ESCAIDE

ABSTRACT BOOK



European Scientific Conference on Applied Infectious Disease Epidemiology

Stockholm, Sweden,
27-29 November 2019

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EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

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Welcome to ESCAIDE 2019!

A warm welcome to Stockholm and the 2019 ESCAIDE conference! I hope you will find the programme to be stimulating and rewarding, and that you have an enjoyable stay in ECDC's host city.

I would like to acknowledge all the ESCAIDE colleagues who provide invaluable support to the conference. ESCAIDE takes place in the dark days of November, which seem light years away from spring and summer when reviewers kindly volunteered to carry out reviews to assess the submitted work, and the ESCAIDE Scientific Committee were actively engaged in defining plenary sessions content and overseeing the abstract selection process and development of the scientific programme as a whole. Hence the conference is a culmination of efforts by many people throughout the year, and I offer sincere thanks to all who have played a role in the development of the 2019 ESCAIDE programme.

As every year, the 2019 ESCAIDE conference programme is based on the presentation of abstracts, and hence the quality of the conference is heavily reliant on the excellence of the abstracts submitted. Therefore, I would like to thank the 487 authors who made the effort to submit an abstract to the conference; even though many were unsuccessful, the overall quality remains extremely high, and this ensures that the presentations that we will enjoy during the conference are based on scientific excellence, and provide relevant and timely information that I hope you can then apply to support your public health work.

The content of the 2019 plenary sessions aims to give new insight and perspectives on some of the current issues facing infectious disease prevention and control, including continued challenges to global health from emerging infection, confidence in vaccination and opportunities to identify and pursue knowledge gaps through research. Emerging drivers of infection causation and dissemination, and pathways of intervention will also be considered in plenary sessions on climate change and the microbiome. I, as well as my colleagues in the Scientific Committee are greatly looking forward to learning more about these aspects. More generally we are anticipating an exciting 3 days at ESCAIDE 2019 and are excited to engage with you all to better understand the methodology and application of epidemiology, microbiology and other related disciplines in support of communicable disease prevention and control.

ESCAIDE is also an opportunity to meet with old friends and colleagues. This is enjoyable, but also important; revitalising existing connections and building new links is a rather intangible gain, but I know from my own experience that being able to contact trusted colleagues can greatly assist in disease assessment and control. Hence, take the time to speak to both familiar and unfamiliar faces, and reenergise your professional and personal networks!

Finally, I wish you a successful and enjoyable ESCAIDE 2019, and hope that you leave the conference and Stockholm with fond memories, useful contacts and renewed enthusiasm for your role in the fight to address communicable disease.

Prof. Mike Catchpole

Chair, ESCAIDE Scientific Committee

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POSTER ABSTRACTS

Scientific Committee

Mike Catchpole

Chief Scientist at ECDC, Chair of ESCAIDE Scientific Committee, ECDC

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

Aura Timen

Head of the National Coordination Centre for Outbreak Management of the Dutch National Institute for Public Health and Environment and a member of the ECDC Advisory Forum on behalf of EUPHA, National Coordination Centre for Outbreak Management, National Institute for Public Health and the Environment

Aura is the Head of the National Coordination Centre for Outbreak Management of the Dutch National Institute for Public Health and Environment and a member of the ECDC Advisory Forum on behalf of EUPHA. Prior to this role, Aura worked for the Delfland Municipal Public Health Service as a physician in social medicine. She is a medical doctor by training, specializing in communicable disease control, with extensive research experience on crisis management in the Netherlands and abroad. Aura holds a PhD in outbreak management from the Radboud University Nijmegen, The Netherlands

Karl Ekdahl

Head of the Public Health Capacity and Communication Unit, ECDC

Karl is the Head of the Public Health Capacity and Communication Unit at ECDC. He was the first expert to join the European Centre for Disease Prevention and Control in 2005. Within ECDC, he has been Strategic Adviser to the Director (2005-2007), and Head of the Health Communication Unit (2007-2010). From February to April 2010, Karl was the Centre's Acting Director. Karl is a medical doctor and a specialist in infectious diseases. He has a PhD in Infectious Diseases from Lund University in Sweden, a Diploma in Tropical Medicine and Hygiene from Prince Mahidol University, Bangkok, Thailand, and a Master's Degree in Epidemiology from the London School of Hygiene and Tropical Medicine. In 1999 he became Associate Professor and in 2007 Adjunct Professor in Infectious Disease Epidemiology, at the Karolinska Institute in Stockholm.

João André Nogueira Custódio Carriço

Researcher in the Molecular Microbiology and Infection Unit, Medical University of Lisbon

João is currently working as a Researcher in the Molecular Microbiology and Infection Unit at the Instituto de Medicina Molecular in the Faculty of Medicine, University of Lisbon, and teaches at the Instituto Superior Técnico, University of Lisbon. He studied Applied Chemistry, Biotechnology and did his PhD on Microbial typing and data analysis methodologies. João's research interests are in Bioinformatics and the development of novel analysis and visualization methodologies with special focus on microbiology, molecular epidemiology and microbial typing methods

Christopher Barbara

Chairman of the Pathology Department, Mater Dei Hospital, Malta

Christopher is the Chairman of the Pathology Department at Mater Dei Hospital in Malta. He received his medical training in both Malta and the United Kingdom. Furthermore, he is a Consultant Virologist and Head of the Virology Unit in the Department of Pathology. Christopher also lectures in Microbiology at the University of Malta and is a member of various National Health Committees related to Pathology and Infectious Diseases. He is the National Microbiology Focal Point for Malta at ECDC.

Scientific Committee

Amrish Baidjoe

Coordinator of the R Epidemics Consortium, Imperial College London, UK“

Amrish is the coordinator of the R Epidemics Consortium at Imperial College in London, UK. Here they bring together different stakeholders working in the arena of public health emergencies and outbreak responses to jointly develop new tools, methodologies and training exercises for outbreak analyses using R. He currently still actively participates in international assignments in emergency situations and outbreaks. Having a background in both microbiology and field-epidemiology he undertook his EPIET training in 2015 at Institut Pasteur in Paris, France where he was part of the outbreak investigation taskforce. In 2010 he started his PhD. in close collaboration with the Radboud University, Nijmegen, the Netherlands and the London School of Hygiene and Tropical Medicine, London, UK and the Kenyan Medical Research Institute. Here he looked at patterns of heterogeneity of malaria in an area of Kenya in a large multi-partner project, strongly focussing on involvement of local communities. Before that he worked on fundamental influenza research and completed his MSc. and BSc. degree in biology of infectious diseases at Wageningen University in the Netherlands. He has been the elected president of the board of the EPIET Alumni Network (EAN) since November 2017.

Maria Van Kerkhove

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead, Health Emergency Program, High Threat Pathogens Unit, World Health Organization (WHO)

Maria Van Kerkhove, PhD is an infectious disease epidemiologist who specialises in outbreaks of emerging and re-emerging pathogens. Dr Van Kerkhove is from the United States and completed her undergraduate degree at Cornell University, a MS Degree at Stanford University, and a PhD in infectious disease epidemiology at the London School of Hygiene and Tropical Medicine. Dr Van Kerkhove is currently the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead in the World Health Organization’s Health Emergency Program, in the High Threat Pathogens Unit. Dr Van Kerkhove regularly participates in Missions to affected member states, including the Kingdom of Saudi Arabia, Jordan, Qatar and the Republic of Korea. Prior to WHO, she was the Head of the Outbreak Investigation Task Force at Institut Pasteur’s Center for Global Health where she was responsible for establishing public health rapid response teams for infectious disease outbreaks. Dr Van Kerkhove was previously employed by Imperial College London in the MRC Center for Outbreak Analysis and Modelling where she worked closely with WHO on influenza, yellow fever, meningitis, MERS-CoV and Ebola Virus Disease.

Bojana Beović

Specialist in & Professor of infectious diseases, Faculty of Medicine, University Medical Centre Ljubljana & University of Ljubljana Slovenia

Bojana is a specialist in infectious diseases at the University Medical Centre Ljubljana, Slovenia and a professor of infectious diseases at the Faculty of Medicine, University of Ljubljana. She is the chair of the Slovenian Society for Antimicrobial Chemotherapy and the vice-chair of the National Intersectoral Coordinating Mechanism for Prudent Use of Antimicrobials at the Ministry of Health in Slovenia. She is the chair of ESCMID Study Group for Antimicrobial Stewardship (ESGAP). In the hospital Bojana leads the antimicrobial stewardship programme. She is involved in antimicrobial stewardship education on the national and international level. In the research area she is focused on antimicrobial stewardship and hospital-acquired infections.

Frode Forland

Specialist Director, Infectious Diseases and Global Health, Norwegian Institute of Public Health

Maria Van Kerkhove, PhD is an infectious disease epidemiologist who specialises in outbreaks of emerging and re-emerging pathogens. Dr Van Kerkhove is from the United States and completed her undergraduate degree at Cornell University, a MS Degree at Stanford University, and a PhD in infectious disease epidemiology at the London School of Hygiene and Tropical Medicine. Dr Van Kerkhove is currently the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead in the World Health Organization’s Health Emergency Program, in the High Threat Pathogens Unit. Dr Van Kerkhove regularly participates in Missions to affected member states, including the Kingdom of Saudi Arabia, Jordan, Qatar and the Republic of Korea. Prior to WHO, she was the Head of the Outbreak Investigation Task Force at Institut Pasteur’s Center for Global Health where she was responsible for establishing public health rapid response teams for infectious disease outbreaks. Dr Van Kerkhove was previously employed by Imperial College London in the MRC Center for Outbreak Analysis and Modelling where she worked closely with WHO on influenza, yellow fever, meningitis, MERS-CoV and Ebola Virus Disease.

Scientific Committee

Susan Hahné

Head of Department, Early Warning and Surveillance, at the Centre for Epidemiology and Surveillance of infectious diseases, National Institute for Public Health and the Environment (RIVM)

Susan heads the department for Early Warning and Surveillance, at the Centre for Epidemiology and Surveillance of infectious diseases at the National Institute for Public Health and the Environment (RIVM) in the Netherlands. In addition, she is host-site supervisor for EPIET-fellows at RIVM. Susan trained as a health scientist and medical doctor in the Netherlands, and was an EPIET fellow in Wales, United Kingdom. She completed public health specialisation at the Faculty of Public Health in the United Kingdom, and a PhD on hepatitis B at Utrecht University, the Netherlands. Susan's research interests include methods for early warning, surveillance and the epidemiological evaluation of vaccination programmes.

Frantiska Hruba

Scientific Coordinator of the EPIET/EUPHEM Fellowship Programme, ECDC

Frantiska is the Scientific Coordinator of the EPIET/EUPHEM Fellowship Programme at ECDC since June 2017. Within ECDC, she was group leader and expert for general surveillance in the Epidemiological Method Section of the Surveillance and Response Support Unit (2010-2017), involved mainly in surveillance system assessments and use of novel methods for surveillance outputs as ECDC Surveillance Atlas. Before that she worked in public health institutes in the Slovak Republic (1989-2010) as an expert in national surveillance system, a researcher in international and national epidemiological studies, and later also as a senior advisor to the Chief Hygienist and a member the Ministry of Health Committee on eHealth. She holds a PhD in public health on use of GIS and spatial analysis in assessment of risk of diseases from the Trnava University and a Doctor of natural sciences degree from the Comenius University in Bratislava.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2019.

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Invited Speaker Biographies

ESCAIDE 2019 Keynote address: Health security and preparedness: lessons from Ebola

Dr Mike Ryan

Executive Director, WHO Health Emergencies Programme

Dr Mike Ryan has been at the forefront of managing acute risks to global health for nearly 25 years. He served as Assistant Director-General for Emergency Preparedness and Response in WHO‘s Health Emergencies Programme from 2017 to 2019.

Dr Ryan first joined WHO in 1996, with the newly established unit to respond to emerging and epidemic disease threats. He has worked in conflict affected countries and led many responses to high impact epidemics. He is a founding member of the Global Outbreak Alert and Response Network (GOARN), which has aided the response to hundreds of disease outbreaks around the world. He served as Coordinator of Epidemic Response (2000-2003), Operational Coordinator of WHO’s response to the SARS outbreak (2003), and as WHO’s Director of Global Alert and Response (2005-2011),

He was a Senior Advisor on Polio Eradication for the Global Polio Eradication Initiative from 2013 to 2017, deploying to countries in the Middle East.

He completed medical training at the National University of Ireland, Galway, a Master’s in Public Health at University College Dublin, and specialist training in communicable disease control at the Health Protection Agency in London and the European Programme for Intervention Epidemiology Training.

Invited Speaker Biographies

Plenary session B: Vaccine confidence in a post-factual world

Dr Wolfgang Gaissmaier

Professor of Social Psychology and Decision Sciences, University of Konstanz

Wolfgang Gaissmaier (*1977), PhD, has been a Full Professor of Social Psychology and Decision Sciences at the University of Konstanz, Germany, since 2014. His research investigates how people make decisions under uncertainty and how risks can be communicated more successfully to help people make better decisions, particularly in medicine. He received his PhD in 2007 (Free University Berlin) and his habilitation (venia legendi) in 2013 (University of Heidelberg). For many years, he worked as Chief Research Scientist at the Harding Center for Risk Literacy at the Max Planck Institute for Human Development, Berlin. Wolfgang Gaissmaier's work has been published in leading psychological and medical journals, including Annals of Internal Medicine, Annual Review of Psychology, Cognition, Health Psychology, JAMA, PNAS, and Psychological Science. He received numerous awards, including the Otto Hahn Medal for outstanding scientific achievements by the Max Planck Society (2008), a fellowship at the Young Academy of the Berlin-Brandenburg Academy of Sciences and Humanities and the German Academy of Sciences Leopoldina (2012-2017), a rising star nomination by the Association for Psychological Science (2013), and an award for excellent teaching and being a positive role model by the students of the University of Konstanz (2016 and 2019).

