number of cases occurring in the community.

Abstract results

Between 2008 and 2012, 9,753 Salmonella and 4,490 Campylobacter infections were annually reported. The annual number of community cases in France was estimated to be 179,442 (90%CrI 108,955 – 316,970) for Salmonella and 603,217 (90%CrI 328,033 – 1,381,185) for Campylobacter resulting in an annual community incidence of 286 cases/100,000 for Salmonella (90%CrI 174 – 505) and 961 cases/100,000 for Campylobacter (90%CrI 523 –2,201). Annually, there were 4,319 Salmonella and 5,811 Campylobacter associated hospitalisations, leading to 69 and 18 deaths respectively. For every case reported through laboratory surveillance it was estimated that there are 18 cases of Salmonella and 134 cases of Campylobacter in the community.

Abstract conclusion

The burden of illness for Salmonella and Campylobacter infections in France is shown to be high. Surveillance data underestimate the true incidence, in particular for Campylobacter infections. Since the level of underreporting differs substantially by disease, burden of illness studies rather than routine surveillance data should be used for priority ranking. Our work indicates that both infections should rank high on the priority list for public health intervention.

Keywords: Burden of illness, Salmonella, Campylobacter, France

PRESENTED BY: Dieter van Cauteren

ESCAIDE REFERENCE NUMBER: 20142121

Incidence and socio-economic impact of acute gastro intestinal illness, Sweden, 2013-2014

Michael Edelstein[1], [2], Annasara Carnahan[2], Hanna Merk[2], Charlotte Deogan[2], Anders Wallensten[2]

[1] European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden; [2] Public Health Agency of Sweden, Solna, Sweden

Abstract

In Sweden, acute gastrointestinal illness (AGI) incidence, perceived severity, impact on productivity, related healthcare usage and associated costs are unknown. We measured these parameters in 2013-14 in order to assess AGI's socio-economic impact.

Abstract methods

We defined AGI as ≥ 3 episodes of loose stools or vomiting/24 hours or diarrhoea or vomiting with ≥ 2 other gastrointestinal symptoms. Between November 2013 and May 2014 we asked participants of Hälsorapport, a representative cohort of the Swedish population, to report symptoms weekly. After each AGI episode, we used a questionnaire to collect information about perceived severity, healthcare use and work/school absenteeism. We calculated age-calibrated incidence rates and AGI-attributable absenteeism, with 95% confidence intervals (CI). We estimated AGI-associated costs, taking productivity loss and healthcare usage into account, with sensitivity analysis around incidence.

Abstract results

The 3,236 participants reported 1025 AGI episodes (Incidence: 0.98/100 person-week, 95% CI 0.88-1.1), highest in under fives (‹5s; 3.2/100 person-week, 95%CI 3.0-3.4). We received a completed questionnaire for 92% of the AGI episodes. Among 700 episodes in ‹5s, 28% were perceived as mild, 64% moderate and 8% severe; 10.9% led to primary care consultations, 1.4% to hospital admissions. Among 233 episodes in over five years of age 20% were perceived as mild, 63% moderate and 17% severe; 7.7% led to primary care consultations, 0.9% to hospital admissions. AGI led to 3.0 days home/100 person-week (95%CI 2.5-3.5). AGI cost €493,000,000 (€222,000,000-€765,000,000) nationally for the study period, mainly through productivity loss.

Abstract conclusion

In Sweden, most cases perceive AGI as a moderate to severe illness. AGI burdens the healthcare system and causes productivity loss, with high associated costs. Sweden and other countries may consider these estimates when prioritising public health interventions.

Keywords: Sweden, cohort studies, gastroenteritis, incidence, economics

PRESENTED BY: Michael Edelstein

ESCAIDE REFERENCE NUMBER: 20142239

Outbreaks (1)

Non-heat-treated frozen raspberries, most likely vehicle of a norovirus outbreak in Oslo, Norway, November 2013

Margot Einoder Moreno[1], Heidi Lange[1], Meera Grepp[2], Elin Osborg[3], Kirsti Vainio[1], Line Vold[1]

[1] Norwegian Institute of Public Health, Norway; [2] Department of Public Health, Health Agency, Municipality of Oslo, Norway; [3] Norwegian Food Safety Authority, Oslo, Norway

Abstract

On the 11th November 2013, the municipal medical officer of Oslo reported to the Norwegian Institute of Public Health a norovirus outbreak following two meetings held on 4th November in a conference centre. Common food and drinks were served during the two meetings. We investigated the outbreak to identify the vehicle of infection.

Abstract methods

Meeting participants completed an online questionnaire on consumption of food and drinks. We asked symptomatic participants to provide a stool sample. We defined a case as a meeting participant, who developed diarrhoea and/or vomiting between November 4th 12pm and November 7th, and had no household contact with a gastroenteritis case the week before symptoms onset. We calculated attack rates (AR) and adjusted risk ratios (RR) with 95% confidence intervals (95%CI), using binomial regression. We conducted food trace-back investigations and tested relevant food items for norovirus.

Abstract results

Overall, 147/168 (88%) meeting participants responded; 124 (84%) were female, 109 (74%) were 40- 59 years old and 74 (50%) met the case definition. All five stool samples provided were norovirus positive. No kitchen staff reported being sick. The risk of illness was higher among those who consumed raspberry mousse (RR=3.4;95%CI=1.4-8.4), sliced fresh fruit (RR=1.8;95%CI=1.2-2.6) and carrot-cake (RR=1.6;95%CI=1.1-2.3). In the binomial regression, only raspberry mousse (RR=3.4;95%CI=1.4-8.2) and sliced fresh fruit (RR=1.9;95%CI=1.3-2.8) remained significant. Of all cases, 70 (95%) consumed raspberries. No food item from the kitchen could be tested. Frozen raspberries used for the mousse were imported and not heat-treated before consumption. After trace-back, the raspberries batch tested negative for norovirus.

Abstract conclusion

Non-heat-treated frozen raspberries were the most likely vehicle of the outbreak. Heat-treatment of frozen berries before consumption could prevent future norovirus infections.

Keywords: Outbreak, Norovirus, Berries, Foodborne Diseases

PRESENTED BY: Margot Einoder Moreno

ESCAIDE REFERENCE NUMBER: 20141953

An outbreak of hepatitis A linked to berry-mix cake in Norway 2014: Methodological approach that addressed recall bias

Margot Einoder Moreno[1], Bernardo Guzman Herrador[1], Laila Jensvoll[2], Heidi Lange[1], Solveig Myking[1], Karin Nygård[1], Kathrine Stene-Johansen[1], Line Vold[1]

[1] Norwegian Institute of Public Health, Norway; [2] Norwegian Food Safety Authority, Ås, Norway

Abstract

Recall bias can challenge investigations of food-borne hepatitis A outbreaks because of long incubation period. Products consumed in places visited for reasons other than food purchase may be especially hard to remember. In March 2014, Norway detected an outbreak with a strain involved in an ongoing European outbreak linked to frozen berry-mix. We here present our methodological approach to minimize recall bias and identify the source of the outbreak.

Abstract methods

Hypothesis generated with trawling questionnaires were tested in a matched case-control study (CC1), calculating matched odds ratios (mOR) and 95% confidence intervals (95%CI). Based on follow-up interviews and food trace-back/trace-forward, we SMSed/emailed a picture of the most suspected product to CC1-participants, prompted them regarding consumption, and ran a second (CC2) analysis. We checked cases' credit card food purchases six weeks before onset.

Abstract results

The trawling interviews of 14/21 outbreak-cases pointed to berries, fruits, herbs and salads. Trace-back/trace-forward indicated that three cases had eaten imported frozen berry-cake from one distributor. The cake was topped with non-heat-treated berry-mix. While berry-cake was not associated with disease in CC1 (CC1-mOR=1.1;95%CI=0.3-4.5), CC2 pointed to the cake (CC2-mOR=13;95%CI=1.7-110, 76% of cases exposed). Credit card information identified dates of cake purchase, and subsequently suspected batches, mainly distributed to shopping centers, cafes and cruise ships in a pattern consistent with the geographical distribution of cases.

Abstract conclusion

The use of food trace-back/trace-forward information, focused questions with pictures of the suspected product and cases' credit card information, addressed the recall bias, identified the source and allowed the Norwegian food authority to withdraw the cake and send an international alert. Information from credit card purchases should include both food and other purchases to detect unrecalled food consumed outside home.

Keywords: Outbreak, Hepatitis A, Berries, Foodborne Diseases

PRESENTED BY: Margot Einoder Moreno

ESCAIDE REFERENCE NUMBER: 20141965

An outbreak investigation of Cryptosporidiosis in Dorset, England, in April-May 2013: a case-control study strengthened epidemiological evidence.

Benedetto Simone[1], Naomi Boxall[2], Linda Booth[3], Sooria Balasegaram[1]

[1] Field Epidemiology Services (Victoria), Public Health England, UK; [2] Health Protection Agency – South East, UK; [3] Wessex Public Health England Centre, Hants, UK

Abstract

We investigated an outbreak of cryptosporidiosis in Dorset, England, in April/May 2013. Descriptive analysis pointed at one of the water sources (A) which supply Water Company X, serving the area where most cases lived. Additionally, low levels of oocysts had been detected in Source A. Demographic and behavioural characteristics of the affected population could however confound the observed geographical link. Our objective was to measure the association between illness and exposure to Source A, accounting for possible confounders.

Abstract methods

We defined cases as adult residents in the area served by Company X with microbiologically-confirmed cryptosporidiosis. We compared each case with three controls, selected from the same area via sequential digit dialling, in terms of demographic characteristics, foods eaten, amounts of water imbibed from different sources and contact with animals in the 10 days prior to symptom onset. We fitted the variables associated with the occurrence of illness ($p<0.20$) in a logistic regression model to provide adjusted odds ratios and 95% confidence intervals (aOR;CI).

Abstract results

We included 15 cases and 53 controls and found an association between illness and residence in households supplied by Source A (aOR=25.8; CI:2.2-306.2), age (aOR=0.9; CI:0.9-1.0) and contact with animal faeces (aOR=8.5; CI:1.7-43.8). We were unable to demonstrate a dose-response effect with the amount of water imbibed from Source A.

Abstract conclusion

Our case-control study confirmed the association between cryptosporidiosis and the water source and excluded confounding by the other factors investigated. This would not have been possible just using descriptive methods. Albeit resource-intensive, we recommend using case-control studies to investigate similar outbreaks to strengthen epidemiological evidence. Subsequent to the outbreak, a review of water treatment took place and an ultra-violet treatment system was installed.

Keywords: Cryptosporidiosis, outbreak, water supply, case-control study

PRESENTED BY: Simone Bernedetto

ESCAIDE REFERENCE NUMBER: 20141969

Outbreak of food-borne Streptococcus pyogenes infection in 21 factories: Bursa Province, Turkey, June 2013

Dilek Cemil Goktas[1], Orhun Kalkan[1], Nihat Demiralp[1], Hamdiye Yılmaz[1]

[1] Public Health Institution of Turkey, Turkey

Abstract

On 20June 2013, several factories in Bursa Province, northwestern Turkey, reported an outbreak of flu-like illness with nausea and joint pain. We investigated to determine the diagnosis, cause and mode of transmission, and to implement control measures.

Abstract methods

We defined a suspected case as onset of fever and sore throat during 18-30 June 2013. We contacted all hospitals in Bursa Province for case-finding.In four cooperating factories we conducted a face-to-face cohort investigation to determine potential exposures. We swabbed the throats of case-patients and food-handlers at Catering Company X, which supplied food to all 21 affected factories, and cultured the specimens for S. pyogenes.

Abstract results

Doctors in 21 factories reported 1010 patients (attack rate: 20%, 1010/5075). The epidemic curves indicated point-source exposures, peaking on 19 June in three of the four factories and on 23 June in the fourth. The 124 case-patients we interviewed had flu-like symptoms plus joint pain (74%) and nausea (33%). Manti (miniature dumplings containing minced beef) was the common food item consumed in three factories; 75% (88/118) of exposed persons and 31% (9/29) of non-exposed persons developed illness (RR=2.5, 95% CI: 1.4-4.2). In the fourth factory, 64% (23/36) of persons who consumed Hasanpasa Meatball (beef meatball mixed with mesh potato and vegetables), compared with 20% (3/15) of persons who did not consume Hasanpasa Meatball developed illness (RR=3.2, 95% CI: 1.1-9.1). S. pyogenes was identified from the throat swabs of 6 case-patients and 2 food-handlers.

Abstract conclusion

This outbreak of S. pyogenes infection was caused by consumption of food containing contaminated minced meat. Food-handlers at the catering company were educated on safe practices for food preparation and preservation.

Keywords: Streptococcus pyogenes, Outbreaks, Foodborne, Cohort studies

PRESENTED BY: Dilek Cemil Goktas

ESCAIDE REFERENCE NUMBER: 20141986

Were Salmonella hiding in spiced ketchup? Nationwide outbreak of Salmonella Manhattan, Germany 2013

Jakob Schumacher[1], Dirk Werber[1], Peter Roggentin[2], Wolfgang Rabsch[1], Angelika Fruth[1], Rita Prager[1], Christina Frank[1]

[1] Robert-Koch-Institut, Wernigerode, Germany; [2] Institute for Hygiene and the Environment, Hamburg, Germany

Abstract

On 7/10/2013 the Institute for Environment and Hygiene in Hamburg informed the Robert Koch Institute about 10 Salmonella Manhattan isolates, received during one month (usually <=1 case/month) from patients from Northwest Germany. Suspecting a widespread foodborne outbreak, we started an investigation for vehicle identification and outbreak control.

Abstract methods

Cases had gastroenteritis with stool samples positive for Salmonella Manhattan notified in Germany from 26/9/13 to 24/11/13. We elicited food-histories seven days prior to diarrhoeal onset from early cases with a 557-item-questionnaire to generate hypotheses. For food-items frequently mentioned during hypotheses generation we subsequently conducted a case-control study between not-previously-interviewed cases and age- and region-matched controls (1:4 ratio), calculating food-specific matched odds ratios (mOR) and 95%-confidence-intervals (CI). Household leftovers were tested for Salmonella. A subset of isolates was tested by pulsed-field gel electrophoresis (PFGE).

Abstract results

We found 41 cases in 10 of 16 federal states with disease onsets 7/9/13 to 28/10/13. Median age was 55 years, 18 (44%) were female. Seven of nine full-food-history cases reported eating spiced ketchup of company X (ketchup X). In the case-control study, five of 10 cases compared to four of 29 controls reported eating ketchup X (mOR 4.8; CI 0.85-27). PFGE-patterns of seven case isolates were identical. Six ketchup X household specimens were Salmonella negative.

Abstract conclusion

Epidemiological investigations suggested ketchup X as the outbreak vehicle, but were not corroborated by food microbiology. Possible explanations for this include insufficient detection methods for Salmonella in ketchup or a false epidemiologic lead. Suspected microbiologically inhospitable food vehicles should be investigated by suitable detection methods. A comprehensive registry of foodborne outbreak investigation results unaffected by publication bias could strengthen evidence for food-items previously unrecognized as vehicles for Salmonella.

Keywords: Salmonella, Infectious Disease Outbreaks, ketchup, Germany

PRESENTED BY: Jakob Schumacher

ESCAIDE REFERENCE NUMBER: 20141996

Follow the Food Flow – Investigational Tracing for Outbreak Clarification

Ursula Huber[1], Petra Luber[1]

[1] Federal Office of Consumer Protection and Food Safety, Germany

Abstract

Several recent foodborne outbreaks have been caused by food vehicles of vegetable origin. Because of their short shelf-life and perishability these foods are often no more available for testing once an outbreak is detected. Moreover, sometimes the plant food matrix leads to performance failures of laboratory methods. In those cases investigational tracing can be the key for clarifying the outbreak.

Abstract methods

The analysis of food flows in supply chains can display epidemiological correlations, show the extent of events and rapidly contain outbreaks. Three examples will be presented.In two major German foodborne outbreaks in 2011 and 2012 where the causative agent and/or the transmitting vehicle were unknown batch-precise traceability studies first helped to narrow down the list of questionable foods and later to identify the causative vehicles.

Abstract results

During the EHEC outbreak forward-tracing of sprouts from a suspicious producer proved a correlation with all outbreak clusters and thus identified the food. Trace-back of seeds identified the relation between German and French outbreaks and its common source. For the complex Norovirus outbreak an investigational trace-back in combination with epidemiological information on food preparation practices rapidly identified the contaminated strawberries and successfully stopped the outbreak. In a German crisis management exercise a combination of food flow analysis and batch-precise trace-back rapidly identified a contaminated food batch. Within hours an additional forward-tracing revealed that this batch was not delivered to all outbreak clusters and that further contaminated foods must have been supplied.

Abstract conclusion

Investigational tracing of food flows is a powerful tool for rapid outbreak clarification and specifically helpful in the case of foods that are easily perishable and/or contaminated with viruses.

Keywords: Outbreaks, foodborne diseases, epidemiology, vegetables, food chain

PRESENTED BY: Petra Luber

ESCAIDE REFERENCE NUMBER: 20142040

Vaccine coverage, effectiveness and safety (1)

Do we need monitoring of immunisation delay?

Oystein Riise[1], *Ida Laake*[1], *Inger Lise Haugen*[1], *Marianne Bergsaker*[1], *Hanne Nøkleby*[1], *Jann Storsaeter*[1]

[1] Norwegian Institute of Public Health, Norway

Abstract

Norway reports a high incidence of pertussis; in addition pneumococcal disease and measles occur in young children. Although vaccination coverage at age 2 years is ≥93% for individual vaccines (9 diseases) this does not reflect the proportion vaccinated according to the schedule. We wanted to present the proportion delayed programme vaccinations in children aged < 2 years.

Abstract methods

Information on all vaccinations given to children born in 2010 (n=63382) before age < 2 years was obtained from the Norwegian Immunisation Registry. Vaccinations were considered delayed from 1 month after the recommended age in the schedule.

Abstract results

A total of 28336 (44.7%) children were delayed for at least one vaccination, mean 139 days. Pertussis (2nd dose), pneumococcal (2nd dose) and measles (1st dose) vaccines were delayed in 16.8%, 18.6% and 29.2% respectively. Children who based on month of birth were scheduled for vaccines in July (summer holiday) were more frequently delayed than others (1st dose measles vaccine 38.1% vs. 22.7%, risk ratio (RR) 1.68 (95% CI 1.61, 1.74)). Immigrants (risk group for tuberculosis, vaccinated) had increased risk for delayed vaccines 52.3% vs. 41.5% RR 1.26 (95% CI 1.24, 1.29). The two counties with the highest proportion of children with delayed vaccinations 58% reached vaccination coverage on national level at age 2 years.

Abstract conclusion

Almost 50% of children received vaccines later than recommended. The proportion of children with delayed vaccinations varied by county, season and immigrant status. Monitoring of delayed vaccines is a tool to improve the vaccination programme.

Keywords: Vaccination, Public Health, measles, pertussis, pneumococcal infection

PRESENTED BY: Oystein Riise

ESCAIDE REFERENCE NUMBER: 20141925

Rubella outbreak at a child-care center in Shimane prefecture, Japan, 2013

Hiroaki Ito[1], *Atsuhiro Kanayama*[1], *Kazutoshi Nakashima*[1], [2], *Keiko Tanaka-Taya*[1], *Setsuko Iizuka*[3], *Motoko Tsunematsu*[3], *Sae Miwa*[3], *Yoichiro Fukuzawa*[3], *Makoto Takeda*[1], *Yoshio Mori*[1], *Kazunori Oishi*[1]

[1] National Institute of Infectious Disease, Japan; [2] Department of Infection Control and Laboratory Diagnostics, Tohoku University Graduate School of Medicine, Japan; [3] Shimane Prefectural Government, Japan

Abstract

During 2007-2012, only one rubella case was reported from Unnan health center in Shimane, Japan. In May 2013, seven rubella cases were reported to the health center from a child-care center accommodating 94 children. Five of the cases had received one dose of measles-rubella (MR) vaccine. We report on the outbreak investigation.

Abstract methods

A case was defined as a child at the child-care center with rubella virus infection confirmed by virus isolation, RT-PCR, or detection of specific IgM with onset from April 1 to June 30, 2013. A retrospective cohort study was conducted to assess MR vaccine effectiveness (VE) against rubella infection among 69 children aged ≥1 year.

Abstract results

Fourteen cases were identified; while four had generalized rash and fever (typical cases), ten developed general rash without fever or focal rash with fever (atypical cases). MR vaccine coverage for children aged one year (73%) was lower than that in children aged two to five years (98%). VE was lower among those aged one year (VE=38%, 95% Confidence interval (CI) 0-64%; VE restricted to typical cases=75%, 95%CI 0-95%)) compared to those aged two to five years (VE=93%, 95%CI 82-97%; VE restricted to typical cases=100% (no case among vaccinated)). Among the cases, there was no apparent association with a particular vaccine lot, location where vaccination was conducted, or vaccination date.

Abstract conclusion

VE was modified by age. Lower VE may be associated with sharing of items that increase exchange of secretions particularly for one year olds, as observed. Nevertheless, given the higher VE against typical clinical rubella cases, MR vaccine should continue to be strongly recommended.

Keywords: Rubella outbreak, vaccine effectiveness, effect modification

PRESENTED BY: Hiroaki Ito

ESCAIDE REFERENCE NUMBER: 20142183

Improving trust in immunizations – Establishing a national surveillance of vaccine injury compensation in Germany

Michaela Diercke[1], *Anja Takla*[1], *Andreas Gilsdorf*[1], *Ole Wichmann*[1], [2]

[1] Robert Koch Institute, Germany; [2] Vaccine European New Integrated Collaboration Effort (VENICE) Project, Germany

Abstract

Monitoring adverse events following immunization (AEFI) is necessary to ensure the safety of vaccines after their widespread use. In Germany, suspected AEFI-cases are reported to the National Regulatory Authority (NRA), where vaccine safety signal detection and further assessments are performed. Independent from NRA-assessments, persons affected by AEFI with sequelae can apply for compensation at the pension and social security authorities (PSSA) in their respective federal state. Vaccine injury compensation (VIC) is based on causality and assessed by external or PSSA-experts in a NRA-independent evaluation. So far, VIC numbers and trends are not available at national level. We analyzed how VIC surveillance could be implemented in Germany to supplement the existing AEFI-surveillance and further increase trust in immunizations.

Abstract methods

We contacted all 17 federal PSSA and conducted telephone interviews using a semi-standardized questionnaire to assess documentation mode and parameters routinely collected in the VIC process.

Abstract results

All PSSA agreed to participate in the new surveillance system. PSSAs' data management differed by state. All use an electronic system for documentation, including basic case-based parameters (e.g. age and sex), number of compensation claims and approved VIC. Only 4 PSSA have electronic data on type of vaccine and AEFI.

Abstract conclusion

For nationwide VIC surveillance, electronically documented parameters in the 17 PSSA first need to be standardized. Parameters should be selected that also allow for potential linkage with NRA-data. The future VIC surveillance system should incorporate claimed and approved VICs and be designed as comprehensive, passive, electronic, case-based and publicly accessible. The establishment of a national VIC surveillance system, thereby supplementing the existing AEFI surveillance, will increase transparency and may reduce vaccine skepticism regarding potential severe AEFI in the population.

Keywords: Immunization, vaccination, adverse effects, surveillance

PRESENTED BY: Michaela Diercke

ESCAIDE REFERENCE NUMBER: 20142003

Effectiveness of alternative vaccines in healthy non-responders to hepatitis B vaccination; a multicentre randomised controlled trial in The Netherlands

Stijn Raven[1], *Christian Hoebe*[2], [3], *A.H.E. Roukens*[4], *L.G. Visser*[4], *Jeannine Hautvast*[1], *A.C.T.M. Vossen*[5], *J.E. Steenbergen, van*[6]

[1] Academic Collaborative Centre for Public Health AMPHI, Radboud University Medical Center, Nijmegen, The Netherlands; [2] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg Public Health Service, Geleen, The Netherlands; [3] Department of Medical Microbiology, School of Public Health and Primary Care, Maastricht University Medical Center, Maastricht, The Netherlands; [4] Department of Infectious Diseases, Leiden University Medical Centre, Leiden, The Netherlands; [5] Department of Medical Microbiology, Leiden University Medical Centre, The Netherlands; [6] Academic Collaborative Centre for Public Health NZH, Leiden University Medical Centre, The Netherlands

Abstract

Five to thirty per cent of healthy adults fail to develop an adequate immune response after vaccination against hepatitis B virus (HBV). Strategies to increase the immune response in non-responders (NR) have been studied, such as the administration of additional doses or other adjuvants; but it still remains unclear which regimen is most effective. We determined the efficacy of 3 different vaccines to induce protective immunity as measured by anti-HBs antibody titres in NR after a primary series of recombinant vaccination against HBV.

Abstract methods

In a multicentre randomised controlled trial participants were randomised to either repeating initial series (HBVAXPRO 10 µg or Engerix-B 20 µg) as control, or Twinrix 20 µg, Fendrix 20 µg or HBVAXPRO 40 µg. All schedules were identical with intramuscular vaccinations at month 0,1 and 2. Anti-HBs antibody titres were measured at 0, 1, 2 and 3 months.

Abstract results

Of 166 included participants, so far 69 anti-HBs titres were available at month 3. The geometric mean titre of the control group (45.4 IU/l) differed from HBVAXPRO-40 (88.2 IU/l; P= 0.36), Twinrix (85.9 IU/l; P=0.13) and significantly from Fendrix (145.1 IU/l; $P<0.05$) after controlling for potential confounders (sex, age, BMI and smoking). The proportion of responders to anti-HBs >10 IU/l ranged from 71% (control), 77% (Twinrix), 80% (HBVAXPRO-40) to 93% (Fendrix) and did not differ significantly in a logistic regression model.

Abstract conclusion

Preliminary results show seroconversion in at least 71% of the revaccinated. These first results are based on small numbers of participants and different laboratory tests. Therefore, at this moment no final conclusions can be drawn. More definite conclusions will become available after standardised testing of an extended number of participants.

Keywords: Hepatitis B Vaccines, Randomised controlled trial, Serology

PRESENTED BY: Stijn Raven

ESCAIDE REFERENCE NUMBER: 20142075

Vaccine coverage and determinants of incomplete vaccination in children aged 12-23 months in Dschang, West Cameroon

Gianluca Russo[1], Alessandro Miglietta[1], Rodrigue Mabvouna Biguioh[2], Martin Sanou Sobze[1], Paola Stefanelli[3], Vincenzo Vullo[1], Patrizio Pezzotti Giovanni Rezza[5]

[1] Department of Public Health and Infectious Diseases, "Sapienza" University of Rome, Italy; [2] Department of Biomedical Sciences, University of Dschang, Cameroon; [3] Department of Infectious, Parasitic and Immune-mediated Diseases, Istituto Superiore di Sanità, Rome, Italy; [4] National AIDS Unit – Italian National Institute of Health, Rome, Italy; [5] Istituto Superiore Di Sanita, Italy

Abstract

Vaccine preventable diseases remain a concern in Cameroon. At 6 August 14, nine wild poliovirus-1 cases have been reported in the Country. Our study was performed in November 2013 in Dschang, West Cameroon, in order to estimate the immunization coverage and to identify risk factors for incomplete vaccination among children aged 12-23 months.

Abstract methods

We conducted a cross-sectional survey using the Expanded Programme on Immunization coverage cluster survey design. A questionnaire was used to obtain information from parents. Immunization status was assessed from the vaccination card (where available) or by parental history. A multilevel logistic regression model was performed to calculate adjusted odds ratios of determinants of incomplete immunization status.

Abstract results

3,248 households were visited and 502 children divided in 65 clusters were enrolled. Children fully vaccinated were 85.9% (95%CI 82.4-89.3) and 84.5% (95%CI 79.5-89.5) according to card plus parent's history and card only respectively. Unvaccinated children were not found. 73.4% (95%CI 67.6-78.4) of children had completed vaccine schedule before one year of age. In the final model, determinants statistically significant associated with incomplete immunization status were: retention of immunization card, mother's utilization of antenatal care services, birth order, mother's age, parents' attitude towards immunization and parents' exposure to information on vaccinations. Distance from the vaccination centers was just at the limit of statistical significance.

Abstract conclusion

Despite high coverage, 1 of 7 children had incomplete vaccination status and 1 of 4 did not complete vaccinations within 1 year of age. In order to increase the coverage and proper (timely) vaccine administration is necessary to strengthen prenatal care and delivery services, improve parents' information and attitude towards immunization targeting younger parents and families living far away from vaccination centers.

Keywords: Cameroon, Cross-Sectional Studies, Health Knowledge, Attitudes, Practice, Immunization Programs/utilization, Risk Factors

PRESENTED BY: Alessandro Miglietta

ESCAIDE REFERENCE NUMBER: 20142019

Prevention of infant pertussis in the Netherlands: attitude and anticipated regret determine new parents' intention to accept vaccination.

Olga Visser[1], Janneke Kraan[2], Jeannine Hautvast[1], Koos van der Velden[1], Marlies Hulscher[3]

[1] Radboud University Medical Center, The Netherlands; [2] Municipal health service Utrecht region, The Netherlands; [3] Scientific Institute for Quality of Healthcare (IQ Healthcare), Radboud University Medical Centre, Nijmegen, The Netherlands

Abstract

Pertussis is a potentially lethal infectious disease for young infants under the age of 6 months, since they are not yet fully vaccinated. One strategy to prevent transmission of pertussis to the infant is to vaccinate parents of young infants, and is called 'cocooning'. Several countries adopted this strategy. However, in these countries, uptake of the vaccination is a problem. In the Netherlands, the topic is on the agenda of the National Health Council. In order to develop an optimal vaccination implementation strategy, this study aims to assess new parents' intention to accept pertussis vaccination and to quantify factors that may influence acceptance.

Abstract methods

Based on earlier qualitative data and the Reasoned Action Approach (RAA), a questionnaire was developed that assessed new parents' vaccination intention and its' psychosocial and personal determinants. The questionnaires were distributed among a representative sample of child welfare centres, where health care professionals asked visiting parents to complete them. We calculated factors influencing intention through multivariate regression analysis.

Abstract results

The parents returned 282 questionnaires. Intention of vaccination in this group was 78%. Multivariate analyses showed that most important psychosocial determinants positively influencing intention were attitude (beta 0,446, $p<.001$); direct perceived norm (beta 0,130, $p<.001$); anticipated regret (beta 0,466, $p<.001$) and ambivalence (beta 0,197, $p<.001$).

Abstract conclusion

In conclusion, this study shows that intention of acceptance of pertussis vaccination as part of a (possible future) cocooning strategy in new parents is 78%. Although intention is rather high, it is important to secure that intention is translated into actual uptake by addressing attitude, direct perceived norm, anticipated regret and ambivalence in the vaccination implementation strategy.

Keywords: Diphtheria-Tetanus-Pertussis Vaccine, Mass Vaccination, Public Opinion, Health Knowledge, Attitudes, Practice, Parents

PRESENTED BY: Janneke Kraan

ESCAIDE REFERENCE NUMBER: 20142144

Food and water-borne diseases & Zoonoses (1)

Domestic acquisition of hantavirus in England may be more common than previously thought: a serological survey of individuals with close contact with rats; 2013-2014

Rebecca Close[1], [2], [3], Lucy McCann[1], Jackie Duggan[1], Deborah Wright[1], Noel McCarthy[1], Trish Mannes[1], Andre Charlett[1], Amanda Walsh[1], Martin Keys[1], Tim Brooks[1]

[1] Public Health England, United Kingdom; [2] EPIET; [3] TV PHEC

Abstract

From 2012 to 2014, six cases of confirmed Seoul hantavirus infection without history of foreign travel but with exposure to wild or pet rats suggest this infection is emerging in the UK. We estimated hantavirus seroprevalence in England among groups with close contact with rats to assess risk and inform public health advice.

Abstract methods

We compared random samples of stored blood specimens (group 1) with owners/breeders of pet rats (group 2), persons with occupational exposure to pet rats (group 3) and persons with occupational exposure to wild rats (group 4), with the aim of sampling 300 participants per group. Individuals were recruited using a combination of sampling at events and through professional bodies, occupational health and specialist groups. We collected information using a questionnaire on the nature and extent of contact with rats. We measured hantavirus immune response using a commercial immunofluorescence assay. We calculated prevalences along with 95% confidence intervals (CI).

Abstract results

Between October 2013-May 2014, we sampled 795 individuals: 300 in group 1, 81 in group 2, 170 in group 3 and 244 in group 4. Preliminary results suggested that hantavirus seroprevalence varied from 0% in group 1 (95% CI: 25-45%), 35% in group 2 (95% CI: 25-45%) to 1.4% in group 4 (95% CI: 0.5-3.9%).

Abstract conclusion

The variation in seroprevalence across different exposure groups suggests low risk from occupational exposure to wild rats. However, domestic acquisition of hantavirus may be more common than previously thought, requiring awareness raising among clinicians and owners and breeders of pet rats. Additional testing of pet rat owners and breeders and surveillance will allow a better understanding of the epidemiological situation.

Keywords: Hantavirus, Seroprevelance, Rats, Seoul hantavirus

PRESENTED BY: Rebecca Close

ESCAIDE REFERENCE NUMBER: 20142034

An Outbreak Investigation of Oropharyngeal Tularemia in a Village in Western Turkey-Izmir Province, Turkey, 21-25 April- 2014

Haldun Suha Gorpelioglu[1], Nihat Demiralp[1], Bekir Celebi[1], Figen Sezen[1], Metin Kizilelma[2], Canan Kaynak[2], Mert Aydin[2], BaoPing Zhu[3], Fehminaz Temel[1], Mustafa Bahadir Sucakli[1], Cigdem Simsek[1]

[1] Public Health Institution of Turkey, Turkey; [2] Izmir Provincial Public Health Directorate, Turkey; [3] World Health Organization, Turkey

Abstract

On 14 April 2014 Turkish Early Warning Response System (EUWS) reported 7 cases from Hamamkoy Village, Izmir who were tested positive for Tularemia. We investigated to identify the cause and mode of transmission, and to implement control measures.

Abstract methods

We made a retrospective cohort investigation with 189 residents in one neighborhood of Hamamkoy Village where first 7 cases were reported. Those who were not living in the village since 1st of January 2014, below 12 months of age, who refused to do inquiry or give blood sample were excluded from the investigation. Face to face interviews were made and blood samples were taken.F. tularensis-specific antibody by microagglutination test was used to detect confirmed cases of F. tularensis.Rodent and water samples were analyzed by bacterial culture and Real-time multiplex PCR. ELİSA and Brucella cross-reaction tests were also performed for cases.

Abstract results

Of the 189 residents we identified 16 confirmed cases in 12 of 65 houses. The attack rate was 8.5% during the likely exposure period. The spring water which was located in this neighborhood of the village was associated with the disease (RR=6.3, 95% CI=1.9-21.4). Analysis showed a significant linear trend for drinking spring water, mixed water, and tap-water, respectively (20%, 16.4%, 2.9%, p=0.002). No other exposures assessed were associated with the disease. IgM and IgG were positive and Brucella cross-reaction tests were negative for Tularemia cases.

Abstract conclusion

Drinking contaminated spring water caused this outbreak. At our recommendation, the control measures for spring-water and use of tap water as drinking water were implemented by local health authorities and municipality. Villagers were informed for Tularemia and rodent activity by local Ministry of Food, Agriculture and Livestock authorities.

Keywords: Tularemia, Outbreaks, Water, Cohort Studies, Turkey

PRESENTED BY: Haldun Suha Gorpelioglu

ESCAIDE REFERENCE NUMBER: 20142146

Seroprevalence study on leptospirosis in high risk groups of Casablanca Region , Morocco

Mohamed Anouar Sadat[1], Zakia Abadane[2], Bouchra Assarag[2], Mohamed El Azhari[3], Kamal Marhoum[4], Abdelaziz Barkia[5], Imad Charkaoui[5], Pascale Bourhy[3], Mathieu Picardeau[6], Naima El Mdaghri[3], Abderahmane Maaroufi[5], Chakib Nejjari[2]

[1] ENSP; [2] National School of Public Morocco, Morocco; [3] Institut Pasteur Morocco, Morocco; [4] Department of Infectious Disease Hospital Averroes Morrocco, Morocco; [5] Directorate of Epidemiology Morocco, Morocco; [6] Institut Pasteur French, France

Abstract

Leptospirosis is a bacterial zoonosis of public health concern worldwide associated occupational activities. This is a first study conducted in Morrocco with an objective to determine the seroprevalence of leptospira among high-risk groups and to identify their risk factors.

Abstract methods

We conducted a cross-sectional study in three sites. Sera were collected during february 2014 from 209 professional volunteers in the municipal saughterhouse, 125 in a poultry market and 155 in the port of Casablanca and tested by both ELISA (IGM,IGG) and the Microscopic agglutination test (MAT) with a cut point of 1:50. Information on risk factors including personal data, place of residence, clinical history, potential exposure and preventive measure use were recorded in a questionnaire.

Abstract results

The seroprevalence considering a seropositivity by either ELISA or MATwas highest among poultry workers (23.73%) than in fishing workers (11.49%) and abattoir workers (6.21%) (χ^2= 19.93, P <0.0000). 10 serovars were identified (7 icterohaemorrahgiae, 1 australis, 1hardjobovis, 1 non identified). In the multivariate analysis by logistic regression only a specific place of residence from all the city was found independently associated with seropositivity by either ELISA or MAT(p=0.02). Most of the serovar icterohaemorrahgiae were identified in subjects from a particular professional category (poultry peelers) living in this specific area located near the poultry market.

Abstract conclusion

This study demonstrated that poultry market workers were at substantial risk of exposition to leptospirosis because of bad hygienic conditions and presence of rodents in both their workplace and their place of residence. Preventive measures should be taken by local authorities targeting high risk area.

Keywords: Leptospirosis,high risk work,seropositivity, ELISA, MAT, Morocco.

PRESENTED BY: Mohamed Anouar Sadat

ESCAIDE REFERENCE NUMBER: 20142232

Hantavirus outbreak associated with experimental rodents in Jagiellonian University (UJ), Poland, 2009-2012

Sylwia Kamińska[1], Joanna Ostrek[1], Michał Czerwiński[1], Lucyna Jurczyk[2], Danuta Gieracka-Pażucha[2], Małgorzata Sadkowska-Todys[1]

[1] NIPH-NIH, Poland; [2] Provinical Sanitary Station, Krakow, Poland

Abstract

In December 2012, the District Sanitary Station in Krakow was informed about two confirmed hantavirus cases among students of the Jagiellonian University (UJ). They had been exposed to bank voles with confirmed Puumala virus infection kept at the UJ laboratory. Bank voles from this colony were also delivered to three other universities in Poland. We investigated to find exposed persons and identify risk factors for infection.

Abstract methods

We defined the population at risk as persons who had contact with suspected experimental bank voles from UJ between October 2009 and December 2012. We conducted a retrospective cohort study using a self-administered questionnaire. A case was a person at risk with hantavirus-specific IgG antibodies. To investigate potential exposures related to suspected experimental rodents held at UJ, we excluded: (1) persons affiliated with other universities, (2) cases with occupational contact with rodents prior to October 2009. We calculated attack rates, relative risks (RRs) and 95% confidence intervals (CIs) for each exposure.

Abstract results

We interviewed 117 persons at risk; of these, 93 (79.5%) provided blood specimens. Twenty-five persons were excluded. We identified 33 cases (AR=48.5%). The most affected group were animal care takers (AR=89%) and students (AR=58%). Remaining in areas where animals were present (RR=2.56, 95% CI: 1.43-4.6), particularly frequenting these areas at least once per week (RR=2.83, 95% CI: 1.62-4.95) or staying there over one hour each time (RR=2.06, 95% CI: 1.38-3.08) were the main risks factors.

Abstract conclusion

We investigated a large outbreak of hantavirus in a research institution. Maintaining a large population of experimental animals for teaching and scientific purposes requires introduction and following adequate procedures to prevent human infections.

Keywords: Hantavirus, outbreak, laboratory, animals, Poland.

PRESENTED BY: Sylwia Kamińska

ESCAIDE REFERENCE NUMBER: 20142071

A primary school outbreak of tinea capitis in Belgium, May 2013: challenges in prevention and case management.

Amber Litzroth[1], [2], Koen De Schrijver[3], [4], Goedele Andries[5], Ann Packeu[1], Monique Detandt[1]

[1] Scientific Institute of Public Health, OD Public Health and Surveillance, Epidemiology of Infectious Diseases, Brussels, Belgium; [2] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; [3] Infectious Disease Control Antwerp, Public Health Authorities Flanders, Antwerp, Belgium; [4] Epidemiology and Social Medicine, University of Antwerp, Antwerp, Belgium; [5] Pupil Guidance Centre Het Kompas, Mechelen, Belgium

Abstract

Tinea capitis is a fungal infection of the scalp mainly affecting children and requiring oral antifungal treatment. In May 2013, a school doctor alerted Infectious Disease Control Antwerp of tinea capitis cases in a primary school. In March 2013 the index case was diagnosed with Microsporum canis, which is not transmitted between humans and therefore did not trigger public health response. We investigated this outbreak to determine its extent, evaluate follow up of treatment recommendations and describe risk factors.