Dr Robb Butler

WHO Regional Office for Europe

Robb Butler is a social scientist and public health advocate with working experience in public health, social protection and humanitarian assistance in developing and transitional states. Robb's specialist areas of experience and knowledge include behavioural and community insight methodology/application, and social science interventions in public health – particularly with regard to communicable disease prevention and vaccine acceptance and demand.
He has presented regularly on vaccine hesitancy at ESPID since 2010. Between 2009 and 2014 Robb spearheaded WHO's efforts to strengthen vaccine demand support to countries in the European Region and represented WHO globally as a spokesperson on vaccine hesitancy, acceptance and demand. Between 2014-2018 Robb managed the Vaccine-preventable Diseases and Immunization Programme at the WHO Regional Office for Europe. The Programme, WHO/Europe's largest, delivers normative guidance and technical assistance to 53 Member States. The programme is globally recognized for establishing capacity in behavioural insights and the application of social science approaches to improve coverage, close immunity gaps and generate demand for vaccination in countries.
Having recently established a global vaccine demand hub with UNICEF, Robb currently serves on the incoming Regional Director for WHO/Europe‘s Transition Team.

Invited Speaker Biographies

Plenary session C:
The microbiome: what you need to know

Assist Prof Dr Sean Gibbons

Assistant professor, Institute for Systems Biology, Seattle

Sean Gibbons earned his PhD in biophysics from the University of Chicago in 2015. He completed his postdoctoral work at MIT in 2018. Sean is now an assistant professor at the Institute for Systems Biology, in Seattle. His lab studies the ecology and evolution of microbial communities. In particular, Sean is interested in how host-associated bacterial communities influence the health and wellness of the host organism. His group designs computational and wet-lab tools for studying these complex systems. Ultimately, the Gibbons Lab aims to develop strategies for engineering the ecology of the gut microbiome to improve human health.

Prof Debby Bogaert

Chair of Paediatric Medicine, University of Edinburgh

Since September 2019, Prof Debby Bogaert has been Chair of Paediatric Medicine at the Centre for Inflammation Research. Furthermore, she works as a physician scientist in paediatric infectious diseases at the University of Edinburgh, the Royal Hospital for Sick Children, Edinburgh, and at the UMC Utrech in the Netherlands.

In 2009, they embarked on a new adventure studying the ecosystem (microbiome) of the respiratory tract in relation to health and disease. So far, they have performed multiple cross-sectional studies in children, adults and elderly, and started several intensive microbiome-driven follow-up studies including birth-cohort studies in healthy infants, premature infants, newborns with cystic fibrosis and children with NEONS (n=150). One of the findings was an important ecological link between risk factors and respiratory health in children as well as adults. Moreover, they found that during serious viral infections such as RSV inflammation, the severity of infections appears driven by co-signaling of the microbial ecosystem.

Currently, they are analysing the development of other ecological niches, like oral, and gut microbiome, as well as the mycobiome and resistome, in relation to (un)beneficial drivers and health consequences such as respiratory and oral health, growth and development, and neurological development. Their aim is to develop new diagnostic tools and new strategies to prevent and/or treat acute and chronic respiratory infections.

Prof Debby Bogaert has a current research portfolio funded by the Dutch government (NWO/ZonMW), the Scottish government (CSO/NRS), UK Medical Research Council (MRC), Wellcome, NIHR global health research units (MPRU and RESPIRE), GCRF, and Bill and Melinda Gates Foundation. She is the author of approx. 100 peer-reviewed papers, nearly 8000 cites, and an H-index of 39.

Invited Speaker Biographies

Plenary session D:
How should public health research priorities be defined, and what should they be?

Dr Jean- Claude Desenclos

MD, PhD, Scientific director, deputy to the general Director, Santé Publique France

Dr. Desenclos moved to public health in 1988 after several years of medical general practice and international humanitarian involvement through Médecins Sans Frontiéres. After working for 3 years at the US CDC as a medical epidemiologist, he joined the newly created French national surveillance institute (Institut de Veille Sanitaire [InVS]) in 1993. He was the head of the InVS Department of infectious Diseases for 12 years and became the Scientific Director of InVS in 2008. He then became the scientific director, deputy to the general director at the creation of the new French public health Agency (Santé Publique France) in 2016. Dr. Desenclos is the author or co-author of 210 international scientific publications and editor of a French textbook in epidemiology. He is affiliated with the Paris Doctoral School of Public Health where he supervises PhD students. He is a member of numerous scientific committee and advisory boards in France and in Europe. He is associate editor to the “European Journal of Epidemiology” and the French journal “Santé Publique”. Dr. Desenclos currently serves as Secretary General of the International Association of National Public Health Institutes.

Ed Whiting

Director of Strategy, Wellcome Trust

Ed is responsible for working with teams across Wellcome to align Wellcome’s activity with their mission and ensure that Wellcome’s impact is greater than the sum of its parts. This includes working with Wellcome’s senior teams to set and communicate short, medium, and long-term priorities and put resources and plans in place to deliver them. As part of Ed’s role, Ed is also the Executive Leadership Team sponsor of Wellcome’s policy function, strategic partnerships, and mental health priority area.

Before joining Wellcome in September 2016, Ed worked in a number of Whitehall social and financial policy departments, including HM Treasury’s financial stability team during the 2008-09 financial crisis. He was most recently at 10 Downing Street as Deputy Principal Private Secretary to the Prime Minister, leading on public services.

Assist Prof Lina Moses

PhD MSPH, Assistant Professor, Department of Global Community Health & Behavioral Sciences, Tulane University School of Public Health & Tropical Medicine

Lina Moses is an Assistant Professor at the Tulane University School of Public Health & Tropical Medicine. Trained in Tropical Medicine, Community Health and Environmental Health, Moses’ research focuses on the prevention and control of zoonotic diseases. She has spent over a decade in West Africa overseeing epidemiology and surveillance activities for Ebola virus disease, Lassa fever, and monkeypox. Moses is a member of the GOARN Steering Committee and will assume leadership of the GOARN-Research Working Group in January 2020.

Invited Speaker Biographies

Plenary session E:
Climate change: Addressing the public health challenge in Europe

Dr. Henriette de Valk

MD, MPH, DTMH, head of the vectorborne, foodborne and zoonotic infections department, Santé publique France

Henriette de Valk, MD, MPH, DTMH is the head of the vectorborne, foodborne and zoonotic infections department at Santé publique France, the French Public Health Agency. She earned her degrees from the University of Leyden, The Netherlands, the London School of Hygiene and Tropical Medicine in the United Kingdom, and the Institute of Tropical Medicine in Antwerp, Belgium, and she is alumna of the European Programme for Intervention Epidemiology Training (EPIET). Prior to working at Santé publique France she worked for the NGO Médecins Sans Frontières in emergency relief programs in Sudan, Uganda and Mali. For five year she was public health advisor for the German Technical Co-operation (GTZ) in Cameroon. She was a medical officer for the World health Organisation in Indonesia at the control programmes for diarrhoeal diseases and respiratory infections.

As head of the vectorborne, foodborne and zoonotic infections department, she participates in the national working groups developing guidelines for surveillance, prevention and control of vectorborne agents such as West Nile, chikungunya, dengue and Zika viruses, as well as the national plan for tick borne diseases. She was involved in the investigation of a large number of vectorborne disease outbreaks, some of which were massive such as the outbreak of chikungunya in 2006 in La Réunion, in the Indian Ocean, and the chikungunya and Zika virus outbreaks in the French Caribbean in 2014 and 2016. She is serving on the national committee nominating the National Reference Centres (laboratories) for infectious agents in France and in Belgium. She is an associate editor of the journal “Eurosurveillance”.Focal Person for EU projects: Episout/Episouth Plus and MediPIET I/MediPIET II.

Plenary Session Abstracts

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Plenary Session Abstracts

PLENARY SESSION B
DAY 1, Wednesday 27. November
17:00-18:30

Plenary Session B:

Chairs:
Prof. Dr. Bojana Beović (University of Ljubljana Slovenia)
Dr. Frantiska Hruba (ECDC)

"Vaccine confidence in a post-factual world"

Presented by

Prof. Dr. Wolfgang Gaissmaier,
University of Konstanz
Dr. Robb Butler,
WHO Regional Office for Europe

Abstract

Wolfgang Gaissmaier: Vaccination has been one of the major medical breakthroughs in history, probably only matched by hygiene and the development of antibiotics. Despite overwhelming scientific evidence favoring vaccination, vaccine hesitancy remains a major obstacle in many countries across the world and is considered to be among the ten most important health problems worldwide by the World Health Organization (WHO). Why do people hesitate? One problem is the public (mis-)perception of risk: People often fear the wrong things and are not worried about vaccine-preventable diseases anymore. Furthermore, both experts and laypeople often fail to understand the relevant statistical evidence. But even if the evidence is understood, we observe a shortage of evidence culture in our society, including among the highly educated. People dismiss scientific evidence that does not fit to their beliefs, be they political or religious. Fundamental misperceptions of randomness and causality fuel superstitions and conspiracy theories about vaccination. Finally, the interpretation of scientific evidence is shaped by social processes, which can amplify misperceptions and lead to polarized beliefs. What can be done? I will argue that a transparent communication of the underlying scientific evidence is necessary, but not sufficient to convince people. The evidence will need to be complemented with good stories highlighting the risks of the disease (rather than the probabilities). It is generally advised to set positive messages rather than repeating myths when trying to correct them. Also, it helps to highlight the social benefit for others, especially those who cannot be vaccinated (e.g., newborns), rather than just focusing on the individual benefit. Finally, making getting vaccinated the default and lowering the barriers for people to do so will likely boost vaccination rates.

Robb Butler: Today, nine of every 10 children in the Region receive at least a basic set of vaccinations during infancy and as a result lead healthier, more productive lives. Furthermore, significant advances have been made in developing and introducing new vaccines and expanding the reach of immunization programmes. More people than ever before are being vaccinated and access to and reception of vaccines by people other than infants is increasing. However, a resurgence of some vaccine-preventable diseases in the Region over the past two to three years has served as a wake-up call. As health authorities seek to promote and deliver equitable access to vaccination and empower immunization programmes through new and ambitious strategies, I will briefly present the status of measles elimination in the Region before considering how vaccine hesitancy manifests itself in the European Region, the tools we have to combat it, and the degree that vaccination refusal and hesitancy have contributed to outbreaks.

Plenary Session Abstracts

PLENARY SESSION C
DAY 2, Thursday 28. November
9:00-10:30

Plenary Session C:

Chairs:
Dr. João André Carriço (Medical University of Lisbon, Portugal)
Dr. Christopher Barbara (Mater Dei Hospital, Malta)

“The microbiome: what you need to know”

Presented by

Assist Prof Sean Gibbons,
Institute for Systems Biology, United States of America
Prof. Debby Bogaert,
The University of Edinburgh, United Kingdom

Abstract

Assist Prof Sean Gibbons:
Please add the abstract of Sean Gibbons as well:
We are walking ecosystems, inoculated at birth with a unique set of microbes that are integral to the functioning of our bodies. The physiology of our commensal microbiota is intertwined with our metabolism, immune function, and mental state. The specifics of this entanglement remain largely unknown and are somewhat unique to individuals, and when any one piece of this complex system breaks, our health can suffer. There appear to be many ways to build a healthy, functional microbiome and several distinct ways in which it can break. Despite the hundreds of associations with human disease, there are only a handful of cases where the exact contribution of the microbiome to the etiology of disease is known. In this talk, I describe recent progress made by my group in leveraging multi-omic data and mechanistic modeling to better define microbiome health and disease. Furthermore, I describe new approaches for engineering the composition and function of the microbiome to mitigate disease risk and optimize wellness.

Prof. Debby Bogaert:
Over the past 15 years, researchers have begun to unravel the causes and consequences of variation within the human microbiome, and how these might influence the pathogenesis of diseases. Most studies have focused on the gut microbiome and how this is linked to metabolism, immune maturation and modulation, as well as control of infectious agents. Recent studies however, have also shown a complex microbial community in both the upper and lower airways, with clear associations with susceptibility to and severity of infections.
In early life, assembly of the human microbial ecosystem is strongly dependent on a breath of host and environmental drivers, where alterations on microbial community composition and development are thought to mediate susceptibility to and severity of acute infections as well as long-term inflammation-driven diseases.
Here I will discuss the current body of evidence regarding human microbiome signatures in early life that are associated with respiratory health over time. I will discuss the potential protective role of microbial communities within different body habitats, how these might be interrelated, and ultimately affect health outcome. Finally, I will discuss how this novel information might lead to development of new diagnostic tools and novel intervention strategies.

Plenary Session Abstracts

PLENARY SESSION D
DAY 3, Friday 29. November
9:00-10:30

Plenary Session D:

Chairs:
Dr. Maria Van Kerkhove (World Health Organisation)
Dr. Frode Forland (Norwegian Institute of Public Health)
Amrish Baidjoe (WHO-South-East Asia Regional Office)

“How should public health research priorities be defined, and what should they be?”