Abstract methods

We screened all pupils. We referred suspect cases to their physician, recommending oral treatment in case of tinea capitis. Cases were defined as pupils clinically diagnosed with tinea capitis after referral. We retrieved personal data from the school and clinical and local laboratory data from the physicians. Three weeks after screening, we collected specimens from symptomatic pupils for testing at a specialised laboratory. We conducted a retrospective cohort study among all pupils. We calculated adjusted risk ratios (aRR) and 95% confidence intervals (CI) using log binomial regression.

Abstract results

Among 291 pupils, we identified 19 (6.5%) cases. Fourteen (73%) were prescribed oral treatment. Having a contaminated sibling (aRR 11; 95% CI 5.4-22.5) and classmate (aRR 4.6; 95% CI 1.6-12.8) were associated with illness. Of 15 cases tested, six (31.6%), including the index case, tested positive for human-to-human transmitted Microsporum audouinii. Two more cases had been originally misdiagnosed at a local laboratory.

Abstract conclusion

A quarter of cases did not receive oral antifungal treatment. Misdiagnosis and intrafamilial transmission occurred and contributed to the spread of the outbreak. We recommend developing guidelines for physicians on case management, placing additional focus on preventing intrafamilial transmission and involving a specialised mycology laboratory.

Keywords: Tinea capitis, outbreak, Microsporum, Belgium

PRESENTED BY: Amber Litzroth

ESCAIDE REFERENCE NUMBER: 20142053

Declining seroprevalence of Q fever in the south of the Netherlands might have contributed to large outbreaks in 2007-2010.

Diederik Brandwagt[1], Christian Hoebe[2], [3], Volker Hackert[2], [3], Wim van der Hoek[4]

[1] Municipal Health Service region Utrecht, Department of Infectious Disease Control, The Netherlands; [2] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg Public Health Service, Geleen, The Netherlands; [3] Department of Medical Microbiology, School of Public Health and Primary Care, Maastricht University Medical Center, Maastricht, The Netherlands; [4] Department for Respiratory Infections. Centre for Infectious Diseases, Epidemiology and Surveillance. National Institute for Public Health and the Environment (RIVM), The Netherlands

Abstract

A 1983 seroprevalence survey estimated the seroprevalence of antibodies against Coxiella burnetii in the general population of the Netherlands at 44.0%, using an indirect immunofluorescence assay (IFA) developed in-house. This was remarkably high compared to the 2.4% found for 2007, using commercial assays. Due to methodological issues and the high seroprevalence found, the results from 1983 are challenged.

Abstract methods

Since the 1983 samples couldn't be retested, we tested 380 historical samples from 1987 from the south of the Netherlands, using a contemporary commercial IFA. The results were compared with the Maastricht subgroup of the 1983 survey. Furthermore, the results were compared with seroprevalence surveys from 2008 and 2010, that had been carried out in the same study region, using commercial IFAs.

Abstract results

For 1987, 57 samples tested positive for antibodies against C. burnetii, resulting in a seroprevalence of 15.0% (95% CI 11.7-19.0). This was significantly lower than the 61.7% (55.6-67.8) estimate for 1983, but significantly higher than the 2008 and 2010 estimate, with 0.8% (0.2-2.0) and 2.7% (1.4-4.0) respectively. Within all study populations, no significant differences were found between age groups and gender.

Abstract conclusion

Due to methodological issues, the 1983 results are not accurate and are probably an overestimation. The seroprevalence estimated for 1987 is remarkable, being as high as during the peak of the large 2007-2010 epidemic of Q fever in the Netherlands. In contrast, the number of cases of Q fever was low in the 1980s. There must have been an unknown exposure, leading to a high number of asymptomatic infections. Apparently, this exposure diminished since 1987, resulting in lower estimates for 2008 and 2010. This waning immunity might have contributed to the Q fever epidemic.

Keywords: Seroepidemiologic Studies, Coxiella burnetii, Q Fever, The Netherlands

PRESENTED BY: Diederik Brandwagt

ESCAIDE REFERENCE NUMBER: 20142152

Vaccine – preventable diseases

Serotype distribution and antibiotic profiles of invasive Streptococcus pneumoniae in Hungary, 2012 – 2013

Zoltan Kis[1], Brigitta Berta[1], Ágnes Csohán[1], Ivelina Damjanova[1], Katalin Krisztalovics[1], Zsuzsanna Molnár[1], Tamás Tirczka[1]

[1] National Center for Epidemiology, Hungary

Abstract

Introduction of pneumococcus conjugate vaccines (PCV) have significantly reduced disease burden globally. In Hungary PCV-7 was available for children aged ›2y from 2008, replaced by PCV-13 in 2010. The estimated vaccination coverage in 2013 among children ‹6y was about 90%; information on adult vaccine uptake is unavailable. Before 2010, the most frequent serotypes among ‹6y were: 19A, 7F, 3, 23F and among 64y‹:3, 9V, 6A, 8, 14, 23F. Our objectives were to monitor country-wide circulating serotypes and antimicrobial susceptibilities across all age groups and compare to previous years (2008-2010).

Abstract methods

A total of 403 IPD isolates representing the entire country from sterile sites (across all age groups) with unknown vaccination status were submitted voluntarily to the National Reference Laboratory. Serotypes were determined using the Quellung reaction. Penicillin, ampicillin, erythromycin, clindamycin, meropenem and ceftriaxon susceptibilities were determined by gradient diffusion and MIC interpreted according to EUCAST.

Abstract results

40.0% of strains were isolated from patients ›64y where predominant serotypes were 3 (32.1%), 8 (6.4%) and 11A (5.8%); amongst the age group ‹6y: 19A (18.6%), 3 (16.3%) and 1, 10A, 15C (both 9.3%). Among all ages the proportion of serotypes included in PCV-7, PCV-10 and PCV-13 were 11.6%, 19.9% and 56.3%, respectively. The percentage of isolates resistant to penicillin, ampicillin, erythromycin, clindamycin, meropenem and ceftriaxon were 2.8%, 1.0%, 18.9%, 13.7%, 0.3% and 0.5%, respectively.

Abstract conclusion

Our data proposes a potential effect of PCV in the decrease of serotypes included in PCV13 and we therefore recommend mandatory vaccination of infants with PCV13. Overall antimicrobial resistance was low. Maintaining laboratory based surveillance, monitoring changing trends in serotype distribution and antimicrobial resistance are essential to measure the impact of a national vaccine program.

Keywords: Streptococcus pneumoniae, Invasive Pneumococcal Disease, Anti-Bacterial Agents, Pneumococcal Vaccines

PRESENTED BY: Zoltan Kis

ESCAIDE REFERENCE NUMBER: 20142045

Prevention of hepatitis A and hepatitis B in Bulgaria

Teodora Georgieva[1], Radosveta Filipova[2], Savina Stoitsova[1], Anna Kurchatova[1], Mira Kojouharova[1]

[1] National Centre of Infectious and Parasitic Diseases, Sofia, Bulgaria; [2] Ministry of Health of Bulgaria, Bulgaria

Abstract

Introduction of the routine children immunization is the most effective way to control hepatitis A and hepatitis B infections. In Bulgaria, a universal hepatitis B infant immunization program was introduced in 1992. Hepatitis A immunization is not mandatory and recommended only for certain risk groups. The aim of this study is to analyze epidemiological characteristic of hepatitis A and hepatitis B during the period 1984-2013.

Abstract methods

The age-specific annual data on acute clinically manifested cases of hepatitis A and hepatitis B reported to the National surveillance system and data on immunization coverage were used in a retrospective analysis.

Abstract results

Hepatitis A is the most common viral hepatitis, constituting 79.04% of all hepatitis cases, registered in Bulgaria during the period 1984-2013. Its incidence follows the natural dynamics of hepatitis A infection, with cyclical increases and decreases in 3-5 year periods (varying between 11.88 and 239.24/100,000 in the study period). Incidence remains highest in children between 1 and 19 years of age (78.52/100,000, 54.19% of all cases in 2013). Average incidence rate for hepatitis B has declined from 30.35/100,000 in the prevaccination period to 4.15/100,000 in 2013 (86.39% reduction). The incidence shifted to older age groups and in 2013 the highest incidence was registered among persons from 20 to 29 years of age (7.92/100,000) who were born before the routine immunizations.

Abstract conclusion

The significant reduction in hepatitis B incidence rates in Bulgaria demonstrates the capability of the country's health system in successfully implementing routine immunization programs. Together with the high hepatitis A incidence rates, this underlines the serious positive potential of introducing a strategy for universal childhood immunization against hepatitis A.

Keywords: Hepatitis A, hepatitis B, immunization

PRESENTED BY: Mira Kojouharova

ESCAIDE REFERENCE NUMBER: 20142037

Viral Co-Infection in Children Hospitalized for Age in which Rotateq Vaccine Strains were Detected in Stool Samples.

Timo Vesikari[1], Matti Uhari[2], Marjo Renko[2], Maria Hemming[1], Marjo Salminen[1], Laurence Torcel Pagnon[3], Susanne Hartwig[3], Hélène Bricout[3]

[1] University of Tampere, Vaccine Research Center, Finland; [2] University of Oulu, Department of Pediatrics, Finland; [3] Sanofi Pasteur MSD, Epidemiology Department, France

Abstract

Finland introduced universal rotavirus (RV) vaccination in September 2009, with exclusive use of the pentavalent human–bovine reassortant RV vaccine RotaTeq®. A prospective hospital-based surveillance was conducted in two hospitals from 2009 to 2013 to identify less than 16 years children with acute gastroenteritis. All stool samples were tested for RV by ELISA and RT-PCR. Samples positive for RV vaccine strains were additionally tested for other viruses.

Abstract methods

Stool samples were collected and analysed centrally for RV by ELISA and genotyped by RT-PCR. RV AGE cases were differentiated to wild and RotaTeq® vaccine strains. Samples positive for vaccine type were tested for other viruses (adenovirus, astrovirus, bocavirus, coronavirus, norovirus, sapovirus).

Abstract results

687 AGE cases were included, 592 of them were tested for RV by ELISA and PCR. In 15 cases a RV vaccine strain was identified (12 were ELISA negative, 2 positive, 1 unknown). A co infection was observed in 10 of these cases (1 coronavirus, 2 sapovirus, 7 norovirus); for 3 samples material was insufficient to perform all the additional tests, and in 2 cases no other viruses were detected: a 2-month-old girl tested positive for RV by ELISA 4 days after the first vaccine dose administration and a 1-month-year-old unvaccinated girl tested negative for RV by ELISA.

Abstract conclusion

Few RVGE cases were admitted to hospitals during the surveillance and most were in unvaccinated children. Cases with vaccine strains were observed, but the causal relationship is uncertain as co-infections with other viruses were detected in some cases and ELISA test for RV were negative in most of the cases suggesting a low RV virus load.

Keywords: Rotavirus, strain, shedding, gastroenteritis, vaccination

PRESENTED BY: Hélène Bricout

ESCAIDE REFERENCE NUMBER: 20142240

Measles in Canada, 2010 to 2014: a post-elimination country in a pre-eradication world.

Lindsey Sherrard[1], Amanda Shane[1], Jenne Cunliffe[1]

[1] Public Health Agency of Canada, Ottawa, Canada

Abstract

Having achieved elimination of indigenous measles in 1998, Canadian measles activity is dictated by importation from other countries, where endemic or outbreak circulation of the virus continues to occur. This is a descriptive summary of Canadian measles experience from 2010 to 2014, as a post-elimination country in a pre-eradication context.

Abstract methods

Data from January 03 2010 to May 06 2014 were obtained from the Canadian Measles and Rubella Surveillance System (CMRSS). Data management was carried out in MS Access, and analysis through MS Excel.

Abstract results

From 2010 to 2014, a total of 1098 cases of measles were reported in Canada. Eight provinces reported 78 importations from 23 different countries, most frequently from France (n=16), the Philippines (n=16), and India (n=8). Importations were typically agedOf the 78 documented importations, 16 (20%) are known to have led to an outbreak. Importations from Europe led to 3 of the largest outbreaks in recent Canadian history. Conversely, importations from other regions generally resulted in relatively limited spread, if any. Outbreaks ranged in size (2 to 686 cases, median: 3), and duration (2 and 41 weeks, median: 3). Adolescents aged 10 to 19 years accounted for 60% of outbreak-associated cases. Cases were primarily unimmunized (61%).

Abstract conclusion

Overall, Canada experienced a number of importations from a variety of countries, the majority of which did not result in secondary transmission. However, a small number of importations from Europe led to significant measles activity. Understanding the risk of international measles epidemiology on Canada, and identifying mechanisms to prevent importations and transmission in Canada, will contribute to development of effective public health strategies to maintain measles elimination.

Keywords: Measles, Canada, Epidemiology, Elimination

PRESENTED BY: Lindsey Sherrard

ESCAIDE REFERENCE NUMBER: 20142249

Hepatitis A Outbreak of Same Genotype from Human and Water Samples in a Tourist Spot in Southern Philippines, February 2014.

Ruth Alma Ramos[1]*, Vikki Carr De Los Reyes*[1]*, Ma Nemia Sucaldito*[2]*, Enrique Tayag*[1]

[1] FETP-Philippines, Philippines; [2] Department of Health Philippines, Philippines

Abstract

An outbreak of symptomatic viral Hepatitis A was reported to the National Epidemiology Center from a municipality in Southern Philippines with a request for epidemiologic investigation.A month long food festival celebration was held last December 2013.

Abstract methods

Review of records and active case finding was done. A case control study was done. Serum samples were collected and sent to RITM for EIA/Anti-HAV IgM testing. Water and stool samples collected were sent to RITM-Tohoku Collaborating Research Center for detection of Hepa A virus by RT-PCR and DNA sequencing.

Abstract results

170 suspect hepatitis A cases were identified. 58% were males. Age of cases range from 2 to 58 years old (median=15). Most affected age group was the 11-15 years old (29%). Masagana Village has the highest attack rate (19/1000 population). 161 (57%) serum samples were reactive for EIA/Anti-HAV IgM. Twenty-three (17%) food handlers screened were also reactive. Hepatitis A virus was detected in all stool samples and in two of the 18 water samples collected. All DNA sequence of both water and stool samples were the same and belong to genotype 1A. Risk factors identified were buying ready to eat food/cooked food (OR=3.4057) and water source near a septic tank (OR=2.7436).

Abstract conclusion

There was hepatitis A outbreak of Genotype 1A in a tourist spot in Southern Philippines. Infected food handlers have unknowingly contaminated food and water sources. Chlorination of water sources and health information campaign were started and planning for level III water supply construction in the town have been initiated.

Keywords: Hepatitis A genotype 1A outbreak, Human and water samples, Risks factors, RT-PCR

PRESENTED BY: Ruth Alma Ramos

ESCAIDE REFERENCE NUMBER: 20142191

Poster Session B 15.20 – 16.20 Thur 6

Antimicrobial Resistance (2)

We can still get Escherichia coli highly susceptible to antibiotics in the tribal villages of India

Sandeep S Narkar[1], Ashok J Tamhankar[1], Smita U Khedkar[2], Cecilia Stålsby Lundborg[1]

[1] Karolinska Institutet, Dept of Public Health Sciences, Sweden; [2] Bac-test Laboratory, India

Abstract

Antibiotic resistance has become a serious global public health concern. There are several reports of high antibiotic resistance from municipal water and various community water sources. In many tribal areas of the world, bacterial contamination of water is of common occurrence. In these tribal areas, the use of antibiotics is low and there, bacteria also get low exposure to antibiotics. Therefore we analyzed antibiotic resistance of Escherichia coli from water samples of a tribal community in India.

Abstract methods

A prospective observational study was conducted during 2011-12 for one year in six tribal villages of India. Water samples from a total of seven open dug community water wells were analyzed for coliform contamination at monthly interval. From contaminated samples, Escherichia coli was isolated and five representative colonies were subjected to test its resistance to 34 antibiotics belonging to different groups by Vitek2 instrument.

Abstract results

Out of a total of 76 water samples, 35 were found to be contaminated with Escherichia coli. Amongst all E. coli isolates, 63% were totally susceptible to all 34 antibiotics tested and 17% were resistant to only one group of antibiotics. Only 8 % isolates were found to be multidrug resistant.

Abstract conclusion

There was a high level of susceptibility to antibiotics in the analyzed E. coli isolates from the included tribal villages. This is an important finding to have susceptible strains in the environment, when high resistance is reported in most of the studies. We have undertaken the genetic analysis of these strains. The genetic information of these strains is of public health significance as it may be helpful in the management of antibiotic resistance in future.

Keywords: Antibiotic resistance, water, E. coli, tribal

PRESENTED BY: Sandeep S Narkar

ESCAIDE REFERENCE NUMBER: 20142164

SHV-5-like extended-spectrum beta-lactamase (ESBL) in a Greek isolate belonging to the emerging monophasic Salmonella enterica subsp.enterica serovar Typhimurium 4,[5],12:i: European clone

Georgia Mandilara [1], Kyriaki Tryfinopoulou [2], Panagiota Giakkoupi[3], Alkiviadis Vatopoulos[4]

[1] National Reference Centre for Salmonella, Shigella, VTEC, Greece; [2] Central Public Health Laboratory, Greece; [3] Antimicrobial Resistance and HAI Laboratory, Central Laboratory of Public Health, HCDCP – Vari,Attica-Greece, Greece; [4] National School of Public Health, Greece

Abstract

Emerging resistance to Extended-Spectrum Cephalosporins (ESCs) in Salmonella spp. is of public health concern. Multiresistant S. monophasic Typhimurium has become increasingly important recently, ranking among the 10 most common serovars isolated from humans in EU. Herein we present an ESCs resistant clinical S. monophasic Typhimurium isolate from Greece.

Abstract methods

One Salmonella spp clinical isolate was sent to the National Reference Centre for Salmonella for further testing. Serotype was determined according to Kauffmann-White-Le Minor scheme. Confirmation of the serotyping result was performed using the PCR protocol proposed by EFSA. Antimicrobial susceptibility testing and phenotypic test for the detection of ESBLs were performed using the disk diffusion method and the double-disk synergy tests (DDST), respectively. Conjugation experiments were carried out in broth cultures and on solid medium at 30oC and 37oC. PCR and subsequent DNA sequencing of the PCR products were applied for the detection and characterization of the bla gene.

Abstract results

The isolate was serotyped as S. monophasic Typhimurium, and was found resistant to ampicillin, streptomycin, sulfonamides, tetracycline, ceftazidime, cefotaxime . β- lactam resistance was transferred by conjugation only on solid medium and at 30oC. In both the clinical isolate and the transconjugants, DDST appeared positive indicative of ESBL production and the PCR and sequencing revealed the presence of blaSHV-5-like gene.

Abstract conclusion

The isolate belonged to the European clone of S. monophasic Typhimurium , with the resistance pattern of ASSuT. As far as we know this is the first report of the presence of blaSHV-5-like in a multidrug resistant S. monophasic Typhimurium isolate. Owing to the spread of this multiresistant clone, the acquisition of bla genes is of great concern and deserves attention from the public health authorities.

Keywords: Salmonella monophasic Typhimurium, extended – spectrum beta lactamase, blaSHV-5

PRESENTED BY: Kyriaki Tryfinopolou

ESCAIDE REFERENCE NUMBER: 20142258

Comparative analysis of Escherichia coli sequence type 131 from humans, animals, and the environment

Ivana Jamborova[1], James R. Johnson[2], Monika Dolejska[3], Brian Johnston[2], Connie Clabots[2], Lenka Micenkova[4], Ivan Literak[3]

[1] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic; Veterans Affairs Medical Center and University of Minnesota, Minneapolis, Minnesota, United States; [3] University of Veterinary and Pharmaceutical Sciences Brno, Czech Republic; [4] Department of Biology, Faculty of Medicine, Masaryk University, Brno, Czech Republic

Abstract

Escherichia coli sequence type 131 (ST131) is currently the world's most studied bacterial lines of clinical importance. Comparative analysis of phenotypic, genotypic, and clonal characteristics of 168 E. coli ST131 isolates collected during various studies from diverse sources such as human community and nosocomial settings (n=130), wildlife (19), and waste water (19) was used to determine whether wild animals and the environment share identical strains with humans, implying exchange of ST131 between humans and the environment, including wildlife.

Abstract methods

Susceptibility to 34 antimicrobials was determined by combination of disc diffusion method and standard microdilution method. Genes encoding resistance to beta-lactams, quinolones, and other antibiotics, plus 52 virulence genes, including fimH30,were detected by PCR and sequencing. Epidemiological relatedness was determined by XbaI pulsed-field gel electrophoresis (PFGE).

Abstract results

Most isolates carried blaCTX-M-15 or blaCTX-M-27, together with other genes typical for this pandemic clone (blaTEM, blaOXA, aac(6')-Ib-cr). Overall, 110 (65%) isolates belonged to the rapidly expanding H30-Rx ST131 subclone, which is characterized by more extensive resistance. Seventy-five (45%) isolates, from all 3 sources, exhibited a conserved virulence profile (afa/dra, iha, fimH, sat, fyuA, iutA, kpsII, traT, usp, ompT, malX). Certain (n=12; 32%) wild animal and waste water isolates corresponded with the globally predominant, human-associated pulsotypes 812 and 968.

Abstract conclusion

This extensive genetic commonality among ST131 isolates from diverse sources suggests that wild animals and the environment may contribute to the global dissemination of this pandemic clone.This study was supported by CEITEC (CZ.1.05/1.1.00/02.0068), IGA VFU Brno (12/2014/FVHE), IGA MZ (NT14398), and the Office of Research Development, Department of Veterans Affairs (JRJ).

Keywords: Antibiotic Resistance, Enterobacteriaceae, ST131, Molecular Epidemiology

PRESENTED BY: Ivana Jamborova

ESCAIDE REFERENCE NUMBER: 20142189

Antibiotic prescribing and its cost for the inpatients of orthopaedic departments of two private, tertiary care hospitals in central India

Yeonji Ma[1], Senia Rosales Klintz[2], Cecilia Stålsby Lundborg[2], Basant K Bhuyan[3], Megha Sharma[4]

[1] Karolinska Institutet/Center for Medicine and Korean Reunification, Seoul National University; College of Medicine, Korea; [2] Global Health (IHCAR), Department of Public Health Sciences, Karolinska Institutet, Stockholm, Sweden; [3] Deaprtment of Orthopedics, R D Gardi Medical College, India; [4] Global Health (IHCAR), Sweden

Abstract

Patients who have undergone an orthopaedic surgery are considered more vulnerable to healthcare associated infectious, compared to other patients; thus often are major antibiotic consumer. High use of antibiotics favours the emergence of antibiotic resistance and increases treatment costs. There is a general lack of studies, especially from low-middle income countries providing data on antibiotic prescribing with cost estimations.

Abstract methods

A prospective, cross-sectional study was conducted for 3 years in orthopaedic departments of a teaching (TH) and a non-teaching hospital (NTH), using a specifically developed form. Data was collected manually by trained nurses and analysed using SPSS 21.0 (USA). Antibiotics were classified using WHO Anatomical Therapeutic Chemical code (ATC) methodology.

Abstract results

Out of total 4394 patients admitted in the orthopedic departments (TH-2434 patients and NTH-1960) more than 80% underwent minor or major surgery. Antibiotics were prescribed to 59% patients in the TH and 81% in the NTH ($p<0.001$). FDCs accounted for 22% of the antibiotics in the TH and 35% in the NTH ($p<0.0001$). Generic name prescribing was significantly lower in the NTH (1%), than in the TH (33%, $p<0.001$). Average cost per antibiotic prescription was 120 and 170 Indian rupees, at the TH and the NTH respectively.

Abstract conclusion

The study indicates lower generic name prescribing, frequent prescribing of FDCs and high cost of prescriptions in the orthopedic department of the NTH, compared to the TH. Despite of more severe situation in the NTH, same issues are applicable to the TH. Relevant interventions such as implementation of prescribing guidelines, antibiotic stewardship program, trainings and regular prescription monitoring are recommended to improve the situation in the settings.

Keywords: Antibiotic prescribing, fixed dose combinations, cost of antibiotic prescriptions, orthopedic departments, private hospitals, India

PRESENTED BY: Megha Sharma

ESCAIDE REFERENCE NUMBER: 20142209

Emergence of multiple drug-resistant uropathogens in neurological rehabilitation wards: a retrospective anaylisis focusing on clinical risk factors

Matteo Ricco’[1], Federica Pezzetti[2], Domenico Nicolotti[1], Chiara Latini[2], Francesca Spagnoli[2], Sara Visciarelli[2], Carlo Signorelli[2]

[1] Azienda Sanitaria Locale di Parma, Italy; [2] University of Parma, Italy

Abstract

Multiple drug-resistant uropathogens (MDR: non-susceptible to ≥1 agent in ≥3 antimicrobial categories) show elevated risk of morbidity/mortality in neurological wards, mainly for spinal cord injury (SCI)-associated urinary tract infections (UTIs). Studies investigating their risk factors are therefore essential for a more rational approach.

Abstract methods

Retrospective analysis involved 637 patients admitted to a specialized neurological ward (“G.Verdi Hospital”, Villanova sull’Arda, Northern Italy) between 10/2009 and 05/2014 (M:385, F:252; mean age:56.2±19.3 y): 358 SCI (56.2%), 147 (27.1%) stroke cases and 132 post-surgery rehabilitation cases. 25,120 person-days were collected for a mean hospital stay of 75.3±65d. Personal and clinical data (e.g. site and type of SCI; voiding methods; comorbidities) were retrieved from medical records. All urine samples and their antimicrobial sensitivity were analyzed. Risk factors for MDR infections were evaluated through regression analysis.

Abstract results

424 UTIs cases (16.9 infections/1,000 person-days) were identified, the most frequent being E.coli (n=232), K.pneumoniae (n=101), P.aeruginosa (n=46), P.mirabilis (n= 39); 141 (33.3%) fullfilled MDR definition; 49 were (11.6%) MDR+carbapenem-resistant (CPR) and 11 with MDR+CPR+tigecycline-resistant (2.6%). UTIs were associated with hospital stay ≥60 days (OR=2.95 95%CI:1.9-3.8), urinary incontinence (OR=2.19 95%CI:1.2-4.1) and SCI (OR=2.45, 95%CI:1.8-4.4). SCI, stroke, age ≤65 year, male sex were also at higher risk for MDR (p<0.001) and MDR-CPR (p<0.001). Voiding system, diabetes, level/etiology of SCI and stroke, aphasia, apraxia, spatial neglect (all p>0.05) were not associated with an increased risk for MDR-infections.

Abstract conclusion

Our retrospective analysis is consistent with the globally increasing prevalence of MDR/CPR infections and confirms the increasing threat for more extended resistance profiles. Our data hint urinary incontinence and prolonged hospital stays, irrespective of their etiology, as the main risk factors for MDR/CPR infections.

Keywords: Neurological rehabilitation wards, Spinal cord injury, MDR (multiple drug resistant), Stroke, UTIs (Urinary tract infections)

PRESENTED BY: Matteo Ricco

ESCAIDE REFERENCE NUMBER: 20142213

Imipenem Resistance Among Pseudomonas aeruginosa Isolates: Risk Factors for Infection and Impact of Resistance on Clinical Outcomes in Intensive care units, Casablanca, Morocco.

Majida Hanine[1], Mohammed Akrim[2], Imad Cherkaoui[3], Khalid Zerouali[4], Abderahmane Maaroufi[3], Chakib Nejjari[1]

[1] National School of Public Health, Morocco; [2] National Public Health School, Morocco; [3] Directorate of Epidemiology, Morocco; [4] Laboratory of Microbiology, Ibn Rochd University Hospital, Morocco

Abstract

Antimicrobial resistance is an emerging problem with Pseudomonas aeruginosa We have no information on such problems in Morocco. The aim of this study was to determine the risk factors for nosocomial infections of imipenem-resistant Pseudomonas aeruginosa (IRPA) and impact of resistance on clinical outcomes in intensive care units.

Abstract methods

A retrospective case-control study was performed from January to December 2013 in all intensive care units at university hospital, in Casablanca, Morocco. The patients with nosocomial P. aeruginosa infection were included in the study. Patients with IRPA infections were compared to those with imipenem-sensitive P. aeruginosa (ISPA) infections. Demographics, comorbidities, device utilization and antibiotic use were analysed.

Abstract results

IRPA was isolated from 35 (38.5 %) patients, and ISPA was isolated from 56 (61.5%) patients during the study period. In multivariate analysis by logistic regression, male gender (odds ratio [OR] = 7.18; 95% confidence interval [CI] = 1.2-42.68, p = 0.03);a longer duration of hospital stay until P. aeruginosa isolation (OR=1.11; 95% CI= 1.04-1.19; p=0.001); immunosuppression (OR, 12.76; 95% CI, 2.25-72.32; p=0.004); fluoroquinolones (OR,9.05;95% CI,1.77-46.05, p=0.008) and imipenem (OR, 11.18; 95% CI=1.73-72;p=0.011) treatment within the 28 days before isolation of IRPA were independently associated with imipenem resistance. Compared with patients infected with ISPA, patients infected with IRPA had longer hospitalization durations (41.5 days vs 22.9 days; p<0.001) and a greater rate of mortality 85.7% vs 55.36% (relative risk, 1.54; 95% CI, 1.18-2.03; p< 0<001).

Abstract conclusion

Creation of antimicrobial stewardship and resistance committee, an emphasis on appropriate use of the imipenem and fluoroquinolones and effective infection control measures in patients with presence of immunosupression are needed to reduce the incidence of nosocomial infections caused by these organisms.

Keywords: Pseudomonas, Risk Factors, Imipenem Resistance, nosocomial infections

PRESENTED BY: Majida Hanine

ESCAIDE REFERENCE NUMBER: 20142224

HIV-STI

Survival, causes of death, and risk factors associated with mortality in Barcelona HIV new diagnoses. 2001-2013

Cesar Garriga[1], Patricia García de Olalla[2], Roser Clos[3], Pilar Gorrindo[3], Macarena Garrido-Estepa[4], Joan A. Caylà[2]

[1] National Centre for Epidemiology, Spain; [2] Public Health Agency of Barcelona/ Biomedical Research Centres Network Consortium, Spain; [3] Public Health Agency of Barcelona, Spain; [4] Field Epidemiology Training Program, Infectious Diseases Surveillance Department, National Center for Epidemiology, Carlos III Health Institute, Spain

Abstract

The antiretroviral treatment has supposed a decrease in HIV-related mortality. We assessed factors related to survival in HIV individuals. Causes of death (CoD) in HIV individuals were described.

Abstract methods

Deaths registered in the Census until 30.06.2013 and 2001-2012 new diagnoses from Barcelona HIV Register were included in the analysis. The CoD were obtained from Death Register. The CoD were classified in external (ICD-10: X), HIV-related (B20-B24, B44.9, C83.7 and C85.9) and non-HIV-related (other codes) causes. Mortality rate was calculated as follow-up person-year per 1000 and its 95% confidence interval (M; 95%CI). Association with mortality of socio-demographic, clinical and epidemiological variables were studied using Cox regression [hazard ratio (HR); 95%CI].

Abstract results

Among 3533 new HIV diagnoses, 168 (5%) died (M:8.2; 95%CI: 6.9-9.4). CoD was available in 93 (55%). Among those, 43% died by non-HIV-related causes (M:1.9; 95%CI:1.3-2.5); 42% by HIV-related causes (M:1.9; 95%CI:1.3-2.5), and 15% by external ones (M:0.7; 95%CI:0.3-1.0). Worse survival was observed in injecting drug users (IDU)(HR:4.7; 95%CI:2.9-7.7) and heterosexual (HTS) men (HR:2.4; 95%CI:1.4-3.9), Spaniards (HR:2.5; 95%CI:1.6-4.0), Gràcia district residents (HR:2.0; 95%CI:1.1-3.7), illiterate/primary education individuals (HR:1.5; IC95%:1.1-2.2), and <200 CD4 subjects (HR:1.8; 95%CI:1.2-3.0). HIV-related CoD were due to infections (48%): most common in men who have sex with men (MSM) (63%), followed by HTS women (60%). Non-HIV-related CoD were cancer (29%): more prevalent in men (32%), people with have secondary/university studies (39%) and HTS men (50%); cardiovascular diseases (22%): in HTS women (57%) and illiterate/primary education individuals (35%) and; liver diseases (19%): in IDU (37%).

Abstract conclusion

Mortality was associated with being IDU, HTS man, Spaniard, with low educational level and damaged immune system. CoD frequencies in HIV-related and non-HIV-related were similar

Keywords: HIV Infections, Viral/epidemiology, Cause of Death, Follow-Up Studies, Registries

PRESENTED BY: Cesar Garriga

ESCAIDE REFERENCE NUMBER: 20142102

How can we establish routine chlamydia testing in general practice for young adults? Exploring the barriers in 4 European countries.

Ellie Ricketts[1], Pia Touboul Lundgren[2], Hans Fredlund[3], Anneli Uuskula[4], Katy Town[1], Nina Ockendon [1] Cliodna McNulty [1]

[1] Public Health England, UK; [2] Département de Santé Publique Hôpital de l'Archet, France; [3] University Hospital Orebro, Sweden; [4] University of Tartu, Estonia

Abstract

Testing rates for Chlamydia trachomatis are low in European general practices, despite high rates of infection and European recommendation for active case finding to detect and treat asymptomatic cases. A qualitative study using the Theory of Planned Behaviour sought to identify barriers in personal attitudes, subjective norms and behavioural controls that could influence GP staff in 4 EU countries implementing routine opportunistic testing for chlamydia with young adult patients. The data was gathered to inform development of a European chlamydia training package for GP staff.

Abstract methods

52 GPs and practice nurses were individually interviewed using a semi structured schedule (England 22, Estonia 8, France 14 and Sweden 8). Interviews were transcribed in their original language and a thematic analysis was undertaken in each country to establish barriers regarding routine chlamydia testing of young adults.

Abstract results

Barriers held a high degree of commonality across the 4 countries. They concerned beliefs about young patients not attending general practice and preferring to receive sexual health services elsewhere, beliefs that sexual health had low status among colleagues, low knowledge derived from limited testing culture, and time pressures and forgetting to offer resulting in low testing. Staff supported receiving training in chlamydia testing, preferring in practice delivery.

Abstract conclusion

As the barriers to chlamydia testing are similar across Europe development of a common European training package is appropriate and feasible. The training package should challenge incorrect beliefs, model brief interventions and provide resources to support the normalisation of testing, and be adaptable for inter country differences in policy and culture.

Keywords: Chlamydia, General Practice, Young adult, Education

PRESENTED BY: Ellie Ricketts

ESCAIDE REFERENCE NUMBER: 20142116

HIV testing data suggest unmet prevention needs among men who have sex with men (MSM) in Poland

Anna Marzec-Bogusławska[1], Mirosław Wysocki[2], Magdalena Rosinska[2]

[1] The National AIDS Center, Poland; [2] National Institute of Public Health – National Institute of Hygiene, Poland

Abstract

Effective diagnosis remains one of the main targets of HIV prevention strategy. Men who have sex with men (MSM) in Poland report to test mainly in the network of voluntary testing and counselling (VCT) sites. We aimed to identify subgroups of MSM with the highest HIV detection rate suggesting the need of enhanced prevention.

Abstract methods

Data on MSM were extracted from the database of clients attending any of the 31 VCT sites located across Poland in 2010 – 2011. Data were collected anonymously on standardized forms filled by trained counsellors supplemented by self-administered questionnaire. We compared proportion of positive tests by demographic characteristics using chi-square test and multivariable logistic regression (p-values from logistic regression are reported) in STATA 13.1.

Abstract results

In 2010 – 2011 6379 HIV tests among MSM were performed in VCT network, 302 (4.9% of valid tests) were positive. Older age, lower educational status and urban residence independently predicted higher proportion of positive tests. The highest rates were noted among MSM 40 years old or older (10.7%, $p< 0.001$ vs younger MSM) and those with vocational education (9.1%, $p=0.012$ vs high school or university education). These two groups constituted respectively 7.1% and 4.9% of all tested MSM. In comparison in general population men aged 40 or older constituted 33% of men aged 15-60 and men with vocational education – 30% of all men >15.

Abstract conclusion

High detection rates among less educated and older MSM may result from high incidence or low prior testing rates. The latter is consistent with low numbers of clients from these groups suggesting the need to promote testing and target prevention messages at them.

Keywords: HIV infection, testing, men who have sex with men, Poland

PRESENTED BY: Magdalena Rosinska

ESCAIDE REFERENCE NUMBER: 20142254

Chlamydia trachomatis tests in males in 5 Federal States of Germany, 2008-2013

Katja Alt[1], Sandra Dudareva-Vizule[1], Andrea Sailer[1], Karin Haar[2], Alexandra Hofmann[1], Ioannis Karagiannis[1], Viviane Bremer[1]

[1] Robert Koch-Institut, Germany; [2] European Centre for Disease Prevention and Control, Sweden

Abstract

In Germany, infections with Chlamydia trachomatis (CT) are not notifiable, and there is no screening policy for males. A nationwide voluntary sentinel among laboratories conducting routine CT-diagnostics was initiated by Robert Koch-Institute in 2010 collecting data retro- and prospectively. We analyzed information on tests conducted in symptomatic males from 5 Federal States with representative data (>20% invoiced tests) to identify trends in CT-diagnostic practices.

Abstract methods

We included information on number of conducted tests, test result, specimen type and demographics of patients from laboratories with continuous data delivery for the years 2008-2013. We calculated proportion of positive tests (PPT) for age-groups and tested materials. We estimated trends for counts with linear regression and trends for rates with Poisson regression.

Abstract results

Results for 93.444 tests from 12 laboratories were included. Overall, 9.035 (9.7%) test results were positive. Men aged 15-29 years were most frequently tested (40% of tests). PPT among men aged 20-24 years was 16% (2.661/16.208). Tested specimens were unspecified swabs (28%), urine (21%) semen (7%), urethral (6%), rectal (3%) and pharyngeal (2%) swabs. PPT was 12% in rectal swabs, 10% in unspecified swabs, 9% in urethral swabs and 8% in urine specimens. Between 2008-2013 the total number of tests increased from 8.289 to 19.470, average 3.555/year ($p<0.01$). Positive tests increased by 312/ year on average ($p<0.01$). PPT decreased from 11% in 2008 to 9% in 2013, overall average 2.3%/year ($p<0.01$); 2.8%/year in age-group 25-29, 5.6%/year in urine specimens.

Abstract conclusion

The decline of overall PPT is probably due to increased testing of urine specimens from young men. Given the high proportion of rectal infections we recommend focus testing for CT on men who have sex with men.

Keywords: Chlamydia trachomatis, men, msm sentinel

PRESENTED BY: Katja Alt

ESCAIDE REFERENCE NUMBER: 20142059

HPV testing using Dried Urine Spot as cervical cancer screening tools in low-income countries

Elena Rosanna Frati[1], *Daniela Colzani*[1], *Silvia Bianchi*[1], *Marianna Martinelli*[1], *Ester Fasoli*[1], *Elisabetta Tanzi*[1]

[1] University of Milan, Department of Biomedical Sciences for Health, Italy

Abstract

The aetiological cause of nearly all cervical cancer is Human Papillomavirus (HPV). Different screening strategies are applicable but in low-income countries inadequate resources, educational levels and misconceptions of women are barriers to their success. Previous studies have shown that urine sample, non-invasive and more acceptable, is useful to detect HPV infection. The aim of this study was to evaluate the performance of HPV testing using Dried Urine on Spot (DUS).

Abstract methods

88 first voided urine samples were collected from migrant women in Milan. 56/88 (63.6%) samples were HPV-DNA positive.Each urine sample was spotted on a filter paper, dried for 3 hours at RT and stored in a plastic zip-lock bag before analysis. HPV-DNA was detected at one and four weeks using an in house ORF-L1-nested-PCR assay.The sensitivity and specificity of HPV-DNA test were presented as percentages with IC95% and the proportion of agreement between urine and DUS testing using the Kappa (k) statistic.

Abstract results

HPV-DNA was detected in 55/56 (98.21%, IC95%: 90.56-99.68) and in 54/56 (96.42%, IC95%: 87.88-99.01) DUS at one and four weeks, respectively.Considering HPV-DNA testing in urine samples as gold standard, the sensitivity of HPV-DNA test in DUS samples was 98.21% (IC95%: 90.56-99.68) and 96.42% (IC95%: 87.88-99.01) at one and four weeks, respectively. The specificity was 100%. An “almost perfect” agreement (K statistic ≥0.81), both at one and four weeks, was found.

Abstract conclusion

The HPV testing using DUS shown an elevated sensibility, specificity and a high concordance rates with HPV-urine test. These data suggest that a DUS-based assay would be a suitable and effective tool for epidemiological surveillance and screening programs especially in low-income countries bypassing the socio-cultural barriers and sampling issues.

Keywords: Cervical cancer screening, Low-income countries, HPV testing, Dried Urine Spot

PRESENTED BY: Elena Rosanna Frati

ESCAIDE REFERENCE NUMBER: 20142086

Outbreak of syphilis in men who have sex with men living in rural North Wales associated with the use of social media

Daniel Thomas[1], *Christopher J Williams*[1], *Claire M Midgley*[1], *Ushan Andrady*[2], *Valerie Anderson*[1], *Sioned Humphreys*[1], *Noel Craine*[1], *Chris Whiteside*[1]

[1] Public Health Wales, UK; [2] Betsi Cadwaldr University Health Board, UK

Abstract

Like other countries in Europe, the United Kingdom has observed a re-emergence of syphilis, primarily affecting men who have sex with men (MSM) living in urban conurbations. However, in recent years there have been a number of outbreaks reported outside these areas.

Abstract methods

On 2 December 2013, Public Health Wales was notified of an increase in syphilis in North West Wales, a predominantly rural area of the UK, and an outbreak control team was convened. Routinely collected surveillance data were used to describe the outbreak and sexual network diagrams were constructed.

Abstract results

In 2013, 30 cases of infectious syphilis were diagnosed in sexual health services in Betsi Cadwaldr University Health Board, compared to a mean of seven cases per year in the previous years. To date, a further 16 cases have been diagnosed in 2014. Most cases were white males, self-reporting as MSM (median age: 34 years, range: 19-56). Most cases acquired their infections locally, though some individuals reported acquiring their infection outside Wales, including three European countries. The use of mobile applications, allowing users to locate other MSM within close proximity, was a common feature in the network. Cases reported using 10 different mobile applications.

Abstract conclusion

Two factors appear to be important in the epidemiology of this outbreak: A high degree of mobility in a proportion of the MSM population in North Wales with links to sexual networks in North West England and further afield, and the use of social media to create local sexual networks. Interventions have included active contact tracing, awareness-raising, the introduction of near-patient syphilis testing at MSM venues, and a health promotion campaign targeting users of MSM mobile applications.

Keywords: Syphilis, outbreak, epidemiology, surveillance, sexually transmitted infection

PRESENTED BY: Daniel Thomas

ESCAIDE REFERENCE NUMBER: 20142106

Healthcare associated infections (2)

Determining the Effect of Social Deprivation on the Prevalence of Healthcare Associated Infections in Acute Hospitals: a multivariable analysis of a linked data set

Simon Packer[1], Shona Cairns[1], Chris Robertson[1], Jacqui Reilly[1], Lorna Willocks[2]

[1] Health Protection Scotland, UK; [2] NHS Lothian, UK

Abstract

Healthcare associated infections (HAI) endanger patient safety by increasing morbidity, mortality, and length of hospital stay. Health inequalities are a serious concern worldwide and a well characterised association exists between increasing social deprivation and poor health outcomes. This association, however, has not been examined for HAI. This study aims to determine the association between social deprivation and HAI prevalence, in inpatients admitted to a Scottish acute hospital on a single day across September and October 2011.

Abstract methods

This study linked Scottish data from the 2011 European Point Prevalence Survey of HAI and Antimicrobial Prescribing to the Scottish Morbidity Record, a national dataset with Scottish Index of Multiple Deprivation (SIMD) included. Multivariable logistic regression was used to model HAI prevalence against SIMD quintile.

Abstract results

A significant difference was found between HAI prevalence across SIMD quintile in patients undergoing surgical procedures; with higher prevalence observed with increasing deprivation. No overall association was found between SIMD quintile and prevalence of HAI. Variables found to be associated, whilst controlling for SIMD, were: male sex, ICU admission, very remote rural location, surgery since admission, and minimally invasive surgery.

Abstract conclusion

This study found a significant difference in HAI prevalence across SIMD quintile in patients undergoing surgery. This could be due to different level of bacterial colonisation or poor health status of deprived patients. This identifies a clear risk group for which a targeted intervention can be implemented. To our knowledge this is the first study to examine the overall association between HAI and SIMD. Further study, utilising complete patient follow up, is required to further establish this association. Deprived surgical patients could be offered decolonisation prior to procedures. This intervention could help narrow the health inequalities gap.

Keywords: Healthcare-associated infections, epidemiology, social deprivation, point prevalence survey, prevalence, risk factors

PRESENTED BY: Simon Packer

ESCAIDE REFERENCE NUMBER: 20141968

Attributing gastroenteritis morbidity to 16 enteropathogens in children attending day care

Remko Enserink[1], Cees van den Wijngaard[1], Patricia Bruijning-Verhagen[2], Liselotte van Asten[1], Lapo Mughini-Gras[1], Erwin Duizer[1], Titia Kortbeek[1], Rianne Scholts[3], Nico Nagelkerke[4], Henriette Smit[5], Mirjam Kooistra-Smid[6], Wilfrid van Pelt[1]

[1] National Institute for Public Health and the Environment (RIVM), The Netherlands; [2] Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, The Netherlands; [3] Laboratory for Infectious Diseases, Department of Research and Development, Groningen, The Netherlands; [4] Institute of Public health, United Arab Emirates University, United Arab Emirates; [5] Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, The Netherlands; [6] Department of Medical Microbiology, University of Groningen, University Medical Center Groningen, The Netherlands

Abstract

Children attending day care experience substantial gastrointestinal morbidity due to enteropathogens circulating in the day care environment. The lack of a pathogen-specific clinical presentation of gastroenteritis in these children, together with the large variety of putative enteropathogens involved, complicates the assessment of their individual contributions. We aimed at estimating the proportion of day care attendees experiencing gastroenteritis attributable to a range of enteropathogens circulating in day care centres in the Netherlands during 2010-2013.

Abstract methods

Generalized estimating equation models were used to analyse longitudinal data from a nationwide laboratory- and syndrome-based surveillance system for major childhood illnesses in Dutch day care centres. We studied the variation in prevalence of 16 enteropathogens of bacterial (8), viral (5) and parasitic origin (3) circulating in day care in relation to the variation in gastroenteritis incidence among children attending day care.

Abstract results

The prevalence of rotavirus, norovirus, astrovirus, Giardia lamblia and Cryptosporidium spp. was significantly associated with gastroenteritis incidence among day care attendees. Of the 1802 children that experienced gastroenteritis during the study period, 1090 (61%) were attributable to the seasonal baseline of the model and 711 (39%) to the aforementioned 5 enteropathogens. Although their pathogen-specific attributable proportions varied over seasons and study years, overall 199 (11%) gastroenteritis cases were attributable to rotavirus, 175 (10%) to norovirus, 131 (7%) to astrovirus, 143 (8%) to Giardia lamblia, and 63 (3%) to Cryptosporidium spp.

Abstract conclusion

We concluded that these 3 viruses and 2 parasites, but no bacteria, contribute most substantially to seasonal gastroenteritis among children attending day care.

Keywords: Childcare, gastroenteritis, enteropathogens, The Netherlands, day care

PRESENTED BY: Lapo Mughini-Gras

ESCAIDE REFERENCE NUMBER: 20142013

Increased short-term, but decreased long-term risk of hospitalization for gastroenteritis in children attending day care: a registry-based cohort study

Remko Enserink[1], Jacob Simonsen[2], Lapo Mughini-Gras[3], Wilfred Van Pelt[3], Kåre Mølbak[4]

[1] Center for Infectious Disease Control (Epidemiology and Surveillance Unit), The Netherlands; [2] Department of Epidemiology Research, Statens Serum Institute, Denmark; [3] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands; [4] Department of Infectious Disease Epidemiology, Statens Serum Institute, Denmark

Abstract

Many studies provide evidence that children experience a short-term increased risk of mild gastroenteritis episodes around the time they start attending out-of-home child day care. Very few studies however, have examined the long-term risk of attending day care for the most severe clinical manifestations of gastroenteritis. Here, we assessed the short- and long-term risk of cumulative day care attendance, age at first enrolment, and type of childcare facility on hospitalization rates for gastroenteritis.

Abstract methods

Cox proportional hazard regression was used to estimate the hazard ratios (HRs) of being hospitalized for gastroenteritis in two nationwide cohorts of preschool (6 year-old) children in Denmark (1994-2011). Together, the cohorts accounted for 14,703 hospitalizations and contributed over 1,7 million child-years of observations.

Abstract results

Until 6 months of cumulative day care attendance, preschool children attending day care institutions displayed a 1.6 times higher short-term risk of hospitalization for gastroenteritis than children that never attended day care. From 6 months of cumulated attendance onwards however, attending either a day care institution or a day care home was associated with a 0.8 times lower long-term risk of being hospitalized for gastroenteritis. This long-term effect was confined to children that started attending day care before the age of one, and extended throughout the preschool, but not the elementary school years.

Abstract conclusion

Compared to permanent home-care, attending (large) day care institutions, but not (small) day care homes, is associated with a significantly higher short-term risk for gastroenteritis hospitalization up to 6 months from first enrolment. If these children experience this short-term risk before the age of one, they experience a lower long-term risk of being hospitalized for gastroenteritis during their preschool years.

Keywords: Gastroenteritis, hospitalization, long-term, child day care

PRESENTED BY: Remko Enserink

ESCAIDE REFERENCE NUMBER: 20142018

An outbreak of multidrug-resistant Pseudomonas aeruginosa in a long-term care hospital in Osaka prefecture, Japan

Atsuhiro Kanayama[1], Ayako Tabuchi[1], Takuya Yamagishi[2], Kenzo Goto[3], Yumiko Kobaru[3], Masako Takano[4], Kazutoshi Morisada[4], Ryuji Kawahara[5], Akira Ukimura[6,7,] Fumiko Kawanishi[6], Tamano Matsui[2], Kazunori Oishi[2]

[1] Field Epidemiology Training Program, National Institute of Infectious Diseases, Japan; [2] Infectious Disease Surveillance Center, National Institute of Infectious Diseases, Japan; [3] Shinsei Hospital, Japan; [4] Takatsuki city health center, Japan; [5] Division of Bacteriology, Osaka Prefectural Institute of Public Health, Japan; [6] Infection Control Center, Osaka Medical College Hospital, Japan; [7] Department of General Internal Medicine, Osaka Medical College, Japan

Abstract

Multidrug-resistant Pseudomonas aeruginosa (MDRP) is a pathogen known to cause outbreaks in large tertiary-care hospitals. However, little is known about MDRP outbreaks in small long-term care facilities. We investigated an outbreak of MDRP infections that occurred at a long-term care hospital.

Abstract methods

A case was defined as a patient positive by culture for P. aeruginosa with carbapenem, fluoroquinolone and amikacin resistance in the hospital from January 2013 to January 2014. Descriptive analysis, a case-control study and molecular analysis of the isolated strains were performed.

Abstract results

A total of 23 cases including 11 fatalities were identified in five of six wards. All were aged over 60 years with underlying condition. Sixteen cases were positive for MDRP in sputum. Sharing a portable oral suction device among patients appeared to be associated with MDRP transmission in sputum. Hand hygiene of healthcare workers was violated when performing multiple medical procedures related to oral or wound care. Use of an oxygen mask was associated with acquisition of MDRP in sputum (OR=12.0; 95% confidence interval 1.6–92.3). Among the 11 isolates, all were indistinguishable or closely related by pulsed-field gel electrophoresis. After conducting active surveillance, enhancing training, discontinuing the use of suspected medical devices, and withholding admission of critical patients, additional cases were not found since January 30, 2014.

Abstract conclusion

An outbreak of MDRP infection in a long-term care facility appeared to occur through inappropriate procedures and poor hygiene. Frequent handling of oxygen masks may increase the risk of MDRP infection under certain conditions. With increasing evidence of MDRP outbreaks in hospitals in Japan, discussions are currently underway to implement case-based surveillance of MDRP infections for timely detection and response.

Keywords: Pseudomonas aeruginosa, multidrug resistance, carbapenemase, long-term care, oral hygiene, surveillance

PRESENTED BY: Atsuhiro Kanayama

ESCAIDE REFERENCE NUMBER: 20142052

Control actions in first hospital outbreak of *Clostridium difficile ribotype 027* in Saxony-Anhalt, Germany 2013-2014

Carina Helmeke[1], Claudia Kohlstock[2], Christina Runck[2], Hanns-Martin Irmscher[2], Henning Preisler[3], Bettina Weiß[4], Sebastian Haller[4], Hanna Oppermann[2]

[1] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm [2] State Agency for Consumer Protection of Saxony-Anhalt, Germany; [3] Local Health Office Jerichower Land, Germany; [4] Robert Koch-Institute Berlin, Germany

Abstract

In December 2013, a Local Health Office in Saxony-Anhalt, reported an outbreak of Clostridium difficile infection (CDI) in a 200-bed hospital. Morbidity and mortality among patients was high. We conducted an outbreak investigation to control the outbreak and to prevent further infections.

Abstract methods

After confirmation of initial reported severe cases (notifiable disease in Germany), we undertook case finding using the German guidelines case definition for CDI and severe CDI. We inspected hospital hygiene SOPs, the affected ward rooms and the implementation of hygiene measures. With the responsible hospital and hygiene management staff, we discussed appropriate measures, risk factors e.g. use of antibiotics or gastric acid inhibitors and the need of CDI surveillance in accordance to German and federal guidelines.

Abstract results

Between December 2013 and February 2014, we identified 20 suspected cases mainly on the geriatrics and early rehabilitation wards. Seventeen cases were confirmed (median age 78 years; 29% male; 75% hospitalized in past 3 months) including 9 severe cases (67% died). Among 15 cases with ribotyped strains including 7 severe cases, six belonged to R027. Hospital hygiene SOPs existed but measures were not always implemented accordingly; e.g. hand washing was not performed in addition to disinfection. Despite requirements, there was no CDI surveillance system in the hospital.

Abstract conclusion

We identified the highly virulent ribotype 027 for the first time in a hospital in Saxony-Anhalt and informed local medical officers about this. Assuming that nosocomial transmission was due to inadequate implementation of hygiene measures we recommended CDI monitoring. We established a laboratory-based intensified CDI surveillance from March to August 2014 to identify new cases, describe a potentially endemic situation and to raise CDI awareness among hospital staff.

Keywords: Clostridium difficile, Enterocolitis, Pseudomembranous, Infections, Hospital, Diarrhea

PRESENTED BY: Carina Helmeke

ESCAIDE REFERENCE NUMBER: 20142083

Quantifying the burden of paediatric hospital-acquired bloodstream infection in England by using a multistate analysis of linked routine data

Nathan Green[1], Berit Muller-Pebody[1], Alan Johnson[1], Katherine Henderson[1], Simon Thelwall[1], Mike Sharland[2], Sarah Deeny[1]

[1] Public Health England, UK; [2] Pediatric Infectious Diseases Unit, St George's Hospital, UK; [3] Freiburg Center for Data Analysis and Modeling, Germany

Abstract

Hospital-acquired bloodstream infection (HA-BSI) is associated with substantial morbidity, mortality and healthcare costs in all patient populations. Young children have been shown to have a high rate of healthcare-associated infections compared to the adult population. We aimed to quantify the excess mortality and length of stay in paediatric patients from HA-BSI.

Abstract methods

We analysed data collected retrospectively from a probabilistically-linked national database of paediatric (1 month-18 years) in-patients with a microbiologically-confirmed HA-BSI in England between January-March 2009. A time-dependent Cox regression model was fit to determine the presence of any effect. Further, a multistate model, adjusted for the time to onset of HA-BSI, was used to compare outcomes in patients with HA-BSI to those without infection. We further adjusted for patients' characteristics as recorded in hospital admission data.

Abstract results

The dataset comprised 297,973 patients, with 251 cases of HA-BSI. After adjustment for time to HA-BSI and co-morbidities, the daily probability of discharge (dead or alive) from hospital for patients with HA-BSI was 0.8 times (95% confidence interval CI: 0.7-0.9) that of non-infected patients. Excess length of stay associated with all-cause HA-BSI was 4.3 days (95% CI: 1.2-7.4), although this varied by pathogen. HA-BSI patients had a 3.9 (95% CI: 1.5-10.2) times higher daily chance of in-hospital death, than non-infected patients.

Abstract conclusion

HA-BSI increased the length of stay and mortality of paediatric inpatients. The results of this study provide an evidence base to judge the health and economic impact of programs to prevent and control HA-BSI in children.

Keywords: Bacteremia, pediatric, length of stay, health care cost

PRESENTED BY: Berit Muller-Pebody

ESCAIDE REFERENCE NUMBER: 20142182

Knowledge, Attitude, and Practice (KAP) surveillance on phlebitis prevention among nurses in large hospital in Baku, Azerbaijan

Yagut Garayeva[1]

[1] Hospital, Azerbaijan

Abstract

There are no national guidelines on prevention of peripheral intravenous catheters (PIC) related phlebitis in Azerbaijan. We surveyed nurses of a large private hospital in Baku to determine their knowledge, attitudes, and practices of nurses on prevention of phlebitis from PIC before offering trainings based on "Guideline for the Prevention of Intravascular Catheter-related infections" (CDC 2011).

Abstract methods

In October 2013, we conducted a cross-sectional survey, randomly selecting 80 out of 157 nurses; of these, 73 (91%) responded. We asked about age, education, work departments, and questions related to knowledge, attitudes and practices on PIC-related phlebitis.

Abstract results

On average nurses were 31 years-of-age, with 9 years professional experience. 27(38%) worked in medical department, 22 (30%) in intensive care unit, 17 (23%) in surgical unit and 6 (8%) in emergency. No participants had previous training on phlebitis prevention. 37 (51%) of nurses routinely inserted 1-3 PICs daily; only 2 (3%) inserted more than 11 PICs daily. Compared to others, nurses working in medical-surgical departments showed better practice in PIC placement, prevalence rate ratio (PRR)=0.4 (CI 95%: 0.2-0.7), and had better knowledge about phlebitis risks, PRR=0.4 (95%CI: 0.2-0.9). Correct responses on 12 phlebitis risk-related questions ranged from 8% to75%. 56 (76.7%) gave less than 50% correct responses, 15 (21%) gave 51% to 70%, and only 2 (3%) gave 75% to 90% correct answers. For example, only 41% correctly answered about the need to wear gloves when inserting PICs.

Abstract conclusion

Nurses' knowledge on PIC-related phlebitis is inadequate. We recommend using the survey results to design professional education to reduce risk of catheter-associated phlebitis, and to initiate surveillance for phlebitis. National guidelines on PIC-related phlebitis prevention should be developed and implemented in Azerbaijan.

Keywords: Phlebitis, peripheral intravenous catheters, Azerbaijan, KAP survey, nursing

PRESENTED BY: Yagut Garayeva

ESCAIDE REFERENCE NUMBER: 20142222

Epidemiology and microbiology driving public health policy

Polio stool surveillance for refugee children from Syria, Pakistan, Somalia and Afghanistan coming to Rhineland Palatinate from January until April 2014

Florian Burckhardt[1]*, Maja George*[2]*, Sabine Diedrich*[3]

[1] Landesuntersuchungsamt Rheinland-Pfalz, Germany; [2] Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany; [3] Robert Koch Institute (RKI), Berlin, Germany

Abstract

Polio cases increased by 80% between 2012 (n=223) and 2013 (n=405) with reintroductions in previously polio-free countries.Outbreaks in Syria prompted federal recommendations in Germany in October 2013 to sample stool from Syrian refugees born after 2011 to prevent potential reintroduction. We expanded the surveillance criteria for refugees coming to the State of Rhineland Palatinate (RP) to include older children from additional polio circulating countries. Our goals were detection of refugees excreting poliovirus and estimating its statistical accuracy.

Abstract methods

We provided the National Reference Centre for Poliomyelitis and Enteroviruses (NRZ) with stool samples from children born after 2008 in Pakistan, Somalia, Syria and Afghanistan and arriving in RP as refugees between January 1st and April 30th 2014. NRZ first screened for Enterovirus with PCR and analysed positive samples for polio viruses (wild-type vs vaccine). We calculated 95% confidence intervals (CI) using Fisher's exact methods (for CI including zero: 97.5% one-sided).

Abstract results

Of 57 eligible children we received 51 (89%) stool samples. We lost three to follow up (6%). Of 48 tested, six (12%) were from Afghan and Pakistani children each, seven (14%) from Somali and 29 (60%) from Syrian children. Five (Afghanistan:3, Syria:2) tested positive for Enterovirus, however all were polio negative. CI for polio cases ranged from 0-0.46 for Afghani and Pakistani, 0-0.41 for Somali and 0-0.12 for Syrian children.

Abstract conclusion

We could confirm that children from Syria, Pakistan, Somalia or Afghanistan coming to RP during the study period were polio-free. However, our estimates lacked power and thus come with uncertainty. The efforts of stool surveillance for refugees from countries with endemic or reintroduced polio need to be balanced against the benefits of a more accurate estimate.

Keywords: Poliomyelitis, Surveillance, Refugees, Germany

PRESENTED BY: Florian Burckhardt

ESCAIDE REFERENCE NUMBER: 20142048

Tularemia in Sweden 1984-2012, epidemiologic trends and spatial correlation with ecological factors

Amélie Desvars[1], Maria Furberg[2], Marika Hjertqvist[3], Linda Vidman[4], Anders Sjöstedt[5], Patrik Rydén[4], Anders Johansson[5]

[1] Umeå University, Sweden; [2] Department of Public Health and Clinical Medicine, Epidemiology and Global Health, Umeå; University, Sweden; [3] The Public Health Agency of Sweden, Solna, Sweden; [4] Mathematics and Mathematical Statistics, Computational Life Science Cluster (CLiC), Umeå University, Sweden; [5] Department of Clinical Microbiology, Clinical Bacteriology, and Laboratory for Molecular Infection Medicine Sweden (MIMS), Umeå University, Sweden

Abstract

The zoonotic disease tularemia, caused by the bacterium Francisella tularensis, is endemic to large areas of the Northern Hemisphere. Yet factors influencing its spatial distribution remain poorly understood. This study aims to describe the spatial epidemiology of tularemia and to identify ecological risk factors for tularemia incidence.

Abstract methods

We analyzed 29 years (1984–2012) of nationwide surveillance data from Sweden. For each tularemia case, longitude/latitude of the location of disease contraction as well as a disease onset date were determined. The spatial distribution of cases was compared to a regularly distributed set of points determined by the Swedish underlying population.

Abstract results

Out of 4,830 laboratory confirmed cases 3,524 were considered in this study. The mean age of the patients was 47.6 years. The lowest incidence was observed at 20-25 years and the highest at 55-69 years. The males/females tularemia risk ratio was 1.39. Comparing the first and the second half of the study period, nationwide mean incidence was ten-fold higher in 1999-2012 (2.47/100,000 persons) than in 1984-1998 (0.26/100,000, $p<0.001$). Case spatial distribution was uneven. The mean incidence was significantly higher in the north (2.30 cases/100,000 persons/year) than in the south (0.28 cases/100,000 persons, $p<0.001$). Denser case aggregates were found in northeast areas and in a belt around the southern border of the boreal forest region. Tularemia incidence was positively correlated with altitude ($p<0.001$) and the presence of lakes and rivers ($p<0.001$). Population-adjusted number of cases was higher than expected in the boreal and alpine ecological regions ($p<0.05$).

Abstract conclusion

Identification of high risk areas for tularemia and characterization of ecological niches favorable to Francisella are essential steps for outbreak modeling and prevention programme management.

Keywords: Tularemia, Francisella, Sweden, epidemiology, vector-borne disease

PRESENTED BY: Amélie Desvars

ESCAIDE REFERENCE NUMBER: 20142214

Cholera outbreaks in Ibadan, Oyo State, Nigeria- 2013: Identification of circulating strain and its antimicrobial susceptibility pattern

Abiodun Ogunniyi[1], Najeem Fasina[2], Olubunmi Olopha[3], Olufemi Ajumobi[4], Gabrielle Ponggesee[1]

[1] Nigeria Field Epidemiology Laboratory Training Programme,Asokoro, Abuja, Nigeria; [2] Medical Microbiology Department, University College Hospital, Ibadan. Oyo State, Nigeria; [3] Public Health Nursing Department, University College Hospital, Ibadan, Nigeria; [4] National Malaria Elimination Program. Abuja., Nigeria

Abstract

Cholera outbreaks were reported in Ibadan the capital of Oyo State shortly after a flood in the state.Reported figures showed a total of 207 cases and 15 deaths from 2011 to 2012. Year 2013 has recorded three outbreaks at different locations of the city with 84 cases and 11 deaths. We conducted laboratory investigation during the outbreak in Egbeda area of Ibadan to obtain laboratory confirmation of cause, determine the likely circulating strain of Vibrio cholerae and its antimicrobial susceptibility.

Abstract methods

Rectal swabs (3) and stool (5) samples collected from suspected cases were transported to the laboratory in alkaline peptone water. After macro and microscopic examinations, culture was done and incubated at 37°C for 24 hours. Biochemical tests were done. Organism identification confirmation was done using Microbact method. Serological typing against polyvalent 01 and 0139, inaba and ogawa antisera was done. Antimicrobial susceptibility testing of the isolate was done using agar disk diffusion method and compared with that of previous outbreaks in the same year.

Abstract results

Two of the rectal swabs and three stool samples culture yielded growth of Vibrio cholerae. The serological typing revealed the strain to be Vibrio cholerae 01 Ogawa. When compared with V. cholerae isolated from previous outbreaks, similar antimicrobial susceptibility pattern was obtained which showed sensitivity to Tetracycline, Gentamycin, Ciprofloxacin and Ceftriaxone but resistant to Erythromycin and Ceftazidime.

Abstract conclusion

The cholera outbreak was confirmed. Given the similar antimicrobial susceptibility pattern, the circulating strain in the city could be Vibrio cholerae 01 Ogawa. Antimicrobial susceptibility pattern is comparable with the previous outbreaks. Health professionals need be informed about the susceptibility pattern of circulating strains. Surveillance should include resistance testing.

Keywords: Cholera, outbreak, microbiology, microbial sensitivity tests, Nigeria

PRESENTED BY: Abiodun Ogunniyi

ESCAIDE REFERENCE NUMBER: 20142268

Trends of human monophasic Salmonella Typhimurium 1,4,[5],12:i:- in Finland, 2003-2013

Anni Vainio[1] Taru Lienemann[1], Aino Kyyhkynen[1], Saara Salmenlinna[2]

[1] National Institute for Health and Welfare, Finland; [2] Department of Infectious Diseases Surveillance and Control, National Institute for Health and Welfare (THL), Finland

Abstract

Monophasic Salmonella Typhimurium with the antigenic structure 1,4,[5], 12:i:- has increased since mid-1990s in Europe, and it has important role as a source of human infection. We report laboratory based surveillance data on monophasic S. Typhimurium in Finland in 2003-2013.

Abstract methods
In Finland, notification of Salmonella is mandatory. Background data collected includes age, gender, and travel information. Isolates were also collected for serotyping, phage typing and antimicrobial sensitivity testing. Multilocus variable number tandem repeat analysis (MLVA) was performed for subset of the isolates.

Abstract results
A total of 924 monophasic S. Typhimurium cases were detected in 2003-2013. The yearly number of cases increased from 15 to 189 (range 6-189). The median age of the patient was 38 and 50 % were female. Fifteen percent of infections were acquired domestically and 83 % were imported. Majority of imported infections (81 %) were from Thailand. The proportion of monophasic S. Typhimurium among all Salmonella increased from 0,8 % to 11 %. Multiresistance occurred in 81 % of monophasic isolates and in 87 % of domestic isolates. Among 818 isolates, 19 different phage types were found, FT193 (43 %) and FT195 (23 %) being the most prevalent ones. MLVA was performed for 67 mainly domestic isolates and was able to identify 26 different types. The most prevalent MLVA types were 3-13-11-NA-0211 (N=10) and 3-12-9-NA-0211 (N=9). One domestic epidemic caused by monophasic S. Typhimurium was recognized.

Abstract conclusion
Multiresistant monophasic S. Typhimurium 1,4,[5],12:i:- showed an increasing trend. Sources of this emerging serovar causing domestically acquired infections remain unknown.

Keywords: Monophasic S. Typhimurium, multiresistance, serotype, laboratory based surveillance

PRESENTED BY: Anni Vainio

ESCAIDE REFERENCE NUMBER: 20142067

Which is the most important marker to assess when predicting the severity of an STEC infection, the shigatoxin subtype or serotype?

Cecilia Jernberg[1], Camilla Sundborger[1], Ingela Hedenström[1]

[1] Public Health Agency of Sweden, Sweden

Abstract
Infection with shigatoxin producing E. coli can vary in severity of symptoms from mild infections, even without symptoms, to death. A correlation of specific subtypes of the shigatoxin genes (stx1 and stx2), specifically subtypes of the stx2 gene, have previously been reported to be connected to more severe infections.

Abstract methods
All clinical isolates from patients infected with STEC during a one year study period (October 2012 – October 2013) were subtyped regarding serotype and shigatoxin subtype. In addition, isolates belonging to the O157 serogroup were specifically analysed for clade 8, a genetic subgroup that has been shown to cause more severe infection. A questionnaire was sent out to all cases assessing foremost the symtoms of the cases. The epidemiological data was collected via the national surveillance system SmiNet. Only cases whith an STEC isolate were included.

Abstract results
In total, 475 isolates were subtyped. The distribution between stx1 or stx2 positive isolates showed only a slight higher number of stx2 positive isolates. Approximately 20% of the isolates were both stx1 and 2 positive. 88 isolates harboured both stx2a and c subtype and the majority belonged to serotype O157:H7, the most common serotype in Sweden. The most common subtype of stx2 was stx2a followed by 2c. There was a strong correlation between rare serotypes and rare stx subtypes. In addition, these rare subtypes were often isolated from cases infected abroad.

Abstract conclusion
More studies from different countries coupling the severity of infection to specific subtypes are needed and the added value of these could be used as a tool in risk assessments for STEC, both on the human side as well as on the food and animal side.

Keywords: STEC, subtyping, stx1, stx2 risk assessment

PRESENTED BY: Cecilia Jernberg

ESCAIDE REFERENCE NUMBER: 20142263

Varying implementation and guidelines for screening for infectious disease among newly arrived migrants: A need for EU-level guidelines?

Tommi Kärki[1], [2], Christian Napoli[2], Flavia Riccardo[2], Massimo Fabiani[2], Maria Grazia Dente[2], Manuel Carballo[3], Teymur Noori[4], Silvia Declich[2]

[1] European Programme for Intervention Epidemiology Training (EPIET), European Centre for disease Prevention and Control (ECDC), Stockholm, Sweden; Istituto Superiore di Sanità (ISS), National Centre for Epidemiology Surveillance and Health Promotion (CNESPS), Rome, Italy; [3] International Centre for Migration, Health and Development, Geneva, Switzerland; [4] European Centre for Disease Prevention and Control, Sweden

Abstract

Screening is one possible tool for monitoring infectious diseases, such as tuberculosis, among migrants. However, there is limited information whether EU/EEA/EFTA-countries perform screening among newly arrived migrants, a population defined as asylum-seekers, refugees and economic migrants. We assessed the implementation and expert opinions on screening, and investigated whether the proportion of asylum-seekers in the population was associated with the implementation of screening programmes.

Abstract methods

We sent a questionnaire to migrant health experts from 28 EU/EEA/EFTA-countries asking whether they currently had screening implemented among migrants within the first year from arrival, and their opinions on screening. We acquired data on asylum-seeker and resident populations from EUROSTAT, divided the countries equally into groups of low, medium and high proportion of asylum-seekers, and estimated the association between these groups and the implementation of screening programmes using the chi-squared test.

Abstract results

Twenty-seven of 28 country experts responded (96%). Of the countries, 16 (59%) had implemented screening programmes and 15 (56%) had national guidelines. Twenty-five country experts (96%) considered screening among migrants useful, especially at holding level (e.g. migrant centres), and 24 (92%) would welcome EU-level guidelines for screening. Eight (89%) of the high proportion (>92/100,000), six (67%) of the medium proportion (16-92/100,000), and two (22%) of the low proportion (<16/100,000) countries had implemented screening programmes. High proportion of asylum-seekers was significantly associated with the implementation of screening programmes (p=0.014).

Abstract conclusion

Although experts consider screening useful, the implementation of screening programmes varies among EU/EEA/EFTA-countries, as does the existence of relevant guidelines. According to our analysis, this variation can partially be explained by the national migration patterns. We recommend establishing EU-level guidelines for screening, taking into account the differences in the arriving migrant populations.

Keywords: Screening, immigration, refugees, migrants, communicable diseases

PRESENTED BY: Dieter van Cauteren

ESCAIDE REFERENCE NUMBER: 20142122

Influenza & influenza vaccination (1)

Outbreak of Mass Psychogenic Illness at a High School-- Amhara Region, Ethiopia, April, 2010

Belay Bezabih[1], Aschalew Teka[2], Basazinew Alemu[3], Masaki Ota[4], Richard Luce[5]

[1] Amhara Regional State Health Bureau, Ethiopia; [2] World Health Organization, Ethiopia; [3] Amhara Regional State Health Bureau, Ethiopia; [4] JICA Amhara Region Infectious Disease Surveillance Project, Ethiopia; [5] Ethiopian Field Epidemiology and Laboratory Training Program (EFELTP), Addis Ababa University, Ethiopia

Abstract

Mass psychogenic illness has been recognized for centuries and has the potential for significant adverse public health consequences. The objectives of this investigation were to determine if an outbreak of clinical illness was due to psycho-social factors, guide interventions and improve understanding and recognition of similar events.

Abstract methods

Local health officials requested assistance with a suspected outbreak at a high school in rural eastern Ethiopia in April 2010. Data was collected using a line-list containing socio-demographic characteristics and clinical symptoms reported by case-patients. Detailed discussions were also conducted with the school principal, administrators, teachers, local disease surveillance officers. The data were analyzed using EpiInfo v3.3.2.

Abstract results

The outbreak began on 7April 2010 and cases continued to occur for 22 days. Forty four case-patients were identified. All were females; the median age was 16 years old, and 33 (75%) were Muslims. The major clinical symptoms were breathlessness, fear and crying, anxiety, and inability to move limbs. The median duration of illness was 3 hours with a range of 2 to 96 hours; 13 (27.3%) and 6 (13.6%) of the cases reported the cause of the disease to be “evil-devil force” and stress respectively, however 26 (59.1%) replied ‘I don’t know’. No environmental toxicity, food-borne illness, infectious disease or societal conflicts were identified as causal factors.

Abstract conclusion

This outbreak was appeared to be the result of mass psychogenic illness. Socio-cultural beliefs in supernatural forces, together with academic pressures, may have been triggering factors. Conducting an investigation, providing immediate reassurance, and timely psychiatric support and counseling at the school and community level could minimize the impact of such events in the future.

Keywords: Hysteria, Epidemiology, Disease outbreaks, Ethiopia

PRESENTED BY: Belay Bezabih

ESCAIDE REFERENCE NUMBER: 20142157

Early influenza vaccine effectiveness: a good proxy for final estimates in Spain in the last four seasons 2010 – 2014

Silvia Jiménez Jorge[1], Salvador de Mateo[2], Concepción Delgado-Sanz[2], Francisco Pozo[3], Amparo Larrauri[1]

[1] National Centre for Epidemiology, Instituto de Salud Carlos III, Spain; [2] National Center of Epidemiology, ISCIII/Ciber Epidemiología y Salud Pública (CIBERESP), Ministerio de Economía y Competitividad, ISCIII, Madrid-España., Spain; [3] National Center of Microbiology, ISCIII, Madrid-Spain, Spain

Abstract

Early estimates of influenza VE can help to guide health authorities in influenza prevention and provide useful information for the WHO strain selection process. The agreement between early and final influenza VE estimates would support the use of interim assessments as a proxy for final VE results. The objective was to compare early and final VE estimates in Spain in the last four influenza seasons.

Abstract methods

We carried out two test-negative case-control studies using data from the observational cycEVA study and from the Spanish Influenza Sentinel Surveillance System (SISS) for 2010/11 to 2013/14. We compared early and final adjusted VE estimates obtained with cycEVA (real-time) and SISS (retrospectively). Sensitivity analyses were carried out by influenza type/subtype and by population (entire/targeted for vaccination).

Abstract results

Early influenza vaccine coverage was ±1% of the final values, except for 2011-12 with decreasing coverage (2-3%) in both studies. The percentage of population targeted for vaccination included into the early analysis changed to the final analysis (range of change: 4-18%). Differences among early/final estimates ranged 4-11% (cycEVA) and 3-9% (SISS) for the entire population and 2-31% (cycEVA) and 6-14% (SISS) for those targeted for vaccination. In general, early A(H1N1)pdm09 and A(H3N2) estimates were higher than final estimates.

Abstract conclusion

In Spain, early VE estimates over 2010 – 2014 seasons were a good proxy of the final protective effect of the vaccine. Differences among early and final estimates were lower for the entire population compared to those targeted for vaccination using cycEVA and SISS. In general, early estimates were higher than final for A(H1N1)pdm09 and A(H3N2) viruses. Differences observed could be explained for differences in the characteristics of the study population (early and end-season).

Keywords: Influenza, vaccine effectiveness, case-control studies, sentinel networks

PRESENTED BY: Silvia Jiménez Jorge

ESCAIDE REFERENCE NUMBER: 20142044

Low to moderate vaccination coverage for seasonal influenza, pneumococcal disease and pertussis among adult population at risk, Ireland, 2013

Coralie Giese[1], Jolita Mereckiene[1], S. Cotter[1], Derval Igoe[2], Joan O´Donnell[1], Darina O'Flanagan[1]

[1] Health Protection Surveillance Centre, Dublin, Ireland; [2] HSE, Ireland

Abstract

The Health Services Executive in Ireland recommends and provides cost-free: 1) influenza and pneumococcal vaccines for individuals at risk due to age (≥65 years) or underlying medical conditions; 2) influenza and pertussis vaccines for pregnant women. In 2013, we conducted a national survey to estimate vaccination coverage (VC) among those vaccination target groups.

Abstract methods

We used computer-generated lists of random land-line and mobile telephone numbers and a quota survey methodology to obtain a representative sample of the Irish population at risk. We conducted telephone interviews among non-institutionalised individuals ≥18 years of age to collect self-reported information on vaccination and health status. We calculated prevalence and prevalence ratios (PR) using binomial regression.

Abstract results

Of 1,770 participants, 84% (95%CI:82–86) were ‹65 years old. Among them, 325 (22%; 95%CI:20–24) and 264 (18%; 95%CI:16–20) had medical risk conditions for which influenza or pneumococcal vaccines, respectively, were recommended. Of these, 28% (95%CI:23–33) and 16% (95%CI:12–21) were vaccinated. Among participants aged ≥65 years, 60% (169/282; 95%CI:54–66) were vaccinated against influenza and 36% (98/271; 95%CI:30–42) against pneumococcal disease. Among pregnant women, 22% (10/45; 95%CI:9.6–35) received influenza and 2.3% (1/43; 95%CI:-2.3 –7.0) pertussis vaccines. Influenza VC was 2.5 times (PR=2.5; 95%CI:2.1–3.0) higher among individuals at risk who had been recommended influenza vaccine by a doctor.

Abstract conclusion

VC for influenza and pneumococcal disease in at risk groups was low, except moderate for influenza among individuals ≥65 years old. VC for pertussis in pregnant women was low. Recommendation of influenza vaccination by a doctor was associated with increased coverage. Doctors should routinely identify and recommend influenza vaccination to their at risk patients annually.

Keywords: Influenza, pneumococcal, pertussis, vaccination coverage, cross-sectional survey, risk groups

PRESENTED BY: Coralie Giese

ESCAIDE REFERENCE NUMBER: 20142115

Factors Associated with Adverse Reactions to the Flu Vaccine in Health Personnel

José L. Carretero-Ares[1], Isidra Tenza-Iglesias[1], Jóse L. Mendoza-García[1], M. El Attabi[1], Vicente García-Román[1], CO. Villanueva-Ruiz[1], E. López-González[1], J. Barrenengoa-Sañudo[1], José Sánchez Payá[1]

[1] Hospital General Universitario de Alicante, Spain

Abstract

Beside avoiding medical treatment, adverse effects (AE) and self-confidence on immunological defenses are the most common causes explained by health personnel (HP) for not being vaccinated against flu. Factors associated with AE appearance are not well studied, so our objective is to study these after flu vaccination of HP.

Abstract methods

Cohort series study in HP that turned to immunize from 2009-2010 to 2013-2014 flu vaccination campaigns. Explanatory variables were: flu vaccination campaign (2009-2010 seasonal, 2009-2010 pandemic, 2010-2011, 2011-2012, 2012-2013, 2013-2014), age (<45, ≥45), sex, job class (MD, nursery, clinical assistant, others) vaccinated or not in the last campaign, and vaccine type (adjuvanted or not). Outcome variable was AE appearance; in order to detect these, HP was telephoned a week after being vaccinated to ask about AE appearance in the 72 hours after vaccination. Raw and adjusted odds ratio (OR) were used to evaluate the relationship between explanatory variables and AE using a logistic regression model, with a 95% confidence interval.

Abstract results

AE were evaluated in 85.2% of immunized HP. AE frequency was 33.6%. 2013-2014 was considered the reference campaign, and adjusted OR were: 2009-2010 seasonal: 1(0.8-1.3), 2009-2010 pandemic:0.6 (0.1-4.7), 2010-2011: 1.1 (0.9-1.4), 2011-2012: 1.4(1.2-1.8), 2012-2013: 1.2 (1.0-1.6); age (<45): 1.5(1.3-1.7); sex (male): 0.7 (0.6-0.8); statement (others as the reference category): MD: 1(0.8-1.2), nursery: 1.1 (0.9-1.4) clinical assistant: 1.2 (0.9-1.5); vaccinated in the last campaign (yes): 0.9 (0.8-1.1); and vaccine type (adjuvanted): 25.4 (2.9-222.0).

Abstract conclusion

2011-2012 campaign, age, sex and adjuvanted vaccine are associated to AE appearance in HP, being the vaccine with adjuvant the highest magnitude item. Obtained information is essential to evaluate "advantages/disadvantages" of flu vaccination in HP.