Presented by

Ed Whiting,
Wellcome Trust, United Kingdom
Assist Prof Dr. Lina Moses,
School of Public Health & Tropical Medicine/ Tulane University, United States of America
Dr. Jean- Claude Desenclos,
IANPHI, Public Health France

Abstract

Jean-Claude Desenclos:
Santé publique France is the National Public Health Agency for France and therefore belongs to the wide family of national public health institute (NPHI) that are science-based organizations that provide national leadership and expertise to protect and improve population health. While their scope and size vary, NPHIs use scientific evidence for policy development and resource allocation, and are accountable to national governments and the public. Their key functions include surveillance, prevention, health promotion and education, together with contributing to health protection by timely detection and investigation of, and response to health threats. In order to achieve these functions, NPHI have dedicated capabilities in either applied research, training, behavior change science and laboratory methods. My approach of the questions raised for this plenary session on research to enhance public health will takes the perspective of a NPHI, Santé publique France, which is defined as a knowledge based organization for health protection and improvement through evidence based actions and prevention. Although it is not a research structure, Santé publique France contributes to knowledge generation through its population based surveillance and studies, and health prevention & promotion activities in all fields of public health. It also interacts with research and academic entities to support its public health strategy. The research perspective is applied that is “high quality knowledge generation that aims to provide evidence for direct transfer to health policies/decisions and problem solving”. This is done in “peace time” and during emergency situations (epidemic, acute environmental exposure, disasters…). The priorities of this applied research agenda should be aligned with the strategic priorities of the Agency that are revised periodically according to national priorities. Currently, priorities include environmental determinants of health, climate change, innovation in and effectiveness of preventive interventions, vaccine hesitancy, control of antibiotic resistance, data science challenges, community participatory approaches, the economy of prevention, social and territorial health inequities…Options and mechanisms to achieve these goals include a variety of actions that range from maintaining a sustainable surveillance, study and investigation capacity including innovation, to active partnerships with public health research units or centers to develop knowledge to fill identified gaps. Investing in European projects/consortium which have an applied perspective is of major importance but needs an active human resource investment of the Agency which is sometimes overlooked. As an example, the incoming H2020 call on vaccine hesitancy offers a unique opportunity. The Challenge of matching the pace of research with rapid needs for evidence based public health actions is almost a day to day dilemma for health protection activities. Although it remains an important need and challenge for outbreak & epidemic response, it is more & more pressing for health effects of acute chemical exposures, emergencies, disasters, terrorist attacks…for which knowledge gaps are numerous and the social demand rapidly growing. It requires a priori flexible research preparedness capacity with fast share, before publication, of new data & knowledge. Besides the applied public health research dimension, there remains an insufficiently met mid to long term public health research agenda at national & European level. This is not only an issue of fund, but as much (even more) of a human research capacity which takes time to develop and infrastructures (large cohorts, biobanks, data repository, new methods…) for which an active and coordinated advocacy remains needed.

Ed Whiting:
Ed’s remarks will explore this question from the perspective of a global research funder. In order to enable science and research to create the greatest possible positive impact on human health, funders need to create incentives both to bring forward diverse curiosity-driven hypotheses and propositions from researchers, and to support rapid development, translation and implementation of insights that could improve health. To work successfully in both of these ways and drawing on experience from recent disease outbreaks, funders must form enduring partnerships with national and regional Governments, global normative bodies, academic institutions and the private sector – supporting a long-term shift of the ‘centre of gravity’ for priority-setting closer to the areas where disease burden is most keenly felt, and in a way that encourages the sustainable growth of Government support for science and research in those settings. Ed will discuss Wellcome’s experience in pursuing these objectives and reflect on how funders can support priority-setting for public health in future.

PLENARY SESSION E
DAY 3, Friday 29. November
17:00-18:30

Plenary Session E:

Chairs:
Dr Susan Hahné (National Institute for Public Health and the Environment)
Prof. Dr. Aura Timen (National Institute for Public Health and the Environment and Free University of Amsterdam)

"Climate change: Addressing the public health challenge in Europe"

Presented by

Dr. Henriette De Valk,
Public Health France

Abstract

During the first decades of the 21st century, the situation of vector-borne diseases in Europe has changed. Invasive mosquitoes, such as Aedes albopictus, have become widely established across Europe and ticks and Phlebotomus sandfly species have changed their geographical distribution. Vector borne diseases have increased substantially in their incidence and distribution in Europe since the beginning of this century. Exotic mosquito borne diseases such as Chikungunya, dengue and Zika virus disease have emerged in southern Europe. West Nile fever is now endemic in a large number of predominantly southern and eastern countries and the virus caused several multi-country outbreaks, with more than 1600 cases reported in 2018. Malaria is no longer endemic but outbreaks of P. vivax malaria occurred in Greece. The incidence of tick borne diseases such as Lyme borreliosis has increased in several countries and tick-borne encephalitis is spreading northwards.

Vector-borne diseases are highly sensitive to changes in weather and climate. However, climate change is only one of several drivers. Changes in land-use, infrastructure and the environment and socioeconomics such as travel and trade and their globalization, are important determinants of disease risk. Lessons from the recent outbreaks of West Nile, chikungunya and Zika virus disease emphasize the need to prepare strategies for the prevention or mitigation of these risk. Adaptation to the risk of emerging infections requires several actions, including (i) improved and integrated surveillance of human and animal cases and vector species, (ii) regular updates of the risk assessment of vector-borne disease risks as new data become available, including forecasts based on vector, disease, climate and sociodemographic and travel data, and (iii) contingencies for disease emergence and outbreaks.

Other issues to be addressed are the sharing of data on vectors and vector-borne diseases throughout Europe and globally, the capacity and networking of diagnostic laboratories, the importance of transdisciplinary research and the need to involve the community as early as possible.

Parallel Session Abstracts

Parallel Session Abstracts

Parallel Session Abstracts

Parallel Session 1
DAY 1, Wednesday 27. November 2019
11:00-12:40

Emerging and vector-borne diseases: surveillance approaches

Moderator

Tamás Bakonyi

Abstracts

1.1. Using epidemiological information to map outbreak networks and inform public health action during the 2018/19 Ebola outbreak in the Democratic Republic of the Congo (DRC)

R. Hams [1]

[1] Public Health England

Background:

During the ongoing Ebola outbreak in the DRC, epidemiologists based in WHO Geneva, utilised a new approach to outbreak network analysis using locally collected data, helping identify healthcare facilities (HCFs) with potential infection prevention and control (IPC) lapses to initiate swift public health actions.

Methods:

We collated information from field teams on case demographics, symptoms and use of HCFs. After data cleaning, we created a transmission database, mapping exposures and links between cases and HCFs. We presented networks by health zone using a rolling three-week reporting period, visualised using Cytoscape software. Issues at HCFs of potential concern (including transmission to HCF staff, nosocomial transmission, delayed referral and failed referral to Ebola treatment centres) were highlighted at operational meetings including senior incident management, epidemiology and IPC teams and through internal weekly reports at all levels of the outbreak response.

Results:

As an example, in one reporting period after initiating the approach, 66 unique HCFs were attended by 76 cases, 27/66 (41%) HCF's had been flagged before for IPC concerns, a further 26/66 (40%) were flagged as new possible concerns. This information supported direct public health action in the field including additional training of HCF staff, strengthening triage, alerting and isolation practices and temporarily closing HCFs in serious breach of IPC standards.

Conclusions: Visualisation of outbreak networks enabled identification of HCFs with potential IPC lapses, and together with other health intelligence supported prioritisation of HCFs for interventions aimed to halt transmission. Network analyses incorporating visualisation improved risk communication, helping to encourage rapid action in a dynamic outbreak, and should be considered as part of a package of epidemiological tools to support field level decision making during outbreaks.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: outbreak, network analysis, visualisation, infection prevent and control

ABSTRACT ID: 185

PRESENTED BY: R. Hams / rebecca.hams@phe.gov.uk

1.2. Strengthening preparedness for West Nile Virus in Europe following the 2018 transmission season: an ECDC protocol to conduct After Action Reviews

F. Riccardo [1]

F. Bolici [2], M. Fafangel [3], V. Jovanovic [4], M. Socan [5], P. Klepac [6], D. Plavsa [7], M. Vasic [8], A. Bella [9], L. Rosi [10], P. Pezzotti [11], X. Andrianou [12], M. Di Luca [13], G. Venturi [14], D. Pervanidou [15], O. Cenciarelli [16], A. Baka [17], J. Young [18], T. Bakonyi [19], J. Suk [20]

[1] National Institute of Health (Istituto Superiore di Sanità, ISS), Department of Infectious Diseases, Rome

[2] UNICLAM, Cassino

[3,5,6] Nacionalni institut za javno zdravje, Ljubljana

[4,7,8] Institut za Javno Zdravlje Srbije Dr Milan Jovanovic Batut, Belgrade

[9,10,11,12,13,14] National Institute of Health (Istituto Superiore di Sanità, ISS), Department of Infectious Diseases, Rome

[15] National Public Health Organization, Athens

[16,17,18,19,20] European Centre for Disease Prevention and Control (ECDC), Stockholm

Background:

Early, increased transmission of West Nile virus (WNV) was documented in several European countries during the summer-autumn of 2018. This led to the highest number of cases ever recorded to date in some countries (e.g. Italy, Serbia, Greece) and to the novel identification of autochthonous circulation in others (e.g. Slovenia).

In order to systematically identify current and emerging preparedness gaps, best practices, and lessons learned, we developed an ECDC after-action review (AAR) protocol covering key public health preparedness and response dimensions for WNV, including One Health aspects and blood safety.

Methods:

The protocol, developed on the basis of 2018 ECDC and WHO guidance, proposes a mixed-method approach, blending the working group and key informant interview WHO AAR formats with inclusion of an event storming exercise. We developed a stakeholder matrix to identify key informants and a semi-structured questionnaire to guide interviews. We suggested using Business Process Model and Notation to construct concise and consensually agreed-upon visualizations of existing processes across/within sectors. The protocol meets the ECDC standards for AAR methodological rigour.

Results:

At the time of submission, AARs using the ECDC protocol have been scheduled for Serbia in May 2019 and have been successfully implemented in Slovenia and Italy during April 2019. A fourth AAR, drawing from the approach described in this protocol, will be performed in Greece as part of an additional ECDC project.

Conclusions:

In Slovenia and Italy, the methods used successfully brought stakeholders together to discuss the public health response to the WNV 2018 transmission season. Common priority areas, identified so far, for improving preparedness include: increasing knowledge to solve controversial issues around vector-control measures, bolstering risk communication activities and strengthening coordination across sectors/admin levels.

Subject: Preparedness (e.g. preparedness planning, simulation exercises, after action reviews)

Keywords: West Nile Virus,Preparedness,After Action Reviews

ABSTRACT ID: 326

PRESENTED BY: Flavia Riccardo / flaviariccardo@hotmail.com

1.3. Automatic information extraction and relevance evaluation of epidemiological texts using natural language processing,

Auss Abbood[1]
A. Ullrich [2], R. Busche [3], S. Ghozzi [4]

[1] Robert Koch Institute|University Osnabrück
[2] Robert Koch Institute
[3] University Osnabrück
[4] Robert Koch Institute

Background :

According to the WHO, around 60% of all outbreaks are detected using informal sources. Thus, a group of epidemiologists at the Robert Koch Institute evaluates such sources as part of event-based surveillance (EBS). They read several online articles and store key information from relevant articles in a database which is a time-consuming process. To support our colleagues, but also to gain insights into what makes an article and the event it describes relevant, we developed a framework for automated information extraction and relevance scoring.

Methods :

First, we scraped all articles from relevant sources referenced in the EBS database. Afterwards, we used the EBS database to label those articles that exist in the EBS database as relevant outbreak articles. For the extraction of keywords of an article (disease, country, confirmed cases, and date of the case counts), we used EpiTator, an open- source epidemiological annotation tool. To reduce the extracted keywords by EpiTator to key information of the article, we trained a naive Bayes classifier on labelled sentences containing possible keywords. For relevance scoring, we compared different text classifiers on relevant and irrelevant articles.

Results :

We have implemented methods that successfully extract keywords and relevance from epidemiological texts. The relevance evaluation reached an F1 score of 0.72. We integrated these functionalities into a web app where relevant sources (like WHO DON and ProMED) are automatically evaluated and stored in a database. Additionally, it allows custom evaluation of articles given their URL.

Conclusions: We showed that natural language processing can improve EBS. Further research should focus on the performance of the classifier and the interpretability of classification decisions to understand which parts of the text lead to the final relevance score.

Subject: Surveillance

Keywords: Public Health Surveillance, Natural Language Processing, Machine Learning, Medical Informatics Applications

ABSTRACT ID: 564

PRESENTED BY: Auss Abbood / a.abbood94@gmail.com

1.4. The role of Epidemic Intelligence in Portugal: Analysis of the reported events in the National Weekly Threats Bulletin, Report on Observations, News, Data and Alerts (RONDA),

Vasco Ricoca Peixoto[1]
A. Firme [2], I. Marinho Falcão [3], A. Sentis [4], P. Vasconcelos [5]

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[2,3,5] Directorate-General of Health, Lisbon, Portugal

[4] Directorate-General of Health, Lisbon, Portugal |2- European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background:

Epidemic intelligence (EI) ensures early detection, assessment and communication of Public Health threats. In Portugal the Directorate-General of Health (DGS) is responsible for EI and publishes a weekly public health threat bulletin (RONDA).Similar reporting activities are developed in other European Member States. This work identifies main reported threats, contributing to the visibility of EI outputs, allowing discussion of usefulness, methods and dissemination procedures among national and international stakeholders

Methods:

We used the database of threats reported in RONDA. We selected threats based on risk of importation and dissemination in Portugal and cross-border threats. We described reported threats 2016-2018 by type of event, ECDC disease groups, place of occurrence and origin, geographic extension, number of cases, information sources, number of published updates, among other variables.

Results:

In total, 196 threats were reported, mostly outbreaks (78%). Most common disease groups were Emerging and Vector- borne Diseases (EVD, 29.1%), Food and Waterborne Diseases (FWD) (25.5%) and Vaccine-preventable Diseases (VPD, 8.7%) and were increasing since 2016. Most updates were on average Influenza and Respiratory Virus (5.9), EVD (3.1), and VPD (2.3). Most reported threats occurred in other European Countries (35.7%) and Portugal (31.6%). The main information sources were DGS/Regional Health Authorities (83.9%) for threats occurring in Portugal and ECDC (56.1%), WHO (23.5%),and Early Warning Response System (EWRS, 18.4%) for threats occurring elsewhere.

Conclusions:

Most reported threats occurred outside Portugal and the most frequently reported threats (EVD, FWD and VPD) can guide on preparedness and response priorities. We recommend the evaluation of usefulness and stakeholders' opinion at regional and local level. Furthermore, similar processes and outputs in different Member States can be compared to improve EI reporting activities and accountability.