Keywords: Influenza Health Personnel Vaccination Adverse Reactions

PRESENTED BY: José Sánchez Payá

ESCAIDE REFERENCE NUMBER: 20142220

Health Related Quality of Life and Influenza in a Fragile Population

Anna Lugner[1], Yolanda van Weert[1], Marianne van der Sande[1]

[1] RIVM, The Netherlands

Abstract

Residents in nursing homes are at risk for serious complication from an influenza infection. This study, nested in a controlled randomised trial (RCT) to assess the effectiveness of oseltamivir, measured the health-related quality of life (HRQL), and we assessed whether individuals becoming ill with influenza had a lower HRQL before illness than individuals not becoming ill.

Abstract methods

The multi-centre double-blinded RCT began when one resident in a unit was diagnosed with influenza. Consenting residents at the same unit received either oseltamivir or placebo as prevention against infection, and were followed-up for 10 days. The responsible nurse filled in a diary including the EQ-5D-5L-instrument, at day of inclusion and end of study. The EQ-5D-5L descriptive system comprises 5 dimensions: mobility, self-care, usual activities, pain/discomfort and anxiety/depression. Each dimension has 5 levels: no problems, some problems, moderate problems, severe problems, and extreme problems/unable to.

Abstract results

The HRQL was measured at least twice for the 98 respondents, and 55% of the observations included at least two responses on the 4th or 5th level of one of the dimensions. Comparing the HRQL at inclusion between the residents that did develop ILI during follow up (n=10, HRQL=0.67) with those that did not develop ILI (n=88, HRQL=0.39) showed a difference in initial HRQL (p=0.02). Both groups showed a higher HRQL after the trial than before (respondents developing ILI, mean improvement HRQL=0.08, p=0.07; no illness, mean improvement HRQL=0.04, p=0.04).

Abstract conclusion

The results did not confirm the hypothesis that residents developing ILI had a lower HRQL at the onset than those not becoming ill. We can only speculate over the reason for this contra intuitive result: do less fit residents have less contact with others?

Keywords: Nursing homes, prevention, oseltamivir, clinical trial

PRESENTED BY: Anna Lugner

ESCAIDE REFERENCE NUMBER: 20142199

Modelling Individual Protective Decisions within an Influenza Epidemic

Jennifer Badham[1], *Nigel Gilbert*[1]

[1] Centre for Research in Social Simulation, University of Surrey, UK

Abstract

The European funded TELL ME project (Transparent communication in Epidemics: Learning Lessons from experience, delivering effective Messages, providing Evidence) is intended to provide advice about communication in response to influenza pandemics. One output from the project will be a simulation model for use by agencies in assessing different communication plans.

Abstract methods

The simulation will have two components. A spatially explicit SEIR compartment model will track disease progression. An agent based model will simulate the adoption by individuals of protective behaviour such as vaccination or improved hand hygiene. This component implements aspects of several cognitive models from psychology: Theory of Planned Behaviour, Health Belief Model, and Protection Motivation Theory.The two components are coupled, mutually influencing each other over time. Increased protective behaviour will reduce the local force of infection and hence epidemic spread, and regional incidence will be considered by the agents in their behaviour decisions.The agents will also respond to a simplified description of possible communication plans, thus enabling users to consider their potential impact on behaviour and epidemic spread.

Abstract results

The model is designed and currently under development. The presentation will focus on the model rules; how understandings from social sciences are being used to extend standard epidemic models. A prototype will also be presented.

Abstract conclusion

The TELL ME model will be the first simulation that combines standard compartment models of epidemics with a behaviour model that allows for heterogeneous decisions that depend on the situation in which each simulated individual is embedded. It is scheduled for release in January 2015.

Keywords: Computer Simulation Models, Psychological Models, Theoretical

PRESENTED BY: Jennifer Badham

ESCAIDE REFERENCE NUMBER: 20142074

Novel methodological approaches for disease investigation, surveillance and control (1)

Web-based questionnaire valuable for timely outbreak response in a gastrointestinal outbreak in Copenhagen, January 2014

Julita Gil Cuesta[1], *Morten Lisby*[2], *Steen Ethelberg*[3], *Jannik Fonager*[3], *Kåre Mølbak*[3], *Luise Müller*[3]

[1] Statens Serum Institut/European Programme for Intervention Epidemiology Training (EPIET), ECDC, Denmark; [2] Food Control Office of Copenhagen, Denmark; [3] Statens Serum Institut, Denmark

Abstract

On 24 January, the Copenhagen Food Control Office was notified of an increase in gastrointestinal illness (GI) among customers of a company canteen. We investigated to determine the magnitude and identify the source of the suspected outbreak.

Abstract methods

Between 28 January and 5 February, we conducted a cohort studyamong employees who had used the canteens, using a web-based questionnaire. We asked about GI and food items consumption. We defined cases as persons developing vomiting or diarrhea who ate in any of the canteens from 21-24 January. We described the response rate by days, cases by person, place and time, calculated attack rates (AR), relative risks (RR) and 95% confidence intervals (CI) by day and canteen.

Abstract results

Out of 750 persons at risk, 445 responded within the first 24 hours and 75 persons in the following week (response rate 70%). We identified 134 cases (AR 26%). Symptoms peaked on 23 January between 18-24 hours. No infectious agent was identified among cases. The univariable analysis showed that six buffet items, including eating from the salad-bar during any of the three days (RR 4.1 CI 1.6-10.8) were associated with illness. One kitchen worker prepared the salad and denied illness. No differences in RR were observed between the canteens or the different days.

Abstract conclusion

The use of a web-based questionnaire allowed an early description of the magnitude of the outbreak, place and time of exposure and food items consumed, and pointed at several food items as the source of the outbreak most likely contaminated from one kitchen worker. We recommend the use of web-based questionnaires in similar cohort settings to allow rapid epidemiological investigation with a high response rate using limited resources.

Keywords: Outbreaks, Cohort studies, Foodborne Diseases, Questionnaires

PRESENTED BY: Julita Gil Cuesta

ESCAIDE REFERENCE NUMBER: 20141958

Recall period and kind of serving influence recall error in self-reported food consumption histories – relevance for outbreak investigations, Germany, 2013

Maximilian Gertler[1], Irina Czogiel[1], Klaus Stark[1], Hendrik Wilking[1]

[1] Robert Koch-Institut, Germany

Abstract

Poor recall during investigations of foodborne outbreaks may lead to misclassifications in exposure ascertainment. We conducted a simulation study to assess the frequency and determinants of recall errors.

Abstract methods

Visitors of a bank cafeteria using exclusively cashless payment reported daily selection from 13 food items during the three preceding weeks using self-administered paper questionnaires. We compared responses with electronic payment information (gold standard) obtaining true, false-positive (reported "yes" but not paid), false-negative (reported "no" but paid) and indecisive recalls. We calculated sensitivity and specificity of recall and estimated the effect of recall-period (3-21 days), age, sex, education level, dietary habits and food-type using multivariable logistic regression.

Abstract results

We included 145/226 (64%) respondents (58% female, median age: 41 years, range 22-64 years) who reported about consumption of 24,917 food items. Sensitivity of recall was 73%, specificity 96%. In multivariable analysis, for each additional day of recall period, the chance for false-negative recall increased by 8% (OR: 1.1; 95%-CI: 1.06–1.1), for false-positive recall by 3% (OR: 1.03; 95%-CI: 1.02–1.05), for indecisive recall by 12% (OR: 1.1; 95%-CI: 1.08–1.15). Indecisive recall was higher among 20-29 year olds compared to 50-65 year olds and in vegetarians compared to non-vegetarians (OR: 4.3; 95%-CI: 1.2-15.9). Sex and education level had no significant effect. False-negative recall was lower for main courses compared to all other servings (OR: 0.3; 95%-CI: 0.3-0.4).

Abstract conclusion

Forgetting to report consumed foods is more frequent than reporting food-items actually not consumed. Forgetting is strongly enhanced by delay of interviews and may make hypothesis generation and testing very challenging after more than two weeks. Side dishes are more easily missed than main courses. If available, electronic payment data can improve food-history information.

Keywords: Outbreak, foodborne, food history, electronic device for outbreak detection, recall error

PRESENTED BY: Maximilian Gertler

ESCAIDE REFERENCE NUMBER: 20142078

Use of a market research panel for control recruitment in a case-control study provides time and resource savings: national outbreak of Salmonella Mikawasima, United Kingdom, 2013

Piers Mook[1], Sanch Kanagarajah[1], Helen Maguire[1], Bob Adak[1], Gavin Dabrera[1], Alison Waldram[1], Rachel Freeman[1], Andre Charlett[1], Isabel Oliver [1]

[1] Public Health England, UK

Abstract

Recruiting population controls in a timely fashion can be difficult in outbreak investigation resulting in delays identifying the source or vehicle of infection and limitations in terms of potential bias. We evaluated the timeliness and cost of market research panels as a sampling frame for recruiting controls in a case-control study in a national outbreak of Salmonella Mikawasima.

Abstract methods

In parallel to the Outbreak Control Team's approach to recruit controls from among Public Health England (PHE) staff by telephone (PHE controls), we deployed via e-mail a web-based control questionnaire to targeted members of a market research panel (MRP controls). The target was 122 controls, frequency matched to cases (n=61; 2:1 ratio of controls to cases) in terms of age, gender and region. Access to the questionnaire was restricted once the target was achieved. Time to recruitment and measurements of direct costs (not including opportunity costs) for staff time per PHE control and payment to the market research firm per MRP control were calculated.

Abstract results

The target 122 MRP controls were recruited within 14 hours of deployment of emails compared to 15 days to complete paper-based questionnaires for PHE controls. The average direct cost per completed questionnaire for MRP controls was £3.60 compared to £3.78 per PHE control. Further time and resource was required to double-enter data for PHE controls into a database.

Abstract conclusion

Recruiting market research panel controls offers potential time and resource savings. More rapid source or vehicle elucidation would enable more prompt implementation of control interventions in outbreak settings. We recommend this approach be used where appropriate to further assess the method.

Keywords: Case-Control Studies, Disease Outbreaks, Methods, Research Design, Salmonella

PRESENTED BY: Piers Mook

ESCAIDE REFERENCE NUMBER: 20142095

Event Mobile Application (EMA-i): A novel tool for field rapid disease reporting and information sharing

Fairouz Larfaoui[1], Noelina Nantima[2], Joseph Sserugga[2], Alessandro Colonna[1], Sabina Ramazzotto[1], Sam Okuthe[3], Juan Lubroth[1], Julio Pinto[1]

[1] Food and Agricultural Organization of the United Nations, Rome, Italy; [2] National Animal and Disease Diagnostics and Epidemiology Center (NADDEC), Uganda; [3] Food and Agricultural Organization of the United Nations (FAO), Nairobi, Kenya

Abstract

Early detection and timely reporting of animal diseases, including zoonoses, are a challenge in developing countries, where weak infrastructure combined with a lack of human resources and capacities have an impact on effectively implementing adequate disease surveillance and reporting. FAO has developed an Event Mobile Application (EMA-i) for data collection and real-time reporting. EMA-i has been piloted in Uganda to support veterinary services in improving their existing surveillance system.

Abstract methods

EMA-i was customized for the national animal health authorities in Uganda; a workflow was established according to the existing reporting procedure from the field to the decision makers and equipment was provided. Participants included District Veterinary Officers (DVOs), the National Animal Disease Diagnostics and Epidemiology Center (NADDEC) and the Chief Veterinary Officer (CVO). Ten districts out of 112 participated and 16 diseases were selected by the participants based on their impact on livestock production and Public Health. Several zoonoses were included, such as anthrax, brucellosis, Rift Valley fever, trypanosomosis and rabies. Smartphones with EMA-i installed were delivered to DVOs to collect data from farmers. The collected information was then transmitted to the EMPRES-i web platform, an animal disease information system developed by FAO, where it was subsequently verified and validated by NADDEC. After validation, reports from EMPRES-i were sent to the CVO, NADDEC and DVOs.

Abstract results

In only 6 months, i.e. from July to December 2013, 126 livestock disease reports were submitted in real-time to NADDEC. This compares to 45 and 56 monthly reports NADDEC received in 2012 and 2011, respectively.

Abstract conclusion

Piloting EMA-i in Uganda demonstrates major improvements with regards to number and timeliness (i.e. from monthly to real-time) of reports received from districts. In addition, a wide range of diseases was reported. Interaction and communication between the field and decision makers was significantly improved.

FAO is supporting developing countries in the implementation of EMA-i and providing training, data server, maintenance and further support for data analysis.

Keywords: Mobile applications, Public Health, Zoonoses, Animal diseases, Surveillance, Data reporting

PRESENTED BY: Fairouz Larfaoui

ESCAIDE REFERENCE NUMBER: 20142225

Medi+board – the public health dashboard for early warning, risk assessment and response

Patty Kostkova [1]

[1] UCL, UK

Abstract

Big data, real-time streams from new situation-aware signals from social media, online searches, loyalty cards, mobile/sensor networks and citizens' participatory surveillance systems need more effectively complement traditional surveillance to enhance preparedness, risk assessment and more effective response. The medi+board is a public health dashboard system screening real-time data sources for early detection of infection threats, cross-validating sources by correlating data streams and displaying results in an integrated format presented by means of an interactive dashboard.

Abstract methods

An integrated digital public health infrastructure was designed for multiple data-streams with dynamic components for data-mining, threat detection, verification, correlation of threats. Monitoring and detection of multiple channels requires different computational methods according to their structure, timelessness and reliability . Our algorithm is expressed in the form of a directed acyclic graph which can be programmed by the analyst in a visual designer to prevent the need of writing code.

Abstract results

medi+board functionality was shown on a simulation of the swine flu pandemics in 2009. We used three datasets: the HPA surveillance data from RCGP, Google News API, and Twitter dataset collected during the pandemics in 2009. We illustrated the three data streams in a dynamic way while statically illustrating other important segments of data at two key points of the pandemics (containment phase in the UK when the demographics study of initial cases 'FF100' was conducted; and control phase in the autumn monitoring the distribution of the anti-virals as well as calls to the dedicated "fluline").

Abstract conclusion

Demonstrated on three data streams from the swine flu 2009, the medi+board integrated public health dashboard provides a simulation illustrating how such system could substantially enhance future public health operations.

Keywords: Public health, surveillance, risk assessment, integrated dashboard, swine flu

PRESENTED BY: Patty Kostkova

ESCAIDE REFERENCE NUMBER: 20142266

A multidisciplinary team approach to control an outbreak due to multidrug-resistant Pseudomonas aeruginosa.

Mireia Puig-Asensio[1], Josep Maria Sánchez-García[2], Dolores Rodríguez-Pardo[3], Nieves Larrosa[4], José Manuel Collado [5], Anna Rey[6], Juan José González-López[4], Magda Campins[2], Benito Almirante[3]

[1] Hospital Universitari Vall d´Hebron, Spain; [2] Department of Public Health, Hospital Universitari Vall d´Hebron, Universitat Autònoma de Barcelona, Barcelona, Spain; [3] Infectious Diseases Department, Hospital Universitari Vall d´Hebron, Medicine Department, Universitat Autònoma de Barcelona, Barcelona, Spain; [4] Microbiology Department, Hospital Universitari Vall d´Hebron, Universitat Autònoma de Barcelona, Spain; [5] Department of Plastic Surgery and Burns, Hospital Universitari Vall d'Hebron, Universitat Autònoma de Barcelona, Spain; [6] Neurotraumatology Intensive Care Unit, Hospital Universitari Vall d´Hebron, Barcelona, Spain

Abstract

During March-April 2012 an increasing frequency of a multidrug-resistant strain of Pseudomonas aeruginosa (MDR-PA) was detected in the Burn Unit of a 1000-bed hospital (Hospital Vall d´Hebron, Barcelona, Spain). This strain was resistant to anti-pseudomonal beta-lactams, tobramycin, ciprofloxacin and gentamicin. An investigation of a suspected outbreak was started in order to identify a potential source and stop transmission.

Abstract methods

A retrospective case finding was performed. Cases were patients who had been admitted to the Burn Unit from August 2011 onwards and had any positive sample for MDR-PA. Pulse field gel electrophoresis (PFGE) of isolates was used to confirm the presence of a clonal strain. An integrated approach was implemented: 1) environmental swabs from mattresses and water were taken; 2) infection control measures were audited and recalled to health-care personnel; 3) a stewardship program with prudent use of broad-spectrum antibiotics and discontinuation of selective digestive tract decontamination in intubated patients was carried out.

Abstract results

From August 2011-July 2012, 13 patients were found to be MDR-PA positive (5 retrospectively identified). PFGE revealed that all strains belonged to the same clone.The transmission map showed a constant overlap of Burn Unit stay between case-patients. One mattress was positive for PA, but the electrophoretic band pattern was different from that obtained from case-patients. New cases decreased with the strengthening of infection control measures and new antibiotics policy. The outbreak terminated following the discharge of the last infected patient from the Unit. In the absence of demonstrable environmental source for the outbreak, we believe that transmission patient to patient, via staff contamination, was the most likely way of spread.

Abstract conclusion

An integrated approach proved highly efficient to control outbreaks due to multidrug-resistant bacteria.

Keywords: Drug resistant, Pseudomonas aeruginosa, outbreak, Burn Units

PRESENTED BY: Mireia Puig-Asensio

ESCAIDE REFERENCE NUMBER: 20142151

Outbreaks (2)

Outbreak of Salmonella infantis associated with consumption of laverbread in Wales, 2014: case-case study supported temporary product withdrawal

Chris Williams[1], BW Mason[1], M Evans[1], Simon Cottrell[1], R Smith[1], M Simmons[1], C Lane[1], B Gregory[1], D Beynon[2], J Hoffmann[1]

[1] Public Health Wales, UK; [2] City and County of Swansea, UK

Abstract

On 19/3/2014, the microbiologist in Swansea, UK, reported a cluster of six cases of Salmonella with an unusual serotype; at interview, 4/6 reported having eaten a local dish of laverbread (Porphyra umbilicalis) and cockles. As descriptive epidemiology was insufficient to enforce withdrawal recommendations, we conducted an analytic study to confirm the source.

Abstract methods

We compared cases of Salmonella serotype O6,7 with date of report after 3/3/2014, with cases of Campylobacter, in persons aged over 40 resident in the outbreak area. We interviewed cases and controls by telephone to ascertain food exposures and calculated odds ratios for each exposure, and stratified by potential confounders. Environmental health staff inspected the production site, and obtained samples of laverbread for microbiological testing. The UK reference laboratory further typed isolates.

Abstract results

We interviewed 12 cases (onset 6-19 March) and 13 controls; mean case age was 65 (range 46-79 years). Cases were more likely to have consumed laver bread (Odds Ratio:65, 95% Confidence Interval 4-3024) and cockles (OR:13, 95% CI 1.1-642) than controls. The association with cockles was not significant when stratified by laver bread consumption (Mantel-Haenszel OR:4.1, 95% CI 0.1-154). All cases had consumed laverbread from the same producer, purchased between 4/3/2014 and 12/3/2014. The mean incubation period was 1.7 days (range 0-3 days). No pathogens were isolated from any laverbread samples. All cases were typed as Salmonella Infantis.

Abstract conclusion

Epidemiological and human microbiological evidence confirmed laverbread from a single producer as the source of infection. The epidemiological findings supported the subsequent active withdrawal of product and a public alert including the producer's name. Descriptive epidemiology suggested time-limited contamination, and production of this traditional food has recommenced with no further cases reported.

Keywords: Foodborne illnesses, Product Recalls and Withdrawals, Salmonella infections, case-control studies

PRESENTED BY: Chris Williams

ESCAIDE REFERENCE NUMBER: 20142036

Nationwide outbreak of listeriosis in Sweden 2013-2014 associated with cold cut meat

Viktor Dahl[1], [5], [6] Jakob Bergström[1], Per Follin[3], Ingela Hedenström[1], Cecilia Jernberg[1], Mats Lindblad[2], Anna Lindqvist[3], Margareta Löfdahl[1], Henrik Mellström[3], Håkan Ringberg[4], Lena Sundqvist[1], Susanne Thisted Lambertz[2], Anders Wallensten[1]

[1] The Public Health Agency of Sweden, Stockholm, Sweden; [2] The National Food Agency, Uppsala, Sweden; [3] Regional Office of Communicable Disease Control and Prevention, Västra Götaland, Gothenburg, Sweden; [4] Regional Office of Communicable Disease Control and Prevention, Region Skåne, Malmö, Sweden; [5] European Programme for Intervention Epidemiology Training (EPIET), Stockholm, Sweden; [6] European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Abstract

In January 2014, the Public Health Agency of Sweden observed a nationwide increase in notified listeriosis cases beginning October 2013. Isolates from eight cases had identical Pulsed Field Gel Electrophoresis (PFGE) patterns, suggesting a common source. We investigated the outbreak to describe its characteristics and identify the source.

Abstract methods

We included listeriosis cases with the identified PFGE pattern notified between 1 October 2013 and 1 September 2014. Cases notified after 15 December 2013 were frequency-matched by age-group and sex to controls sampled from a representative cohort of residents of Sweden. Cases were asked about food items consumed two weeks prior to symptom onset via email questionnaires. Controls received the same questionnaire and were asked about food items consumed in the previous two weeks. After 11 February 2014, The Swedish National Food Agency typed Listeria isolates found by food producers by PFGE.

Abstract results

We identified 44 cases with identical PFGE patterns. Their median age was 78 years and 28 (64%) were female. Thirty-six (82%) were notified after 15 December 2013. Twenty-three (64%) of them responded to the questionnaire and were included in the analysis with 125 controls. 100% of cases had eaten cold cuts compared to 72% of controls (P=0.004). Listeria with the outbreak PFGE pattern were found in cold cuts from one food producer.

Abstract conclusion

Epidemiological and microbiological results indicate cold cuts as the likely source of the outbreak. The food producer recalled food items and closed the affected production line. We reminded risk groups through media that cold cuts can be associated with listeriosis. However, new cases with the outbreak PFGE pattern were reported thereafter and the outbreak investigation continues.

Keywords: Listeriosis, Listeria, Foodborne disease, Disease outbreak, Public Health, Sweden

PRESENTED BY: Viktor Dahl

ESCAIDE REFERENCE NUMBER: 20142041

An Outbreak in a Primary School Associated with Consumption of a Traditional Food, Ankara, Turkey, March 2014

Meltem Akin[1], Gulsen Barlas[1], Ayla Aydin[2], Fehminaz Temel[1], Bahadir Sucakli[1]

[1] Public Health Institution of Turkey, Turkey; [2] Ankara Provicial Health Directoriate, Turkey

Abstract

On 26 March 2014, a gastroenteritis outbreak affecting students (aged 8 ± 1 year) in an elementary school was reported in Ankara City, Turkey. We investigated to identify the cause and mode of transmission, and implement control measures.

Abstract methods

A probable case was onset of abdominal pain or vomiting during 25-28 March in case-patient's classes. We designed a retrospective cohort study and used questionnaire by face to face interview. Among 346 students, 260 individuals participated the study. We took food samples and tap water samples. We gathered water and swab samples from water dispensers.

Abstract results

Among 346 students, 111 probable cases were identified (attack rate: 32%). The main symptoms included abdominal pain (90%), vomiting (62%), self-reported fever (37%), and diarrhea (29%). The epidemic curve showed a peak after lunch. Lunch menu of school included creamy mushroom soup, sarma (yogurt and stuffed grape leaves with meat and rice), spaghetti with sauce and apple on March 25th. The attack rate among students who ate sarma was twice compared to the ones who did not eat (RRcrude=1.5, 95% CI: 1.1-2.7). Students who ate sarma were 3 times more likely to develop the disease (ORadj=2.6, 95% CI: 1.3-5.2) after controlling for dispenser water and place of refectory, by using conditional logistic regression. We could not isolate any pathogen in the samples.

Abstract conclusion

This outbreak was likely due to consumption of contaminated sarma in a school. Investigation could not reveal the contamination source and the agent. Food-handlers at the catering company were educated on safe practices for food preparation and preservation.

Keywords: Outbreaks, foodborne diseases, cohort study, primary school

PRESENTED BY: Meltem Akin

ESCAIDE REFERENCE NUMBER: 20142056

An outbreak of foodborne intoxication caused by Staphylococcus aureus at a large community fair in Toronto, Canada

Anne Arthur[1], Effie Gournis[1], Sylvia Ota[1]

[1] Toronto Public Health, Canada

Abstract

Toronto, Canada hosts the Canadian National Exhibition (CNE), a large annual fair with approximately 1.4 million visitors. The CNE offers carnival rides, games, and the opportunity to taste unique culinary creations. On August 20, 2013, Toronto Public Health was notified of several reports of acute gastrointestinal illness among visitors to the CNE. Many of those ill reported consuming a highly profiled speciality burger, the 'cronut'. The vendor selling this item closed on the same day. This summarizes the public health investigation undertaken to confirm the source of illness.

Abstract methods

Reports of ill individuals who attended the CNE and experienced gastrointestinal illness were received after considerable media coverage of the outbreak. Symptoms, onset dates, and food histories were collected using a standardized questionnaire and analysed using SAS V9.2. The environmental investigation focussed on the CNE vendor, and two food establishments which supplied components of the cronut. Laboratory testing was conducted on food and stool samples.

Abstract results

In total, 146 outbreak-associated cases were identified; 99% of confirmed cases reported eating the cronut. The mean incubation period for all cases was 4.5 hours. Microbiological tests identified the presence of enterotoxin-producing Staphylococcus aureus in the bacon jam – the main cronut condiment prepared by an off-site supplier. Review of the supplier's food handling and storage practices identified several opportunities for contamination of the bacon jam.

Abstract conclusion

Epidemiological and environmental investigation results suggested S. aureus intoxication as the likely cause of illness. The bacon jam topping on the cronut was identified as the probable outbreak source. Collaborations with the vendor and CNE were essential to successful outbreak management. Ensuring safe food handling and storage practices can prevent future outbreaks.

Keywords: Infectious Disease Outbreaks, Foodborne Diseases, Staphylococcus aureus, Public Health Surveillance

PRESENTED BY: Anne Arthur

ESCAIDE REFERENCE NUMBER: 20142127

Relapsing fever outbreak investigation in Bahir-Dar, Amhara region, Ethiopia, 2012

Addisu Workineh Kassa[1], Masaki Ota[2], Belay Bezabih[1]

[1] Amhara Regional State Health Bureau, Ethiopia; [2] JICA Amhara Region Infectious Disease Surveillance Project, Ethiopia

Abstract

Ethiopia is one of the main endemic focus of louse borne relapsing fever. It occurs as epidemic under conditions of poor socio-economic status, overcrowding, draught and famine. An outbreak investigation on relapsing fever was conducted in Bahir Dar, Ethiopia in 2012. A descriptive epidemiology anda case-control studies were conducted to identify possible risk factors related to relapsing fever.

Abstract methods

A case was defined as a person who was diagnosed as relapsing fever based on laboratory confirmations conducted at the local health centre from 15 October to 15 November 2012. A control was defined as a person who had no previous history of relapsing fever.Statistical analysis was conducted using EpiInfo 3.5.1.

Abstract results

Sixty-eight patients and 136 controls were enrolled in the study. Of the 68 cases, all presented with fever, 64 (94.1%) chills, 63 (92.6%) headache, and 56 (82.45) vomiting and no death. Median age of the cases was 20 years (SD 7.14). Fifty one (75%) patients and 37 (27.2%) controls did not wash their clothes at least weekly (adjusted odds ratio [AOR]=13.23, 95%CI [5.51-31.75]) and 54 (79.4%) patients and 87 (64%) controls did not bathe at least weekly (AOR = 8.01, 95%CI [3.51-18.29]).

Abstract conclusion

Poor personal hygiene contributed to the occurrence of the outbreak. The outbreak was contained due to prompt interventions taken. It was recommended that the local government should raise personal hygiene of the residents to prevent future outbreaks of relapsing fever.

Keywords: Relapsing fever,hygiene,Ethiopia, vector bourne disease

PRESENTED BY: Addisu Workineh Kassa

ESCAIDE REFERENCE NUMBER: 20142248

Robin Hood takes aim at the mode of infection, food-borne versus person to person transmission in a Norovirus outbreak in Rhineland-Palatinate, 2014

Maja George1, Christin Lutz2, Marina Hoehne3, Florian Burckhardt4

[1] Robert Koch Institute, Berlin, Germany; [2] Primary School Offenbach, Germany; [3] Department for Infectious Diseases, Robert Koch Institute, Berlin, Germany; [4] Landesuntersuchungsamt Rheinland-Pfalz, Germany

Abstract

On 13/03/2014, local health authorities were notified of a gastroenteritis outbreak among participants of a school trip to a castle-style youth hostel from 10-12/03/2014. We investigated the outbreak to identify its source and prevent further spread.

Abstract methods

We conducted a retrospective cohort study among 4th grade pupils (9-10 years) and teachers with two self-administered questionnaires completed at school, asking on consumption of food-items during their stay at the hostel and participation in Robin-Hood-style activities such as archery or abseiling on 11/03/2014. Cases were defined as participants of the trip reporting at least one of: vomiting, diarrhea or stomachache between 10-17/03/2014. We calculated relative risks (RR) using Fisher's exact test. Available stool samples of kitchen staff and cases were tested for gastroenteric pathogens and positive isolates finetyped.

Abstract results

Fifty pupils and three teachers completed the questionnaires. Of 37 cases (AR: 70%) 18 were females. Two pupils reported symptoms onset 10/03/2014 and 11/03/2014, all others on 12/03/2014 or 13/03/2014. Eleven cases (30%) reported secondary infections among close family members. We could not identify an association between any of the 98 food items and illness. However, 31/44 pupils (excluding the two early cases) participating in any activity fell ill afterwards compared to 2/6 pupils not participating (RR=2.11; 95%CI: 0.67-6.66; p=0.16). One early case vomited during the activity. Three cases tested positive for Norovirus genotype 1.3 with identical sequences. Kitchen staff tested negative.

Abstract conclusion

Descriptive and microbiological investigations indicate a common source outbreak; analytical epidemiology suggests spread of disease during group activities implicating close contact. Before and during school trips teachers should remind pupils of regular hand-washing, encourage them to notify gastrointestinal symptoms and supervise pupils' hand-washing in case of sickness.

Keywords: Norovirus, person-to-person transmission, youth hostel, Rhineland-Palatinate

PRESENTED BY: Maja George

ESCAIDE REFERENCE NUMBER: 20142205

Vaccine coverage, effectiveness and safety (2)

Decline in invasive meningococcal disease in Ireland: a review of the epidemiology, 1999-2013

Margaret Fitzgerald[1], Piaras O'Lorcain[1], S. Cotter[1], Robert Cunney[2], Darina O'Flanagan[1]

[1] Health Protection Surveillance Centre, Dublin, Ireland; [2] Irish Meningococcal and Meningitis Reference Laboratory, The Children's University Hospital Temple Street, Dublin, Ireland

Abstract

In the late 1990s, the annual incidence of invasive meningococcal disease (IMD) exceeded 12 cases per 100,000 population in Ireland. Serogroup B (SgB) and serogroup C (SgC) accounted for most of the cases (2:1 ratio). In October 2000, the meningococcal C conjugate (MCC) vaccine was introduced. We aimed to review the epidemiology of IMD, to guide vaccination policy.

Abstract methods

We analysed enhanced surveillance data on IMD cases from 1999-2013 and described trends in incidence rates and mortality. We calculated incidence rate ratios (IRR) and 95% confidence intervals (95%CI) using Poisson regression.

Abstract results

Between 1999-2013, 3,330 cases of IMD were notified, 3.9% of whom died. In that period, IMD incidence declined by 88% (IRR=0.12, 95%CI: 0.10-0.16) and the number of IMD deaths fell by 76% (95%CI: 50-93%). Between 1999-2013, SgC and SgB incidence fell by 99% (IRR 0.01, 95%CI: 0.00-0.04) and by 81% (IRR=0.19, 95%CI: 0.15-0.25), respectively. In 2013, SgB and SgC accounted for 93% and 1% of IMD cases, respectively. The highest SgB incidence was in infants aged <1 year (32/100,000), representing 34% of SgB cases. In 2013, there were four IMD deaths (case-fatality=4.9%), all due to SgB, including one death in an infant.

Abstract conclusion

SgC incidence has dramatically declined since the introduction of MCC vaccine. SgB incidence has also been declining, with the highest burden in infants. The recently-licensed meningococcal B vaccine could prevent SgB disease in infants and is being considered for inclusion in the national schedule. However, the current low disease burden may impact negatively on the cost-effectiveness of the vaccine. Continued enhanced surveillance is essential to monitor IMD epidemiology and the impact of current and future vaccines.

Keywords: meningococcal infections, meningococcal C conjugate vaccine, epidemiology, surveillance

PRESENTED BY: Margaret Fitzgerald

ESCAIDE REFERENCE NUMBER: 20142005

Changes in seroprevalence of pneumococcal serotypes during the pre-vaccine era

Annemarijn van Ginkel[1]*, K.E. Elberse*[1]*, Guy Berbers*[1]*, I. Tcherniaeva*[1]*, H.E. de Melker*[1]*, M.J. Knol*[1]

[1] National Institute of Public Health and the Environment (RIVM), The Netherlands

Abstract

Knowledge of natural fluctuations in carriage before the implementation of pneumococcal conjugate vaccines (PCVs) contributes to the understanding of the impact of PCV. Since pneumococcal carriage can elicit an antibody response, seroprevalence indicates that subjects have encountered the serotype at least once. This study investigated differences in concentrations of pneumococcal antibodies between two studies conducted in the pre-vaccine era in the Netherlands.

Abstract methods

Two cross-sectional population-based serosurveillance studies were conducted in the Netherlands in 1995-1996 (N=1780) and 2006-2007 (N=6159). Subjects were aged between 0 and 79 years and donated a blood sample. The pneumococcal IgG antibody concentrations against the 13 serotypes included in the PCV13 vaccine were measured using fluorescent-bead based multiplex assay. To match the Dutch population distribution the geometric mean concentrations (GMCs) were weighted for age, gender, degree of urbanization and ethnicity.

Abstract results

The GMCs were significantly higher in the 2006-2007 study compared to the 1995-1996 study for serotype 1, 6A, 6B, 9V, 18C, 19A, 19F and 23F and lower for serotype 3. The overall differences in GMC between the studies were also found in the different age groups, except for serotypes 3, 7F and 19A. The GMCs were higher in the 1995-1996 study for age groups 5-9, 10-19 and 20-39 years for serotype 3 and 10-19 years for serotype 7F and lower for age group 5-9 years for serotype 19A.

Abstract conclusion

When comparing the IgG concentrations in 1995-1996 with 2006-2007 the IgG concentrations against PCV13 serotypes increased. The differences between serotypes and age groups indicated that the distribution of pneumococcal serotypes is dynamic and not only influenced by vaccination. This is important to consider when studying the impact of PCV implementation.

Keywords: Streptococcus pneumonia, cross-sectional, antibodies, seroepidemiologic studies

PRESENTED BY: Annemarijn van Ginkel

ESCAIDE REFERENCE NUMBER: 20142010

Effect of pneumococcal conjugate vaccines on hospitalisations associated with pneumonia and myringotomy with ventilation tube insertion, Ireland, 2005-2013

Margaret Fitzgerald[1]*, Tara Kelly*[1]*, S. Cotter*[1]*, Robert Cunney*[2]*, Darina O'Flanagan*[1]

[1] Health Protection Surveillance Centre, Dublin, Ireland; [2] Irish Meningococcal and Meningitis Reference Laboratory, The Children's University Hospital Temple Street, Dublin, Ireland

Abstract

In September 2008, Ireland introduced the 7-valent pneumococcal conjugate vaccine (PCV7), which was replaced in December 2010 by the 13-valent vaccine (PCV13). We estimated the effect of PCV7/PCV13 on hospitalisation rates due to (a) all-cause pneumonia and (b) myringotomy with ventilation tube insertion (MVTI).

Abstract methods

We searched the national hospital discharge database to identify hospitalisations with relevant ICD-10 codes between July 2005 and June 2013. We compared hospitalisation rates by age-group in the pre-PCV7 (July 2005-June 2008), post-PCV7 (July 2009-June 2011) and post-PCV13 (July 2011-June 2013) periods. We conducted interrupted time series analysis adjusting for seasonality and secular trend and calculated incidence rate ratios (IRR) and adjusted IRR (aIRR) using negative binomial regression on the monthly hospitalisation rates.

Abstract results

We identified 78,848 pneumonia hospitalisations; 6% in <2 year old children. Compared with pre-PCV7 and before adjusting for trend, pneumonia hospitalisation rates in <2 year old children declined by 33% (IRR=0.67; 95%CI: 0.53-0.85) post-PCV7 and by 47% (IRR=0.53; 95%CI: 0.42-0.67) post-PCV13. Compared with pre-PCV7, trend-adjusted pneumonia hospitalisation rates in this age group did not change (aIRR=1.1; 95%CI: 0.81-1.5 post-PCV7 and aIRR=1.2; 95%CI: 0.75-1.8 post-PCV13). We identified 29,800 MVTI hospitalisations; 89% in <18 year olds. In <2 year old children, compared with pre-PCV7, MVTI hospitalisation rates declined by 36% (aIRR=0.64; 95%CI: 0.53-0.78) post-PCV7 and by 46% (aIRR=0.53; 95%CI: 0.40-0.72) post-PCV13. In 2-17 year olds compared with pre-PCV7, MVTI-hospitalisation rates were stable (aIRR=0.99; 95%CI: 0.86-1.1 post-PCV7 and aIRR=1.1; 95%CI: 0.92-1.4 post-PCV13).

Abstract conclusion

Trend-adjusted time series analysis suggested that PCV7/13 vaccination reduced hospitalisations for MVTI in <2 year old children, but the effect on pneumonia hospitalisations was unclear. Underlying secular trends must be considered when assessing the impact of new vaccines.

Keywords: Streptococcus pneumoniae, pneumococcal vaccines, pneumonia, middle ear ventilation, interrupted time series

PRESENTED BY: Margaret Fitzgerald

ESCAIDE REFERENCE NUMBER: 20142015

Antibody responses to pertussis vaccine antigens in two population-based studies conducted in The Netherlands, 1996 and 2006

Rita De Sousa[1], Gabi Smits[1], Liesbeth Mollema[1], Guy Berbers[1]

[1] National Institute for Public Health and the Environment (RIVM), The Netherlands

Abstract

Whooping cough remains a global health problem. Previous studies in the Dutch population (>9 years of age) showed that the levels of IgG antibodies against pertussis toxin (PT), which are indicative of active or a recent infection in the last 6-12 months (≥ 62.5 EU/ml), doubled from 1996 to 2006.Our aim is to analyse the antibody response profiles to three other B. pertussis antigens: filamentous heamagglutinin (FHA), fimbriae (FIM) and pertectin (PRN), which are associated with the different IgG-PT levels of antibodies analysed in the previously studied population.

Abstract methods

We analysed 2000 serum samples collected in 1996-97 and 6386 in 2006-07 from two population-based cross-sectional studies conducted in the Netherlands. We measured the levels of IgG antibodies against FHA, FIM, and PRN antigens using a fluorescent bead-based multiplex immune assay. Since a cut-off for these antibodies, indicative of a specific infection by B. pertussis, has not yet been established, we compared the levels of these antibodies with other variables by specific age-groups associated with different categories of IgG-PT levels. Kruskal–Wallis and Mann-Whitney tests were used for statistical analysis.

Abstract results

In adolescents and adults there are significant differences in the median antibody levels against FHA, PRN, FIM between the IgG-PT < 20 EU/ml group and the IgG-PT≥62.5 EU/ml group. Higher levels of these antibodies were detected in the IgG-PT≥62.5 group. However, in this group, no statistical differences were found in the median of antibody levels against PT, PRN, FIM and PRN between the persons who had cough versus those who did not have cough. Detailed findings will be discussed.

Abstract conclusion

Understanding how the level of antibodies correlates with infection is crucial to improving vaccination strategies.

Keywords: Bordetella pertussis, antibodies, Pertussis toxin, filamentous heamagglutinin, fimbriae, pertectin

PRESENTED BY: Rita De Sousa

ESCAIDE REFERENCE NUMBER: 20142231

Meningococcal disease among military conscripts in Finland 2003-2012: need to expand immunization programme?

Maija Toropainen[1], Tuula Hannila-Handelberg[2], Markku Kuusi[1], Hanna Nohynek[1], Ilkka Mäkitie[2]

[1] National Institute for Health and Welfare, Finland; [2] Finnish Defence Forces, Centre for Military Medicine, Finland

Abstract

Vaccination against Neisseria meningitidis (meningococcus) in Finland is currently recommended for persons with high-risk medical conditions, travellers to countries with endemic meningococcal disease, and contacts of meningococcal cases. Military recruits receive a compulsory tetravalent ACYW polysaccharide vaccine when entering service. We assessed the disease burden of invasive meningococcal disease (IMD) among military conscripts in Finland during a non-epidemic period in 2003-2012.

Abstract methods

Cases with ICD-10 diagnoses compatible with IMD in 2003–2012 were identified from electronic register of the Finnish Defence Forces and used for estimation of IMD rates among conscripts. Case validation was done by reviewing individual case histories and comparing data on isolated organism to data in the National Infectious Disease Register (NIDR). For comparison, data were retrieved from the NIDR to calculate the IMD rates among age and calendar year matched cohorts.

Abstract results

In 2003–2012, a total of 29 IMD cases occurred among conscripts. The average age of onset was 19.3 years (range 19–21 years). The mean annual incidence of IMD was 17 (5.1-29) per 100,000 population, compared to 2.7 (1.5-3.7) among all 18-21 year olds. All culture confirmed cases (28/29; 97%) were caused by serogroup B. In 1993-2012, five deaths occurred with an annual death rate of 1.4 (0-6) per 100,000 person years.

Abstract conclusion

Despite the use of tetravalent polysaccharide vaccine, IMD continues to cause significant disease burden among military conscripts in Finland. Since most cases were caused by serogroup B, conscripts could benefit from vaccination with the recently approved, protein based meningococcal vaccine targeted against serogroup B.

Keywords: Neisseria meningitidis, meningococcus, vaccination, military conscripts

PRESENTED BY: Maija Toropainen

ESCAIDE REFERENCE NUMBER: 20142039

Serogroups B, W-135 and Y Invasive Meningococcal Disease in Canada, 2002-2011

Yuanyuan Anita Li[1]*, Heather Deehan*[1]

[1] Public Health Agency of Canada, Canada

Abstract

Following the implementation of routine childhood immunization programs and various catch-up programs with monovalent meningococcal C conjugate vaccines in Canada, the incidence rate of Serogroup C invasive meningococcal disease (IMD) is now at an all-time low, and serogroups B, W-135 and Y are now most commonly reported. The purpose of this study is to analyse the trend of IMD caused by serogroup B, W-135 and Y in Canada from 2002 to 2011.

Abstract methods

IMD data was obtained from the national Enhanced Invasive Meningococcal Disease Surveillance System. National population estimates were obtained from Statistics Canada. Incidence rates (IRs) were calculated per 100,000 population. Multivariate Poisson regressions were used to estimate the incidence rate ratios (IRRs).

Abstract results

During the study period, the IR ranges of IMD serogroups B, W-135 and Y were 0.26-0.40, 0.02-0.05, and 0.07-0.12, respectively. The overall IRRs of serogroups B, W-135 and Y were 1.01 (CI: 0.99-1.04, p=0.18), 0.98 (CI: 0.94-1.02, p=0.25) and 0.96 (CI: 0.90-1.02, p=0.16), respectively. Among individuals at 60 years and over, the IRs of serogroup W-135 and Y decreased 9% (IRR=0.91, CI: 0.84-0.99, p=0.02) and 7% (IRR=0.93, CI: 0.88-0.98, p=0.006) each year, respectively.

Abstract conclusion

The overall trends of IMD serogroups B, Y and W-135 did not change significantly over the study period. The decreasing trends of IMD caused by W-135 and Y among the elderly in Canada are different than what has been reported in other countries. Further research is needed to better understand the pattern of IMD to inform public health policy and immunization programs.

Keywords: Epidemiology, Neisseria meningitidis, Meningitis, Meningococcal, Canada,

PRESENTED BY: Anita Li

ESCAIDE REFERENCE NUMBER: 20142137

Surveillance (1)

Evaluation of the sentinel practitioner's network in Reunion Island, 2005-2012

Elise Brottet[1]*, Harimahefa Razafimandimby*[2]*, Laurent Filleul*[1]

[1] French Institute for Public Health Surveillance, Reunion, France; [2] Ministry of Health, Madagascar

Abstract

The sentinel general practitioner's (SGP) surveillance network in Reunion Island was set up in 1996. Sixty SGPs distributed across the Island report weekly influenza, gastroenteritis, chickenpox and dengue-like syndromes to the regional office of the French Institute for Public Health Surveillance in order to detect and monitor seasonal outbreaks and influenza viruses circulating, and guide public health measures. We evaluated the surveillance system in order to assess its performance and propose improvements.

Abstract methods

We used the CDC guidelines for evaluating public health surveillance systems. We focused the evaluation on influenza surveillance for the 2005-2012 period. We sent a standardized questionnaire to participating SGPs and all recipients of the feedback. To assess sensitivity, specificity and positive predictive value (PPV), we built a gold standard based on virological and hospital emergency departments surveillance data.

Abstract results

The proportion of SGP weekly participation was 76%. Participating SGPs represented 5.4% of all GPs registered on the island. SGPs thought that the reporting forms are easy to fill. We estimated sensibility, specificity and PPV to be 100.0%, 91.1% and 48.3% respectively. Virological surveillance provided information on the circulating types of influenza viruses, contributing to the vaccination campaign strategy. The network proved useful when it was mobilized during the 2005 chikungunya outbreak.

Abstract conclusion

The SGP network is an essential tool for influenza and public health surveillance in Reunion Island. Our results suggest that it is useful, simple, flexible, acceptable and stable. It detects outbreaks, monitor and quantify their impact. Our evaluation suggests that it will benefit from a new recruitment campaign among GPs to improve representativeness, and from the use of a statistical epidemic threshold to improve timeliness of outbreak detection and response.

Keywords: valuation, Sentinel surveillance, Sensitivity and Specificity, Influenza, General Practitioners, Reunion Island

PRESENTED BY: Elise Brottet

ESCAIDE REFERENCE NUMBER: 20141930

Trends and epidemiological patterns of hepatitis E infections in Hungary, 2002-2013

Agnes Feher[1], Ágnes Csohán[1]

[1] National Center for Epidemiology, Hungary

Abstract

Before 2002, acute viral hepatitis E was rarely diagnosed in Hungary. We described trends and epidemiological features of reported hepatitis E cases in Hungary between 2002 and 2013.

Abstract methods

We analyzed aggregated data from the national communicable disease and laboratory registers. We defined cases as persons with acute hepatitis and anti-HEV IgM. We calculated rates using census data and analyzed by time, place and person. We examined trends using Poisson regression and compared 2002-2007 with 2008-2013 in terms of morbidity and seasonal patterns.

Abstract results

In 2002-2013, 456 hepatitis E cases were reported (mean age: 54 years, range: 5-90 years, 62% males, 70% hospitalized and 1.1% deaths). Reported rates per million increased from 1 in 2002 to 9 in 2013. The annual trend increased (incidence rate ratio=1.3; 95% confidence interval: 1.2-3.4). Highest rates were among 60-69 years old (3.3/million) in 2002-2007 and among 50-59 years old (15.1/million) in 2008-2013. Rates differed across counties (median: 0.93/million, range: 0.18-3.1/million). An average number of counties reporting cases was 6 between 2002-2007 and 16 between 2008-2013. The number of regional laboratories performing HEV serological tests increased from 2 in 2002-2007 to 5 in 2008-2013.

Abstract conclusion

During 2002-2013 reported rates of hepatitis E virus increased continuously and significantly. The highest rates were among elderly. Future surveillance efforts will require uniform capacity to diagnose in the laboratory and to collect information on risk factors. We also need to determine how the increased laboratory capacity may have accounted for some of the increase in hepatitis E diagnoses.

Keywords: Hepatitis E, retrospective descriptive analyses, morbidity, epidemiological trends

PRESENTED BY: Agnes Feher

ESCAIDE REFERENCE NUMBER: 20141964

Seroepidemiology in Foodborne Campylobacter Infections

Kåre Mølbak[1]

[1] Statens Serum Institut, Denmark

Abstract

Measuring incidence of foodborne campylobacter infections is affected by biases inherent in passive laboratory surveillance as reflected in the surveillance pyramid. The attributes of the surveillance pyramid are different in different countries and therefore it is often misleading to compare reported figures of culture confirmed cases between countries. To overcome this problem, we hypothesized that seroepidemiologic methods could provide a stringent approach to measure the force of infections in humans, and be used as a tool to measure the impact of control activities in the poultry production on human incidence.

Abstract methods

We developed a mathematical model that enabled a backcalculation of the annual seroincidence from measurements of specific antibodies (IgG, IgA, IgM), and applied this model to about 7,500 serum samples collected from populations in 11 different European countries.

Abstract results

Only a two-fold difference was observed: Greece had the lowest seroincidence (0.55 infections per year) and Poland the highest (1.11 infections per year). There was an inverse correlation with the reported national incidence of campylobacter infections in humans (p=0.008), and the data did not correlate with prevalence data of campylobacter in broilers. Seroincidence tended to correlate with Swedish figures of country-specific risk of travel-associated campylobacter infections (p=0.089).

Abstract conclusion

The finding of no correlation between campylobacter seroincidence and prevalence of contaminated broiler carcasses in the corresponding countries indicates that seroepidemiology is not suitable to address the impact of control activities of campylobacter aimed at the poultry reservoir. These data challenge our current understanding of the epidemiology of campylobacteriosis.

Keywords: Campylobacter, seroepidemiology, humans, poultry

PRESENTED BY: Kåre Mølbak

ESCAIDE REFERENCE NUMBER: 20142068

Latvia needs to strengthen its surveillance of acute flaccid paralysis to ensure its polio-free status

Ieva Kantsone[1], Irina Lucenko[1], Jurijs Perevoscikovs[1], Dzintars Mozgis[1]

[1] Centre for Disease Prevention and Control, Latvia

Abstract

In 1998, Latvia implemented acute flaccid paralysis (AFP) surveillance to certify its polio-free status and detect eventual wild poliovirus re-introduction. Until 2008, AFP surveillance was active and passive, since 2009 it was passive only. We assessed Latvia's AFP surveillance against key WHO-developed performance indicators to identify areas for improvement.

Abstract methods

We analysed all AFP cases notified during 1998 – 2013. We calculated the annual AFP detection rate by dividing the number of notified AFP cases by the population of children 1/100 000 children. We calculated the proportion of cases for which two stool samples were collected at least 24 hours apart, within 14 days after AFP onset (expected ≥80%), and the proportion of stool specimens from which non-polio enterovirus was isolated.

Abstract results

From 1998 to 2013, physicians reported 60 AFP cases (mean age 8.4 years). Expected AFP detection rate wasn't achieved the recent three years and some years before and ranged between 0.34 in 2011 and 2.33 in 2010. In 72% of cases, two stool samples were collected 24 hours apart within 14 days of symptom onset. The National Microbiology Reference laboratory investigated all (100%) specimens virologically. No polioviruses were found. Non-polio enteroviruses were isolated only in three specimens.

Abstract conclusion

Although AFP cases were detected each year, Latvia needs to improve AFP detection rates to maintain its polio-free status and detect possible re-introduction of wild poliovirus from several African and Middle-Eastern countries. We will carry out systematic explanatory work with health professionals, pointing out the importance of AFP surveillance, especially since the recent re-emergence of polio. We recommend a detailed evaluation of the system to identify gaps in AFP ascertainment, reporting and timely investigation.

Keywords: Acute flaccid paralysis, surveillance, poliovirus

PRESENTED BY: Ieva Kantsone

ESCAIDE REFERENCE NUMBER: 20142257

Stool screening for wild polio viruses (WPV) among Syrian refugees and asylum seekers, Germany, 2013/2014

Katrin Neubauer[1], Sindy Boettcher[2], Armin Baillot[3], Gabriele Rieder[4], Maja Adam[5], Konrad Beyrer[6], Gerhard Falkenhorst[1], Sabine Diedrich[2]

[1] Department for Infectious Diseases, Robert Koch Institute, Berlin, Germany; [2] Robert Koch Institute (RKI), Berlin, Germany; [3] Governmental Institute of Public Health of Lower Saxony (NLGA), Hannover, Germany; [4] Bavarian Health and Food Safety Authority (LGL), Oberschleissheim, Germany; [5] Governmental Institute of Public Health of Baden-Wuerttemberg (LGA), Stuttgart, Germany; [6] Governmental Institute of Public Health of Lower Saxony (NLGA), Hannover, Germany; Chair of German National Certification Commission for Poliomyelitis Eradication (NCC), Germany

Abstract

In Germany, proof of polio free status is based on enterovirus (EV) surveillance. In response to the WPV outbreak in Syria 2013 and high number of refugees coming from Syria to Germany, on 01/11/2013 RKI additionally advised stool screening for EV of asymptomatic Syrian refugees/asylum seekers aged <3 years. Furthermore, the necessity of polio (IPV) vaccination for all residents and staff of asylum seeker reception centres and shelters (RC/S) was re-emphasized.

Abstract methods

Enterovirus (including PV) diagnostic of stool samples was performed at the National and WHO Reference Laboratory for Poliomyelitis and Enteroviruses at RKI (NL/RRL) and three labs of the established German EV-laboratory network using molecular and virological methods. Characterization of EV-positive samples as well as differentiation between vaccine and wild PV was performed at the NL/RRL.

Abstract results

Labs received samples from more than 100 RC/S and public health offices from all 16 German federal states. From Nov 2013 to Apr 2014, stool samples from 629 Syrians were tested. Of these, 92 (14.6%) were EV-positive. Vaccine like PV strains were detected in 12 persons indicating a recent polio (OPV) immunization. WPV were not identified.

Abstract conclusion

Results of stool screening indicated a very low risk for WPV importation by Syrian refugees and asylum seekers during a period of six months. Due to OPV vaccination campaigns implemented in Syria and neighbouring countries presence of vaccine like polioviruses in arriving asylum seekers/refugees was expected. Assessment of stool surveillance demonstrated that an immediate and sound response by German NCC and RKI due to an urgent situation as well as a good cross-functional cooperation between RKI, public health authorities and services, lab network and RC/S staff is feasible.

Keywords: Polio, surveillance, refugees, Syria, Germany

PRESENTED BY: Katrin Neubauer

ESCAIDE REFERENCE NUMBER: 20142245

A two-year active surveillance of community-acquired pneumonia among adults >64 years old, Puglia region, Italy: ad interim analysis, January 2013 – February 2014

Vanessa Cozza[1], Francesca Fortunato[2], Maria Giovanna Cappelli[3], Anna Sallustio[3], Maria Chironna[3], Domenico Martinelli[4], Rosa Prato[1]

[1] Sector of Hygiene, Department of Medical and Surgical Sciences, University of Foggia, Foggia, Italy; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Sweden; [2] Sector of Hygiene, Department of Medical and Surgical Sciences, University of Foggia, Italy; [3] Department of Biomedical Sciences and Human Oncology, University of Bari, Italy; [4] Sector of Hygiene, Department of Medical and Surgical Sciences, University of Foggia, Italy

Abstract

Worldwide, Streptococcus pneumoniae is the most commonly identified cause of community-acquired pneumonia (CAP) among the elderly. Little is known about the burden of CAP in Italy. Starting 2000, Puglia recommended the 23-valent pneumococcal polysaccharide vaccine (PPV23) to adults aged >64 years; in 2011, 13-valent conjugate vaccine (PCV13) was also introduced. By August 2013, the overall vaccination coverage in this age groupwas 10%. We investigated the epidemiology of CAP in Puglia in order to assess the potential impact of increasing pneumococcal vaccination coverage on CAP incidence among the elderly.

Abstract methods

In January 2013, we implemented a two-year active sentinel surveillance among a convenient sample of thirty GPs and pneumologists region-wide to identify residents in Puglia aged >64 years with suspected CAP. For each case, physicians collected informed consent, clinical information, medical and vaccination history (web-based form), nasopharyngeal swabs, sputum and/or blood specimens. Specimens were tested by PCR. We calculated frequencies in an ad interim analysis after 14 months of data collection.

Abstract results

We identified 115 CAP cases between January 2013-February 2014 (65-96 years; median 79 years; 60% males); 41 (36%) were vaccinated with PPV23 and 11 (10%) with PCV13; 53 (46%) had one or more risk factors for developing pneumonia and 101 (88%) had one or more comorbidities. Blood and/or sputum were collected for 102 CAP cases; of these, 38 (37%) were positive for S. pneumoniae and 15 (15%) for Haemophilus influenzae. PCV13 contained serotypes were detected in 31 (82%) of S. pneumoniae positive samples.

Abstract conclusion

S. pneumoniae was the most frequently identified pathogen in CAP cases. The high proportion of vaccine-contained serotypes demonstrates the potential impact of increasing PCV13 vaccination coverage in this age group.

Keywords: Community Acquired Infections, Pneumonia, sentinel surveillance, Streptococcus pneumoniae, pneumococcal vaccines

PRESENTED BY: Vanessa Cozza

ESCAIDE REFERENCE NUMBER: 20141970

Poster Session C 14.50 – 15.50 Fri 7

Influenza & influenza vaccination (2)

Estimates of influenza vaccine effectiveness in Hungary, 2013-14: as part of a multi-centre European case control study (I-MOVE)

Judit Krisztina Horvath[1], Péter Dancs[1], Annamária Ferenczi[1], Beatrix Oroszi[1], Eva Herczeg[2]

[1] Office of the Chief Medical Officer, Hungary; [2] National Centre for Epidemiology, Hungary

Abstract

The reformulation of influenza vaccine is considered yearly to ensure its closest possible match with circulating influenza strains. Influenza vaccine effectiveness (IVE) needs to be measured annually. We conducted case control studies to estimate IVE in 2013-14 in Hungary in the 18+ population as part of the European I-MOVE (Monitoring of IVE) project.

Abstract methods

General practitioners contributing to sentinel influenza surveillance in Hungary interviewed and collected swabs from a systematic sample of patients presenting with influenza-like illness (ILI). Cases are ILI patients laboratory-confirmed by reverse transcription polymerase chain reaction (PCR) as influenza. Controls are those who tested negative for influenza. The outcome of interest is medically attended, laboratory confirmed influenza. Influenza vaccination is defined as having received one dose influenza vaccine more than 14 days before onset of symptoms. IVE is estimated as 1-odds ratio. Logistic regression is used to adjust for possible confounding factors.

Abstract results

During the study period (between 13 January and 27 April 2014), influenza was detected by PCR in 86/349 (24.6%) participants. Six (7.0%) cases had received vaccination against seasonal influenza more than 14 days before the date of symptom onset, compared with 40/263 (15.2%) controls. All were vaccinated with adjuvanted trivalent vaccine containing inactivated whole virus, licensed in Hungary. The adjusted IVE was 69.8% (95% confidence int **l, case control studies**

PRESENTED BY: Judit Krisztina Horvath

ESCAIDE REFERENCE NUMBER: 20142073

Seasonal Influensa Vaccine Effectivness 2011-2014: A Population Cohort Analysis from 2.3 Million Individuals in Stockholm County

Amy Leval[1], Maria-Pia Hergens[1], Karin Persson[1], Åke Örtqvist[1]

[1] Department of Communicable Disease Control and Prevention, Stockholm County, Sweden

Abstract

In Stockholm County, seasonal influenza vaccination is recommended and available at no individual out-of-pocket costs to those over age 65, or to younger individuals with certain underlying risk profiles. Estimates of seasonal influenza vaccine effectiveness (VE) are important for determining future vaccination policies and programs, preferably from several seasons since the effectiveness varies substantially between years. In addition, analysis during a specific influenza season may permit early detection of vaccine failure due to a poor virus-vaccine match.

Abstract methods

All individuals living in Stockholm County as of October 1st of the 2011-2012, 2012-2013 and 2013-2014 season were included. Vaccination status was obtained from Stockholm's vaccine register. Main influenza outcome variables (ICD-10 codes J09-J11) and comorbidities were obtained from in-patient, out-patient and primary care databases. VE was assessed with seasonal vaccination as a time-varying exposure using Cox multivariate analyses adjusting for age, sex, comorbidity status and previous flu vaccinations including the pandemic influenza A (H1N1) pdm09 vaccine (Pandemrix®).

Abstract results

For those vaccinated for the 2011-2012 season, hazard ratio (HR) for influenza inpatient and outpatient care was 0.86 (95% CI 0.74-1.01) compared to unvaccinated. For those vaccinated for the 2012-2013 season, HR were 0.56 (95% CI 0.41-0.77) for influenza inpatient and outpatient care compared to unvaccinated. Preliminary analyses for the 2013-2014 season show a HR of 0.66 (95% CI 0.49-0.88) for inpatient and outpatient care compared to unvaccinated.

Abstract conclusion

In 2012-2013 and 2013-2014, seasonal influenza vaccination provided substantial protective effects on hospitalization for influenza and outpatient care whereas significant VE were not found in the 2011-2012 season.

Keywords: Vaccine effectiveness, seasonal influenza, cohort study

PRESENTED BY: Maria-Pia Hergens

ESCAIDE REFERENCE NUMBER: 20142093

The attitudes of health care workers towards seasonal influenza vaccination for programming an effective communication campaign: the experience of a tertiary referral paediatric hospital, Italy, 2013-2014

Vanessa Cozza[1], Valeria Alfonsi[2], Maria Cristina Rota[2], Marta Luisa Ciofi degli Atti[3],

[1] Sector of Hygiene, Department of Medical and Surgical Sciences, University of Foggia, Italy; [2] Istituto Superiore di Sanità (ISS), National Centre for Epidemiology Surveillance and Health Promotion, Rome, Italy; [3] Clinical Epidemiology Unit, Medical Direction, Bambino Gesù Children's Hospital, Rome, Italy

Abstract

Despite recommendations for seasonal influenza vaccine for health care workers (HCWs), the paediatric hospital observed a progressive decline in vaccine uptake among HCWs over the last three years. In October 2013, we started a communication campaign for vaccine promotion using information leaflets, posters and an intranet web-banner. Free-of-charge vaccination was offered to HCWs at the hospital. In December 2013, we investigated HCWs' attitudes towards influenza vaccination and their opinion regarding the campaign.

Abstract methods

We performed a cross-sectional survey in a random sample of non-critical inpatient units (7/33), and five intensive care units. We surveyed physicians, nurses and other HCWs via an anonymous self-administered questionnaire on their socio-demographic and professional characteristics, vaccination history, attitudes towards and uptake of influenza vaccine, and their opinion regarding the campaign. We used odds ratios (ORs) with 95% confidence intervals (95%CI) to compare vaccine uptake and access to communication tools among HCWs.

Abstract results

Overall, 191 HCWs responded. Sixty-eight (36%) had at least one influenza vaccination during their life; 49 (72%) between 2008-2011. Physicians were 2.3 times more likely to have received vaccination (95%CI=1.1-4.9) compared to other HCWs. Patient protection was the main reason for vaccination (34%); considering influenza a mild disease was the main reason for non-vaccination (37%). Overall, 75% saw at least one communication tool; of these, 66% found the information useful. Compared to nurses and physicians, other HCWs were more likely not to have seen any tools (OR=2.4; 95%CI=1.1-5.5).

Abstract conclusion

Misperceptions about severity of influenza was the main reason for non-vaccination. We recommend developing targeted information on influenza and implementing strategies that make communication tools more visible to a wider audience. Future studies are needed to measure their impact on vaccination uptake.

Keywords: Cross-sectional studies, Influenza vaccines, health personnel, Attitude

PRESENTED BY: Vanessa Cozza

ESCAIDE REFERENCE NUMBER: 20142168

Evolution of Adverse Reactions to the Influenza Vaccination in Health Personnel in the Period 2006-2013

Malika El Attabi[1], José L. Carretero-Ares[1], CO. Villanueva-Ruiz[1], E. Javier Silva-Contreras[1], Isidra Tenza-Iglesias[1], Jóse L. Mendoza-García[1], Vicente García-Román[1], José Sánchez Payá[1]

[1] Hospital General Universitario de Alicante, Spain

Abstract

Adverse reactions (AR), avoidance of medication and rely on own defenses are the most frequent reasons of health personnel (HP) for refusing flu vaccination, hence the importance of monitoring. The aim of this work is to study the frequency and type of AR to influenza vaccination in HP during 2006-2013.

Abstract methods

Serial cohort study in HP immunized against flu during vaccination campaigns 2006-2007 to 2013-2014. To detect AR, a nurse telephoned every worker (five times, if necessary) a week after vaccination and asked about emergence of local pain, malaise, myalgia, fever or other AR (scored as an open answer) appeared within three days after vaccination. Frequency of each AR, and the overall, were calculated for every campaign. Chi-square test was used to study the association between campaign and emergence of AR.

Abstract results

We evaluated AR in 81.2% of HP. There were not statistical differences in age, sex and job class between HP evaluated and non evaluated. Frequency of AR ranged from 24.7% (2013-1014) to 80.5% (2009-2010 pandemic). Pain, from 15.8% (2009-2010, seasonal) to 74.6% (2009-2010, pandemic); fever, from 0.8% (2012-2013) to 5.9% (2009-2010, pandemic); general discomfort, from 4.7% (2009-2010, seasonal) to 21.5% (2009-2010); myalgia, from 1.3% (2008-2009) to 15.1% (2009-2010, pandemic); other, from 2% (2013-2014) to 16.5% (2009-2010, pandemic).

Abstract conclusion

Frequency of AR to influenza vaccination in HP (25-30%) remained stable throughout the studied period (apart from pandemic 2009-2010 influenza season, when the frequency was significantly higher), being the most common AR pain in the injection site. All AR were mild. Given the frequency and characteristics of the AR, this should not be a reason to justify the refusal of influenza vaccination among HP.

Keywords: Influenza, Health Personnel, Vaccination, Adverse Reactions

PRESENTED BY: José Sánchez Payá

ESCAIDE REFERENCE NUMBER: 20142200

Influenza Outbreaks in Long-term Care Facilities during the 2013/2014 Influenza season in the Health Service Executive (HSE) East region of Ireland: a prospective study.

Lois O Connor[1], Mairin Boland[1], Helen Murphy[1], Elizabeth Montague[1]

[1] Health, HSE East, Dr Steevens, Dublin 8, Ireland

Abstract

Influenza outbreaks are a major cause of morbidity and mortality among residents of long-term care facilities (LTCFs). Atypical presentations and reduced vaccine response are complicating factors. We describe epidemiological features and challenges in managing outbreaks of influenza in LTCFs in the HSE East region (population 1.4 million) during the 2013/2014 season.

Abstract methods

An email questionnaire was sent to each LTCF (n=28) reporting an outbreak of influenza in the 2013/2014 influenza season and was supplemented with input from the relevant public health infection control nurse and specialist. Telephone follow-up enhanced completion rate.

Abstract results

There was a 78.57% response rate. Fifteen(68.20%) of respondents advised that they were prepared for an influenza outbreak. Most (n=14,63.6%) outbreaks were due to Influenza AH3. Outbreaks lasted on average 19 days. Mean number of cases was 18 (range 4-37) with mean attack rates of 34.46% and 9.22% in clients and staff respectively. Anti-viral medication was used in 18 (81.80%) of outbreaks. In total 399 clients and staff had influenza-like illness. Overall 29 (7.27%) of cases required hospitalisation and 10(2.51%) deaths occurred. Prior to the outbreaks mean vaccination rates were 90.34% in clients and 40.78% in staff. Challenges identified by LTCFs included case isolation, visitor restriction difficulties and educating staff on infection control measures including influenza vaccination. Difficulties faced by public health included late notification of outbreaks, low staff vaccination rates, anti-viral non-availability and prescribing variations.

Abstract conclusion

Influenza outbreaks occur in LTCFs on an annual basis despite facility preparation, high client vaccination rates and staff vaccination rates approaching the current HSE target of 40%. Identified challenges include improving staff vaccination rates and managing anti-viral prescribing processes.

Keywords: Influenza, human, Disease outbreaks, Infection control, Influenza vaccine, Long term care

PRESENTED BY: Lois O Connor

ESCAIDE REFERENCE NUMBER: 20142099

Distribution of influenza virus types and subtypes during summer is associated with the distribution during upcoming winter season, EU/EEA, 2005-2014

Eeva Broberg Broberg[1], Chantal Quinten[2], Cornelia Adlhoch[3], Phillip Zucs[2]

[1] European Influenza Surveillance Network (EISN), Sweden; [2] European Centre for Disease Prevention and Control, Sweden; [3] ECDC, Sweden

Abstract

Distribution of influenza subtypes varies every influenza season and different subtypes have different impact on the population. Little is known about how the circulation between seasons relates to the upcoming winter season.

Abstract methods

Sentinel and non-sentinel influenza virological surveillance data reported to The European Surveillance System from all EU/EEA countries during 2005-2014 were analysed. We assessed the association of A(H1), A(H3) and B virus-specific proportions of interseasonaldetections (weeks 21-39) with those of the upcoming seasons (week 40-week 20) by (sub) type, surveillance system and period (interseason-season cycle), using analysis of variance (ANOVA) with nine cycles. The level of significant association was set at $p>0.05$.

Abstract results

The proportion of influenza detections varied by (sub)type across the nine periods, being highest for the A(H1) subtype during the 2009 influenza pandemic with 93% of all samples studied during the 2009 interseason and 73% during the season 2009-2010. The A(H3) detections were at their lowest during the 2009-2010 season (<1%) and highest during the 2011-2012 season (67%). The highest proportion of influenza B was observed in the interseason 2005 (96%). For all (sub) types detected through sentinel surveillance, there was a statistically significant association between the interseason and the upcoming season proportion ($p>0.05$), when removing the 2009 influenza A(H1N1) pandemic. The association was evident also for A(H1) and A(H3) in the non-sentinel detections.

Abstract conclusion

The virological influenza detection data reported in 2005-2014 in Europe suggest that influenza A(H1), A(H3) and B virus circulation during the interseasons is associated with the distribution of (sub)types circulating in the forthcoming influenza season. With a deeper interseason knowledge, an early assessment of the season may be possible for mitigation of the impact by vaccination and communication campaigns.

Keywords: Influenza, surveillance, infection, epidemic

PRESENTED BY: Eeva Broberg

ESCAIDE REFERENCE NUMBER: 20142140

Intervention studies in public health

Determinants of non-response in infectious disease public health programmes in primary health care – HCV screening in the general population

Natalia Parda[1], Małgorzata Stępień[1], Magdalena Rosinska[1]

[1] National Institute of Public Health – National Institute of Hygiene, Poland

Abstract

Considering the widespread prevalence of HCV infections in Poland, there is a need for screening in general population in addition to programmes targeting high-risk groups. We analysed preliminary data on implementation of HCV screening in primary health care units (PHCUs) to determine individual and unit-based factors associated with participation refusal.

Abstract methods

We analysed the dataset of invitations to ongoing HCV screening programme in 52 randomly selected PHCUs. Each unit performed systematic sampling from the list of registered adult patients. We used multivariable logistic regression in STATA 13.1 with refusal as the outcome variable and patients demographic, unit size, staff workload, private/public ownership and unit's prior experience in prevention programmes as predictors.

Abstract results

A total of 17,144 individuals were contacted in March 2013 – April 2014, of whom 15,121 (88.2%) agreed to participate in the study. Male gender (adjusted odds ratio, AOR 1.9 95%CI 1.6 – 2.2), age 5000 patients registered (AOR 4.9, 3.9-6.1) and those who have participated in public health programmes (AOR 2.0, 1.4-3.0). Dedicating over 5h/week to the programme was associated with reduced refusal rate (AOR 0.39, 0.33-0.46) contrary to the number of staff involved which remained statistically insignificant.

Abstract conclusion

Refusal rate was particularly low in small, public units located in countryside, which may suggest better contact between the staff and the patients there. The increased risk of refusal in PCHUs, which conducted other public health programmes indicates the need to coordinate between programmes to avoid patients' tiredness.

Keywords: HCV infection, screening, primary health care, refusal, Poland

PRESENTED BY: Magdalena Rosinska

ESCAIDE REFERENCE NUMBER: 20142255

Survey of Knowledge, Attitude and Practice (KAP) on anthrax in Gakh – Azerbaijan 2012

Etibar Zeynalov[1], Mariam (Marika) Geleishvili[1], Tom Rush [2] Ed Maes[3]

[1] State Veterinary Services of Azerbaijan, Azerbaijan; [2] SC-FELTP, UK; [3] Centre of Diseases Control , United States; [4] CDC/CGH/DGHPWD, United States

Abstract

Anthrax is a serious zoonotic disease. 14 confirmed and probable cases among humans and 1 case among cattle were reported in August and September in the Gakh region of Azerbaijan. We conducted a cross-sectional survey of Knowledge, Attitude and Practice on anthrax.

Abstract methods

Design of study: cross-sectional, sampling with the probability proportional to the size of population. Data collection: structured questionnaire and analysis using EpiInfo 3.5.

Abstract results

560 households were involved. Out of those interviewed men made up 253 (45.3%), 117 (24.2%) had >12 years education. 385 (69.9%) people kept animals, 370 (69.4%) were directly involved in animals handling. 333 (88.6%) of 385 animals were vaccinated. 309 (92.8%) of 333 were vaccinated against anthrax. The veterinary service was available for 368 (96.8%) from 380 and a regularly visiting veterinarian was available to 47 (12.2%) out of 385. 182 persons from 390 used some form of personal protection equipment (PPE) during the slaughtering process. 168 (30.3%) from 555 respondents stated: "I know something about anthrax". The knowledge among men was higher, than among women (RR=1.35 95%CI 1.05-1.74). With regard to animal keepers, almost no difference was found in KAP between groups (RR=1.1). Knowledge in the group with higher education (> 12 years) was 2.2 times higher than in group with < 12 years of education (RR=2.25 95%CI 1.76-2.88). 93 people (16% of respondents) declared they knew the clinical symptoms of anthrax, and 55% reported "knowing" something about anthrax (not statistically significant).

Abstract conclusion

On the basis of the conducted work and data analysis, it was decided to make recommendations on increasing the awareness of the population concerning anthrax and to create a notification system through the public health services.

Keywords: Anthrax, cross-sectional, public health, KAP,

PRESENTED BY: Etibar Zeynalov

ESCAIDE REFERENCE NUMBER: 20142029

Health Assessment Survey of Selected Evacuation Centers and Health Facilities in Affected Areas Post Typhoon Haiyan – November, 2013

Ruth Alma Ramos[1], Vikki Carr De Los Reyes[1], Enrique Tayag [1], Ma Nemia Sucaldito[2]

[1] FETP-Philippines, Philippines (FETP-Philippines, Philippines); [2] Department of Health Philippines, Philippines (FETP Philippines, Philippines)

Abstract

Typhoon Haiyan was an exceptionally powerful tropical cyclone that has devastated the Philippines. The deadliest typhoon on record it has caused thousands of deaths, catastrophic destruction and many have been left homeless in the Visayas Region. A team from the National Epidemiology Center- Department of Health was sent to conduct Rapid Health Assessment Survey (RHAS) of evacuation centers and health facilities.

Abstract methods

A descriptive study was done. Evacuation centers were assessed on the following information: environmental sanitation, drinking water, food supply source, medical services, essential medicines, problems encountered and recommendations. Health facilities were assessed as to its functionality, human resource and existing surveillance. Key informant interviews were conducted.

Abstract results

Twenty evacuation centers with 2,785 families displaced have been surveyed. Of these 10 (50%) were in Tacloban City; 6 (30%) in Leyte Province, 3 (15%) in Western Samar and 1(5%) in Eastern Samar. All do not have a standby medical team. Majority (17, 85%) were not provided mental health and psychosocial services. Majority (17, 85%) do not have vector control activities. Immunization on measles and OPV were started in only thirteen (65%) evacuation centers. Immediate needs identified were additional toilets, medicines, beddings, hygiene kits and family planning kits.Seventeen health facilities were surveyed (11 Rural Health Units and 6 hospitals). Six (30%) of these facilities were totally damaged, however, all (100%) were functional because of assistance from local and international health partners.

Abstract conclusion

The need to address the immediate environmental sanitation in evacuation centers should be attended. Standby medical teams should be formed that will provide the needed mental/psycho-social support and health services. Health facilities were damaged hence immediate rehabilitation and clean-up drive should be done.

Keywords: Tropical Cyclone, Evacuation Centers, Risk Health Assessment Survey, displaced families

PRESENTED BY: Ruth Alma Ramos

ESCAIDE REFERENCE NUMBER: 20142195

Health Protection Surveillance during a summer of Mass Gatherings: The 2013 Experience in Northern Ireland

Naomh Gallagher[1], Anne Wilson[1], Brian Smyth[1], Lewis Shilliday[1], Jillian Johnston[1], Gillian Smith[2], Alex Elliot[2], Helen Hughes[2], Roger Morbey[2]

[1] Public Health Agency, Northern Ireland, UK; [2] Real-time Syndromic Surveillance Team, Public Health England, UK

Abstract

In the summer of 2013 Northern Ireland was presented with a unique major event planning opportunity; three major events of international significance – the G8 Summit, the World Police and Fire Games, and the All-Ireland Fleadh – were hosted over a two month period. Systems of enhanced health protection surveillance were established within tight time constraints, with the aim of minimising potential threats and ensuring vigilance of health protection issues.

Abstract methods

Both new and established surveillance systems were utilised during this period, loosely following the lead from the 2012 Olympic Games. Systems used included routine health protection surveillance, surveillance of event and location-specific incidents, international surveillance, and emergency department syndromic surveillance (EDSSS). The latter was developed in conjunction with colleagues at Public Health England, and was the first time such a system had been introduced in NI.

Abstract results

Daily health protection SitReps were completed using the systems described above and sent to internal and external partners. A detailed risk assessment process was completed daily, with any emerging issues flagged and appropriately actioned. The EDSSS provided real time syndromic information for 30 diagnostic codes, whilst remaining a passive system that presented no increased burden on the health service. Throughout the period there were a number of issues requiring action, however no serious incidents related to the major events occurred.

Abstract conclusion

The system of enhanced surveillance was successful in both development and utility, primarily due to the strength of inter-organisational relationships within NI and the collaboration between the PHA and PHE. Both the enhanced and new systems are continuing within the program of regular surveillance, and present new opportunities to assess health within NI and comparatively with other countries.

Keywords: Mass gatherings, epidemiology, population surveillance, preparedness

PRESENTED BY: Naomh Gallagher

ESCAIDE REFERENCE NUMBER: 20142014

A pilot evaluation of the ECDC's assessment tool for EU candidate countries

Edoardo Colzani[1], Assimoula Economopoulou[1], Graham Fraser[1], Boguslaw Andrzej Suski[1], Maarit Kokki[1]

[1] ECDC, Sweden

Abstract

Following a request from the European Commission (DG SANCO), ECDC has created an internal task force (TFEnA) to perform a comprehensive technical assessment of the communicable disease prevention and control system in the EU enlargement countries in order to meet EU legislation (Eu acquis), and to develop a methodology for this assessment.

Abstract methods

To perform enlargement countries' assessment, TFEnA developed a self-assessment questionnaire (SAQ) for the assessed country comprising of 267 questions covering six technical chapters: health governance; human resource capacity development; surveillance and control; preparedness and response; public health microbiology; and national disease programmes, respectively. The assessment visit lasts 1-2 weeks in which a team of assigned TFEnA experts, together with Commission officials meet with national counterparts and carry out district visits. The assessment team writes the technical report with recommendations to be shared with the Commission and the country.

Abstract results

The EU enlargement countries assessed so far are Croatia, Iceland, Montenegro and Serbia. Some of the most common areas for improvement were: full adoption of EU case definitions; sustainability of epidemiologists workforce; strengthening the infrastructure; capacity of local epidemiological units;development of national communicable disease emergency plans and guidelines for outbreak investigations; integration of national laboratory reporting system with epidemiological surveillance system; adequate operational implementation of national disease programmes.

Abstract conclusion

This is the first attempt to assess the needs for a country to fulfil EU acquis concerning prevention and control of communicable diseases. It is an important chance for ECDC to offer support and identify opportunities for improvement of enlargement countries' national systems. The next steps of the assessment will involve a plan for follow-up on the recommendations provided (including feedback from the candidate countries and milestones).

Keywords: Country assessment, communicable diseases, prevention, international health

PRESENTED BY: Edoardo Colzani

ESCAIDE REFERENCE NUMBER: 20142054

Designing and conducting a cross-border outbreak simulation to practice and enhance cross-border infectious disease control in the Euregion Maas-Rhine (Netherlands, Germany and Belgium)

Henriette ter Waarbeek[1], Chakib Kara-Zaitri[2], Christian Hoebe[3], [4]

[1] GGD Zuid Limburg, The Netherlands; [2] Independent consultant in health informatics Leeds, UK; [3] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg Public Health Service, Geleen, The Netherlands; [4] Department of Medical Microbiology, School of Public Health and Primary Care, Maastricht University Medical Center, Maastricht, The Netherlands

Abstract

The occurrence of (potential) transnational outbreaks challenges public health agencies in cross-border areas to develop ways to consistently cooperate for early detection and response. To enhance cross-border cooperation we designed, executed and evaluated a one-day cross-border simulation in Euregion Maas-Rhine.

Abstract methods

14 time-bound injects were used to stimulate 24 cross-border public health professionals to confirm and respond to a large cross-border hepatitis A outbreak: 58 cases (2 fatalities) – 45 directly linked to contaminated frozen berries from a Belgian supermarket chain servicing Belgium and Germany, causing 7 secondary cases (MSM-contact, food-worker); and 6 other cases caused by a concurrent hepatitis A outbreak (Dutch daycare).Participants of each country were in three separate rooms managed by Exercise Control Room (ECR). Injects included cases notification only, prompting participants to decide on further information needed from ECR and record actions. All intra-room communications were done by filling in Cross-border Alert Templates (CATs). The evolvement of the entire simulation was finally shown in a plenary session using a Dashboard with GIS when individual and group feedback were obtained.