Parallel Session Abstracts

Subject: Surveillance

Keywords: Epidemic Intelligence, Threat Reports, Even-based Surveillance, Threat bulletins, National Epidemic Threat Bulletin, Public Health Surveillance

ABSTRACT ID: 618

PRESENTED BY: Vasco Ricoca Peixoto / vpeixoto@campus.ul.pt

Parallel Session 2
DAY 1, Wednesday 27. November 2019
11:00-12:40

Vaccine-preventable diseases: vaccine coverage, safety and uptake

Moderator

Giri Shankar

Abstracts

2.1. “When you welcome well, you vaccinate well”: Reasons for sub-optimal vaccination coverage in urban settings in Conakry, Republic of Guinea

Julita Gil Cuesta [1]

K. Whitehouse [2], S. Kaba [3], K. Nanan-N’Zeth [4], B. Haba [5], C. Bachy [6],
I. Panunzi [7], E. Venables [8]

[1] Médecins Sans Frontières

[2,3,4,5,6,7,8] Médecins Sans Frontières

Background:

Quantitative surveys have identified low vaccination coverage reached by mass vaccination campaigns (MVC) in urban settings in Sub-Saharan countries. Exploring reasons for this could help to adapt and improve future vaccination strategies. The 2018 measles outbreak in Conakry, Guinea, provided an opportunity to understand sub- optimal vaccination coverage within a MVC among participants through their perceptions and experiences.

Methods:

We conducted Focus Group Discussions (FGDs) with care-givers and key informant interviews (KII) with health-care workers and community leaders in two communes in Conakry. Participants of vaccinated and non-vaccinated children were recruited through purposive sampling. FGDs were conducted in Susu and KIIs in French, until saturation was reached. Informed consent and ethics approval was obtained.

Results:

We conducted 9 FGDs and 13 KIIs which included 68 participants. The majority of participants regarded vaccinations positively, including their preventive benefits. The most common concerns reported related to vaccine side-effects and the subsequent cost of treatment.

The role of community health-workers (CHWs) in vaccine campaigns was also widely discussed. Care-givers suggested recruiting CHWs from local neighborhoods to increase trust during campaigns. The importance of improving CHWs’ knowledge and capacity to provide information about vaccinations was stressed.

Some care-givers stated payment for vaccination was often solicited, and they lacked trust in the health system, particularly after the 2014 Ebola outbreak. Religion and illiteracy were mentioned by key informants as barriers to vaccination.

Conclusions:

In order to increase MVC coverage, we suggest recruiting CHW’s from that community, with better presentation and language skills and to improve their training to ensure comprehensive knowledge about vaccine mechanisms, potential side-effects and their management. This would facilitate information provision to the community and, in turn, help to improve trust.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Vaccination; measles; Qualitative research; Mass vaccination; Vaccination refusal; Vaccination Coverage

ABSTRACT ID: 343

PRESENTED BY: Julita Gil Cuesta / julita.gil@luxembourg.msf.org

2.2. Risk of Guillain-Barré Syndrome after vaccination against human papillomavirus (HPV): a systematic review

Tamara Sonia Boender [1]

B. Bartmeyer [2], L. Coole [3], O. Wichmann [4], T. Harder [5]

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[2,] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

[3] Field Service, National Infection Service, Public Health England, UK

[4,5] Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

Background:

Persistent human papillomavirus (HPV) infection can cause genito-urinary cancers and warts. A large proportion of HPV- associated cancers are preventable through vaccination. Since ~2007, HPV-vaccination programmes have been implemented in most EU countries. While pre-licensure clinical trials did not observe an association between HPV vaccination and Guillain-Barré Syndrome (GBS), a study from France reported an increased risk. We assessed the risk of occurrence of GBS after HPV vaccination through a systematic literature-review.

Methods:

We systematically reviewed studies that reported on the risk of the occurrence of GBS after HPV vaccination (Cervarix, Gardasil-4/-9) in humans aged >=9 years, published between 1 January 2000 and 21 January 2019, indexed in Embase and Medline. No geographical or language restrictions were made. We excluded studies without a comparator group. We assessed studies’ risk of bias, using the revised Cochrane Collaboration’s tool (RoB 2.0) and the ROBINS-I tool. PROSPERO review-protocol registration number: #CRD42019123533.

Results:

Out of 489 identified records, 20 studies were eligible for inclusion. In 17/20 studies, no increased risk of GBS after HPV vaccination was found. In 3/20 studies, a signal of increased risk of GBS after HPV vaccination was identified: #1) incidence rate 1.36 versus 0.37/100,000 person-years, aHR 3.78 (95%CI: 1.79-7.98); #2) incidence rate 1.3-1.5 versus 1.1-1.5/100,000 person-years; aHR 5.31 [95%CI: 0.62-45.39]; #3) 6.6 cases observed versus 0.65-2.57 expected/week per 10,000,000.

Conclusions:

A significant relative increase in the risk of GBS after HPV vaccination was identified in one out of 20 studies. The results of our systematic review indicate that the absolute risk of GBS after HPV vaccination is low. The potential risk of GBS should have minimal impact on the risk consideration for HPV-vaccination programmes, and should reassure vaccine confidence.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Vaccination, Papillomaviridae, Guillain-Barre Syndrome, Systematic Review

ABSTRACT ID: 278

PRESENTED BY: Tamara Sonia Boender / BoenderS@rki.de

2.3. Underreporting of the 5-year tetanus, diphtheria, pertussis and polio booster vaccination in the Danish Vaccination Register

Ida Glode Helmuth [1]

S. Skou Voss [2], C. Hiul Suppli [3], P. Valentiner-Branth [4]

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[2,3,4] Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark

Background:

Surveillance of childhood vaccination coverage in Denmark is conducted using the Danish Vaccination Register (DDV). Reporting of all vaccinations is mandatory and written reminders sent to parents of children missing vaccinations. The objective of this study was to validate the coverage of the 5-year tetanus, diphtheria, pertussis and polio booster and identify reasons for non-vaccination.

Methods:

We identified all children born in 2010 and living in Copenhagen as of July 2018 in the Danish civil registration system including their unique personal identifier used to link to the DDV. In DDV, we identified children not registered with the 5-year booster and an electronic questionnaire was sent to their parents. Using the results of the questionnaire survey we calculated a corrected vaccination coverage for Copenhagen, the largest municipality in Denmark, and used this to produce a national estimate.

Results:

692/6039 children (11%) had not received the 5-year booster. Parents of 340 children (49%) answered the questionnaire. Of those, 186 (55%) reported having received the 5-year booster; 61% had received the vaccination at their general practitioner and 34% were vaccinated abroad. The most common reason for non-vaccination was forgetfulness (31%), whereas 26% had actively declined and 17% were not aware of the vaccination after immigration to Denmark. The corrected vaccination coverage was 91% (95% CI: 90-91%).

Conclusions:

The coverage of the 5-year booster in Denmark is currently underestimated, and national coverage estimates reported to WHO are now adjusted by two percentage points. Despite reminder letters, forgetfulness is still the most common reason for missing vaccines. Denmark will introduce prevaccination reminders in the future. We recommend tailored communication about the vaccination program targeting immigrants to Denmark.

Subject: Surveillance

Keywords: The Danish Vaccination Register,Vaccination Coverage

ABSTRACT ID: 128

PRESENTED BY: Ida Glode Helmuth / idgk@ssi.dk

2.4. Uptake of the second measles-mumps-rubella vaccination by school in Denmark

Palle Valentiner-Branth [1]

L. Riberholdt [2], L. Mortensen [3], T. Krause [4]

[1] Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut

[2,] Methods and Analysis, Statistics Denmark

[3,] Methods and Analysis, Statistics Denmark|Department of Public Health, University of Copenhagen

[4] Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut

Background:

Since 2017 WHO has assessed that measles is eliminated in Denmark. However, with the surging number of measles cases in The European Region there is an increasing risk of spread to Denmark and transmission in areas with low coverage. So far, the uptake of the second measles-mumps-rubella vaccination (MMR2) has only been estimated by municipality level. We assessed the uptake of MMR2 by school in order to identify pockets with an increased risk of measles outbreaks and identified socioeconomic determinants for low school coverage.

Methods:

We combined individual level data from Statistics Denmark on school attendance in 2017 and various sociodemographic determinants for children born in Denmark from 2002 to 2011 with the MMR2 vaccination status retrieved from The Danish Vaccination Register.

Results:

The overall uptake of the MMR2 for the 617,277 children attending 1,873 schools was 89%. Most children, 54%, attended a school with an uptake between 80% and 90%, while 44% attended schools with uptake between 90% and 100%. Under 2% attended a school with a coverage below 80%. A minority of 1% of the children attended 30 schools with an uptake between 50% and 75%. Of these, eleven were antroposophic schools, but also international, various religious, small island and four schools from a single municipality were among the schools with the lowest uptake. Uptake was positively correlated with education and income, and negatively with single parents and large families although these determinants only explained a small part of the low uptake.

Conclusions :

We provide a detailed picture of pockets with low coverage. Identifying schools with low coverage enable the municipalities to target their vaccination interventions to schools with a high risk of measles transmission.

Subject: Surveillance

Keywords: Mumps Measles Rubella Vaccination Schools Denmark

ABSTRACT ID: 639

PRESENTED BY: Palle Valentiner-Branth / PVB@ssi.dk

Parallel Session 3
DAY 1, Wednesday 27. November 2019
11:00-12:40

Healthcare-associated infections: burden and prevention

Moderator

Annalisa Pantosti

Abstracts

3.1. A genomic profile of Mycobacterium abscessus isolates from Cystic Fibrosis patients in Scotland

Elizabeth Dickson [1]

K. Templeton [2], J. Murray [3], C. Peters [4], L. Seagar [5], A. Innes [6], A. Fall [7], I. Laurenson [8], S. Bicknell [9], J. McMenamin [10], M. Holden [11]

[1] European Programme for Public Health Microbiology | Health Protection Scotland

[2,9] West of Scotland Adult Cystic Fibrosis Centre, Queen Elizabeth University Hospital

[3,10] Health Protection Scotland, Meridian Court, Glasgow

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[5,8] Scottish Mycobacterial Reference Laboratory, Royal Infirmary of Edinburgh, Edinburgh

[6] Respiratory Medicine, Western General Hospital, Edinburgh

[7] Paediatric Respiratory Medicine, Royal Hospital for Sick Children, Edinburgh

[7] Health Protection Scotland, Meridian Court, Glasgow | School of Medicine, University of St Andrews, St Andrews

Background:

Mycobacterium abscessus complex infection in Cystic Fibrosis patients leads to chronic infection with limited treatment options. An investigation was undertaken to determine the genomic profile of Scottish M.abscessus isolates from 2000 to 2017 utilising whole genome sequencing (WGS) to support epidemiological data in understanding mode of transmission and evaluate control measures.

Methods:

Clinical M. abscessus isolates (79) referred to the Scottish Mycobacteria Reference Laboratory were sent to University of St Andrews where WGS using the Illumina MiSeq platform was performed. Sequence data was analysed by mapping to a reference sequence using SMALT to identify core SNPs, and maximum likelihood trees prepared with RAxML. MLST was conducted using SRST2. Epidemiological data was collected using TrakCare and Clinical Portal.

Results:

WGS analysis showed that the isolates could be split up into the three known subspecies: M. abscessus supbsp bolletti (4), M.abscessus subsp massillense (18) and M. abscessus subsp abscessus(57). The latter group comprised three main clusters: sequence type (ST) 5, ST9 and clonal complex (CC)24. Epidemiological investigations were performed on ST5 and ST9 as WGS data suggests they are dominant clones capable of causing healthcare–associated infection. The ST5 cluster comprised 10 isolates, two separated by 5 non-recombination SNPs but geographically distant. The ST9 cluster (21 isolates) spanned the entire time period constituting 9 clusters with self- mapping suggesting as few as 1 SNP apart, with epidemiological links to hospital and clinic visits.

Conclusions:

M. abscessus subsp abscessus has two dominant healthcare-associated clones which should be monitored routinely in cystic fibrosis patients. In situations where transmission of infection is suspected and to determine efficacy of infection control interventions, WGS is required to support investigation of M. abscessus in this vulnerable population.

Subject: Burden of disease

Keywords: Mycobacterium abscessus,Cystic Fibrosis,Single Nucleotide Polymorphism,Whole Genome Sequencing,Genomics,Infection Control

ABSTRACT ID: 352

PRESENTED BY: Elizabeth Dickson / elizabeth.dickson2@nhs.net

3.2. Long-term excess mortality after Clostridium difficile infection by place of origin; a nationwide study from Denmark, 2010-18

Sophie Gubbels [1]

I. Johanson [2], M. Chaine [3], B. Olesen [4], J. Engberg [5], S. Persson [6], M. Voldstedlund [7], K. Mølbak [8], B. Kristensen [9], S. Ethelberg [10]

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Background:

Clostridium difficile (CD) can cause severe disease and forms a considerable burden on hospitals, particularly due to hospital outbreaks.

High mortality has been described for the short term (30 days) and middle-long term (up to one year). The objectives of this study were to provide information on long-term CD-related mortality in Denmark and differences in mortality between healthcare-associated and community-associated infections.

Methods:

A retrospective registry-based study was performed using the Hospital-Acquired Infections Database – HAIBA (occurrence of CD infections (CDI) between 2010 and 2018, origin of acquisition), Population registry (mortality data) and Denmark Statistics (death rates in the general population). Cases in HAIBA were classified, based on the European case definition for CDI surveillance: Hospital Onset Healthcare-Associated (HOHA), Community Onset Healthcare- Associated (COHA), Community Onset Community-Associated (COCA) and unknown origin (UNKN). Cox-regression was performed, adjusted for age and sex. Nine years CDI-related excess mortality was calculated by comparing observed and expected survival using the Ederer II method.

Results:

Age and sex adjusted hazard ratio for HOHA was 2.39 (95% CI 2.26 -2.52), for COHA 1.78 (95% CI 1.68 -1.88) and for UNKN 1.42 (95% CI 1.32 -1.52) compared to COCA. CDI-related excess mortality up to 9 years after the first CDI episode compared to the general population was observed for all origin types, except UNKN. Patients with UNKN showed the expected death rate after 8 years.

Conclusions:

The study showed that excess mortality related to CDI could be observed many years after the first CDI episode. Patients with hospital onset had the highest risk. These findings underpin the need for effective preventive measures and outbreak management. Further research is planned to investigate the influence of CD subtypes and co-morbidity.