Abstract results

The design of the exercise engendered focused discussions around cross-border challenges. Interactive investigation via ECR widened the scope of the exercise and captured response actions. Participants managed local cases well but struggled to detect linked cross-border cases, decide when and what to communicate and how to respond collaboratively. CATs containing minimal data and action(s) were perceived as useful for information exchange, confirming Cross-border Risk Alert Levels and (real-time) Dashboard as essential enhancements.

Abstract conclusion

The design and execution of this exercise has heightened cross-border infection control awareness, identified strengths, vulnerabilities and useful cross-border communication and management tools, and reconfirmed the necessity of cross-border training.

Keywords: International, exercise, simulation, infectious disease outbreak

PRESENTED BY: Henriette ter Waarbeek

ESCAIDE REFERENCE NUMBER: 20142211

Emerging & vector-borne diseases

Very active circulation of lineage 2 West Nile virus (WNV) in mosquito vectors in Southeastern Romania 2012-2013

Ani Ioana Cotar[1], [2], Sorin Dinu[1], Elena Falcuta[1], Florian-Liviu Prioteasa[1], Raluca Ioana Gatej[1], Cornelia Svetlana Ceianu[1]

[1] "Cantacuzino" National Institute for Research and Development in Microbiology and Immunology, Bucharest, Romania; [2] European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Abstract

WNV is endemic in South East Romania, where 14 (in 2012), and 24 (2013) human neuroinvasive cases have been documented.The aim of this study was to assess the seasonal dynamics for WNV in mosquito vectors in a natural reservoir and an urban area: Danube Delta and Bucharest city.

Abstract methods

Mosquitoes were collected during May – October 2012 and 2013, pooled by species, screened for WNV genome using real-time RT-PCR, and determination of MIR/1000 mosquitoes (Minimum Infection Rate represents WNV-positive pools/total number of mosquitoes tested). Partial NS5 gene sequences were obtained.

Abstract results

859 mosquito pools (up to 30 mosquitoes/pool) were examined: from Danube Delta 262 (in 2012), 508 (2013), and from Bucharest 89 (2012). 184 were positive for WNV genome. In 23 sequenced samples the virus genome was assigned to lineage 2 WNV, with › 99% sequence identity to Volgograd 2007 strain. In the Danube Delta first infected mosquito pools were detected at the end of July 2012 (MIR 22.92), the infection rate remained high until the end of August (MIR 17.43). In 2013, infected mosquitoes were detected end of June–start of July (MIR 4.19), and MIR increased to 14.3 (end of July), and 15.55 (end of August). In Culex pipiens collected end of summer 2012 in Bucharest, MIR was 1.64, and an infected pool of males was detected (proof of vertical WNV transmission).

Abstract conclusion

Same lineage 2 WNV was circulating in Danube Delta and Bucharest in 2012-2013. Principal and secondary vector species were identified. The high infection rate in mosquitoes could be correlated to the variation of weather conditions. These eco-epidemiological data will be used to improve risk assessment, surveillance and control of WNV.

Keywords: West Nile virus, Minimum Infection Rate, mosquitoes, Romania, Danube Delta, surveillance

PRESENTED BY: Ani Ioana Cotar

ESCAIDE REFERENCE NUMBER: 20141946

Insufficient mosquito protection measures among migrants in an area with re-emerging malaria, Greece 2013

Iro Evlampidou[1], Kostas Danis[1], Annick Lenglet[2], Maria Tseroni[3], Yorgos Theocharopoulos[4], Takis Panagiotopoulos[5]

[1] European Centre for Disease Prevention and Control (ECDC), Sweden; [2] Independent scholar, The Netherlands; [3] Hellenic CDC, Greece; [4] Independent scholar, Greece; [5] National School of Public Health, Greece

Abstract

In 1974, malaria was eliminated in Greece. Since 2009, locally-acquired P.vivax malaria cases occurred in the agricultural area of Evrotas, Laconia. Public health actors implemented a malaria-control program targeting migrants from malaria-endemic countries, including house-to-house visits for active case detection (ACD), advice on mosquito protection methods (MPMs) and distribution of mosquito protection items. In June 2013, we undertook a survey among migrants in Evrotas to assess their MPMs and identify factors associated with mosquito-protection practices to guide prevention activities.

Abstract methods

We selected participants using simple random sampling from a list of all migrants targeted for ACD. We performed face-to-face interviews using a structured questionnaire and trained translators. We defined as personal MPMs the use of long-sleeved clothes and/or mosquito repellent; as household MPMs the presence/use of: 1.mosquito screens, 2.fan/air-condition, 3.indoor repellent/insecticide, 4.outdoor mosquito coils. We calculated prevalence ratios (PR) using poisson regression and allowing for clustering.

Abstract results

One-hundred-thirty migrants (99%) participated (all men; median age: 26 years, range: 18-55; 92% from Pakistan). Sixty-seven (52%) used personal MPMs, 79 (61%) used >2 household MPMs and 95 (73%) >2 overall MPMs. Living in a warehouse/shack (PR=0.7; 95%CI:0.6-0.9), being married (PR=1.2; 95%CI:1.1-1.5), concerns about contracting malaria (PR=1.4; 95%CI:1.1-1.9), awareness of malaria cases in the area before 2012 (PR=1.2; 95%CI:1.0-1.4), and seeking medical care in the previous year (PR=0.6; 95%CI:0.4-1.0) were associated with use of >2 MPMs.

Abstract conclusion

Despite extensive interventions in Evrotas, migrants from malaria-endemic countries used insufficient MPMs. Migrants with better living conditions and malaria awareness were more protected against mosquitoes. Housing conditions should be improved and public health activities should further focus on mosquito protection to increase awareness and reduce the risk of re-establishment of malaria in the area.

Keywords: Malaria, mosquito control, Greece, migrants, cross-sectional survey

PRESENTED BY: Iro Evlampidou

ESCAIDE REFERENCE NUMBER: 20142204

Assessment of distribution of morbidity and mortality due to malaria in Ondo State, south-west Nigeria, 2012: a secondary data analysis

Abiodun Ogunniyi[1], Olufemi Ajumobi[2], Olufunmilayo Fawole[1], Gabrielle Ponggesee[1]

[1] Nigeria Field Epidemiology Laboratory Training Programme, Asokoro, Abuja, Nigeria; [2] National Malaria Elimination Program. Abuja., Nigeria

Abstract

In Nigeria,malaria accounts for an estimated 100 million cases and 300,000 deaths annually. The south-west region of Nigeria, where Ondo State is situated, is classified as holoendemic. We conducted a secondary data analysis to determine distribution of reported morbidity and mortality due to malaria in Ondo State.

Abstract methods

We reviewed malaria data of the Integrated Disease Surveillance and Response system, Ondo State Ministry of Health Nigeria for 500 health facilities from January to December 2012. The data was analysed using Microsoft Excel 2007. We described distribution of cases and deaths by age, high risk group, and local government of origin.

Abstract results

There were 326,860 reported cases and malaria incidence proportion was 8.0 per 100,000 populations. Persons younger than 5 years (U5) and older than 40 years accounted for 57% and 28% of the total morbidity respectively. There were 11,971 (3.7%) severe cases while 12,421 (3.8%) of cases were pregnant women. Akure South LGA had 40% of total morbidity, and highest incidence proportion with 31.1 per 100,000 populations at risk with. With 56 deaths, mortality rate was 1 per 100,000 populations. About 27(49%) and 19(39%) of the total mortality were found among U5 and age group >40 years, respectively. Five deaths (9%) were reported among pregnant women. Okitipupa LGA has the highest mortality rate of 13 per 100,000 populations and accounts for 66% of reported deaths due to malaria in the state.

Abstract conclusion

Reported malaria incidence proportion among children under five years of age in 2012 was higher than what was reported in the same region in 2010. There is need to intensify malaria control/elimination intervention activities in the state especially at Akure and Okitipupa LGA.

Keywords: Malaria, surveillance, morbidity, mortality, Nigeria

PRESENTED BY: Abiodun Ogunniyi

ESCAIDE REFERENCE NUMBER: 20142267

Validation Of Cyscope Microscope, Quantitative Buffy Coat And Rapid Diagnostic Kit For Malaria Diagnosis Among Clinic Attendees In Southwest Nigeria

Abiodun Ogunniyi[1], Oyibo Wellington[2], David Dairo[3], Olufemi Ajumobi[4], Gabrielle Ponggesee[1]

[1] Nigeria Field Epidemiology Laboratory Training Programme, Asokoro, Abuja, Nigeria; [2] College of Medicine, University of Lagos, Nigeria; [3] Epidemiology and Medical Statistics, University of Ibadan, Nigeria; [4] National Malaria Elimination Program. Abuja, Nigeria

Abstract

The unavailability of accurate, rapid, reliable and cost effective malaria diagnostic instruments compels many laboratories to depend on the labour-intensive and time consuming light microscopy (LM) for malaria diagnosis. Alternative instruments like Cyscope fluorescent microscope (Cyscope), Quantitative Buffy Coat fluorescent microscope (QBC), and CareStart Rapid Diagnostic Kit (CareStart) have been developed with the potential to resolve challenges from LM. This study was designed to validate these instruments and assess their cost-effectiveness.

Abstract methods

Blood samples collected from 502 patients who were systematically randomly selected from 1800 patients at three hospitals in southwestern Nigeria, were tested for malaria parasites using the diagnostic instruments mentioned above, with LM as the gold standard. For each instrument,sensitivity, specifcity,positive predictive value(PPV),negative predictive value(NPV), cost per hour of use and turnaround time (TAT) per result output were assessed. Statistical analysis included McNemar chi-square and Kappa statistics as 0.05 significance level.

Abstract results

Malaria prevalence in the samples was 30.7% by LM. Sensitivity of the instruments compared with LM was 76% (CareStart), 95% (Cyscope) and 98.1% (QBC) while specificity was 85.5% (QBC), 87.3% (Cyscope) and 96% (CareStart). PPV for the instruments were 65.2% (QBC), 67.5% (Cyscope) and 84.7% (CareStart) with NPV of 93.6% (CareStart), 98.6% (Cyscope) and 99.4% (QBC). Kappa values were 0.71 (QBC) (OR=28.5; CI=7.54-241.01), 0.72 (Cyscope) (OR=10.0; CI=4.01-32.13) and 0.75 (CareStart) (OR=0.6; CI=0.3=1.13. Cost per hour of use was .04 (Cyscope), .61 (RDT), .89 (QBC) and .77 (LM). The TAT was 5minutes (Cyscope), 10minutes (QBC), 20minutes (CareStart) and 45 minutes (LM).

Abstract conclusion

Cyscope fluorescent microscpy was found to be comparatively accurate, rapid and cost effective for malaria diagnosis in this resource-limited setting and is therefore recommended for routine diagnosis in this elimination phase of malaria.

Keywords: Malaria, Diagnosis, Clinical laboratory techniques, Reliability and validity, Cost-Benefit Analysis, Nigeria

PRESENTED BY: Abiodun Ogunniyi

ESCAIDE REFERENCE NUMBER: 20141939

Chikungunya outbreak in French Territories in the Americas, November 2013 – May 2014: possible risk of international spread

Laure Fonteneau[1], [2], Harold NOEL[1], Audrey Andrieu[3], Vanessa Ardillon[3], Fatim Bathily[3], Alain Blateau[3], Luisiane Carvalho[3], Sylvie Cassadou[3], Elise Daudens[3], Frederique Dorleans[3], Carlos Moreno-Parejo[3], Marion Petit-Sinturel[3], Jacques Rosine[3], Amandine Vaidie[3], Elsa Balleydier[1], Anne Guinard[1], Florence Kermarec[1], Audrey Lemaitre[1], Lucie Leon[1], Remy Michel[4], Cyril Rousseau[1], Véronique Servas[5], Caroline Six[1], Martine Ledrans[3]

[1] French Institute for Public Health Surveillance, Saint-Maurice, France; [2] ECEC, Stockholm, Sweden; [3] French Institute for Public Health Surveillance, Fort de France, Martinique, France; [4] French Army Center for Epidemiology and Public Health, Marseille, France; [5] French Institute of Public Health Surveillance, Aquitaine, France

Abstract

On 6 December 2013, the epidemiology unit of French territories in the Americas reported two autochthonous cases of chikungunya (a mosquito-borne viral disease) on the French part of Saint Martin (Caribbean), for the first time in the Americas. Because of its high epidemic potentialwe enhanced surveillance in all French territories in the Americas to monitor spread, and guide control measures.

Abstract methods

We defined a suspected case as any individual with sudden onset of fever (>38.5°C) and arthralgia not explained by other medical conditions. Cases were confirmed by serology or PCR. When the first autochthonous cases were detected, we actively searched for cases door-to-door. In regions with chikungunya outbreaks,we estimated the total number of suspected cases based on the number of cases reported by sentinel general practitioners. We monitored hospitalized cases.

Abstract results

As of 11 May 2014, we estimated 41,500 suspected cases, 4,800 of which were laboratory-confirmed and 586 hospitalisations, 15% with severe disease. Seven chikungunya-related deaths were reported. The virus has spread to all French territories in the Americas. The 4 Caribbean Islands reported up to 7.1 suspected cases per 1,000 per week. Vector control measures were implemented and strengthened in localities with the highest attack rates.

Abstract conclusion

The chikungunya outbreak spread rapidly despite continued vector control efforts. Because of no pre-existing population immunity and favourable climatic conditions for the vector, the disease may resurge in the Caribbean during the next rainy seasons. High tourist traffic between Europe and the Caribbean increases the risk of chikungunya virus introduction in Mediterranean Europe. We recommend continuation of vector control in French territories in the Americas and strengthening surveillance of chikungunyain European regions where the vector is established.

Keywords: Chikungunya, outbreak, Caribbean region, Americas, viral infection

PRESENTED BY: Laure Fonteneau

ESCAIDE REFERENCE NUMBER: 20142017

Explaining the geographic spread of emerging viruses: a new framework for comparing viral genetic information and environmental landscape data

Simon Dellicour[1], Rebecca Rose[1], Oliver Pybus[1]

[1] University Of Oxford, UK

Abstract

Phylogenetic analysis has become an important tool in the study of pathogenic viruses. It enables researchers to reconstruct epidemic history when surveillance epidemiology data are sparse or non-existent, and can infer epidemiological linkages among infections that may not be evident otherwise. However, a major challenge is to develop a statistical framework within which hypotheses about the effect of environmental factors on transmission and spatial spread can be rapidly investigated and tested. Recently-developed 'phylogeographic' approaches use sampled viral genomes to reconstruct a full history of virus dispersal, including the locations of ancestral infections and the rate and direction of spatial spread.

Abstract methods

We present the development of a new analytical framework that compares viral genetic information and environmental landscape data. First, the abovementioned phylogeographic methods are used to estimate the dispersal history of an emerging pathogen. Each of the inferred paths of dispersal is subsequently assigned a numerical 'weight' based on high-resolution maps of underlying environmental variables. Next, statistical analyses are used to test the impact of environmental factors upon viral movement. Three different randomization procedures are used to assess statistical confidence.

Abstract results

We validated our approach using simulated data and also present its application to a rabies outbreak among North American raccoons. We tested and compared the impact of several environmental factors (including elevation, population density, land cover) on the dispersal rate of this epidemic.

Abstract conclusion

We show that it is possible to integrate viral genomic and geographic data in a single statistical framework, which has the potential to rapidly assess questions concerning the mode and tempo of virus dispersal during emerging epidemics.

Keywords: Molecular epidemiology, viral phylogeography, landscape data, rabies

PRESENTED BY: Simon Dellicour

ESCAIDE REFERENCE NUMBER: 20141919

A Case-Control Study on the First Reported Chikungunya Outbreak in Rapu-rapu, Southern Luzon, Philippines, 2012

Alethea De Guzman[1], Ma. Justina Zapanta[1], Ma Nemia Sucaldito[1], Vikki Carr De Los Reyes[2], Enrique Tayag[2]

[1] Department of Health, Philippines; [2] FETP-Philippines, Philippines

Abstract

The National Epidemiology Center received a report of increasing febrile cases in Rapu-rapu, Albay. Investigation was done to verify diagnosis, determine existence of an outbreak, identify source and mode of transmission, identify risk factors and recommend control and prevention measures.

Abstract methods

A matched for age and sex case-control study was conducted. A suspect case was a previously well individual from Rapu-rapu with ≥2 days fever and joint pains from June 15-October 15, 2012. A confirmed case was a suspect case positive for Chikungunya IgM. Environmental inspection and entomological investigation were done. Data was analyzed using EpiInfo.

Abstract results

There were 124 suspect cases. Eighty-four (68%) were females. Most affected (15%) age-group was the 21-25 years. Fifty-three cases were positive for Chikungunya IgM. Entomological study showed that Breteau and House Indices were higher than the set standard of 20% and 5%, respectively. Majority (59%) of identified larvae was Aedes aegypti. Rapu-rapu is a mining community frequently visited by outside traders. Case-control study showed that cases were more likely to have discarded bottles outside (OR=2.6, p-value=0.02, CI=1.16-5.95). Protective factors were having a Level III water system, garbage collection system and covered water containers.

Abstract conclusion

There was a Chikungunya outbreak in Rapu-rapu. First cases were exposed to a group of traders with history of febrile illness. Outside breeding sites, such as discarded bottles, led to increased breeding sites and vector density as evidenced by high Breteau and House indices. Festivities coincided with the peaks and may have contributed to case propagation. Recommendations include improved sanitation and water system upgrading, which minimizes need for water storage, to lessen breeding sites, regular search and destroy and continuation of surveillance

Keywords: Chikungunya fever, case-control, water system, entomological study

PRESENTED BY: Ma Nemia Sucaldito

ESCAIDE REFERENCE NUMBER: 20142161

Novel methodological approaches for disease investigation, surveillance and control (2)

A social media campaign for gonorrhoea control in Ireland

Susan Donlon[1], *Fionnuala Cooney*[2], *Derval Igoe*[3]

[1] Dublin AIDS Alliance, Ireland; [2] Department of Public Health HSE East, Ireland; [3] HSE, Ireland

Abstract
A multidisciplinary gonorrhoea control group was convened in Dublin in December 2012 in response to an increase in gonorrhoea notifications. Two main risk groups were identified: men who have sex with men (MSM) and young heterosexuals. Although high quality information on gonorrhoea was available for MSM, materials for young heterosexuals was less well developed. For this reason, it was decided to deliver an information campaign about gonorrhoea targeted specifically at young people and delivered using social media.

Abstract methods
A working group was formed of professionals who work with young people and are experienced in digital media. Based on feedback from other campaigns, eye-catching imagery, humour (when appropriate), quick and clear information and positive and non-judgemental messages were used. Materials were tested on a sample of young people who were also asked for the hashtag for the Twitter promotion and invited to model for the creatives/visuals. Both Twitter and Facebook were used with referral to an updated health service website: yoursexualhealth.ie. The campaign was delivered over a two month period, concluding in February 2014 with a St Valentine's competition promotion.

Abstract results
The campaign trended on Twitter. Facebook promoted posts reached tens of thousands of young people, generated hundreds of thousands of impressions, with click-through rates and engagement rates well above average. The campaign website reported a 59% increase in visits. There was considerable media interest from newspapers, radio and television.

Abstract conclusion
This is the first instance of social media being used in STI outbreak control in Ireland. The campaign achieved good reach of the target population and we advocate using social media as an effective model for sexual health promotion activities.

Keywords: Social Media, Neisseria gonorrhoeae, Sexually Transmitted Diseases, Disease Outbreaks, Health Promotion

PRESENTED BY: Susan Donlon

ESCAIDE REFERENCE NUMBER: 20142057

A novel automated data extraction and transmission tool for identification of influenza- and pneumonia-associated diseases based on ICD-10 data from German primary care practices

Aryna Zanuzdana[1], *Karla Koepke*[1], *Walter Haas*[1]

[1] Robert Koch Institute, Department for Infectious Disease Epidemiology, Germany

Abstract
Influenza and community-acquired pneumonia (CAP) pose a considerable burden on German health system causing annually up to 5 million of excess influenza-associated consultations and up to 800 000 cases of CAP. Yet there is a lack of data on diseases and health conditions from the country's outpatient sector. The Robert Koch Institute (RKI) initiated the study to identify population groups at increased risk for influenza or CAP as well as related comorbidities and sequelae.

Abstract methods
A semi-automated data extraction tool (DET) developed on behalf of the RKI extracts anonymized case-based data from the primary health care practice software for all patients meeting the case definition of the codes J09 – J18 of International Classification of Diseases (ICD). The extracted data includes ICD-10-coded information for the period of 6 months before and after the diagnosis of J09-J18, as well as the set of basic demographic characteristic and vaccination status.

Abstract results
Technical functionality of the tool as well as its validity and plausibility of extracted data was successfully tested during the pilot phase in 2013 and rolled out to 70 practices. Since then data from 66.274 patients was collected. A key advantage of the DET is the acquisition of each diagnosis with the date of its coding which allows analyzing the temporal association of disease. Data can be extracted retrospectively and transferred per a mouse click in a timely manner to the RKI.

Abstract conclusion
The developed tool delivers in a standardized fashionICD-10-coded epidemiological data on population-based burden of influenza and CAP in Germany. The main limitation of the tool is that it is not universally compatible with different medical software. Further analysis of data and its quality is carried out.

Keywords: Influenza, Human, Pneumonia, International Classification of Diseases, Primary Health Care

PRESENTED BY: Aryna Zanuzdana

ESCAIDE REFERENCE NUMBER: 20142079

Evaluation of a new automated surveillance tool for hospital acquired urinary tract infections in Denmark

Orla Condell[1], Sophie Gubbels[1], Jens Nielsen[1], Marianne Voldstedlund[1], Robert Skov[1], Brian Kristensen[1]

[1] Statens Serum Institut, Denmark

Abstract

An automated surveillance system, the Hospital Acquired Infections Database (HAIBA), is currently under development in Denmark, as an alternative to the current system for monitoring hospital-acquired (HA) infections; point prevalence surveys (PPS). This study aims to evaluate discrepancies between PPS and HAIBA for urinary tract infections (UTIs), in order to validate the HAIBA case definition.

Abstract methods

HAIBA consists of merged data from the National Patient Registry and the national microbiological database. In HAIBA, a HA-UTI is a urine culture positive for ≤two organisms with at least one at 104CFU/ml and sample date ≥48 hours after admission and ≤48 after discharge. PPS data (2012 and 2013) were obtained for 2,111 patients. PPS and HAIBA data were linked through personal identification numbers.

Abstract results

HAIBA compared to PPS demonstrated a 70.8% (34/48) sensitivity and 97.7% (2015/2063) specificity. The PPS detected 48 HA-UTIs, HAIBA detected 82. Both systems were concordant for 34 cases. Forty-eight were detected by HAIBA only; 24 where laboratory results were unavailable at the time of the PPS, six where the PPS considered the infection as non-clinically relevant because of indwelling catheters, one where the culture was reported as contamination, 17 remained unexplained. Fourteen cases were detected by PPS only; two did not submit urine samples and 12 had negative cultures.

Abstract conclusion

The main discrepancies between HAIBA and PPS were that HAIBA detected cases whose laboratory results were unavailable during the survey, and did not detect cases without a laboratory confirmed results. This study validates HAIBA as a system to monitor HA-UTIs and helped build trust and acceptance amongst end users. HAIBA, unlike PPS, reports geographical trends overtime thus allowing a more rapid response to reduce occurrence of HA-UTI.

Keywords: Surveillance, prevalence, automated, hospital, urinary tract infection.

PRESENTED BY: Orla Condell

ESCAIDE REFERENCE NUMBER: 20142176

Using a social marketing framework to inform education aimed at increasing appropriate antibiotic use amongst 15-18 year olds: an international project

Meredith Hawking[1], Donna Lecky[1], Pia Touboul Lundgren[2], Eman K Aldigs[3], Hind A Abdulmajed[3], Demetra Hadjichambi[4], Eleni Ioannidou[5], Cliodna McNulty[1]

[1] Public Health England, UK; [2] Département de Santé Publique Hôpital de l'Archet, France; [3] College Of Medicine, King Abdulaziz University, Saudi Arabia; [4] Department of Educational Sciences, University of Cyprus, Nicosia, Cyprus; [5] Cyprus International Institute for Environmental and Public Health, Limassol, Cyprus

Abstract

The 2013 Eurobarometer reported that 15 – 24 year olds were the least informed and highest users of antibiotics, but this age group are the most likely to change their minds on antibiotic. e-bug (www.e-bug.eu) does not currently educate 16-18 year olds.We aimed to dertermine young peoples needs for materials to improve their antibitoic use.

Abstract methods

The research was undertaken in the UK, Belgium, France, Cyprus and Saudi Arabia. A social marketing framework approach was used. To determine the most appropriate implementation strategy first each country undertook a detailed review of the provision of information around antibiotics for 15-18 year olds. Qualitative interviews and focus groups were used to explore young adults knowledge and attitudes towards antibiotic use and the competition faced by improving use. Thematic analysis was conducted within each country using the same methodology.

Abstract results

87 students participated in Focus groups and 63 in interviews.Two main antibiotic-related behaviours were common to all countries: taking antibiotics for upper respiratory tract infections and not taking antibiotics as prescribed. In Saudi Arabia and Cyprus students discussed purchasing antibiotics over the counter and sharing antibiotics with friends. Most students knew what antibiotics were, however some confused antibiotics and painkillers and there was low knowledge of the difference between viruses and bacteria.Most students did not understand antibiotic resistance. Their peers treated antibiotics as cure all, and are lazy about taking their antibiotics. Parents have an advisory role and remind students to take their antibiotics.Students in the UK discussed modifying treatment regimens in order to drink alcohol.

Abstract conclusion

Educational resources will be developed by the e-bug team to improve young peoples use of antibiotics thorugh lesson plans and debate cards.

Keywords: Antibiotic use, young people, education, qualitative.

PRESENTED BY: Cliodna McNulty

ESCAIDE REFERENCE NUMBER: 20142120

Informing future surveillance for carriage of multi-resistant gram negative bacteria: problems with recruiting to an English stool sample cross-sectional community prevalence study

Cliodna McNulty[1], Deborah Nakiboneka-Ssenabulya[1], Tom Nichols[1], Li XuMcCrae[1], Sahida Shabir[1], Chung Keun Taik Taik Chung[1], Donna Lecky[1], Lucy Thomas[1], Mike Thomas[2], Stephen Smith[3], Peter Hawkey[1]

[1] Public Health England, UK; [2] Primary Care Research, University of Southampton, UK; [3] Birmingham; Bowel Cancer Screening Programme. University Hospitals Coventry& Warwickshire NHS Trust, UK

Abstract

The rise in infections due to multi-resistant gram negative bacteria is a major public health problem. Monitoring the carriage of such organisms in the asymptomatic population is crucial to informing control efforts. Obtaining stool samples from the asymptomatic population is challenging. We set up a cross-sectional community study to determine the prevalence of extended spectrum beta lactamases producing coliforms in the healthy general population, and determined how this could inform the development of future community surveillance.

Abstract methods

We purposively selected 12 general practices in four areas of England with different ethnic population structures. After stratification of GP lists by age, ethnicity and antibiotic use, randomly selected patients were sent a postal invitation. Respondents who posted back letters of interest in the study were sent a postal stool kit and questionnaire.

Abstract results

Difficulties with the study which may affect future community surveillance programmes:1. Consent and data protection issues made stratification and selection of patients according to age, ethnicity and previous antibiotic use, difficult and time consuming.2. Obtaining information on patients' type of antibiotic use in a format to allow easy stratification of patients was difficult in many practices.3. Stool return rates varied greatly by region: Central Urban Birmingham 2%, Newham in London 4.2%, Southampton (South England) 4.6% and 14.7% Shropshire (Rural Central England). 4. Stool returns were lower in younger patients (18-39y 1.9%. >60y 6.3% and ethnic minorities (Asian 1.5%, black 4.2%, mixed 6.8%, white 12.1%).

Abstract conclusion

Implications: Older, white and mixed ethnicity patients may be recruited by post for future stool based surveillance studies of antimicrobial resistant organisms; other recruitment methods will be needed to recruit younger or ethnic minority.

Keywords: Surveillance, ESBLs, stool samples, community, ethnicity, antibiotic, age

PRESENTED BY: Cliodna McNulty

ESCAIDE REFERENCE NUMBER: 20142125

Evaluation of the EUFRAT risk assessment tool

Dragoslav Domanovic[1], Rabin Neslo[2], Welling Oei[2], Mart Janssen[2]

[1] ECDC, Sweden; [2] Julius center for Health Sciences and Primary Care, UMC Utrecht, The Netherlands

Abstract

The European Up-Front Tool (EUFRAT) is a web-based tool commissioned by the European Centre for Disease Prevention and Control (ECDC) for quantifying the risk within the blood transfusion chain during outbreaks of emerging infectious diseases. An evaluation was deemed necessary before the tool becomes more widely used by transfusion regulators and public health officials.

Abstract methods

A zero test, range test, value test and sensitivity test was applied to the model in order to assess whether the tool produces the correct output for given inputs. Also, warnings for invalid input values, and correct propagation of the uncertainty in input parameters were checked. Six international experts were asked to use the tool to evaluate outbreaks they had analyzed themselves before and to report their experiences.

Abstract results

Testing revealed 14 discrepancies and 2 "bugs" in the model: 6 (Step-1); 2 (Step-2); 1 (Step-3); 4 (Step- 4); 1 (Step -5) and 2 (general concept). Comparison between the risk estimates the experts obtained earlier with the risk they estimated using the tool showed a lower EUFRAT estimate than found previously for hepatitis A. The experts agreed that the tool's usability is good (3/6) or limited to trained persons (3/6). Experts provided 19 comments summarized in 8 findings related to: distinguishing between cumulative and weekly incidence; dealing with unreliable or sparse data; guidance on bias and variation; documentation wording ; parameter references; ability to use of large datasets; outputs explanation and presentation ; tailoring to the need of end-users.

Abstract conclusion

From this evaluation a set of changes to the existing model and associated materials have been recommended. The upgrading of the tool is ongoing and currently funded by the European Blood Alliance.

Keywords: Evaluation, risk, model, transfusion

PRESENTED BY: Dragoslav Domanovic

ESCAIDE REFERENCE NUMBER: 20141955

Outbreaks (3)

Don't count your chicken livers: An outbreak of Campylobacter not associated with chicken liver parfait, UK, November 2013.

Suzan Trienekens[1], Charlotte Anderson[1], Jennifer Duffy[2], Rachel Gill[2], Lisa Harvey-Vince[2], Helen Jones[3], Piers Mook[1], Chikwe Ihekweazu[1], Ishani Kar-Purkayastha[2]

[1] Field Epidemiology Services – Victoria Office, Public Health England, UK; [2] Surrey & Sussex Health Protection Team, Public Health England, UK; [3] Environmental Health – Runnymede Borough Council, UK

Abstract

In December 2013, Surrey and Sussex Health Protection Team received reports of 14 guests with diarrhoea and vomiting (including confirmed Campylobacter), followinga lunch event at a hotel on 21 November, attended by 138 people. Chicken liver parfait, often linked to Campylobacter outbreaks in the UK, was served on the premises. Our objective was to describe the outbreak in place, person and time, describe illness and identify possible risk factors associated with illness.

Abstract methods

Information was collected on demographic characteristics, food exposures and illness history from attendees of the lunch event via online and telephone questionnaires. Cases were defined as "individuals who attended the event on 21 November 2013 and became unwell with diarrhoea and/or vomiting with onset between 21 November and 1 December 2013". We calculated adjusted odds ratios (aOR) for food exposures between cases and non-cases using a negative binomial regression model. Available stool samples were collected and tested for common gastrointestinal pathogens; on-site environmental investigation was performed.

Abstract results

102/138 guests (74%) completed the questionnaire, 46/102 were cases (attack rate: 45%). Median incubation period was two days; 18/46 cases (39%) sought medical care. Food items associated with illness were roast turkey (aOR 3.55, $p=0.045$) and jus (aOR 3.02, $p=0.041$). Campylobacter was detected in 11/14 stool samples analysed. Environmental investigation found adherence with regulatory food handling practices.

Abstract conclusion

This outbreak of Campylobacter had a high attack rate and long symptom duration. Epidemiological analysis identified roast turkey and/or jus as the likely vehicle of the infection. Surprisingly, no association was found between chicken liver parfait and illness. We recommend that other food items should be equally investigated by outbreak control teams in similar circumstances.

Keywords: Infectious Disease Outbreaks, Campylobacter, Gastro-intestinal diseases, Epidemiology

PRESENTED BY: Suzan Trienekens

ESCAIDE REFERENCE NUMBER: 20142104

An outbreak of *Microsporum canis* in two elementary schools in a rural area close to the capital city of Slovenia

Maja Subelj[1], [2], Jana Sveticic Marinko[1], Veronika Ucakar[1], Irena Klavs[1]

[1] National Institute of Public Health of Slovenia, Ljubljana, Slovenia; [2] European Centre for Disease Prevention and Control (ECDC), Sweden

Abstract

Tinea caused by infection with Microsporum canis is endemic in Southern Europe and the Mediterranean. A cluster of cases of M. canis infections occurred among pupils of two elementary schools in Slovenia in 2013. Our objectives were to describe the outbreak, identify factors associated with contracting infection, and to recommend control measures.

Abstract methods

We defined a case as a pupil having attended one of the two elementary schools between 1 October and 1 December 2013, with a skin lesion and probable or confirmed M. canis infection by direct microscopy or culture. We compared cases with controls in two separate case-control studies by calculating odds ratios (ORs) and 95% CI for different exposures. For each case, five controls were randomly selected from the classes infected pupils originated were attending. Skin scrapings and hair plucks from a suspected kitten were examined by direct microscopy.

Abstract results

The outbreak lasted from 4 October to 1 December 2013. All 12 cases occurred among females aged 6-13 years (median 9.5 years). Primary cases were 49 times more likely to have had physical contact with a stray kitten at a birthday party ($p<0.001$). Secondary cases were more likely to have participated in gymnastics classes together with one of the primary cases (OR: 23.2; $p<0.001$) and to have had physical contact with a primary case (OR: 27.5; $p<0.001$). No fungal spores were found by microscopy in samples from the suspected kitten.

Abstract conclusion

The epidemiological findings indicated physical contact with a stray kitten or primary cases and the affected premises as risk factors for acquiring tinea. We recommended keeping the lesions covered until the first negative microbiological result, and hypochlorite-based disinfection of the premises.

Keywords: Microsporiosis, outbreak, case-control study, Slovenia

PRESENTED BY: Maja Subelj

ESCAIDE REFERENCE NUMBER: 20141931

An outbreak of Cholera due to consumption of sachet water in Abeokuta, Ogun state, Nigeria, July 2013.

Oluwatoyin Aiyelotan[1]*, Oluyomi Bamiselu*[1]*, Anayochukwu-Ugwu Ngozi*[1]*, Olufunmilayo Fawole*[2]

[1] Nigeria-FELTP, Nigeria; [2] Epidemiology and medical statistics, University of Ibadan, Oyo state, Nigeria

Abstract

Cholera is an acute dehydrating diarrhoea disease that can be transmitted through consumption of contaminated water. On 27th June 2013, a suspected outbreak of cholera was reported in Abeokuta South Local Government Area, Ogun state. We carried out a case control study to identify source of infection and to institute prevention and control measures.

Abstract methods

We identified a case as any person ›5years of age living in Abeokuta with three or more episodes of acute watery diarrhoea from 25th June to 12th July, 2013. Controls were community members without symptoms during the period. We used a semi structured questionnaire to obtain information on demography, clinical history, symptoms and exposure factors. Stools, water specimen from wells and sachet water were cultured. We performed bivariate, multivariate and unconditional logistic regression to identify risk factors, using Epi info 3.5.3.

Abstract results

Of the 37 cases and 74 controls interviewed, 21 (52.3%) and 46 (62.2%) were females. Age group mostly affected were individuals ‹10years. Mean age for cases and control were 20.5years(SD=19) and 38.8years(SD=15.6) respectively. Vibrio cholerae was isolated from two of the six stool samples and heavy growth of E.coli was found in the water specimens. Protective factors were hand washing with soap and water before eating (OR=0.3, Confidence interval 95%:0.12-0.74) and hand washing with soap and water after using the toilet (OR=0.25, CI 95%:0.11-0.59). However, cases were more likely to have drank sachet water (OR=40.7, CI 95%:12.9-129.9) and had contact with diarrhoea case (OR=6.7, CI 95%:2.7-16.8).

Abstract conclusion

Consumption of sachet water was identified as the key risk factor for infection in this outbreak. Intensive health education was conducted. Immediate sanitary inspection of sachet water factories was recommended to local authority.

Keywords: Cholera, outbreak, case control study, vibrio cholerae, infectious disease

PRESENTED BY: Oluwatoyin Aiyelotan

ESCAIDE REFERENCE NUMBER: 20141971

Outbreak of influenza A in a primary school during a low flu season.

Gayle Dolan[1]*, Russell Gorton*[2]*, Deborah Wilson*[1]

[1] Public Health England, UK; [2] Field Epidemiology Services, Public Health England, UK

Abstract

In January 2014, an outbreak of influenza-like-illness (ILI) was reported to the health protection team by the head teacher of a primary school in North East England. We conducted a retrospective cohort study to investigate the extent of the outbreak and identify the likely mode of transmission.

Abstract methods

All pupils and staff who attended the school were invited to complete a paper-based questionnaire on demographic, clinical and potential exposure variables. Five nasal swabs were obtained from affected pupils and submitted for viral panel testing. We used the ECDC case-definition for ILI and calculated attack rates (AR) and relative risks (RR), with associated 95% confidence intervals (95%CI).

Abstract results

The response rate was 67% (30/45) for staff and 38% (118/311) for pupils. Overall, 43 individuals met the case definition for ILI, including 4 cases with laboratory confirmed influenza A (H1) pdm09. The AR was highest for pupils in the nursery (mean age 3 years) (RR=2.5, 95%CI 1.6-4.1) and lowest for pupils in year 5 (mean age 9 years)(RR=0.22, 95%CI 0.03-1.50) when compared with other pupils in the school (age range 3-11 years). One or more cases were reported in 39 households; 29 (74%) of the primary cases were pupils or staff members at the school.

Abstract conclusion

Schools remain an important setting for transmission of influenza, even when influenza activity in the community is low. Investigating outbreaks in this setting enables identification of transmission dynamics which can inform control measures.

Keywords: Outbreaks, Influenza, Analysis, Cohort, Schools

PRESENTED BY: Gayle Dolan

ESCAIDE REFERENCE NUMBER: 20141979

Outbreak of norovirus GI.3 among lunch guests at a hotel in southern Finland, 2013

Sari Huusko[1], Jani Soini[2], Kaisa Hemminki[3], Aija Pirnes[3], Merja Roivainen[2], Leena Maunula[1], Ilkka Miettinen[2], Ari Kauppinen[2], Salla Toikkanen[2], Ruska Rimhanen-Finne[1]

[1] Department of Infectious Diseases Surveillance and Control, National Institute for Health and Welfare (THL), Finland; [2] National Institute for Health and Welfare, Finland; [3] Food and Environmental Health Unit, Section of Health, City of Espoo, Finland

Abstract

A series of acute gastroenteritis outbreaks among lunch guests at a hotel in southern Finland was notified to the National Institute for Health and Welfare in May 2013. Despite microbiological testing, no cause of illness had been detected. Our investigation was initiated to determine the agent, source and extent of the outbreak.

Abstract methods

Stool, water and surface samples were analyzed in 3 laboratories using several molecular biology methods (quantitative real-time RT-PCR and RT-PCRs). Data from retrospective cohort studies of the outbreaks was combined and analyzed for water exposure as no food was common to the lunches. The hotel had a private well. A case was a lunch guest who developed diarrhea or vomiting within 72 hours after visiting the hotel.

Abstract results

At first, the agent was not recognized by regular quantitative RT-PCR used for norovirus detection from stool specimens. Only by typing RT-PCR were positive results obtained. Virus was typed as norovirus GI.3 according to the capsid sequence. Subsequently, norovirus GI was found in water and surface samples. Out of 590 lunch guests, 355 (60 %) responded and 172 cases were identified. Those that consumed tap water at the hotel lunch before hotel's well was cleaned were 1.8-times (95 % CI 1.3 – 2.4) more likely to become ill than non-exposed.

Abstract conclusion

Epidemiological and microbiological investigations suggest that the outbreak started with contaminated water. Since norovirus was found in hotel surfaces, environmental transmission is also probable. After thorough cleaning of the well and premises, no new gastroenteritis cases were identified at the hotel. The source of water contamination was not identified. The methods used in laboratories participating in outbreak investigations should be up to date and harmonized.

Keywords: Outbreak, norovirus, detection, water, environmental transmission

PRESENTED BY: Sari Huusko

ESCAIDE REFERENCE NUMBER: 20142190

An outbreak of measles in Ondo West LGA, Ondo State, Nigeria. February-May, 2013

Adefisoye Adewole[1], Endie Waziri[2], Olufunmilayo Fawole[2], Patrick Nguku[2]

[1] Lautech Teaching Hospital Ogbomoso Oyo State, Nigeria; [2] Nigeria Field Epidemiology and Laboratory Training Programme(NFELTP), Nigeria

Abstract

On 6th May, 2013, suspected measles cases were reported from Ondo West LGA to State Ministry of Health Akure. We investigated the outbreak to confirm diagnosis of measles, assess the magnitude, identify the source of the infection and institute control measures.