Subject: Burden of disease

Keywords: Clostridium difficile, mortality, Denmark, hospital-acquired, community-acquired

ABSTRACT ID: 548

PRESENTED BY: Sophie Gubbels / gub@ssi.dk

3.3. Healthcare associated infection in home healthcare; what, why and how?

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Background:

The number of patients and clinical conditions treated in home healthcare (HHC) is increasing. Care in home setting presents many challenges, including healthcare associated infections (HAI). Currently, in Belgium, data and guidelines on the topic are lacking. Our objective was to investigate a definition of HAI in HHC, their associated risk factors and recommendations for infection prevention and control (IPC).

Methods:

The study included three consecutive steps: i) a scoping literature review; ii) in-depth interviews with individuals involved in the field of HHC; and iii) a two-rounds Delphi survey online to reach consensus among experts on the results of the previous steps.

Results:

The review included 47 publications. No standard definition was broadly accepted, risk factors identified were limited by methodological flaws and recommendations were therefore inconsistent. The overall evidence was weak.

Nineteen in-depth interviews were conducted, and supported the literature findings, highlighting the lack of agreed definitions, risk factors and guidelines.

The Delphi survey included 21 and 23 participants in each round, respectively, and agreement was reached on the following:

Definition: Any infection specifically linked with providing care, that develops in a patient who receives HHC from a professional healthcare worker, and occurs ≥48 hours after starting HHC.

Risk factors: hand and patient's hygiene; untrained patients and caregivers; presence and management of invasive devices.

Recommendations: adapt and standardise existing IPC guidelines to HHC; perform a national point prevalence study to measure the burden of HAI in HHC in Belgium.

Conclusions:

This study offers an overview of the evidence available and the field knowledge of HAI in HHC. It provides a framework to set-up a prevalence study, and drive future monitoring policies and guidelines on IPC in Belgium.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: SHealthcare associated infection,Home health care,Infection prevention and control,Belgium

ABSTRACT ID: 195

PRESENTED BY: Ana Hoxha / ana.hoxha@sciensano.be

3.4. Incidence of hospital-acquired Clostridium difficile infection and association with antimicrobial consumption in Ireland, 2013-2017,

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Background:

Clostridium difficile infection (CDI) may be acquired in hospital and is associated with high morbidity and mortality. Broad- spectrum antimicrobial exposure is a known risk factor for CDI. We investigated the temporal effect of antimicrobial consumption (AMC) on the incidence of hospital-acquired CDI (HA-CDI) in Ireland, to guide hospitals to set priorities for AMC and prevent CDI.

Methods:

We linked new HA-CDI (2013-2017) cases with quarterly AMC data (from 2012) from the respective national surveillance systems. We expressed AMC as defined daily dose (DDD) and all rates per 1,000 bed days used (BDU). We conducted an ecological study with multi-level time series analysis, allowing for variability between hospitals, trends, seasonality and AMC in previous quarters. We calculated adjusted incidence rate ratios (aIRR), per unit increase in AMC rate, using negative binomial regression.

Results:

There were 3,632 new HA-CDI cases in 34 public hospitals in the study period. Average annual HA-CDI incidence rates varied from 0.21 (2013) to 0.19 per 1,000 BDU (2017) and total AMC rates from 846 (2012) to 822 DDD/1,000 BDU (2017).

Within the same quarter, HA-CDI rates increased with consumption of combinations of penicillins, including beta- lactamase inhibitors (aIRR=1.001; p=0.022), third-generation cephalosporins (aIRR=1.006; p=0.028), carbapenems (aIRR=1.005; p=0.008) and lincosamides (aIRR=1.015; p=0.003). Consumption of carbapenems, lincosamides and macrolides in previous quarters was also associated with increased HA-CDI incidence. No association with fluoroquinolones was found.

Conclusions:

Increased consumption of beta-lactams and lincosamides was associated with increased HA-CDI incidence. The lack of association with fluoroquinolones may reflect a national reduction in consumption since 2009. We recommend using these findings to inform and tailor antimicrobial stewardship initiatives, coupled with continued AMC and CDI surveillance in hospital patients.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Antimicrobial stewardship, time series analysis, Clostridium difficile infection,Beta-lactam antibiotis

ABSTRACT ID: 241

PRESENTED BY: Annalisa Quattrocchi / annalisaquattrocchi@hotmail.com

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3.5. Alerting all neighbours

Aimée Tjon-A-Tsien [1]

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Background:

When there is an outbreak in a healthcare facility, transfers of patients between facilities can lead to exchange of pathogenic or resistant micro-organisms. Facilities do not always share information on ongoing outbreaks when transferring patients to another facility, which undermines timely preventive measures. Various regional healthcare facilities expressed a need for a system that would allow real-time interchange of information on outbreaks between healthcare facilities and regional public health services.

Methods:

We designed a web-based notification system for 3 Dutch regions (~ 2,1 million inhabitants). The aim was to obtain real- time data on infectious disease outbreaks, allowing hospitals and long-term care facilities to be informed and prepared during ongoing regional outbreaks. During each step of the development, we consulted various stake holders from health care facilities on definitions of notification criteria, the computer interface and the outbreak report form. In an iterative design process with the group and a web developer, "MUIZ" was developed in five "sprints".

Results:

"MUIZ" is a user friendly, enclosed system that enables 95% of regional health care facilities to enter real-time data on outbreaks and to be notified of new outbreaks. Relevant information is visible to users (i.e. geographical locations, symptoms, pathogens, total cases). We defined notification criteria: outbreaks of minimally 2 interrelated cases of gastro-intestinal disease, respiratory disease, scabies or carrier/symptomatic resistant micro-organisms. Since February 2017, 228 outbreaks are reported from 404 professionals: 158 gastro-enteritis, 50 respiratory,3 scabies and 17 multi-resistant outbreaks. Participants in the evaluation confirmed that "MUIZ" facilitates timely infection prevention measures.

Conclusions:

"MUIZ" is a unique web-based system that provides real-time data on infectious disease outbreaks and assists regional infection prevention. More Dutch regions are keen to implement MUIZ.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: outbreaks,health-care associated infections,surveillance,real-time,notification system,infection prevention measures

ABSTRACT ID: 419

PRESENTED BY: Aimée Tjon-A-Tsien / aml.tjonatsien@rotterdam.nl

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Parallel Session 4
DAY 1, Wednesday 27. November 2019
14:30-15:30

Antimicrobial resistance and Healthcare-associated infections: epidemiology

Moderator

Kåre Mølbak

Abstracts

4.1. Descriptive epidemiology of carbapenemase-producing enterobacteriaceae in Northern Ireland, 2012 to 2017

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Parallel Session Abstracts

Background:

Carbapenemase-producing enterobacteriaceae (CPE) present a major public health challenge through the limited availability of treatment options due to their resistance to last line antibiotics (carbapenems). Voluntary notification of CPE to the Public Health Agency (PHA) in Northern Ireland (NI) began in 2011; positive CPE isolates from screening and clinical samples are reported to PHA with additional case information collected from healthcare providers. Our aim is to describe the epidemiology of CPE in NI from 2012 to 2017 as part of an evaluation of CPE reporting in NI, to inform development of regional guidelines.

Methods:

Data was collected on species and carbapenemases detected, specimen type, patient demographics, and known CPE risk factors. We calculated rates of CPE per 100,000 population from 2012 to 2017, using mid-year population estimates.

Results:

97 confirmed CPE isolates were reported to PHA between 2012 and 2017. 43.2% (42) were Klebsiella pneumoniae, 19.6% (19) were Enterobacter clocae, and 9.3% (9) were E. coli. 42.3% (41) of CPE reported produced NDM. 32.0% (31) were detected in urine, 21.6% (21) in rectal swabs, 8.2% (8) from faecal samples and 5.2% (5) in blood. Annual incidence ranged from 0.3 isolates per 100,000 population in 2012 to 1.5 per 100,000 in 2014, with 1.0 per 100,000 in 2017.

Conclusions :

The rate of CPE in NI has fluctuated over time and is lower than reported incidence in England and the Republic of Ireland (ROI) (5.4 and 11.4 per 100,000 in 2017, respectively).The carbapenemases detected in isolates in NI also differ from ROI and England. Because of this variation, we recommend further engagement with microbiology and infection prevention/control teams to better understand CPE screening, detection and reporting within NI.

Subject: Surveillance

Keywords: Carbapenem-Resistant Enterobacteriaceae,Health Care Associated Infections, Antimicrobial resistance , Surveillance

ABSTRACT ID: 113

PRESENTED BY: Joseph Pett / joseph.pett@phe.gov.uk

4.2. Defining nosocomial E. coli transmission using an integrated genomic and epidemiological approach

Catherine Ludden [1]

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Background:

E. coli is the leading cause of bloodstream infections, a proportion of which are nosocomial. Here, we examine acquisition via transmission in a hospital setting using genomic surveillance.

Methods:

We prospectively identified and followed 149 hematology patients admitted to a hospital in England for 6 months. Patient stools were taken at intervals and cultured for E. coli. We collected all E. coli bloodstream isolates. We sequenced 970 E. coli isolates (686 non-ESBL, 284 ESBL) from 152 stools/97 patients and 123 isolates (88 non-ESBL, 35 ESBL) from 45 blood cultures/32 patients. We used within-host diversity to define a SNP threshold to infer transmission and applied this to patient epidemiological data.

Results:

Ninety different sequence types (STs) were identified in stool samples, with 30% of samples containing >2 STs. Thirty of 101 patients (30%) with ≥2 stool samples acquired one or more E. coli STs through a total of 50 acquisition events. A maximum within-host diversity of 17 SNPs was identified based on pairwise core genome comparison of isolates from the same patient/same ST. Network analysis using 17 SNPs as a transmission cut-off showed that 20/97 patients positive had genomic links with at least 1 other patient, with 10/20 also having a strong epidemiological link supporting nosocomial transmission. During the 6-months, 17/97 patients were positive for ESBL-producinEg. coli with bla$_{\text{CTX-M-15}}$ and bla$_{\text{CTX-M-14}}$ present in 12 and 2 cases respectively, and bla$_{\text{CTX-M-1}}$, bla$_{\text{CTX-M-27}}$ and bla$_{\text{SHV-12}}$ identified in one patient only.

Conclusions: Our findings reaffirm the importance of whole-genome sequencing to accurately detect bacterial acquisition and transmission. On-going work will characterise whether mobile elements encoding bla$_{\text{CTX-M-15}}$ and bla$_{\text{CTX- M-14}}$ were shared between different lineages.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Antimicrobial resistance, E. coli, Transmission, Genomics, Epidemiology, ESBL ,Plasmids

ABSTRACT ID: 792

PRESENTED BY: Catherine Ludden / catherine.ludden@lshtm.ac.uk

4.3. Molecular epidemiology of community- and healthcare associated Clostridium difficile infections in Jönköping, Sweden, October 2017 – March 2018

Theresa Enkirch [1]

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Background:

Clostridium difficile infections (CDIs) are mostly hospital-acquired (HA) with high morbidity and mortality. Limited knowledge is available for community-acquired (CA) infections. We investigated the molecular epidemiology of clinical isolates of CA-CDI and HA-CDI in order to improve the Swedish national surveillance of CDI in the community.

Methods:

We collected isolates (n=156) and data of CDI patients (n=130) attending the hospital in Jönköping, October 2017-March 2018, and classified them as CA (hospital onset <=2 days after admission and >12 weeks after discharge; community onset >12 weeks after hospitalization) or HA (onset >3 days after hospital admission or within 4 weeks after discharge). Molecular characterisation of isolates included PCR ribotyping (n=156) and single nucleotide polymorphisms (SNP) analysis on whole genome sequencing results (n=53). Adjusted risk ratios (aRR) were estimated using logistic regression.

Results:

We classified 94 isolates (60.3%) as HA-CDI and 62 (39.7%) as CA-CDI. CA-CDI was more common in male (61.3%). Between HA-CDI and CA-CDI isolates, we observed no statistically significant difference for age (RR 1.0; 95% CI: 0.97-1.00), 30-day mortality (RR 0.8; 95% CI: 0.42-1.42) and recurrence (RR 1.2; 95% CI: 0.77-1.75). Ribotype 002 (aRR 2.3; 95% CI: 1.24-4.22), 014 (aRR 2.1; 95% CI: 1.27-3.39), 005 (aRR 3.7; 95% CI: 2.31-6.05) and 020 (aRR 2.4; 95% CI: 1.45-3.89) were higher associated with CA-CDI than HA-CDI. SNP analysis identified six clusters (0-2 SNP difference) involving 16/53 isolates of HA-CDI (n=4) or CA-CDI (n=4) or both (n=8).

Conclusions: Molecular epidemiology differed between CA-CDI and HA-CDI and the cluster identification in SNP analysis suggests transmission events of CDI not only in the hospital but also in the community. Our results demonstrate that CA-CDIs are underestimated and need to be closely monitored.

Subject: Surveillance

Keywords: Clostridium difficile, community-associated infections, hospital-associated infections, enhanced surveillance, Whole Genome Sequencing

ABSTRACT ID: 751

PRESENTED BY: Theresa Enkirch / theresa.enkirch@gmail.com

Parallel Session 5
DAY 1, Wednesday 27. November 2019
14:30-15:30

Emerging and vector-borne diseases: epidemiology

Moderator

Kostas Danis

Abstracts

5.1. High subsequent mortality of Ebola virus disease survivors in Guinea: a nationwide retrospective cohort study

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Background:

The 2013-2016 West African Ebola outbreak left a record number of Ebola survivors. A range of post-Ebola sequelae in survivors have been reported, but little is known about their subsequent mortality. The aim of the study was to describe subsequent mortality from the Guinea outbreak and identify associated risk factors.

Methods :

The Guinean national Ebola survivors' monitoring program contacted all survivors and recorded deaths from December 2015. Survivors were followed up until September 2016. We investigated deaths using verbal autopsy interviews and calculated the age-standardised mortality ratio (SMR) compared to the Guinean population. We assessed whether length of hospitalisation (divided in number of days above or below the median) was a risk factor for mortality using survival analysis and Cox regression.

Results:

Information was retrieved on 1130/1270 Guinean Ebola virus disease survivors (follow-up rate 89%). Enrolled survivors were followed-up for a mean of 21 months after ETU discharge. Survivors had an over five-fold increased risk of dying, compared to the Guinean population (SMR 5.2, 95% CI 4.0-6.8), a mean of one year of follow-up after ETU discharge, with no increase in risk for the subsequent 9 months. Mortality rates were increased in all age groups and were similar for males and females. Of the 59 deaths, main contribution to death was assigned to renal failure for 37 and was unknown for 7. Longer hospitalisation in the ETU was associated with an increased risk of subsequent death (adjusted hazard ratio 2.6, 95% CI 1.4-4.8).

Conclusions:

Our results suggest that systematic follow up of survivors should be implemented for at least one year after their recovery, when the risk of subsequent death is highest.

Parallel Session Abstracts

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Ebola, Survivor, Resurgence, Surveillance, Guinea, Kidney, Mortality, late death

ABSTRACT ID: 284

PRESENTED BY: Lorenzo Subissi / lorenzo.subissi@sciensano.be

5.2. Cross-Protection of Dengue Virus Infection against Congenital Zika Syndrome, Northeastern Brazil,

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Background:

The catastrophic Zika virus (ZIKV) outbreak in Latin America has a major impact on maternal and child health due to ZIKV-associated congenital malformations summarized as Congenital Zika syndrome (CZS). For unknown reasons, CZS incidence was particularly high in northeastern Brazil. Data from in vitro studies and mouse models suggest that dengue virus (DENV)-mediated immune enhancement may affect CZS formation, potentially explaining the accumulation of CZS in northeastern Brazil. Our goal was to examine whether preexisting DENV immunity did affect CZS formation within a case-control framework in northeastern Brazil.

Methods:

We analyzed all available historical DENV genomic data to compare genomic signatures from northeastern Brazil with other Brazilian regions. Moreover, we performed comprehensive serological testing within the case-control framework by performing plaque-reduction neutralization tests (PRNT90). Serotype-specific neutralization testing for DENV and ZIKV was conducted for 29 ZIKV-seropositive mothers of CZS cases and 108 ZIKV-seropositive controls from northeastern Brazil.

Results:

No unique DENV genomic signature was evident for northeastern Brazil, refuting differential anti-DENV immunity to affect CZS incidence. There were neither statistically significant differences of DENV PRNT90 titers between cases and controls, nor between the four DENV serotypes. In contrast, DENV seroprevalence was significantly higher in controls (92%) than in cases (66%; $p=0.0003$). The median number of neutralized DENV serotypes was two for cases and four for controls ($p<0.0004$). Serotype-specific DENV neutralization was neither correlated with ZIKV titers, nor with heterologous DENV titers, suggesting robustness of the serological data.

Conclusions:

Our study strongly suggests a complex interaction between ZIKV and DENV immunity and a protective effect of strong preexisting multitypic DENV immunity of the mother on CZS development in the fetus during the Zika virus outbreak in northeastern Brazil.

Subject: Microbiology

Keywords: Cross-protection, antibody dependent enhancement, congenital Zika syndrome Dengue virus, Zika virus, Brazil

ABSTRACT ID: 431

PRESENTED BY: Carlo Fischer / carlo.fischer@charite.de

5.3. Surveillance of hospitalisations during a large outbreak shows severe dengue remains stable, La Réunion, 2018-2019,

Eve Robinson [1]

A. Etienne [2], M. Vincent [3], J. Donikian [4], M. Lafont [5], Y. Koumar [6], G. Mourembles [7], C. François [8], E. Balleydier [9], . Vilain [10], L. Menudier [11]

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Background :

La Réunion, in the Indian Ocean, is a French overseas department. Dengue serotype-2 (DENV-2) has been circulating since 2017 leading to a large outbreak with 6,801 laboratory-confirmed cases in 2018. In 2019 a second epidemic wave is onging, with 9,200 cases as of week 16, including a DENV-1 cluster. We implemented surveillance of hospitalisations to monitor outbreak severity.

Methods:

We aimed to identify cases hospitalised for greater than 24 hours or severely ill. Laboratories routinely notified diagnoses and we investigated those originated from a hospital service. Clinicians were also encouraged to spontaneously report hospitalisations. We collected data on clinical and biological signs, risk factors, and outcomes using a standardised form. We classified severity using WHO definitions.

Results:

In 2018 we identified 156 hospitalisations (2% of cases) compared to 273 (3% of cases) as of week 16, 2019. Across both periods the male-to-female ratio was 0.9 and the median age was 62 years. Among those with a returned surveillance form, the proportion of severe dengue was 18% for both periods (34/196 in 2019; 27/156 in 2018). The most frequent severe complications were renal impairment (39%), liver impairment (24%), and hemorrhage (18%). Alert signs were reported for 67% of non-severe cases in 2018 and 61% in 2019. In both periods, 3 of 6 deaths amongst hospitalised cases were directly attributable to dengue.

Conclusions:

Thus far the proportion of hospitalisations identified in 2019 exceeds that of 2018, potentially due to improved sensitivity. The similar proportion of severe cases, does not suggest increased severity. This surveillance improved the understanding of the outbreak and its burden on the population and should continue, particularly given the risk of endemisation and co-circulation of other serotypes.

Subject: Surveillance

Keywords: Dengue; severe dengue; surveillance; Indian Ocean

ABSTRACT ID: 516

PRESENTED BY: Eve Robinson / eveprobinson@gmail.com

Parallel Session 6
DAY 1, Wednesday 27. November 2019
14:30-15:30

Food- and waterborne diseases and zoonoses: outbreaks (1)

Moderator

Therese Westrell

6.2. E. coli O157 and leafy green outbreaks in Canada, 2015-2019

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Background:

E. coli O157 remains an important foodborne pathogen in Canada. While beef has traditionally been a common source of outbreaks, fresh leafy greens are frequently implicated in foodborne illness outbreaks in Canada. We describe the trends, lessons learned and challenges associated with E. coli O157 and leafy green outbreaks in Canada since 2015.

Methods:

The National Microbiology Laboratory identifies multi-jurisdictional clusters of E. coli, using multiple-locus variable number tandem repeat analysis (MLVA) and whole genome sequencing (WGS), and prior to 2018, pulsed-field gel electrophoresis (PFGE). We reviewed multi-jurisdictional E. coli outbreak investigations in Canada from 2015 to 2019. For outbreaks associated with leafy greens, details on the investigation were summarized, including commonalties, challenges and lessons learned.

Results:

There have been 11 multi-jurisdictional E. coli national outbreak investigations in Canada since 2015. One outbreak was a non-O157 investigation associated with flour; the remaining ten were due to E. coli O157. Five of the ten outbreaks did not have a source identified, one was associated with beef, and four were associated with leafy greens. Three outbreaks in a 12 month period (2017-2018) were associated with romaine lettuce. Key challenges in investigations associated with leafy greens included the wide range of produce exposures reported by cases, the short shelf life of leafy greens and the complexities of the associated traceback investigations.

Parallel Session Abstracts

Conclusions:

Recent outbreak investigations in Canada have demonstrated the importance of considering sources other than beef when investigating E. coli infections, especially leafy greens. Leafy green outbreaks are challenging to investigate and traceability improvements are necessary to improve the response to leafy greens-related outbreaks. Specific product information gathered from cases during the initial interview is critical to inform the investigation.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: E. coli, Leafy greens,outbreaks

ABSTRACT ID: 590

PRESENTED BY: Philippe Bélanger / philippe.belanger@canada.ca

6.3. Investigating salmonella contamination in frozen feeder mice being supplied to the UK market

Matt Edmunds [1]

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Background:

Two large human outbreaks of Salmonella associated with frozen reptile feeder mice have been documented in the UK. As part of ongoing investigations into the second outbreak, linked to a single breeding farm in another country, we sought to identify whether mice from other farms supplying the UK were potential sources of human Salmonella.

Methods:

Breeding farms were identified via a supply chain analysis conducted with industry stakeholders. Six bags each of 25 “pinks”/“fluffs” (feeder mice sizes) were requested from each identified farm. The Animal Plant and Health Agency pooled and tested 10 mice from each bag. Isolates were sent to the National Salmonella Reference Service for whole genome sequencing (WGS) and single nucleotide polymorphism (SNP) typing, for comparison with human isolates.

Results:

Three farms submitted 24 bags: 3/6 pooled batches of fluffs from one breeder were contaminated with Salmonella Enteritidis. All other samples tested negative. All isolates fell into a single five SNP cluster (1.1.2.43.195.358), not closely genetically related to the current outbreak strain. Isolates for 42 human cases from the national gastrointestinal database fell within the same 5-SNP cluster. Routine questionnaires were available for eleven cases; four reported contact with a pet fed feeder mice and three reported travel. Phylogenetic analysis suggested human cases arose from multiple sources.

Conclusions:

Combined microbiological/epidemiological evidence suggests that that some human cases forming part of a new 5-SNP cluster may be associated with mice from a different farm. This previously unrecognised association indicates frozen feeder mice may be a larger contributor to the Salmonella disease burden in the UK than previously known. Further assessment of sources of contaminated rodents and improved risk management information for reptile owners is warranted.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella Enteritidis, Outbreak, Reptiles, Feeder mice

ABSTRACT ID: 477

PRESENTED BY: Matt Edmunds / matt.edmunds@phe.gov.uk

Parallel Session 7
DAY 2, Thursday, 28. November 2019
11:00-12:40

Food- and waterborne diseases and zoonoses: public health microbiology and surveillance methods

Moderator

Marc Struelens

Abstracts

7.1. Interactive application to explore time series of European infectious disease surveillance data for signal detection: the ECDC EpiSignalDetection R-package

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Background:

The monitoring of multi-country routine surveillance data has the potential to detect important changes in a disease’s epidemiology, including outbreaks. Using the European Surveillance System data (https://atlas.ecdc.europa.eu), our goal was to develop an interactive tool for epidemiologists to monitor surveillance data time series for outbreaks.

Methods:

We used the R-package ‘surveillance’ to implement the algorithms. Based on expert review, we selected the so-called Farrington Flexible and the Generalized Likelihood Ratio for the Negative Binomial (GLRNB) algorithms. We developed an interactive application using the ‘shiny’ R-package. R-Markdown allowed production of automated integrated reports. We encapsulated the scripts in an R-package and developed a user manual and package vignette. We chose the statistical computing platform R in order to make the tool as broadly available as possible: free, open source and portable on any platform.

Results:

We developed the 'EpiSignalDetection' R-package (https://CRAN.R-project.org/package=EpiSignalDetection) including an interactive application to import external data, explore time series through a set of parameter choices (study period, time unit, geographical level, detection period and algorithm) and perform basic signal detection analysis. The tool automatically produces a graph presenting the time series of number of cases over the study period, an interactive table of signals to assess and a report summarising the results of the analysis.

Conclusions:

'EpiSignalDetection' can assist epidemiologists in timely monitoring of surveillance data. Statistical signals generated constitute a rapid and efficient way of screening a large number of disease-specific time series for outliers. However, a signal by itself is of little use and need to be embedded in a protocol for what happens with the signals, e.g. further assessment and verification. Interactive tools can play a valuable role in this process.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Public Health Surveillance,Signal Detection,Disease Outbreak,Automated reporting,R,R Shiny

ABSTRACT ID: 256

PRESENTED BY: Joana Gomes Dias / l.merdrignac@epiconcept.fr

7.3. Evaluation of national legionellosis surveillance in Norway, 2008 to 2017

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Background:

In Norway, Legionnaire's disease (LD) is reportable upon clinical suspicion to public health authorities, and mandatorily notifiable through the Norwegian Surveillance System for Communicable Diseases (MSIS). While several European countries reported increases in incidence of LD in 2017, this was not observed in Norway. We evaluated MSIS to assess if it meets its objective of detecting changes in LD incidence.

Methods:

We retrieved MSIS data from 2008 to 2017: timeliness was calculated as days from test result to notification, and internal completeness as the proportion of observations with any value, for key variables. Where possible, we assessed internal validity on the presence of a plausible value. To describe acceptability and representativeness, we surveyed doctors in hospitals that notified LD in 2013-2017, on their units' diagnostic and notification procedures, and their use of MSIS.

Results:

There were 438 MSIS-notified LD cases. Internal completeness and internal validity were high (>=95%). The median delay from test-positive to notification was 4 days (10th-90th percentile 1-16 days). Forty-seven respondents, representing 28/39 hospitals, described testing procedures. These were inconsistent: 29 (62%) reported no systematic application of criteria for requesting legionella testing; 18 (38%) reported testing all patients with suspected pneumonia and a travel history. For acceptability, 31 (66%) found the notification criteria clear. Thirty-nine (83%) found MSIS incidence data useful, and 24 (51%) reported that data are easy to access.

Conclusions:

While data quality and timeliness were good for notified cases, we identified differences in diagnostic practices, and limited acceptability, which could result in sub-optimal representativeness. This evaluation suggests that MSIS may not be sufficiently sensitive to changes in LD occurrence in Norway. We recommend comparing MSIS against another data source, to estimate sensitivity.

Subject: Surveillance

Keywords: Legionnaires' disease, legionellosis, surveillance, outbreak

ABSTRACT ID: 333

PRESENTED BY: Cecilia Wolff / cecilia.mia.wolff@fhi.no

7.4. Genomic Comparisons to Investigate Virulence Differences Between Australian and International Strains of O157 Shiga Toxin-Producing Escherichia coli

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Background:

Shiga toxin-producing Escherichia coli (STEC) causes a wide spectrum of disease, due to the immune competence of the individual affected, and to the genetic heterogeneity found within STEC which involves several known virulence factors. The presence, absence, or variation of these virulence factors within strains can affect the severity of disease. Heterogeneity in virulence is observed between Australian and many international strains of O157 STEC, where Australian strains are typically associated with mild disease and fewer outbreaks than international. Here, genomic analysis is used to examine genetic attributes that might contribute to the difference in virulence between Australian strains of O157 STEC and international strains.