Abstract methods

We conducted a descriptive study. Suspected cases were line listed from the hospital register of Mother and Child Hospital, Ondo. Five (5) blood samples were collected from suspected cases and analyzed using enzyme linked immunosorbent assay (ELISA) technique. Data were analyzed using Microsoft Excel.

Abstract results

31 cases were identified. Mean age was 20 months. Out of 31 cases, 17 (54.8%) were males. The estimated population of Jilalu ward is 18,712 with under 5 children population of 3,742 resulting in an attack rate of 0.8/100,000 populations. There were 2 deaths reported (Case fatality rate: 6.4%). Males (54.8%) were more affected than females. Age distribution of children affected during the outbreak was: – less than 6 months (3.2%), 6 and 11months (22.6%) and over 12mths (74.2%). The first case was on 23rd February, followed by a rapid increase in the number of cases leading to a peak on 3rd May and a progressive decrease. The last reported case was on 22nd May, 2013. Immunization coverage for measles antigen in the affected local government between February-May 2013 was 85%, 65%, 38% and 60% respectively. Measles-specific immunoglobulin M (IgM) was detected by in three (60%) samples.

Abstract conclusion

The low coverage of immunization might be identified as one of the key risk factor for the measles outbreak. Daily immunization services were commenced at the Mother and Child Hospital Ondo for children.

Keywords: Measles, Outbreak, Immunization and ELISA

PRESENTED BY: Adefisoye Adewole

ESCAIDE REFERENCE NUMBER: 20142192

Vaccine coverage, effectiveness and safety (3)

Rapid Vaccination Coverage Post-typhoonHaiyan: The Challenges in Measles Elimination-Tacloban City, Samar, Philippines, 2013

Paola Katrina Ching[1]

[1] Field Epidemiology Training Program, Philippines

Abstract

After the typhoon Haiyan struck Eastern Visayas, a vaccination activity to prevent outbreak was conducted in Tacloban City from November 26 to December 5, 2013. This targeted children ages six to 59 months for measles vaccination, oral polio vaccine (OPV) and Vitamin A administration. On Dec. 5, 2013, a team conducted rapid vaccination coverage survey.

Abstract methods

A cross sectional survey was done. A purposive sampling was utilized with highest priority based on active evacuation centers and communities which included the coastal areas, lowlands, mountains and national roads. Twenty households with eligible children were interviewed using a standard questionnaire. A survey on the knowledge, attitude & practices (KAP) regarding vaccination was also done among caregivers.

Abstract results

A total of 456 children inten evacuation centers and nine communities surveyed. Two hundred sixty-four (58%) were unvaccinated with measles. Three-hundred nine (68%) did not received OPV and 277 (61%) had no Vitamin A. Reasons for missing vaccination were lack of awareness about the vaccination activity (56%), child was away (12%) and child was sick (8%). Seventy-six caregivers were interviewed for KAP survey. Sixty-one (80%) knew about the activity and were informed through visits by vaccinators (38%). Majority (57, 75%) subjected their child for vaccination as protection for diseases. Majority (73%) who had positive attitude towards vaccination had their children vaccinated (56%).

Abstract conclusion

There was a large percentage of missed children present with the measles campaign only at 36%. Possible accumulation of susceptible children can result from the mobility of the displaced population and inadequate coverage.There is a need to conduct a wider coverage of mop-up vaccination with framework on the targets and strategies to cover ambulatory population and isolated areas.

Keywords: Rapid vaccination coverage, measles, Typhoon Haiyan, Tacloban City

PRESENTED BY: Paola Katrina Ching

ESCAIDE REFERENCE NUMBER: 20142277

Cost of public health management of sporadic invasive meningococcal disease, Baden-Wuerttemberg, Germany

Lukas Murajda[1], *Elisabeth Aichinger*[1], *Wiebke Hellenbrand*[2]

[1] State Health Office Baden-Wuerttemberg, Germany; [2] Robert Koch-Institute, Germany

Abstract

Incidence of sporadic invasive meningococcal disease (IMD) in Germany decreased from 0.73/100,000 in 2001 to 0.38/100,000 in 2013, but public health management still requires resources for contact tracing and post-exposure antibiotic prophylaxis (PEP). For household settings, ECDC estimated 284 (a) contacts require PEP to prevent one case. We estimated the cost of IMD management in the federal state of Baden-Wuerttemberg for modelling the cost-effectiveness of meningococcal B vaccination.

Abstract methods

We surveyed local public health authorities (LHA) to estimate number of household contacts in need of PEP/case (b) and time spent by medical officers and other staff on management of contacts of IMD cases in 2012. We costed this time in EUR according to the Civil Service Wage Agreement (e), estimated antibiotic costs in EUR (f) using minimum price per dose, and included cost of visit to hospital emergency services (g). We excluded costs of visits to GP and vaccination of contacts. Cost of preventing one IMD was calculated as (a/b)*(e+f+g).

Abstract results

On average, each IMD case had 11 contacts in need of PEP (range 0-51), of which 3.6 were household contacts. Average cost of staff at LHA for contact management was 440.33/case. The average cost of antibiotics for contacts was 219.14/case. The cost of a visit to emergency department was 161.70/case. Thus, cost of management of IMD contacts was estimated at 821.17/case. Preventing one IMD case would cost 284/3.6*821.17=~65,000.

Abstract conclusion

Substantial staff time is dedicated to manage contacts of sporadic IMD cases. However, overall incurred costs are moderate due to low IMD incidence. The high cost of preventing secondary cases can be justified in view of the severity and high treatment costs of IMD.

Keywords: Meningococcal infections, public health practice, Germany, cost effectiveness

PRESENTED BY: Lukas Murajda

ESCAIDE REFERENCE NUMBER: 20142147

Knowledge-practice gap in public health management of invasive meningococcal disease contacts in Baden-Wuerttemberg, Germany

Lukas Murajda[1]*, Elisabeth Aichinger*[1]*, Guenter Pfaff*[1]*, Wiebke Hellenbrand*[2]

[1] State Health Office Baden-Wuerttemberg, Germany; [2] Robert Koch-Institute, Germany

Abstract

In Germany, local public health authorities trace and manage contacts of invasive meningococcal disease (IMD). National guidance recommends post-exposure antibiotic prophylaxis (PEP) for all contacts in a household (-like) or day care setting as well as for other contacts with exposure to nasopharyngeal secretions of the index case. Post-exposure vaccination is additionally recommended for household contacts of cases with a vaccine-preventable serogroup. We evaluated the implementation of these recommendations.

Abstract methods

We surveyed 38 local public health authorities in Baden-Wuerttemberg to evaluate awareness and knowledge of national guidance and actual implementation in IMD contact management in 2012.

Abstract results

Thirty-four public health authorities (89%) responded and reported using guidance documents to manage contacts. Contact management information was available for 41 of 49 IMD cases notified in 2012. Of 154 household contacts, PEP was recommended to 148 (96%) and vaccination to 15 (10%), of which six were contacts of an IMD case with a non-vaccine-preventable serogroup. None of the cases had contacts in a day care setting. Of 83 healthcare workers with any contact to a case, 100% were recommended PEP, and 10% vaccination.

Abstract conclusion

Local health authorities in Baden-Wuerttemberg were familiar with national guidance for IMD contact management. However, PEP and vaccination were underused for household contacts while overused for healthcare workers. Some household contacts were recommended vaccination even when the index case did not have a vaccine-preventable serogroup. We informed the local health authorities and recommend further exploring the reasons for this knowledge-practice gap to improve compliance with the national guidance.

Keywords: Meningococcal infections, public health practice, Germany

PRESENTED BY: Lukas Murajda

ESCAIDE REFERENCE NUMBER: 20142148

Attitude, social norm, autonomy, anticipated regret and ambivalence: a model on vaccination acceptance

Olga Visser[1]*, Jeannine Hautvast*[1]*, Koos van der Velden*[1]*, Marlies Hulscher* [1]

[1] Radboud University Medical Center, The Netherlands

Abstract

The efficacy of a vaccination programme as a public health intervention is determined by its uptake. Yet, acceptance of vaccination is not self-evident. As a pertussis cocooning strategy is considered for implementation in the Netherlands, we aim to explore barriers and facilitators of vaccination acceptance among the target groups for vaccination. Consideration of these factors in the development of a vaccination programme for pertussis cocooning is necessary to optimize uptake.

Abstract methods

We conducted 13 focusgroup and 6 individual semi-structured interviews with members of target groups for pertussis cocooning (i.e. parents, maternity assistants, midwives and paediatric nurses). The topic list was based on literature review and a barrier framework. All interviews were transcribed verbatim and analyzed on thematic content (by two researchers).

Abstract results

Attitude (e.g. perceived risk of pertussis, pertussis vaccination and tranmission to an infant; perceived efficacy of pertussis cocooning; and moral values), social norm, autonomy, anticipated regret and ambivalence were identified as barriers for acceptance of vaccination.

Abstract conclusion

In conclusion, this study shows 5 important constructs influencing intention to accept pertussis vaccination, in the context of a cocooning strategy. The Reasoned Action Approach (RAA) best fitted these results, complemented with anticipated regret and ambivalence. We advise to account for the given constructs in introduction of the pertussis cocooning vaccination programme; and to use this model in introduction of future vaccination programmes and research on vaccination acceptance.

Keywords: Whooping Cough, Vaccination, Patient Compliance, Health Knowledge, Attitudes, Practice

PRESENTED BY: Olga Visser

ESCAIDE REFERENCE NUMBER: 20142130

Impact of vaccination on brucellosis seroprevalence in sheep and goats, Azerbaijan, 2007-2013

Natig Javadov[1], Naile Malakmadze[2], Ed Maes[3]

[1] Baku Veterinary Office, Azerbaijan; [2] NGCIS, United States; [3] CDC/CGH/DGHPWD, United States

Abstract

Azerbaijan reported 7533 (0.32% from tested animals) laboratory-confirmed cases of brucellosis in sheep and goats and 11218 (0.13% from tested) cases in cattle and 2397 (0.03%) cases in humans, in 2007-2013. Increase of seroprevalence among sheep and goats from 289.8 to 489.6 per 100,000 was observed during years 2000-2006. In 2007, Azerbaijan initiated its first annual vaccination against brucellosis in sheep and goats (vaccine Rev-1).

Abstract methods

We used sero-surveillance data to statistical comparisons between sero-prevalences of laboratory-confirmed (screened by Rose-Bengal and all positive by complement fixation) brucellosis among sheep and goats of both sex after the starting vaccination program. Purposive sampling of animals 10% to 15% of annual estimated number of adult sheep and goats in all 65 districts of Azerbaijan was done. Selection of animals was done regardless of vaccination status.

Abstract results

Annual vaccination of female sheep and goats was carried out in all country in 2007-2013, using an alternative schedule of vaccinating only juvenile female animals (3-11 months age) in 2007, 2009, 2010, 2012, 2013 and all adult female animals over 12 months of age in 2008 and 2011. In 2007, seroprevalence among sheep and goats was 375.8/100,000 (95%CI: 363.1-388.4). During 2008-2010 was 312/100,000 (95%CI: 300-323), accounting for 12% decrease, during 2011-2012 seroprevalence was 275/100,000 (95%CI: 258-292), accounting for 17% decrease and in 2013 seroprevalence was 189/100,000 (95%CI: 168-211), accounting for 21% decrease.

Abstract conclusion

A proportion decrease in brucellosis since 2007 demonstrates effectiveness of vaccination program. Purposive sampling and use of surveillance data may underestimate the full impact of vaccination. Introducing random sampling and obtaining information about specific farms of tested animals would provide needed evidence to offer specific recommendations on adjustment of current vaccination schedule.

Keywords: Brucellosis, vaccination, Rev-1, Azerbaijan, sheep, goats

PRESENTED BY: Natig Javadov

ESCAIDE REFERENCE NUMBER: 20142196

Impact of vaccination strategy on the incidence of measles in Slovakia, 1969-2013.

Henrieta Hudeckova[1], Viera Svihrova[1], Jana Zibolenová[1], Eva Malobická Veronika Szabóová[1]

[1] Department of Public Health Comenius University in Bratislava Jessenius Faculty in Martin, Slovakia

Abstract

Measles is a highly contagious disease. In Slovakia vaccination against measles was introduced in 1969. At present we use trivalent vaccine (measles, mumps and rubella), first dose is recommended for children aged 15–18 months and second dose for 10 year olds. Our objectives are to describe the impact of vaccination strategy on measles incidence at national level, to assess risk factors for measles infection and to recommend preventive and control measures.

Abstract methods

Retrospective review of measles cases reported since January 1969 to December 2013. Measles is obligatory reported communicable disease based on the standard criteria of ECDC in Slovakia. The data on morbidity are from the Epidemiological Information System (old versions: 1969-1997, new version: 1997-2013). This study covers and compares 3 periods: 1969-1984 (beginning of vaccination and its balance), 1985-1999 (decrease of endemic cases), 2000-2013 (elimination of measles).

Abstract results

During 1969-2013 were reported 110,565 cases: 108,091(98.8%; average incidence 145.4/100.000) in 1969-1984; 2,474 (2.2%; 3.0/100.000) in 1985-1999; 0 (0.0%) in 2000-2013. The highest age specific incidence was in the group of 0-4 year-old children. The incidence of measles decreased during 1969-1999. In the third period only 23 imported cases were reported. The vaccination coverage was at the highest level (98-99%) in the long term. In last children cohort (born in 2011) 95.8% vaccination coverage was noticed.

Abstract conclusion

Our analysis showed the positive impact of vaccination against measles on the epidemiological situation in Slovakia. Since 1999 measles has been eliminated, only imported cases were reported in our country. Risk factors that influenced the vaccination coverage are: increase of anti-vaccination activities and risk populations (Romany population and migrants). This work was supported by the SRaDA under the contract No. APVV-0096-12.

Keywords: Measles, incidence, vaccination, vaccination coverage, elimination.

PRESENTED BY: Henrieta Hudeckova

ESCAIDE REFERENCE NUMBER: 20142180

Surveillance (2)

Positive predictive value of the German notification system for infectious diseases at the local health department level, Berlin, 2012

Benjamin Bluemel[1], Michaela Diercke[1], Daniel Sagebiel[2], Andreas Gilsdorf[1]

[1] Robert Koch Institute, Germany; [2] Berlin State Office for Health and Social Affairs, Infectious Disease Epidemiology and Environmental Health, Germany

Abstract
The Protection against Infection Act requires notifying cases of infectious diseases to local health departments (LHD). LHDs transmit notifications meeting the case definitions (CD) via the regions to the national health authority (NHA). At the national level, the number of discarded notifications and the associated workload are not known. We quantified the proportion of discarded notifications to estimate the work that LHDs spend investigating them.

Abstract methods
We asked all Berlin LHDs (n=12) to extract all their notifications by disease for 2012. At the NHA, we extracted notifications received in 2012 by disease. We calculated the proportion of cases transmitted by LHDs to NHA among all notifications by disease (positive predictive value of the notification system, PPV). We included diseases with at least 10 notifications. We analysed individual investigation forms for discarded notifications available from one LHD to determine whether they needed thorough investigations (e.g. contacting and interviewing patient or physician, contact tracing).

Abstract results
Nine (75%) LHDs provided data, but we excluded one that did not keep all notifications electronically. Of 10,113 notifications recorded in 8 LHDs, 8,989 were transmitted (PPV=89%; range=77-97% across LHDs). Across diseases, PPV ranged from 30% (Hepatitis B) to 99% (Rotavirus). Of 166 investigation forms for discarded notifications reviewed in one LHD, 57% indicated that the LHD had conducted thorough investigations.

Abstract conclusion
LHDs discard many notifications, of which a large number require thorough investigation. Differences in the nature and notification requirements of diseases under surveillance may explain the range of PPVs. For diseases with low PPV, change in CDs or the legal framework concerning notifications may reduce the high workload associated with discarded notifications.

Keywords: Surveillance, evaluation, predictive value, disease notification, Germany

PRESENTED BY: Benjamin Bluemel

ESCAIDE REFERENCE NUMBER: 20141973

Quantifying workload and data quality of infectious disease notifications at local health department level in Germany

Anna Kuehne[1], Michaela Diercke[1], Benjamin Bluemel[1], Hermann Claus[1], Andreas Gilsdorf[1]

[1] Robert Koch Institute, Germany

Abstract
In Germany local health departments (LHD) contact notified cases and investigate required details to prevent spreading and to classify cases according to case definitions. To quantify this workload we analysed the duration of work process and required changes in notification data; to evaluate data quality we measured achieved data completeness.

Abstract methods
We analysed German notification data processed with SurvNet3@RKI-software (05/2011-05/2014) including all diseases with a total of › 10 cases. Duration from notification to final changes in notification data and number of changes since original notification were analysed by disease. Number of cases and number of changes were multiplied to estimate a rough proxy for workload regarding data-management at LHD-level. Completeness was analysed by reviewing fulfilment of case definition requirements.

Abstract results
Of all notifications in Germany 132,799 cases (12%) were processed with SurvNet3@RKI.Tuberculosis and brucellosis required the highest median process time of more than two months. Cases of listeriosis, Q-fever, Creutzfeldt-Jakob-Disease and brucellosis required a median of more than three changes to notification data. Taking the number of notifications by disease and data-changes into account, norovirus-gastroenteritis caused the biggest workload at LHD-level (38% of workload), followed by campylobacteriosis (17%), rotavirus-gastroenteritis (11%), influenza (7%), salmonellosis (6%), chicken pox and whooping cough (each 2%). Required clinical and laboratory information was lacking most often for cases of norovirus-gastroenteritis.

Abstract conclusion
Although rare diseases seem to require more effort to investigate notified cases than common diseases, common gastrointestinal and vaccine preventable diseases cause the biggest workload at LHD-level. Data quality is worst for the disease requiring most data-entries at LHD-level. Hence adjustments in mandatory notification, case definitions and use of innovative data-entry solutions to reduce workload in big outbreaks should be discussed.

Keywords: Data quality, surveillance, evaluation, disease notification, Germany

PRESENTED BY: Anna Kuehne

ESCAIDE REFERENCE NUMBER: 20141990

Development of a nationwide prospective, laboratory-based active surveillance system on the syndromes of infectious diseases in China

Weizhong Yang[1], Shengjie Lai[2], Luzhao Feng[2], Honglong Zhang[1], Hongjie Yu[2], Yajia Lan[3], Zhongjie Li[1]

[1] Key Laboratory of Surveillance and Early-warning on Infectious Disease, Chinese Centre for Disease Control and Prevention, Beijing, China. labsurv@163.com;
[2] West China School of Public Health, Sichuan University, Chengdu, China. lanyajia@sina.com

Abstract

In 2009, one nationwide prospective, laboratory- and sentinel-based surveillance system, the National Infectious Disease Surveillance Platform (NIDSP), was developed in China. The purpose of NIDSP is to strengthen the core capability of clinical and public health laboratories on etiological surveillance of infectious disease, and to discover the pathogenic spectrum of infectious diseases in China.

The surveillance objects were the patients with any one of the five defined syndromes, including syndromes of respiratory with fever, syndromes of rash with fever, syndromes of hemorrhagic with fever, syndromes of gastrointestinal, and syndromes of meningitis and/or encephalitis. NIDSP collected information on the sampled surveillance objects and various clinical specimens in the 290 sentinel hospitals located throughout the country. Standardized laboratory methods were employed and routinely performed by 92 network laboratories to the specimens to identify >50 kinds of infectious agents. Information regarding cases and laboratory testing results were reported through a web-based reporting system.

From 2009 to 2013, over 289,000 cases, specimens and laboratory results has been collected by NIDSP. And more than 13,000 isolates and 4,000 molecular information of isolates were obtained. Currently, NIDSP had far-reaching public health implications in China. For example, more and more clinical and public health laboratories at national and provincial level had the ability to detect many kinds of pathogens, and preliminary results generated from NIDSP suggested that respiratory syncytial virus (RSV) was common in young children aged <2 years that hospitalized with acute lower respiratory infections (ALRIs), while influenza was the most common one in adults hospitalized with ALRIs, etc.

The innovation of NIDSP to integrate clinical syndromic data with laboratory information could enhance the capacity of infectious diseases surveillance in China.

Keywords: Infectious disease, laboratory-based surveillance, China

PRESENTED BY: Weizhong Yang

ESCAIDE REFERENCE NUMBER: 20141998

Pilot season of a web-based self-reporting influenza like illness surveillance system in Denmark, 2013-14

Charlotte Kjelsø,[1], Michael Galle[1], Henrik Bang[1], Steen Ethelberg[1], Tyra Grove Krause[1]

[1] Statens Serum Institute, Denmark

Abstract

October 2013 we implemented Influmeter, a general population, voluntary, web-based influenza like illness (ILI) self-reporting system. Participants provided personal details upon enrolment and subsequently reported symptoms weekly within predefined categories. We evaluated the system use during the influenza season October 2013-May 2014, in order to decide on its future implementation.

Abstract methods

We compared participants of Influmeter to the Danish population registry in terms of sex, age and educational level. We calculated the weekly proportion of participants reporting. We calculated weekly ILI rates, proportion of ILI cases seeking medical assistance and compared ILI signals and timeliness with existing Danish ILI sentinel surveillance system, using the Danish ILI case definition.

Abstract results

By the end of April 2014, 1089 persons (67% females) had enrolled in Influmeter. Compared to the general population there were more 25-64 year old females (75% vs 51%, $p < 0.001$), more +65 males (28% vs 17%, $p < 0.001$), and fewer children/adolescents aged 0-24 years (11% vs 30%, $p < 0.001$). The proportion of participants reporting weekly declined from 90% in week 44, 2013, to 67% in week 20, 2014. 192 participants (18%) reported ILI symptoms at least once. Among these 22% reported to have consulted a doctor. Signals exceeded signals from the sentinel system and peaks were detected earlier.

Abstract conclusion

Influmeter volunteers were not fully representative of the Danish population but enrolment and commitment was acceptable. Influmeter may contribute valuable information on the burden of ILI in the general population as a high proportion of ILI cases did not consult a doctor. We recommend continuation of the system, and suggest to; adjust future analyses for uneven representation, target under-represented groups for enrolment, encourage continued reporting during the next influenza season.

Keywords: Influenza Human, Internet, Self Report, Volunteers, Burden of Illness.

PRESENTED BY: Charlotte Kjelsø,

ESCAIDE REFERENCE NUMBER: 20142085

Ways forward in meningitis detection and reporting Fes-Boulemane region, Morocco, 2010-2013

Tarik Rhandour[1], Ahmed Bouharras[2], Asmae Khattabi[1]

[1] NSPH (National School of Public Health), Morocco; [2] Provincial Cell of Epidemiology, Morocco

Abstract

Meningitis is a public health problem in Morocco, with an incidence between 1.2 and 3.6/100000 and case fatality around 11%. The fight against meningitis is still a Ministry of Health priority. In Fes-Boulemane region the incidence is higher than the national rate. We aimed at evaluating the surveillance system for meningitis in this region to identify room for improvement.

Abstract methods

We used data from the meningitis investigation forms collected into the regional database in the service of the public health and epidemiologic surveillance, and data from laboratory registry between 2010 and 2013, to describe cases in time, place and persons. We used a self administrated questionnaire to interview the staff of three different hospitals; and surveillance actors to assess simplicity, acceptability, representativeness, timeliness and data quality of the system.

Abstract results

Between 2010 and 2013, we recorded 311 cases, most of them (80,6%) were aged less than 15 years, and 15.4% were laboratory confirmed. Case-fatality was 10.3%. Among confirmed cases, 57% was not reported in the regional database. Of the interviewed staff, 89% completed the questionnaire:74% of clinicians used the case definition for diagnosis. 54% reported completion of the investigation form, 30% did not notify all types of meningitis. The system collected cases from all provinces in the region, all concerned services, and all the stakeholders were using it. Only 46% of the investigation forms were fully completed. The median delay between the case hospitalisation and the investigation was 3 days [2;6].

Abstract conclusion

Effort should be undertaken to strengthen clinicians and laboratory skills in diagnosing and reporting cases. The surveillance tools should be simplified and prompt investigation should be strongly encouraged. Laboratory confirmation should be widely possible.

Keywords: Meningitis, Surveillance, Evaluation, Case fatality rate

PRESENTED BY: Tarik Rhandour

ESCAIDE REFERENCE NUMBER: 20142124

Evaluation of Acute Flaccid Paralysis Surveillance System in Oyo State, South Western Nigeria – 2008-2012

Oluwaseyi Israel[1], Abbass Gbolahan[2]

[1] Nigeria Field Epidemiology Laboratory Training Programme, Abuja, Nigeria; [2] Oyo State Ministry of Health, Nigeria

Abstract

Nigeria remains one of the three countries globally with pockets of circulating wild polioviruses.Acute flaccid paralysis (AFP) is a clinical syndrome, it is the most common sign of acute poliomyelitis. Nationwide AFP surveillance is the gold standard for detecting cases of poliomyelitis. This study evaluated the AFP surveillance system in Oyo State for its attributes and performance.

Abstract methods

We reviewed surveillance data of Oyo state from 2008-2012 obtained from World Health Organization. We used the Centers for Disease and Control guidelines for evaluating surveillance systems. We quantitatively and qualitatively assessed the surveillance system's key attributes. We interviewed seven key informants at the state, local government and health facility levels using a semi-structured self-administered questionnaire. We analyzed the data using Microsoft excel.

Abstract results

The case definition and tools are simple to use and are acceptable to key stakeholders. Data flow from the local to the state is clearly defined and feed-back is regular.A total of 603 cases of AFP aged 0 months to 15 years were reported by the surveillance system between 2008 and 2012. Those below 5 years of age accounted for the largest proportion (76.9%) of cases reported and investigated. Of the 20 cases of laboratory confirmed polio in 2008 and 2009, 60% were male, 65% of them had wild polio virus 1 (WPV1) and 35% had WPV3. 35% of theseconfirmed polio cases had 0 dose of OPV.

Abstract conclusion

The system is sensitive, acceptable, timely, flexible with good data quality but unstable because its donor driven. The resources to maintain the system are inadequate at the state and the district levels. We advocate that the state should be financially committed.

Keywords: Evaluation, Acute Flaccid Paralysis, Poliomyelitis, Surveillance.

PRESENTED BY: Oluwaseyi Israel

ESCAIDE REFERENCE NUMBER: 20142178

Food and water-borne diseases & Zoonoses (2)

Salmonella Enteritidis outbreak in a primary school in Enying, Hungary, October 2013: importance of rapid outbreak response.

Ágnes Feher[1], Erika Krisztián[2], Judit Pászti[1], Maria Herpay[1], Ágnes Csohán[1]

[1] National Centre for Epidemiology, Hungary; [2] Public Health Authority of County Fejér , Hungary

Abstract

On 17/10/2013, a physician in Enying reported an unusually high number of gastroenteritis cases among pupils of a primary school. The same day we started an investigation to identify the source of this outbreak, prevent new cases and avoid recall bias.

Abstract methods

We actively looked for gastroenteritis cases among children absent from school and visiting local physicians. We defined cases as persons having gastroenteric symptoms who ate meals prepared by the restaurant between 13 and 16 October 2013. Between 18 and 19 October we conducted a cohort study among school pupils and personnel. We calculated food-specific attack rates (AR) and risk ratios (RR) with 95% confidence intervals (CIs). We collected specimens from cases, foods and kitchen surfaces.

Abstract results

We identified 116 cases (male/female ratio 0.8, median age 11 years). Eleven cases were admitted to hospital. The risk of gastroenteritis was higher among those who ate grated cheese (RR=2.6; 95% CI: 1.1-6.2), meatballs (RR=2.2; 95% CI: 1.3-3.7) or ate after 2 PM (RR=1.5; 95% CI: 1.16-1.91). 74/87 (85%) stool specimens were positive for S. Enteritidis. FT2 fagetype was identified in 38 cases' specimens and in 4 meals. Food and environmental specimens were contaminated with indicator bacteria.

Abstract conclusion

Due to the quick response we could efficiently identify contaminated foods. People who had eaten at the end of lunch time had higher risk to be come ill, pointing out the possibility of contamination of different meals in their preparation process. As a response to this outbreak, on 18/10/2013, we recommended closing the suspected restaurant and thorough cleaning the school canteen. Rapid investigation of this outbreak was essential to secure food left-over samples, prevent recall bias and implement efficient control measures.

Keywords: Salmonella Enteritidis, outbreak, cohort study, cooperation, contaminated food, environment

PRESENTED BY: Ágnes Feher

ESCAIDE REFERENCE NUMBER: 20141962

Outbreak of food-poisoning caused by *Staphylococcus aureus enterotoxin* --Muğla, Marmaris, Turkey, December 2013

Celal Tutus[1], Gurcan Paracikli[1], Demet Borekci[1], Derya Tetıker[2], Revasiye Gulesen[1], Bao-Ping Zhu[3], Fehminaz Temel[1], Mustafa Bahadir Sucakli[1]

[1] Public Health Institution of Turkey, Turkey; [2] Provincial Public Health Directorate of Mugla, Turkey; [3] World Health Organisation, Turkey

Abstract

On 23rd of December, 2013, 116 patients including students of 2 schools and workers of 17 work places who consumed lunch and/or dinner from the same catering company, applied to Marmaris State Hospital suffering from nausea, vomiting, stomach ache and diarrhea.This investigation was conducted to identify the cause and mode of transmission, and to implement control measures.

Abstract methods

We defined suspected case as onset during 23-24 December 2013 of ≥1 of the following symptoms in a person working in the 17 work places or 2 schools affected by this outbreak: nausea, vomiting, stomach ache, diarrhea, fever. A probable case was onset of vomiting or diarrhea. We conducted face-to-face interviews of 77 probable cases and 113 controls. Controls were chosen among asymptomatic students of the same schools and workers of the same work place willing to participate in the investigation. We took water and food samples, and stool and blood samples to identify the agent. We also took environmental samples from the kitchen of the catering company.

Abstract results

We identified 77 probable cases (attack rate: 16%). The epidemic curve showed that no significant distribution was seen according to sex and age. Of the 77 probable case-persons, 96% (74/77) and of the 113 control-persons, 32% (37/113) ate chicken kebab during lunch and/or dinner on the day of the case-person's illness onset (ORadj= 34, 95% CI= 8,8-129,7), after controlled for mushroom soup and salad. S. Aureus enterotoxin was identified from the leftover chicken kebab.

Abstract conclusion

This outbreak was caused by a S. Aureus enterotoxin in the chicken kebab. Investigations couldn't reveal contamination source. We recommended the catering company to implement control and prevention measures and good hygiene practices.

Keywords: Staphylococcus Aureus, enterotoxin, outbreak, foodborne

PRESENTED BY: Celal Tutus

ESCAIDE REFERENCE NUMBER: 20142033

A Salmonella School Outbreak Associated with Consumption of Éclairs, Osmaniye, Turkey, April 2014

Nalan Karakus[1]*, Nesrin Ata*[1]*, Ali Goktepe*[1]*, Fehminaz Temel*[1]*, Kahraman Tunckol*[2]*, Belkis Levent*[1]*, Eftal Bilge Demir*[2]

[1] Public Health Institution of Turkey, Turkey; [2] Public Health District Directorate, Turkey

Abstract

On 19 April 2014, a diarrheal disease outbreak in a school including students, teachers and staff, was reported to Early Warning and Respond Department by local authorities. We investigated to identify the cause and mode of transmission, and to implement control measures.

Abstract methods

We defined a probable case as onset of diarrhea or 2 of the symptoms: vomiting, self-reported fever, abdominal pain; in the school during 18-20 April; confirmed case as positive stool result for S.Enteritidis We reviewed medical records of the two hospitals and the school in the district, for case-finding. Among 461 students and staff, 444 (96%) participated the retrospective cohort study. We collected food specimens from school refectory and the pastry confectionery from which eclairs were ordered; stool samples for pathogen identification.

Abstract results

We identified 333 probable, 10 confirmed cases (attack rate %79). The main symptoms included diarrhea (98%), abdominal pain (91%), self-reported fever (90%) and vomiting (77%). The epidemic curve showed a peak 11 hours after lunch on 18 April. The attack rate among people who ate éclairs (94%) was 35 times compared to the ones who did not (3 %) (RRadj=34.5, 95% CI: 8.8-135). Salmonella enteritidis was identified in the éclairs and also in the stool samples. The same DNA pattern was identified from the isolates of eclairs and 4 of the stool samples by pulse –field gel electrophoresis.

Abstract conclusion

This salmonella outbreak was likely due to consumption of contaminated éclairs. We recommended the implementation of infection control policies such as training and certification of food handlers. Ministry of Agriculture closed down the confectionery and started the legal proceeding for the school to strengthen food safety measures.

Keywords: Salmonella,outbreak, foodborne, school

PRESENTED BY: Nalan Karakus

ESCAIDE REFERENCE NUMBER: 20142038

A Rotavirus Gastroenteritis Outbreak Caused by Drinking Water from Contaminated City Tap Water – Nigde City, Turkey, March 2014

Ebru Tozan[1]*, Pinar Duman*[1]*, Hanife Demet Elbasan*[2]*, Omur Aktepe*[2]*, Figen Sezen*[1]*, Fehminaz Temel*[1]*, Gulay Korukluoglu*[1]*, Bahadir Sucakli*[1]*, Cigdem Simsek*[1]

[1] Public Health institution Turkey, Turkey; [2] Provincial Public Health Directorate, Nigde, Turkey

Abstract

On March 18-2014, an increase in gastroenteritis patients was reported in Nigde, central Turkey. We investigated to identify the cause and mode of transmission and to implement evidence based control and prevention measures.

Abstract methods

We defined a probable case as onset of vomiting or diarrhea (≥3 episodes/day) among 0-14 age group, resident in Nigde during March 18-30 2014. In case-control study, we compared exposure histories between 88 case-patients randomly selected from 15 neighborhoods with highest attack rates and asymptomatic neighborhood control persons, matched by age groups. Matched (ORMH) and adjusted odds ratios (ORadj) were obtained through conditional logistic regression. We reviewed the hospital records for gastroenteritis-associated ICD-10 codes (A09, R11, K52) during outbreak period.We used bacterial culture, Real-time multiplex PCR to identify pathogens in clinical specimens, and Membrane Filtration Method to assess the quality of water.

Abstract results

In total, 605 excess gastrointestinal illnesses occurred during this outbreak. Of the case-patients, 80.7% (71/88) used tap water as source of drinking water compared with 52.3% (46/88) of control persons (ORMH=4.57, 95% Cl=2¬¬–10.3). Analysis showed a significant linear trend for drinking only tap-water, mixed water, and only bottled water, respectively (72%, 17.3%, 10.6%, p<0.001). When drinking only bottled water was taken as referance, drinking only tap water was 6.4 times higher in case patients compared with the control persons (ORadj=6.4, 95% Cl=2.1–19.1). Of the 10 stool specimens, 4 tested positive for Rotavirus. The water source samples were positive for E. coli and total coliform. Free chlorine level was 0 (zero) ppm in 5 of 7 samples.

Abstract conclusion

Contaminated tap water caused this rotavirus outbreak. We recommended that drinking tap water chlorination and monitoring should be done regularly.

Keywords: Water, Outbreak, Gastroenteritis, Case-Control studies

PRESENTED BY: Ebru Tozan

ESCAIDE REFERENCE NUMBER: 20142100

Surveillance of Hepatitis E virus (HEV) in swine farms and farmers and first identification of genotype 4 in Italy.

Giorgia Angeloni[1], Letizia Ceglie[1], Alda Natale[1], Isabella Monne[1], Giovanni Cattoli[1], Silvia Zamprogna[1], Alessia Schivo[1], Federica Zuliani[1], Erika Rampazzo[1], Katia Capello[1], Nadia Inglese[2], Cristiano Salata[2], Giorgio Palù[2], Lebana Bonfanti[1]

[1] Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Italy; [2] Department of Molecular Medicine, University of Padova, Italy

Abstract

Hepatitis E is an emerging zoonotic disease caused by a positive ssRNA virus, Hepatitis E virus (HEV). In Europe, pigs are the main reservoir. Genotype 3 of HEV (HEV3) has a worldwide distribution while genotype 4 (HEV4) mostly occurs in Asia. However, HEV4 has recently been isolated in pigs and humans in Europe.

Abstract methods

During 2011-2014, a monitoring plan was performed to evaluate the prevalence of HEV infection in different human populations and pigs in Italy. Assuming an expected herd-level seroprevalence of 50%, 175 pig farms were sampled. To detect at least one positive sample assuming a within-herd seroprevalence of 30%, 9 sera were collected and analyzed from each farm. Moreover, in 105 farms HEV presence was investigated collecting 10 fecal pools. In order to understand whether consumption of pork products or/and contact with pigs may represent a risk factor, sera were collected from farmers (no.127), general population(no.131) and vegetarian/vegan group (no.114).

Abstract results

Anti-HEV antibodies were detected in 65.7% (115/175,95% CI:58.2-72.7) of farms, while viral RNA was identified in 24.8% (26/105). Most of the identified strains belonged to HEV3. However, in one farm HEV4 was detected. HEV seroprevalence in humans was significantly different among the 3 groups ($p<0.001$): farmers showing the greatest prevalence (15.75%,95% CI:9.9-23.3) and general population the lowest (2.3%,95% CI:0.5-6.5). No significant differences were found between general population (omnivorous) and vegetarian/vegan group.

Abstract conclusion

The survey confirmed a wide spread of HEV in Italian pig herds. The finding of HEV4 can be an issue of concern, considering that it may cause a more severe clinical course in humans. Moreover, our findings reinforce the opinion that HEV infection in industrial countries could be associated with professional activity.

Keywords: HEV, Surveillance, Zoonoses, Professional risk

PRESENTED BY: Giorgia Angeloni

ESCAIDE REFERENCE NUMBER: 20142149

Hepatitis E virus antibody prevalence in hunters from a district in Hesse, Germany, 2013.

Anika Schielke[1], Veronika Ibrahim[2], Irina Czogiel[1], Mirko Faber[1], Christina Schrader[3], Paul Dremsek[4], Rainer G. Ulrich[4], Reimar Johne[3]

[1] Robert Koch Institute, Germany; [2] Veterinary Officer of Local Authority Wetteraukreis, Friedberg, Germany; [3] Federal Institute for Risk Assessment (BfR), Berlin, Germany; [4] Friedrich-Loeffler-Institut (FLI), Greifswald-Insel Riems, Germany

Abstract

In Germany, 17% of the general population have antibodies to hepatitis E virus (HEV). Pigs and wild boars are the main animal reservoirs of HEV genotype 3. We estimated seroprevalence among hunters with contact to wild boars to identify factors that may be associated with past or present HEV infection.

Abstract methods

In 2013, the local veterinarian authority in Wetteraukreis district (Hesse) engaged hunters who provided blood specimens and completed a questionnaire collecting information on age, sex, hunting-related activities and consumption of wild boar meat. Specimens of wild boars were taken during drive hunts in this district during the season 2012/2013. All specimens were tested for HEV RNA and anti-HEV antibodies. Binomial regression with logarithmic link was used to estimate prevalence ratios (PR).

Abstract results

Of 126 hunters (median age 55; 94% male) 21% tested positive for anti-HEV antibodies (95% confidence interval [CI] 13-28%). In the south-western part of the district, where wild boars had most acute HEV infections and highest anti-HEV prevalence, hunters who frequently used gloves when disembowelling wild boars had a lower anti-HEV prevalence (age-adjusted PR 0.12; 95% CI 0.02-0.86).

Abstract conclusion

Hunters may benefit from barrier protection, including wearing gloves when in contact with blood or body fluids of HEV animal reservoirs. Anti-HEV prevalence among these hunters did not significantly differ from the general population suggesting that other factors play a major role in the epidemiology of HEV in Germany.

Keywords: Hepatitis E virus, seroprevalence, wild boars, protective gloves

PRESENTED BY: Anika Schielke

ESCAIDE REFERENCE NUMBER: 20141957

Latebreaker **Abstracts**

Latebreaker Abstracts 16.10 – 17.10 Fri 7

Syrian refugees in lebanon: a community-based approach describing diseases and symptoms in informal settlements

Rami Malaeb Mohamad K Haidar[1], Folaranmi Ogunbowale[1], Marie-Amélie Degail[1]

[1] Première Urgence – Aide Médicale Internationale, Lebanon

Abstract
In response to the displacement of 996,276 Syrian refugees in Lebanon, PU-AMI intervenes on three acute needs: (i) shelter, (ii) health and (iii) water, sanitation and hygiene. Considering the poor living conditions of the Syrian refugees in the informal settlements (IS), the risk for disease outbreaks to occur called for the implementation of a Community-based health surveillance system (CBSS) in order to inform and adapt further health interventions targeting the Syrian populations living in IS in Lebanon.

Abstract methods
The CBSS is based on a network of 75 focal points designated in their settlement. Individual data was collected daily from 75 IS including demographics, symptoms, dates of onset, health seeking behaviour, drug prescriptions, and the difficulties accessing healthcare including out-of-pocket payments. Data on clusters of cases were reported through line listings – demographics, date of symptoms' onset, recovery, and health seeking behaviour.

Abstract results
During four months, 1,108 cases were reported, where the incidence density of illness reached 40 cases per 1,000 people in 1 month. Among all symptoms, fever had the highest rates (30%), followed by skin rash (17%), while acute watery diarrhoea was present in 10% of the cases. Six clusters of cases were detected in Akkar and Saida including scabies, diarrhoea, respiratory symptoms, and conjunctivitis.