Methods:

Whole Genome Sequences from Australian (n = 47), related to a highly pathogenic UK 2015 outbreak (n = 116), and other international O157 STEC strains (n = 23) were investigated. Core single nucleotide polymorphism (SNP) analysis was performed to create a phylogenetic tree and the Shiga toxin (Stx) profiles and gene presence-absence variation of these strains were noted to compare geographically distinct strains.

Results:

The phylogenetic analysis shows that most Australian sequences formed a distinct clade, separate from other international strains, except for the sequences related to the UK 2015 outbreak. Further comparisons between

Australian and UK 2015 outbreak sequences shows a predominate difference in Stx profiles, with Australian sequences having a stx1a and/or stx2c profile whereas the highly pathogenic UK 2015 outbreak sequences have a stx2a profile.

Conclusions:

These results provide further evidence that stx2a is a major predictor of high virulence in STEC strains. It also raises awareness that STEC strains of mild pathogenicity can become highly pathogenic, as has been reported for the UK 2015 outbreak strains

Subject: Microbiology

Keywords: O157, Genomics, Shiga Toxin-Producing Escherichia coli, Epidemiology, Whole-Genome Sequencing, Virulence

ABSTRACT ID: 546

PRESENTED BY: Alexander Pintara / alexander.pintara@hdr.qut.edu.au

7.5. Benefits of Sentinel Laboratory Surveillance of Human Campylobacter Infections in Ireland, 2019,

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Background:

Campylobacteriosis is the most common cause of bacterial gastroenteritis in Ireland with 2786 cases and an incidence of 58/100,000 in 2017. However, there is no national laboratory database of clinical campylobacteriosis. We set up a national sentinel laboratory surveillance protocol to describe Campylobacter infections using traditional and molecular genomic methods to assess its feasibility for national surveillance.

Methods:

Irish clinical diagnostic hospital laboratories (n=24) submitted cultured Campylobacter human clinical isolates or Campylobacter PCR-positive stools to an agreed sentinel sampling plan. Confirmation and sensitivity testing (erythromycin, ciprofloxacin, tetracycline) was performed on isolates at PHL-HSE-D, followed by whole genome sequencing (WGS) to speciate, identify resistance determinants and detect clusters.

Results:

82 specimens were submitted – 63 stools and 19 isolate swabs. 49 isolates were recovered; 32 (52%) from stools and 17 (90%) from isolate swabs. WGS confirmed Campylobacter jejuni in 92% (n=45/49) and Campylobacter coli in 8% (n=4/49) of isolates. There were 11 clonal complexes, with ST-21 complex the most prevalent at 29% (n=14). C. coli isolates were all ST-828 complex. 49% of isolates (n=24) were susceptible to all three antimicrobials. Phenotypically, 43% (n=21) isolates were resistant to ciprofloxacin, 32% (n=16) were resistant to tetracycline and 2% (n=1) were resistant to erythromycin. There was a majority phenotypic-genotypic antimicrobial resistance data concordance – 100% tetracycline and 63% ciprofloxacin. No genomic clusters of potential public health significance were detected.

Conclusions:

This data indicate that C. jejuni is the predominant cause of campylobacteriosis in Ireland and that macrolides remain the optimum empiric treatment. This dataset provides a baseline for continued phenotypic and genotypic Campylobacter surveillance and a framework for the establishment of a national reference laboratory service.

Subject: Surveillance

Keywords: Campylobacter, Surveillance, Genomics, Microbiology, AMR

ABSTRACT ID: 677

PRESENTED BY: Carina Brehony / carina.brehony@hse.ie

Parallel Session 8
DAY 2, Thursday, 28. November 2019
11:00-12:40

Vaccine-preventable diseases: surveillance (1)

Moderator

Adam Roth

Abstracts

8.1. Vaccination with the 13-valent pneumococcal conjugate vaccine in an outbreak of Streptococcus pneumoniae serotype 4 in a Norwegian shipyard

Anneke Steens [1]

J. Berild [2], B. Winje [3], J. Fjeldheim [4], T. Danielsen [5], E. Nilsen [6], H. Holmemo [7], J. Longva [8], P. Brügger-Synnes [9]

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Background:

Although exposure to metal fumes increases the risk of invasive pneumococcal disease (IPD), work related outbreaks are rare. On March 28, a suspected outbreak of pneumococcal disease among shipyard workers in Norway was notified to the Norwegian Institute of Public Health (NIPH). Local medical officers, the Norwegian Labour Inspection Authority (NLIA), and NIPH investigated the outbreak.

Methods:

We searched for cases of IPD or lower respiratory tract infection caused by pneumococci among persons working at a shipyard in Western Norway. We characterized available pneumococcal isolates using quellungs-reaction and next- generation sequencing, performed chart reviews of admitted patients and conducted an on-site inspection.

Results:

We identified 21 cases with onset of disease between 28.01.2019 and 04.04.2019. Sixteen were hospitalized. We characterized isolates available from 17 cases. Ten isolates were from blood culture specimens. All belonged to serotype 4. Results of sequence typing were available for eight isolates, all were sequence type 801.

On-site inspection found a crowded shipyard and immediate occupational hygiene measures were ordered with short notification. Regulations on tobacco smoking, air quality improvements, and use of correct personal protective equipment were implemented.

Pneumococcal polysaccharide vaccine is recommended for welders. In this outbreak setting with known serotype, the 13-valent pneumococcal conjugate vaccine was offered to prevent further cases. Almost 1900 workers were vaccinated during one week. No cases were notified after the vaccination campaign..

Conclusions:

We detected a large pneumococcal outbreak caused by a vaccine serotype. The outbreak strain has also been found in an outbreak in a North-Irish shipyard in 2015. The present outbreak indicates that the occupational risk of pneumococcal disease is multifactorial. Pneumococcal vaccination of broader occupational groups exposed to metal fumes should be considered.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: pneumococcal infection, 13 valent pneumococcal vaccine, disease outbreak, welders

ABSTRACT ID: 422

PRESENTED BY: Anneke Steens / dive@fhi.no

8.2. The changing face of diphtheria 70 years since vaccine introduction in the United Kingdom

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Background:

This study aimed to describe characteristics of toxigenic diphtheria cases in the UK and review results of toxigenicity testing of Corynebacterium diphtheriae and C. ulcerans isolates by the UK National Reference Laboratory between 2009 and 2017.

Methods:

All human isolates of C. diphtheriae, C. ulcerans and C. pseudotuberculosis identified by microbiological laboratories in the UK are sent for toxigenicity testing to the UK National Reference Laboratory (NRL) for diphtheria. Demographic, clinical and microbiological information is collated on all positive cases from laboratory reports, local and national public health centre records, as part of national surveillance and outbreak management across the UK.

Results:

There were 43 toxigenic cases of diphtheria in the UK between 2009 and 2017; the age range was 4 to 82 years and 51% were female. The majority of toxigenic C. diphtheriae cases were cutaneous (14/18, 78%). Conversely, more than half of C. ulcerans cases had respiratory presentations (8/15, 53%). Disease severity was strongly linked to vaccination status with sixty-five percent (28/43) of cases being inadequately vaccinated. Two cases died, both of whom were unvaccinated. The major risk factor for C. diphtheriae was travel to an endemic area and for C. ulcerans contact with a companion animal. The majority of isolates submitted for toxigenicity testing were non-toxigenic C. diphtheria, however, toxin positivity rates were higher (15/23, 65%) for C. ulcerans than C. diphtheriae (18/469, 4%) isolates.

Conclusions:

Diphtheria is a rare disease in the UK. In the last decade, we have seen an increase in milder cutaneous C. diphtheriae cases. C. ulcerans is more commonly seen in older unvaccinated individuals. Vaccination status was strongly associated with the risk of hospitalisation and death.

Subject: Surveillance

Keywords: corynebacterium; ulcerans; diphtheriae; cutaneous; respiratory

ABSTRACT ID: 682

PRESENTED BY: Charlotte Gower / charlotte.gower@phe.gov.uk

8.3. Effectiveness of 10- and 13-valent pneumococcal conjugate vaccines against invasive pneumococcal disease in children <5 years: lessons learnt from SpIDnet multicentre study

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Background:

SpIDnet conducts enhanced population-based surveillance of invasive pneumococcal disease (IPD) in all age groups. Using surveillance data from 12 European sites, we measured the effectiveness of 10- and 13-valent pneumococcal conjugate vaccines (PCV) against IPD in children under five years of age.

Methods:

We included 2-59 month-old children with IPD reported between January 2011 and December 2017, using a common protocol. We compared the odds of being vaccinated with at least one dose of vaccine for IPD cases caused by PCV10 or PCV13 serotypes (cases) to those caused by nonPCV13 serotypes (controls). We computed vaccine effectiveness (VE) as (1 - pooled odds ratio of vaccination)*100.

Results:

In the PCV13 VE analysis, we included 537 cases and 1648 controls. The PCV13 VE adjusted for age, underlying conditions, notification year and site was 83% (95% confidence interval (CI): 78-87) against PCV13 IPD, 92% (95%CI: 87-95) against PCV7 IPD (n cases/controls = 157/1648) and 78% (95%CI: 70-84) against PCV13nonPCV7 IPD (n=380/1648). In the PCV10 VE analysis, we included 171 cases and 257 controls. PCV10 VE adjusted for age, notification year and site was 81% (95%CI: 61-91) against PCV10 IPD, 86% (95%CI: 66-94) against PCV7 IPD (n=114/257) and 63% (95%CI: -16 to 88) against PCV10nonPCV7 IPD (n=57/257).

Conclusions:

SpIDnet results suggest good PCV10 and PCV13 effectiveness against IPD caused by vaccine serotype categories analysed. Limitations are related to heterogeneity caused by health-care practices, low number of cases and unavailability of data on underlying conditions in sites using PCV10. This method allows monitoring of PCV effectiveness using surveillance data only. Continuous IPD surveillance will help increasing the sample size that will improve the precision of VE estimates and allow measuring serotype-specific PCV effectiveness.

Subject: Surveillance

Keywords: Invasive pneumococcal disease, pneumococcal conjugate vaccine, effectiveness, surveillance, Streptococcus pneumoniae

ABSTRACT ID: 721

PRESENTED BY: Camelia Savulescu / c.savulescu@epiconcept.fr

8.4. Effectiveness of pertussis vaccination during pregnancy against laboratory confirmed pertussis in hospitalised infants aged <61 days in four European countries, PERTINENT, December 2015-December 2018

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Background:

PERTINENT is an active hospital-based surveillance system for pertussis in infants. Four of the six participating European countries (15 hospitals) recommend pertussis vaccination during pregnancy. We aimed to measure the effectiveness of maternal vaccination (VE) against pertussis in hospitalised infants too young to be vaccinated.

Methods:

We included all infants aged <61 days presenting with pertussis-like symptoms from December 2015 to December 2018 with a nasopharyngeal aspirate (NPA) collected. Cases were infants testing positive for Bordetella pertussis by PCR or culture. Controls were those testing negative for all Bordetella species. Vaccinated mothers were those having received a pertussis vaccine during pregnancy. We excluded infants with unknown maternal vaccination status or where mothers vaccinated within 14 days of delivery. We calculated pooled VE as 100*(1-odds ratio of vaccination) adjusted for study-site, onset date in quarters and age group (4-30 and 31-61 days).

Results:

Of 267 infants presenting with pertussis-like symptoms 186 (70%) had a NPA. We included 48 cases and 96 controls with known maternal vaccination status. Eighteen cases (38%) and 17 controls (18%) were aged <31 days (p=0.013). The median-birthweight was 3320g for cases and 3200g for controls (p=0.725). Thirty-eight cases (79%) and 75 controls (79%) were breastfed. The median gestational age at vaccination was 30.3 weeks for cases and 29.4 for controls. Four cases (8%) and 45 controls (47%) had recorded maternal vaccination during pregnancy, adjusted VE was 88% [95%CI: 53-97%].

Conclusions:

This is the first multicenter study on the maternal VE against pertussis in infants. The high VE observed among infants not eligible for primary vaccination suggests that vaccination during pregnancy could reduce pertussis incidence in the first months of life, when the disease is life-threatening.

Subject: Surveillance

Keywords: Whooping cough, Pertussis Vaccine, Vaccine Effectiveness,

Parallel Session Abstracts

Immunity Maternally-Acquired, Pregnancy, Public Health Surveillance

ABSTRACT ID: 251

PRESENTED BY: Marta Valenciano / l.merdrignac@epiconcept.fr

Parallel Session 9
DAY 2, Thursday, 28. November 2019
11:00-12:40

Influenza: vaccination and intervention (1)

Moderator

Hanna Nohynek

Abstracts

9.1. Vaccine effectiveness against influenza A(H1N1)pdm09 and A(H3N2): Results from the 2018/19 European I-MOVE primary care multicentre study

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[23] I-MOVE network

Background:

Influenza A dominated in Europe in 2018/19. The I-MOVE network conducted a multicentre test-negative case-control study using sentinel primary care networks in nine European countries to measure vaccine effectiveness (VE) against influenza A(H1N1)pdm09 and A(H3N2).

Methods:

Primary care practitioners swabbed and interviewed a systematic sample of patients presenting with influenza like illness (ILI), collecting information on demographics, vaccination and clinical characteristics. Cases were RT-PCR positive for influenza A(H1N1)pdm09 or A(H3N2) and controls were negative for any influenza. We calculated VE using logistic regression, adjusting for study site and potential confounders (age, sex, onset time, presence of chronic conditions). We stratified VE by age-group (0–14, 15–64, >=65 years).

Results:

We included 6960 ILI patients of whom 1554 and 1747 were influenza A(H1N1)pdm09, and A(H3N2) positive, respectively.

Adjusted VE (aVE) against influenza A(H1N1)pdm09 was 57% (95%CI: 44–67) overall, and 78% (95%CI: 49–91), 49% (95%CI: 29–64) and 63% (95%CI: 36-78) among those aged 0–14, 15–64 and >=65 years, respectively.

aVE against influenza A(H3N2) was -4% (95%CI: -30 to 16) overall, and 52% (95%CI: 13–73), -38% (95%CI: -83 to -3) and 23% (95%CI: -19 to 50) among those aged 0–14, 15–64 and >=65 years, respectively.