Abstract conclusion
After four months of implementation, the CBSS enabled to inform on the health status of the Syrian refugees in 75 settlements. The findings lead to the opening of two primary healthcare centres in Akkar and Saida and to reach a better integration of PU-AMI activities, enabling to widen the free access to healthcare for Syrian refugees, and the adaptation of health promotion messages disseminated in the settlements.

Keywords: Refugees, Community-based health, Surveillance System, Syria, Lebanon, Disease Outbreaks

PRESENTED BY: Mohamad K Haidar

ESCAIDE REFERENCE NUMBER: 20142502

.

National outbreak of Yersinia enterocolitica O9 infections in military camps and in the general population associated with consumption of mixed salad, Norway 2014

Emily MacDonald[1], Margot Einöder-Moreno[2, 3], Katrine Borgen[1], Lin Thorstensen Brandal[1], Lore Diab[4], Øivind Fossli[5], Bernardo Guzman Herrador[1], Ammar Ali Hassan[5], Gro S. Johannessen[6], Eva-Jeanette Johansen[5], Roger Jørgensen Kimo[4], Tore Lier[7], Bjørn-Leif Paulsen[5], Rodica Popescu[5], Charlotte Tokle Schytte[5], Kristin Sæbø Pettersen[6], Line Vold[1], Astrid Louise Wester[1], Marit Wiklund[7], Karin Nygård[1]

[1] Norwegian Institute of Public Health, Norway; [2] Department of Infectious Disease Epidemiology, Norwegian Institute of Public Health, Oslo, Norway; [3] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden; [4] Norwegian Armed Forces, Norway; [5] Norwegian Food Safety Authority, Norway; [6] Norwegian Veterinary Institute, Norway; [7] University Hospital of North Norway, Norway;

Abstract
In May 2014, two cases of Yersinia enterocolitica (Y. enterocolitica) O9 infections were reported from a military camp in northern Norway. Concurrently, an increase in Y. enterocolitica infections was observed in the Norwegian Surveillance System for Communicable Diseases. In less than one week >20 cases were identified from three military camps. We investigated to ascertain the extent of the outbreak and identify the source in order to implement control measures and prevent further spread.

Abstract methods
A case was defined as a person with laboratory-confirmed Y. enterocolitica infection with the outbreak MLVA-profile since 1 March 2014. We compared cases with controls frequency matched by company (ratio 1:4) in two camps. We calculated odds ratios (OR) and 95% CI using logistic regression. Traceback investigations were conducted to identify common suppliers and products in commercial kitchens frequented by cases.

Abstract results
Between 9 April and 28 May, we identified 133 cases, of which 117 were linked to one of four military camps and 16 were civilians from geographically dispersed counties. Five cases were food handlers employed in the most affected military camp (n=87 cases). Illness was associated with mixed salad (OR=10.0; 95%CI=0.9-124). Traceback investigations indicated that the four military camps and cafeterias visited by 14/16 civilian cases had the same supplier of fresh produce. All kitchens had received salads containing iceberg lettuce or raddichio rosso from a salad processer with significant lapses in hygiene upon inspection. No relevant salad batches were available for sampling.

Abstract conclusion
The most likely source of the outbreak was salad mix containing imported raddichio rosso, due to its long shelf life. This outbreak is a reminder that fresh produce should not be discounted as vehicle in prolonged outbreaks.

Keywords: Food-borne diseases, disease outbreaks, Yersinia enterocolitica, Norway

PRESENTED BY: Emily MacDonald

ESCAIDE REFERENCE NUMBER: 20142518

Outbreak with Listeria monocytogenes Investigated using Whole-Genome Sequencing, Denmark, 2014

Steen Ethelberg[1], Anne Kvistholm Jensen[1], Luise Müller[1], Jonas Torgny Larsson[1], Tenna Jensen[2], Søren Persson[1], Tyra Grove Krause[1], Eva Møller Nielsen[1]

[1] Statens Serum Institut, Denmark; [2] Danish Food and Veterinary Administration, Denmark

Abstract
In Denmark, invasive listeriosis is surveyed clinically and microbiologically; an average of 50 cases occur annually. Outbreaks are rare, but inherently difficult to solve. June 26, 2014, we detected an outbreak in Denmark. We investigated with the aim of removing the source and preventing further cases.

Abstract methods
We performed whole-genome sequencing (WGS) on listeria isolates from patients and available isolates from food. We defined cases and performed comparisons to food isolates using single nucleotide polymorphism (SNP) analysis. Through interviews, we established cases' institution and food exposure histories. Food production facilities were inspected and sampled and we performed trace-back/forward of food delivery.

Abstract results
Case-isolates differed by one or zero SNPs. One isolate obtained from pork roll sausage ('rullepølse') from Company A was identical to the outbreak strain by WGS. An above-normal proportion of cases were infected while hospitalised/institutionalised; institutions were supplied through different wholesalers by Company A. Further testing within this company demonstrated the presence of listeria in 10 of 20 products sampled. Beginning 12 August, all products were traced and recalled from more than 6000 food establishment recipients. The outbreak strain was found in establishments directly supplied by Company A. Cases appeared for a further four weeks; then stopped. As of 21 September 38 cases were known of which four occurred in 2013; 16 cases died.

Abstract conclusion
Sausages from one production facility caused this outbreak. Pork roll sausage is popular among the elderly; serving it at hospitals may have contributed to the high case fatality rate. Typing of food isolates using WGS was instrumental in swiftly locating the source of infections, likely preventing further illnesses/deaths. Isolates from examined food products should be retained for future analysis wherever possible.

Keywords: Outbreaks Sequence Analysis, DNA, Molecular Epidemiology, Molecular Typing, Listeria

PRESENTED BY: Steen Ethelberg

ESCAIDE REFERENCE NUMBER: 20142520

Latebreaker **Abstracts**: Public Health Event

Public Health Event 17.10 – 18.20 Fri 7

Ebola virus disease outbreak in Nigeria: Lessons to learn

Christian Lorenz Althaus[1], Sandro Gsteiger[1], Nicola Low[1]

1 Institute of Social and Preventive Medicine (ISPM), University of Bern, Switzerland)

Abstract

International travel has already spread Ebola virus disease (EVD) to major West African cities as part of the unprecedented epidemic that started in Guinea. An infected airline passenger who arrived in Nigeria on July 20, 2014 caused outbreaks in Lagos and Port Harcourt. By September 13, there were 21 reported EVD cases including 8 deaths.

Abstract methods

We quantified the impact of early control measures in preventing further spread of EVD in Nigeria and calculated the risk that a single undetected case will cause a new outbreak. We extended our EVD transmission model (Althaus, PLOS Curr, 2014 Sept 2) and applied it to the outbreak in Nigeria.

Abstract results

We estimated the basic reproduction number Ro=5.4 (95% confidence interval [CI]: 4.2-6.8). We also found that the reported control interventions including case isolation, contact tracing and surveillance were successful in reducing the reproduction number below unity 15 days (95% CI: 10-21 days) after the death of the index case. Using the estimated value of Ro in Nigeria, we calculated that the risk of an outbreak from a single undetected case was 81% (95% CI: 76-85%).

Abstract conclusion

Ro in Nigeria was substantially higher than in Guinea, Sierra Leone and Liberia. This shows the large number of contacts at risk of infection when EVD is introduced through air travel. Cities at the highest risk of imported cases should have strong surveillance at airports and the capacity to implement intensive control measures.

Keywords: Ebola virus, mathematical model, outbreaks, contact tracing, Nigeria

PRESENTED BY: Christian Lorenz Althaus

ESCAIDE reference number: 20142515

The UK Imported Fever Service: a one stop shop for expert advice and quality assured specialist diagnostics in the management of unwell travellers returning from areas affected by the 2014 Ebola outbreak

Amanda Semper[1], Caoimhe Nic Fhogartaigh[2], Andrew Simpson[1], Emma Aarons[1], Jane Osborne[1], Peter Chiodini[2], Nicholas Beeching[3], Tim Brooks[1]

[1] Public Health England, United Kingdom; [2] Hospital for Tropical Diseases, United Kingdom; [3] Liverpool School of Tropical Medicine, United Kingdom

Abstract

The UK Imported Fever Service (IFS) provides specialist advice and diagnostic tests for unusual infections to support hospital doctors managing febrile returning travellers, including those entering the UK from areas experiencing outbreaks of serious disease, notably the current Ebola virus disease (EVD) outbreak in West Africa.

Abstract methods

The volume of calls to the IFS 24/7 phone line was monitored in July and August 2014. Calls about cases from EVD-affected areas were assessed for VHF risk, clinical management and infection control advice was offered and if needed, samples were referred for IFS tests. Cases with a significant VHF risk were tested using an extended PCR panel [VHFs (Ebola, Marburg, generic filovirus, Lassa fever and CCHF) plus dengue, chikungunya, Rift Valley fever, rickettsia, leptospirosis and malaria].

Abstract results

Routinely the IFS receives ~50 calls/month. Calls climbed in late July 2014, peaking at 282 in August, following increased global awareness of the worsening EVD outbreak. Many calls were enquiries from clinical and public health professionals seeking procedural guidance or reassurance that patients had no credible VHF risk and that full hospital investigation and management should proceed. 59/282 calls in August concerned unwell travellers returning from EVD-affected areas and required a full VHF risk assessment; 24/59 were tested using the extended PCR panel. 1/24, a known case repatriated from Sierra Leone, tested positive for EVD. Negative VHF results were available on the same day as sample receipt, allowing de-escalation of hospital infection control measures. 9/24 tested positive for malaria and 1/24 for leptospirosis; all received prompt treatment.

Abstract conclusion

The IFS is a key component in the UK's national preparedness to detect, investigate, and manage potential Ebola cases in travellers returning from EVD-affected areas.

Keywords: disease outbreaks, hemorrhagic fevers, viral, Ebola hemorrhagic fever, Ebola virus disease, diagnostic services

PRESENTED BY: Amanda Semper

ESCAIDE REFERENCE NUMBER: 20142509

Indexes

Index by Subject

78	The characterization of hepatitis C infections from 1995 to 2013 in Finland	Poster
79	Burden of non-typhoid Salmonella and Campylobacter, metropolitan France, 2008-2012	Poster
79	Incidence and socio-economic impact of acute gastro intestinal illness, Sweden, 2013-2014	Poster

Emerging and vector-borne diseases

32	Awareness of Lassa Fever Transmission and Practices in A Semi Urban Community, Oyo state, Southwest Nigeria. February 2014.	Parallel
33	Targeted Mass Drug Administration of antimalarials to prevent malaria establishment in Lakonia Greece-transmission period 2013	Parallel
33	Validating serological tests for the diagnosis of Visceral Leishmaniasis in an endemic European country	Parallel
125	Very active circulation of lineage 2 West Nile virus (WNV) in mosquito vectors in Southeastern Romania 2012-2013	Poster
126	Insufficient mosquito protection measures among migrants in an area with re-emerging malaria, Greece 2013	Poster
126	Assessment of distribution of morbidity and mortality due to malaria in Ondo State, south-west Nigeria, 2012: a secondary data analysis	Poster
127	Validation Of Cyscope Microscope, Quantitative Buffy Coat And Rapid Diagnostic Kit For Malaria Diagnosis Among Clinic Attendees In Southwest Nigeria	Poster
127	Chikungunya outbreak in French Territories in the Americas, November 2013 - May 2014: possible risk of international spread	Poster
128	Explaining the geographic spread of emerging viruses: a new framework for comparing viral genetic information and environmental landscape data	Poster
128	A Case-Control Study on the First Reported Chikungunya Outbreak in Rapu-rapu, Southern Luzon, Philippines, 2012	Poster

Epidemiology and microbiology driving public health policy

57	Decreased prevalence of carried Streptococcus pneumoniae and genetic shifts of non-vaccine serotypes after changing the 7 pneumococcal conjugate vaccine to the 13-valent vaccine in Norway	Parallel
58	Decision-rules for regional recommendation of vaccination against Tick Borne Encephalitis in Sweden	Parallel
58	Epidemiological impact and cost-effectiveness of vaccination against meningococcal B disease in France	Parallel
59	Evaluating implementation of polio vaccination and stool screening among Syrian asylum seekers, Germany, 2013/2014	Parallel
59	Notifiable disease or not: a tool to help public health policy makers decide	Parallel
101	Polio stool surveillance for refugee children from Syria, Pakistan, Somalia and Afghanistan coming to Rhineland Palatinate from January until April 2014	Poster
102	Tularemia in Sweden 1984-2012, epidemiologic trends and spatial correlation with ecological factors	Poster
102	Cholera outbreaks in Ibadan, Oyo State, Nigeria-2013: Identification of circulating strain and its antimicrobial susceptibility pattern	Poster
103	Trends of human monophasic Salmonella Typhimurium 1,4,[5],12:i:- in Finland, 2003-2013	Poster
103	Which is the most important marker to assess when predicting the severity of an STEC infection, the shigatoxin subtype or serotype?	Poster
104	Varying implementation and guidelines for screening for infectious disease among newly arrived migrants: A need for EU-level guidelines?	Poster

Healthcare Associated Infections

69	Are early deaths following bloodstream infections preventable?	Poster
69	Examining the rate of invasive Candida infection in UK critical care units using multi-level modelling: a prospective cohort study	Poster
70	A large-scale outbreak of viral keratoconjunctivitis related to healthcare-associated transmission in Canada	Poster
70	Outbreak of infections by *acinetobacter baumanii* in a critical care unit	Poster
71	Hospital-acquired Clostridium difficile infection in a Hematology center from Cluj-Napoca, Romania, 2013	Poster
71	Problems associated with the use of antimicrobials: evolution of clostridium difficile infections in the period 2011-2013	Poster
98	Determining the Effect of Social Deprivation on the Prevalence of Healthcare Associated Infections in Acute Hospitals: a multivariable analysis of a linked data set	Poster
98	Attributing gastroenteritis morbidity to 16 enteropathogens in children attending day care	Poster
99	Increased short-term, but decreased long-term risk of hospitalization for gastroenteritis in children attending day care: a registry-based cohort study	Poster
99	An outbreak of multidrug-resistant Pseudomonas aeruginosa in a long-term care hospital in Osaka prefecture, Japan	Poster

100	Control actions in first hospital outbreak of highly virulent Clostridium difficile ribotype 027 in Saxony-Anhalt, Germany 2013-2014	Poster
100	Quantifying the burden of paediatric hospital-acquired bloodstream infection in England by using a multistate analysis of linked routine data	Poster
101	Knowledge, Attitude, and Practice (KAP) surveillance on phlebitis prevention among nurses in large hospital in Baku, Azerbaijan	Poster

HIV and sexually-transmitted infections

45	Molecular epidemiology suggests ongoing transmission of hepatitis B virus in rural parts of the Netherlands, 2009-2013.	Parallel
45	Epidemiology and antimicrobial resistance of gonorrhea in Finland, 2007-2013	Parallel
46	Was there any impact of the ECDC Guidance on Chlamydia control in Europe five years after publication?	Parallel
46	Communicating better with MSM - better prevention of HIV/AIDS/STIs and hepatitis	Parallel
47	Surveillance in the time of austerity; Portuguese HIV/AIDS Surveillance achieves a 30% improvement in efficiency after LEAN inspired changes to processing.	Parallel
93	Survival, causes of death, and risk factors associated with mortality in Barcelona HIV new diagnoses. 2001-2013	Poster
93	How can we establish routine chlamydia testing in general practice for young adults? Exploring the barriers in 4 European countries.	Poster
96	HIV testing data suggest unmet prevention needs among men who have sex with men (MSM) in Poland	Poster
96	Chlamydia trachomatis tests in males in 5 Federal States of Germany, 2008-2013	Poster
97	HPV testing using Dried Urine Spot as cervical cancer screening tools in low-income countries	Poster
97	Outbreak of syphilis in men who have sex with men living in rural North Wales associated with the use of social media	Poster

Influenza

34	Transmission of the first influenza A(H1N1)pdm09 pandemic wave in Australia was driven by undetected infections: pandemic response implications	Parallel
34	Influenza surveillance in animals: What is our capacity to detect emerging influenza viruses with zoonotic potential?	Parallel
35	Pandemic influenza vaccination coverage and severe influenza outcomes during seasons 2009/10 and 2010/11 in five Nordic countries.	Parallel
35	Impact of antiviral therapy on adverse outcomes among hospitalised patients with confirmed influenza A (H1N1)pdm09 during the 2009-2010 pandemic in the UK	Parallel
36	Contact tracing following influenza exposure on aircraft	Parallel
36	Preliminary influenza vaccine effectiveness estimates from the I-MOVE multicentre case-control study in Europe, 2013-14: moderate, but heterogeneous results by country	Parallel
104	Outbreak of Mass Psychogenic Illness at a High School--Amhara Region, Ethiopia, April, 2010	Poster
105	Early influenza vaccine effectiveness: a good proxy for final estimates in Spain in the last four seasons 2010 - 2014	Poster
105	Low to moderate vaccination coverage for seasonal influenza, pneumococcal disease and pertussis among adult population at risk, Ireland, 2013	Poster
106	Factors associated with adverse reactions to the flu vaccine in health personnel	Poster
106	Health Related Quality of Life and Influenza in a Fragile Population	Poster
107	Modelling Individual Protective Decisions within an Influenza Epidemic	Poster
119	Estimates of influenza vaccine effectiveness in Hungary, 2013-14: as part of a multi-centre European case control study (I-MOVE)	Poster
120	Seasonal influensa vaccine effectivness 2011-2014: a population cohort analysis from 2.3 million individuals in Stockholm County	Poster
120	The attitudes of health care workers towards seasonal influenza vaccination for programming an effective communication campaign: the experience of a tertiary referral paediatric hospital, Italy, 2013-2014	Poster
121	Evolution of adverse reactions to the influenza vaccination in health personnel in the period 2006-2013	Poster
121	Influenza Outbreaks in Long-term Care Facilities during the 2013/2014 Influenza season in the Health Service Executive (HSE) East region of Ireland: a prospective study.	Poster
122	Distribution of influenza virus types and subtypes during summer is associated with the distribution during upcoming winter season, EU/EEA, 2005-2014	Poster

Intervention studies in public health

122	Determinants of non-response in infectious disease public health programmes in primary health care - HCV screening in the general population	Poster
123	Survey of Knowledge, Attitude and Practice (KAP) on anthrax in Gakh - Azerbaijan 2012	Poster
123	Health Assessment Survey of Selected Evacuation Centers and Health Facilities in Affected Areas Post Typhoon Haiyan – November, 2013	Poster
124	Health Protection Surveillance during a summer of Mass Gatherings: The 2013 Experience in Northern Ireland	Poster
124	A pilot evaluation of the ECDC's assessment tool for EU candidate countries	Poster
125	Designing and conducting a cross-border outbreak simulation to practice and evaluate cross-border infectious disease control in the Euregion Maas-Rhine (Netherlands, Germany and Belgium)	Poster

Measles

62	The transcontinental spread of measles from the Netherlands to Canada and the United States in 2013/2014: The well-travelled D8 measles genotype	Parallel
63	Cross-border health threat: a measles outbreak on a cruise ship, western Mediterranean sea, 2014	Parallel
64	Measles Elimination in Portugal: data from 2004 to 2013	Parallel
64	Measles Outbreak in Olorunda Local Government-Osun State, Nigeria, January-April, 2013	Parallel
63	2013 Outbreak of Measles in a Non-Immunizing Population in Alberta, Canada: How Preparedness Planning Assisted in Containing Transmission to Ten Households	Parallel

Novel methodological approaches for disease investigation, surveillance and control

22	Application of novel methods to assess the response capacity of front-line laboratories to influenza in the UK, 2013	Parallel
22	Interpretations of associations: Assessing the plausibility of results found in a matched case-control study on sporadic human salmonellosis in Lower Saxony, Germany, 2011-2013	Parallel
23	Transmission dynamic of MERS-CoV: Multiple imputation approach to estimate the date of onset	Parallel
23	Early detection of influenza activity using telephone helpline data	Parallel
24	Effectiveness of interventions that apply new media to improve vaccine uptake and vaccine coverage: a systematic review	Parallel
107	Web-based questionnaire valuable for timely outbreak response in a gastrointestinal outbreak in Copenhagen, January 2014	Poster
108	Recall period and kind of serving influence recall error in self-reported food consumption histories – relevance for outbreak investigations, Germany, 2013.	Poster
108	Use of a market research panel for control recruitment in a case-control study provides time and resource savings: national outbreak of Salmonella Mikawasima, United Kingdom, 2013	Poster
109	Event Mobile Application (EMA-i): A novel tool for field rapid disease reporting and information sharing	Poster
109	Medi+board - the public health dashboard for early warning, risk assessment and response	Poster
110	A multidisciplinary team approach to control an outbreak due to multidrug-resistant Pseudomonas aeruginosa.	Poster
129	A social media campaign for gonorrhoea control in Ireland	Poster
129	A novel automated data extraction and transmission tool for identification of influenza- and pneumonia-associated diseases based on ICD-10 data from German primary care practices	Poster
130	Evaluation of a new automated surveillance tool for hospital acquired urinary tract infections in Denmark	Poster
130	Using a social marketing framework to inform education aimed at increasing appropriate antibiotic use amongst 15-18 year olds: an international project	Poster
131	Informing future surveillance for carriage of multi-resistant gram negative bacteria: problems with recruiting to an English stool sample cross-sectional community prevalence study	Poster
131	Evaluation of the EUFRAT risk assessment tool	Poster

Outbreaks

24	Catering risky food to those at-risk: Salmonella Derby outbreak among the elderly in Berlin, December 2013/January 2014	Parallel
25	A national outbreak of Salmonella Mikawasima in the UK, 2013: did proton pump inhibitors play a role?	Parallel
25	Salmonella foodborne outbreak following a wedding party--Ust-Kamenogorsk City, East Kazakhstan Region, April 19-20, 2013	Parallel
26	MLVA-typing of Yersinia enterocolitica identified Christmas pork as the source of an outbreak in Norway, December 2013 to February 2014	Parallel

26	Are ready-to-eat salads ready to eat? An outbreak of Salmonella Coeln linked to imported, mixed, pre-washed and bagged salad, Norway, November 2013	Parallel
41	Outbreak of Yersinia enterocolitica serogroup O:9 in Norway December 2013 to February 2014, due to a traditional processed Christmas pork	Parallel
40	Investigation of a National Outbreak of Verotoxigenic E. coli (VTEC) in Ireland, 2013.	Parallel
40	A Legionnaires' disease outbreak associated with cooling towers in Warstein, Germany, August 2013	Parallel
41	Norovirus outbreak after corporate birthday party buffet associated with asymptomatic catering staff in Bavaria, Germany, December 2013	Parallel
41	Outbreak of Yersinia pseudotuberculosis O1 infection in Southern Finland associated with raw milk consumption, February- April, 2014	Parallel
42	Sub-clinical pertussis infection in teenage children as a vehicle for transmission; seroepidemiology of recent infection during a school outbreak, UK 2012	Parallel
42	An outbreak of acute gastroenteritis associated with group A Rotavirus in a residential long-term care facility in Slovenia, April 2013	Parallel
43	Cluster of diarrhea following typhoon Haiyan, Philippines, November-December 2013: A four-hour investigation	Parallel
43	A prolonged outbreak of Salmonella Infantis associated with pork products in central Germany, April to October 2013	Parallel
44	Outbreak of Salmonella Goldcoast associated with whelks: a novel vehicle of infection, England, 2013	Parallel
44	The perils of gourmet eating: outbreak of gastroenteritis due to enteric viruses at a high-end London restaurant, January 2014	Parallel
80	No-heat-treated frozen raspberries, main vehicle of a norovirus outbreak in Oslo, November 2013	Poster
80	An outbreak of hepatitis A linked to berry-mix cake in Norway, 2014: how to overcome recall bias?	Poster
81	An outbreak investigation of Cryptosporidiosis in Dorset, England, in April-May 2013: a case-control study strengthened epidemiological evidence.	Poster
81	Outbreak of food-borne Streptococcus pyogenes infection in 21 factories: Bursa Province, Turkey, June 2013	Poster
82	Were Salmonella hiding in Ketchup? Diffuse nationwide outbreak of Salmonella Manhattan, Germany 2013	Poster
82	Follow the Food Flow - Investigational Tracing for Outbreak Clarification	Poster
110	Outbreak of Salmonella infantis associated with consumption of laverbread in Wales, 2014: case-case study supported temporary product withdrawal	Poster
111	Nation-wide outbreak of listeriosis in Sweden 2013-2014 associated with cold cut meat	Poster
111	An Outbreak in a Primary School Associated with Consumption of a Traditional Food, Ankara, Turkey, March 2014	Poster
112	An outbreak of foodborne intoxication caused by Staphylococcus aureus at a large community fair in Toronto, Canada	Poster
112	Relapsing fever outbreak investigation in Bahir-Dar, Amhara region, Ethiopia, 2012	Poster
113	Robin Hood takes aim at the mode of infection, food-borne versus person to person transmission in a Norovirus outbreak in Rhineland-Palatinate, 2014	Poster
132	Don't count your chicken livers: An outbreak of Campylobacter not associated with chicken liver parfait, UK, November 2013.	Poster
132	An outbreak of Microsporum canis in two elementary schools in a rural area close to the capital city of Slovenia	Poster
133	An outbreak of Cholera due to consumption of sachet water in Abeokuta, Ogun state, Nigeria, July 2013.	Poster
133	Outbreak of influenza A in a primary school in the North East of England, January 2014.	Poster
134	Outbreak of norovirus GI.3 among lunch guests at a hotel in southern Finland, 2013	Poster
134	An outbreak of measles in Ondo West LGA, Ondo State, Nigeria. February-May, 2013	Poster

Public health microbiology and molecular epidemiology

75	Detection of diphtheria toxin gene-bearing and non-toxin gene-bearing Corynebacterium diphtheriae and Corynebacterium ulcerans/ Corynebacterium pseudotuberculosis using a quadruplex Rotor-Gene Q PCR assay	Poster
75	Human Papillomavirus (HPV) and Chlamydia trachomatis (Ct) infections in undocumented immigrant women in Milan (Northern Italy)	Poster
76	Development of a Directory of Microbiology Laboratory Services (EULabServe) to support laboratory based surveillance and preparedness in the EU	Poster
76	Factors Influencing Infant Feeding Choices By Mothers Attending Prevention of Mother To Child Transmission of HIV Clinics in Oyo State, Nigeria	Poster
77	Detection of Carbapenem, Cephalosporin, and Quinolone Resistance coding genes in E. coli isolated from hospital waste water : a matter of concern	Poster

77	International External Quality Assessment (EQA) for molecular detection of Lassa virus (LASV) performed in 2013 reveals the need to optimize diagnostic protocols	Poster

Surveillance

52	The use of syndromic surveillance to monitor the incidence of arthropod bites requiring healthcare in England	Parallel
53	Evaluation of the Austrian Measles Surveillance, 2009-2013	Parallel
53	CIDARS: A nationwide web-based automated outbreak early warning system in China	Parallel
54	The impact of new national guidance for public health management of enteric fever in England.	Parallel
54	Mobile-based disease surveillance from formal and informal health care providers in resource-limited settings. Experience from Madhya Pradesh, India	Parallel
60	Public Health Monitoring of the XX Commonwealth Games, Glasgow 2014	Parallel
60	Establishment of Active Disease Surveillance in Areas Affected by Super Typhoon Haiyan - Eastern Visayas, Philippines, 2013	Parallel
61	Implementing a syndromic surveillance system in Kefalonia island, Greece, after destructive earthquakes, February-March 2014. Results and evaluation of the surveillance system.	Parallel
61	Etiology of Influenza-Like Illnesses in Reunion Island, general practitioners sentinel network, 2011 and 2012	Parallel
62	Prevalence of hepatitis E virus infection among blood donors resident in Apennines mountains, central Italy	Parallel
116	Evaluation of the sentinel practitioner's network in Reunion Island, 2005-2012	Poster
117	Trends and epidemiological patterns of hepatitis E infections in Hungary, 2002-2013	Poster
117	Seroepidemiology in foodborne campylobacter infections	Poster
118	Latvia needs to strengthen its surveillance of acute flaccid paralysis to ensure its polio-free status	Poster
118	Stool screening for wild polio viruses (WPV) among Syrian refugees and asylum seekers, Germany, 2013/2014	Poster
119	A two-year active surveillance of community-acquired pneumonia among adults >64 years old, Puglia region, Italy: ad interim analysis, January 2013 - February 2014	Poster
138	Positive predictive value of the German notification system for infectious diseases at the local health department level, Berlin, 2012	Poster
138	Quantifying workload and data quality of infectious disease notifications at local health department level in Germany	Poster
139	Development of a nationwide prospective, laboratory-based active surveillance system on the syndromes of infectious diseases in China	Poster
139	Pilot season of a web-based self-reporting influenza like illness surveillance system in Denmark, 2013-14	Poster
140	Ways forward in meningitis detection and reporting Fes-Boulemane region, Morocco, 2010-2013	Poster
140	Evaluation of Acute Flaccid Paralysis Surveillance System in Oyo State, South Western Nigeria - 2008-2012	Poster

TB and other respiratory diseases (excluding influenza)

29	Previously treated tuberculosis: stable proportion and low treatment success, EU/EEA, 2008-2012	Parallel
30	Laboratory-confirmed cases of tuberculosis and drug-resistance in Greece, 2012	Parallel
30	Tuberculosis outbreak investigation using whole genome sequencing, Finland 2012	Parallel
72	Investigation of an Outbreak of Multidrug-resistant Tuberculosis in a Workplace Setting.	Poster
72	Final results of QuantiFERON-TB Gold In-Tube screening for latent tuberculosis in a cohort of patients with HIV infection.	Poster
73	Molecular surveillance pilot on multi-drug resistant tuberculosis in the EU/EEA	Poster
73	The effectiveness of convalescent plasma for the treatment of severe acute respiratory infections of viral aetiology such as Middle East Respiratory Syndrome coronavirus: a systematic review and exploratory meta-analysis	Poster
74	Far away from the guideline: Diagnostic and preventive treatment of children who had contact to persons with tuberculosis infections. A survey in Lower Saxony, Germany, 2007-2012	Poster
74	Predictors of delay in initiation of treatment among newly-diagnosed pulmonary tuberculosis patients in Karaganda City, Kazakhstan, 2012-2013	Poster

Vaccine coverage, effectiveness and safety

27	Evidence of waning immunity against mumps in vaccinated young adults, France 2013	Parallel
27	Catching the catch-up group - successful HPV vaccination coverage in school-based campaigns, Sweden 2012	Parallel
28	Assessment of Routine Immunisation Programme-Osun State, South-West, Nigeria, January 2008-December 2012	Parallel
28	National seasonal influenza vaccination in Europe. Overview of surveys conducted by VENICE	Parallel
29	High vaccine effectiveness and signs of serotype replacement after the introduction of higher valency pneumococcal conjugate vaccines: results of SpIDnet first year	Parallel
55	Moderate to high seasonal influenza vaccine effectiveness in Ireland: a test-negative case-control study, I-MOVE project, 2013-2014	Parallel
55	Intussusception in Sicily: hospitalization trends before the introduction of rotavirus vaccination, 2003-2012	Parallel
56	A mumps outbreak among adolescents highly vaccinated with two doses, Klatovy, Czech Republic, 2011	Parallel
56	High effectiveness and impact of universal Rotavirus vaccination in Finland 4 years after its introduction into National Immunisation Program (NIP)	Parallel
57	Maternal pertussis vaccination is effective in preventing pertussis in infants: a case-control study in England and Wales, 2012- 2013	Parallel
83	Do we need monitoring of immunisation delay?	Poster
83	Rubella outbreak at a child-care center in Shimane prefecture, Japan, 2013	Poster
84	Improving trust in immunizations - Establishing a national surveillance of vaccine injury compensation in Germany	Poster
84	Effectiveness of alternative vaccines in healthy non-responders to hepatitis B vaccination; a multicentre randomised controlled trial in The Netherlands	Poster
85	Vaccine coverage and determinants of incomplete vaccination in children aged 12-23 months in Dschang, West Cameroon	Poster
85	Prevention of infant pertussis in the Netherlands: attitude and anticipated regret determine new parents' intention to accept vaccination.	Poster
113	Decline in invasive meningococcal disease in Ireland: a review of the epidemiology, 1999-2013	Poster
114	Changes in seroprevalence of pneumococcal serotypes during the pre-vaccine era	Poster
114	Effect of the pneumococcal conjugate vaccination programme on hospitalisation rates due to all-cause pneumonia and myringotomy with ventilation tube insertion among children <2 years of age, Ireland, 2005-2013	Poster
115	Antibody responses to pertussis vaccine antigens in two population-based studies conducted in The Netherlands, 1996 and 2006	Poster
115	Meningococcal disease among military conscripts in Finland: need to extend immunization practices?	Poster
116	Serogroups B, W-135 and Y Invasive Meningococcal Disease in Canada, 2002-2011	Poster
135	Rapid Vaccination Coverage Post-typhoonHaiyan: The Challenges in Measles Elimination-Tacloban City, Samar, Philippines, 2013	Poster
135	Cost of public health management of sporadic invasive meningococcal disease, Baden-Wuerttemberg, Germany	Poster
136	Knowledge-practice gap in public health management of invasive meningococcal disease contacts in Baden-Wuerttemberg, Germany	Poster
136	Attitude, social norm, autonomy, anticipated regret and ambivalence: a model on vaccination acceptance	Poster
137	Impact of vaccination on brucellosis seroprevalence in sheep and goats, Azerbaijan, 2007-2013	Poster
137	Impact of vaccination strategy on the incidence of measles in Slovakia, 1969-2013.	Poster

Vaccine-preventable diseases

37	How many children are unvaccinated in England? Evaluation of a national catch-up MMR campaign in England, April-September 2013	Parallel
37	Estimating the impact of meningococcal group C conjugate vaccine on hospitalization for invasive disease in Italy, 2001-2011	Parallel
38	Immunization coverage assessment and drop-out rates for different vaccines among children in rural Atakumosa, Southwestern Nigeria	Parallel
38	Invasive pneumococcal disease (IPD) and effect of pneumococcal conjugate vaccines in Ireland in 2008-2013	Parallel
39	Introduction of a national herpes zoster (shingles) vaccination programme in Scotland - monitoring the impact on neuropathic pain	Parallel
39	Epidemiological pattern of mumps epidemic waves, associated hospitalizations and complications. Spain, 1998-2013	Parallel

Zoonoses

Index by Presenting Author

Hollo	Vahur	Parallel	29
Horvath	Judit Krisztina	Poster	119
Hudeckova	Henrieta	Poster	137
Huovinen	Elisa	Poster	78
Huusko	Sari	Poster	134
Ibarz Pavon	Ana Belen	Parallel	30
Inns	Thomas	Parallel	44
Israel	Oluwaseyi	Poster	140
Ito	Hiroaki	Poster	81
Jamborova	Ivana	Poster	93
Javadov	Natig	Poster	137
Jernberg	Cecilia	Poster	103
Jiménez Jorge	Silvia	Poster	105
Jurke	Annette	Parallel	40
Kamińska	Sylwia	Poster	87
Kanayama	Atsuhiro	Poster	99
Kantsone	Ieva	Poster	118
Karakus	Nalan	Poster	142
Kark	Malin	Parallel	58
Kärki	Tommi	Parallel	63
Kis	Zoltan	Poster	89
Kissling	Esther	Parallel	36
Kjelso	Charlotte	Poster	139
Ködmön	Csaba	Poster	73
Kojouharova	Mira	Poster	89
Kontula	Keiju	Poster	69
Kostkova	Patty	Poster	109
Kraan	Janneke	Poster	85
Kristin	Kremer	Plenary Session B	17
Kubatova	Anna	Parallel	56
Kuehne	Anna	Poster	138
Kulzhabaeva	Aizat	Parallel	52
Kuma	George Khumalo	Poster	68
Lange	Heidi	Parallel	26
Larfaoui	Fairouz	Poster	109
Le Perff	Hervé	Parallel	23
Lentzos	Filippa	Plenary Session D	18
Li	Zhongjie	Parallel	53
Li	Anita	Poster	116
Li	Yuanyuan Anita	Poster	116
Lin	Yung-Ching	Parallel	53
Litzroth	Amber	Poster	88
López-Perea	Noemí	Parallel	39
Luber	Petra	Poster	82
Lucarelli	Claudia	Parallel	62
Lugner	Anna	Poster	106
MacDonald	Emily	Latebreaker	146
Martinelli	Domenico	Parallel	37
Mateus	Ana	Parallel	35
Matussek	Andreas	Parallel	48
McNulty	Cliodna	Poster	130, 131
Mereckiene	Jolita	Parallel	28, 38
Mexia	Ricardo	Parallel	23
Miglietta	Alessandro	Poster	85
Migone	Chantal	Poster	72
Mikhail	Amy	Parallel	42, 44
Moeller	Eeva	Plenary Session E	19
Mølbak	Kåre	Poster	117
Mook	Piers	Poster	108
Mughini-Gras	Lapo	Poster	98
Muller-Pebody	Berit	Poster	100
Murajda	Lukas	Poster	135, 136
Murdoch	Heather	Parallel	39
Nerkar	Sandeep S	Poster	92
Neubauer	Katrin	Poster	118
Newitt	Sophie	Parallel	52
Nic Lochlainn	Laura	Parallel	50, 62
Nikisins	Sergejs	Poster	77
O Connor	Lois	Poster	121
Odone	Anna	Parallel	24
Ogunniyi	Abiodun	Poster	102, 126, 127
Olugbade	Olukemi	Parallel	32
Oravcova	Veronika	Poster	66
Ozin-Hofsaess	Amanda	Poster	76
Packer	Simon	Poster	98
Parent du Chatelet	Isabelle	Parallel	58
Pärn	Triin	Parallel	41, 45
Patterson	Lynsey	Poster	69
Preußel	Karina	Parallel	51
Puig-Asensio	Mireia	Poster	110
Purriños-Hermida	María Jesús	Poster	66
Ramos	Ruth Alma	Parallel	60
Ramos	Ruth Alma	Poster	91, 123
Raven	Stijn	Poster	84
Rehn	Moa	Parallel	27
Rettenbacher-Riefler	Sophie	Parallel	22
Rhandour	Tarik	Poster	140
Ricco'	Matteo	Poster	94
Ricketts	Ellie	Poster	95

Riise	Oystein	Poster	81
Rosinska	Magdalena	Poster	96, 122
Ruesch-Gerdes	Sabine	Plenary Session B	17
Russell	Katherine	Parallel	54
Saavedra-Campos	Maria	Poster	73
Sánchez-Payá	José	Poster	70,71,106,121
Sanchez-Vivar	Alex	Parallel	60
Sane	Jussi	Parallel	51
Sañé Schepisi	Monica	Poster	72
Savulescu	Camelia	Parallel	29
Scharlach	Martina	Poster	74
Schielke	Anika	Poster	143
Schink	Susanne Barbara	Parallel	47
Schroeder	Sabine	Parallel	43
Schumacher	Jakob	Poster	82
Sekerbaya	Lyazzat	Poster	74
Semper	Amanda	Latebreaker	148
Seychell	Martin	Plenary Session C	18
Sfetcu	Otilia	Parallel	46
Sharma	Megha	Poster	93
Sherrard	Lindsey	Poster	90
Shevyakova	Yelena	Parallel	25
Shivaji	Tara	Parallel	47
Silvestros	Chrysovalantis	Parallel	61
Smit	Pieter	Parallel	30
Soetens	Loes	Parallel	45
Steens	Anneke	Parallel	57
Story	Alistair	Plenary Session B	17
Subelj	Maja	Parallel	42
Subelj	Maja	Poster	132
Suleimen	Sholpan	Poster	74
Suttorp	Vivien	Parallel	64
ter Waarbeek	Henriette	Poster	125
Thomas	Daniel	Poster	97
Toropainen	Maija	Poster	115
Tozan	Ebru	Poster	142
Trienekens	Suzan	Poster	132
Tryfinopoulou	Kyriaki	Poster	68, 92
Tutus	Celal	Poster	141
Usman	Aishat	Poster	76
Vainio	Anni	Poster	103
Van Cauteren	Dieter	Poster	79, 104
van der Wielen	Paul W.J.J.	Parallel	50
van Ginkel	Annemarijn	Poster	114
Vestrheim	Didrik Frimann	Parallel	26
Visser	Olga	Poster	136
Von Dobschuetz	Sophie	Parallel	34
Vygen	Sabine	Parallel	27, 49
Wain-Hobson	Simon	Plenary Session D	18
Williams	Chris	Poster	110
Workineh Kassa	Addisu	Poster	112
Yang	Weizhong	Poster	139
Zanuzdana	Aryna	Poster	129
Zeitlmann	Nadine	Parallel	41, 59
Zeynalov	Etibar	Poster	123

Index by Keyword

5-7 November 2014 Stockholm, Sweden

@ECDC_EU

www.facebook.com/ECDC.EU

ESCAIDE

European Centre for Disease
Prevention and Control (ECDC)

Postal address:
ECDC, SE171 83 Stockholm, SWEDEN

Visiting address:
Tomtebodavägen 11A, Solna, SWEDEN

Tel. +46858601000
Fax +46858601001
http://www.ecdc.europa.eu

An agency of the European Union
http://www.europa.eu