Conclusions:

The 2018/19 aVE against influenza A(H1N1)pdm09 was higher overall and by age-group than aVE against influenza A(H3N2). The lowest aVE point estimate for both influenza A(H1N1)pdm09 and A(H3N2) was among 15–64 year olds. The aVE against A(H3N2) overall and among 15–64 year olds was null. As in previous seasons, the 2018/19 VE against influenza A(H3N2) highlights the need to improve seasonal influenza vaccines so as to achieve acceptable protection levels.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza,Vaccine effectiveness,Multicentre study,Europe,Test-negative design,Influenza A

ABSTRACT ID: 348

PRESENTED BY: Esther Kissling / e.kissling@epiconcept.fr

9.2. Seasonal influenza vaccine effectiveness for the prevention of laboratory-confirmed influenza in asthma during the influenza seasons 2010-16 in Scotland: a test-negative design case-control study

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Background:

Influenza infection is an important trigger of asthma attacks. Influenza vaccination has the potential to reduce the incidence of influenza in people with asthma, but uptake remains persistently low, at least in part, reflecting concerns about vaccine effectiveness (VE).

Methods:

We conducted a test-negative design case-control study to estimate the effectiveness of influenza vaccine in children and adults with asthma in Scotland over six influenza seasons (2010/11 to 2015/16). We used individual patient level data from 223 primary care practices which yielded 1,830,772 patient-years of data, which were linked with hospital and virological (n=5,910 swabs) data.

Results:

Vaccination was associated with an overall 55.03% (95% confidence interval (CI): 45.84-62.66) reduction in the risk of a laboratory-confirmed influenza infection in people with asthma over the six seasons. There was substantial variation in VE between seasons, influenza strains and age groups. The highest VE (76.08%; 95% CI: 55.60-87.12) was found in 2010/11 season where the A(H1N1) strain dominated and there was a good antigenic vaccine match. High protection was observed against A(H1N1) (e.g. 2010/11: 70.68%; 95%CI: 32.46-87.27) and B strains (e.g. 2010/11: 83.17%; 95%CI: 44.31-94.92), but there was lower protection for the A(H3N2) strain (e.g. 2014/15: 26.40%; 95%CI: -12.00-51.64). The highest VE against all viral strains was observed in adults aged 18-54 years (56.98%; 95%CI: 42.25-67.95).

Conclusions:

Influenza vaccination gave meaningful protection against laboratory-confirmed influenza in people asthma across all six seasons. Strategies to boost influenza vaccine uptake has the potential to substantially reduce influenza triggered asthma attacks.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: influenza vaccine,asthma,influenza infection

ABSTRACT ID: 36

PRESENTED BY: Eleftheria Vasileiou / e.vasileiou@ed.ac.uk

9.3. Vaccine effectiveness against influenza A(H3N2) and A(H1N1) in older adults and the effects of age-group and statins: Results from the I-MOVE hospital network, 2018–19

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Background:

Influenza A(H3N2) and A(H1N1)pdm09 viruses co-circulated in Europe in the 2018–19 season. The I- MOVE hospital network conducted a multicentre test-negative case control study in 17 hospitals in eight European countries to measure influenza vaccine effectiveness (IVE) against these subtypes among older adults.

Methods:

Hospital teams swabbed patients aged >=65 years admitted with onset <=7 days of severe acute respiratory infection and collected information on demographics, influenza vaccination status, statin use and underlying conditions. Cases were RT-PCR positive for influenza A(H3N2) or A(H1N1) pdm09; controls were negative for any influenza virus. We calculated IVE adjusted for study site, chronic conditions, sex, age and date of onset; stratified by age-group and statin use. We used interaction to test for differences, where appropriate

Results:

We included 474 A(H3N2) and 250 A(H1N1)pdm09 cases, and 1222 controls. Of 1944 (>99%) patients with available information, 714 (37%)

were on statins. IVE against A(H3N2) was 12% (95%CI:-11–31) overall; -11% (95%CI: -54–21) in those aged 65–79 years and 32% (95%CI: 4–52) in those >=80 years ($p=0.037$). A(H3N2) IVE was 2% (95%CI: -47–35) in statin users, 15% (95%CI: -14–37) in non-users. IVE against A(H1N1)pdm09 was 42% (95%CI: 20–58) overall, 36% (95%CI: 2–58) in 65–79-year-olds, 45% (95%CI: 8–67) in those >=80 years, 39% (95% CI: -3–64) in statin users and 45% (95%CI: 16–64) in non-users.

Conclusions:

Results suggest low to moderate IVE against influenza A among hospitalised patients >=65 years, with age-specific differences in IVE against A(H3N2). Point estimates suggest a lower A(H3N2) IVE among statin users, but results are imprecise. We reinforce the importance of influenza vaccination in older adults, and encourage further research into the effect of statins and age-group on influenza A VE in older adults.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: influenza,vaccine effectiveness,hospital,older adults,age-group,statin

ABSTRACT ID: 424

PRESENTED BY: Angela Rose / demerararose@gmail.com

9.4. Low frequency of reduced neuraminidase inhibitor susceptibility in twelve EU/EEA countries, 2008-2018

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Background:

Neuraminidase inhibitors (NAIs) are used as prophylaxis and treatment against influenza. We analysed the frequency of reduced (RI) or highly reduced (HRI) NAI susceptibility in specimens received through influenza surveillance in the European Union/European Economic Area (EU/EEA) countries to inform the treatment guidelines.

Methods:

Pheno- and genotypic RI and HRI to oseltamivir and zanamivir in 12 EU/EEA countries who submitted influenza antiviral susceptibility data to The European Surveillance System for at least five influenza seasons during 2008/09-2017/18 were included. Comparison of means was performed by Fishcer's exact test for categorical variables (significance, $p<0.05$).

Results:

The overall prevalence of RI/HRI to NAIs was 1.0% in the 27371 analysed influenza viruses. Frequency of RI/HRI varied by season, (sub)type, country, hospitalisation and treatment status, while vaccination status did not affect the susceptibility to NAIs. A(H1N1) viruses showed 74%, A(H1N1)pdm09 1.3%, A(H3N2) 0.2% and B viruses 0.2% RI/HRI to oseltamivir and 0%, 0.1%, 0.2% and 0.2% to zanamivir, respectively. The highest frequency of RI/HRI (2.8%) was detected in season 2010/11. Across the seasons, the proportion of RI/HRI of A(H1N1)pdm09 for oseltamivir was highest in France (3.7%, $p<0.0001$). Of the hospitalised patients, 113 (3.0%; $p<0.0001$) had a virus showing RI/HRI to oseltamivir compared with the 37 (0.5%) of the outpatients. Of the 179 patients with known treatment status with RI/HRI to oseltamivir, 63 (35%; $p<0.0001$ vs treated) had not been treated with NAIs. Amino acid substitutions associated with RI/HRI were mainly H275Y and Y155H in A(H1N1)pdm09 and E119V and R292K in A(H3N2) viruses.

Conclusions:

The low frequency of reduced NA susceptibility supports the use of NAIs against severe influenza. Continuous monitoring of susceptibility is crucial in patients treated and not treated with NAIs.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: influenza, neuraminidase, inhibitor, susceptibility, Europe

ABSTRACT ID: 685

PRESENTED BY: Eeva Broberg / Eeva.Broberg@ecdc.europa.eu

Parallel Session 10
DAY 2, Thursday, 28. November 2019
14:30-15:30

Antimicrobial resistance and Healthcare-associated infections: surveillance

Moderator

Diamantis Plachouras

Abstracts

10.1. External quality assessment (EQA) of Neisseria gonorrhoeae antimicrobial susceptibility testing in primary laboratories in Germany

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Parallel Session Abstracts

Background:

Worldwide, an increase in antimicrobial resistance of Neisseria gonorrhoeae has been observed. In 2018 an EQA protocol was introduced for the first time in Germany. The German Gonococci resistance network (GORENET) performed the EQA in order to assess quality of antibiotic susceptibility testing in primary laboratories in Germany, the type of protocols used and the impact of laboratory procedures on results.

Methods:

The EQA included testing of five strains for susceptibility to cefixime, ceftriaxone, azithromycin, penicillin and ciprofloxacin according to EUCAST standard 8.0. 21 laboratories participated. Minimal inhibitory concentrations (MICs) were compared to reference laboratory results; deviation by +/- one doubling dilution was accepted. Additional data on laboratory procedures were collected via a standardised questionnaire. Generalized linear models and conditional interference trees (CTI) were used to assess relationships between laboratory procedures and testing outcomes.

Results:

Of ciprofloxacin MICs, 96% were reported within accepted deviations, as well as 88% for cefixime, 85% for ceftriaxone, 79% for penicillin and 70% for azithromycin. Testing protocols were diverse and not always in line with EUCAST recommendations and standard literature, e.g. with regard to growth media used. In statistical analysis, incubation time of cultures ›23 hours was associated with incorrect measurements. Regarding azithromycin, incorrect results were associated with 3% CO2 concentration compared to 5%. CTI showed that, depending on the antibiotic tested, incubation time, CO2 concentration and humidity were influencing the outcome.

Conclusions:

German primary laboratories reported correct outcomes for 70%-96% of samples depending on the antibiotic agent. Protocols used were heterogeneous and may explain deviations of testing results from consensus. We recommend SOP implementation based on EUCAST guidelines, reference to updated literature and the outcomes provided by this study's statistical analysis.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Neisseria gonorrhoeae, external quality assessment, antimicrobial susceptibility testing

ABSTRACT ID: 97

PRESENTED BY: Regina Selb / selbr@rki.de

10.2. Use of the automated Danish Clostridium difficile surveillance system for reporting to the manual European surveillance system

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Background:

Surveillance of Clostridium difficile infections (CDI) in Denmark includes a fully-automated system (HAIBA). As its case definition differs in some details from the European case definition, our aim was to determine if HAIBA can be used to report CDI to the European surveillance system (TESSy).

Methods:

We included all patients hospitalized or diagnosed with CDI in Denmark during 2010-2018. We applied TESSy's protocol on Danish data. We linked data on infection date and patient identifier, and compared results on episode definition and infection origin (healthcare-associated, community-associated or unknown). TESSy deems a new episode if two months elapsed since the first positive sample, while HAIBA counts a new episode two months after last positive sample. With that, HAIBA addresses the fact that CDI patients are typically tested several times and a clinical episode can last more than two months.

Results:

There were 43,699 CDI that met both case definitions. Of these, 32,595 (75%) were identical; 7,752 (18%) had a different origin, and 3,352 (7%) were assigned to different hospitals/departments. HAIBA and TESSy use the same definitions for community-associated and unknown origin CDI. However, HAIBA included all (n=6,548 and 4,603, respectively), while TESSy only included CDI followed by hospital admission (n=1,707 (26%) and 1,488 (32%), respectively). TESSy captured all CDI identified from HAIBA, and counted 2,247 (5%) additional CDI, due to different episode definition.

Conclusions:

Despite some differences in definition, the majority of data from HAIBA were compatible with TESSy, suggesting that HAIBA can be used for reporting to TESSy. These findings are important for European surveillance which in future will need to collect data both from automated and manual surveillance systems more often.

Subject: Surveillance

Keywords: Clostridium difficile, Public Health Surveillance, Denmark, automated surveillance, healthcare-associated infections

ABSTRACT ID: 346

PRESENTED BY: Manon Chaine / manc@ssi.dk

10.3. Hospital outbreaks of group B streptococcal (GBS) infection: a systematic review

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Background:

Outbreaks of invasive group B streptococcal (GBS; Streptococcus agalactiae) disease in healthcare settings are presumed to occur infrequently. We reviewed the literature to inform future identification and management of such outbreaks.

Methods:

Systematic review (PROSPERO reg. CRD42018096297) of all publications in MEDLINE, EMBASE, EMCARE, COCHRANE, TRIP, SCOPUS, and CINAHL up to 08/08/2018 without language restriction, using search terms for GBS and outbreak, cluster, cross-infection or acquisition in any healthcare setting (hospital, neonatal intensive care unit (NICU), special care baby unit, nursery).

Results :

Twenty-three references were included describing 25 GBS hospital clusters from 9 different countries between 1966-2018. Of the 23 references, 20 described neonatal clusters (13/20 in NICUs) and 3 reported clusters in adult specialties/wards. We identified 17 clusters involving cross-infection between unrelated neonates. These described an early (<7 days of life; n=3) or late (7-90 days; n=11) onset or colonized (n=3) index case followed by one or more late onset cases. The median serial interval between cases in neonatal outbreaks was 9 days (IQR 3-17, range 0-50 days, n=38). Links between cases were determined by phage typing in 3 clusters, PFGE in 3, MLST in 1, PCR in 2, WGS in 4 and non-molecular methods in 4 clusters. The most commonly implicated routes of transmission in neonatal clusters were via staff and shared equipment, particularly during periods of crowding and high patient-to-nurse ratio. Of the 3 adult clusters, one (respiratory cases) was attributed to droplet spread and one to staff.

Conclusions:

GBS clusters may occur more frequently in neonatal units than presumed because intervals between consecutive cases can be long. Enhanced surveillance supported by genotyping should be established to identify and investigate cross- infection.

Subject: Surveillance

Keywords: Streptococcus agalactiae, group B streptococcal disease, neonatal sepsis, hospital outbreak, healthcare- associated infection, systematic review

ABSTRACT ID: 631

PRESENTED BY: Simon Collin/ simon.collin@phe.gov.uk

Parallel Session 11
DAY 2, Thursday, 28. November 2019
14:30-15:30

Late breakers

Moderator

Karl Ekdahl

Abstracts

11.1. Rapid data sharing and cross-border collaboration identifies likely vehicle of Yersinia enterocolitica O3 outbreak, Sweden and Denmark, March 2019

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Background:

Infection with Yersinia enterocolitica (YE), found in the throat and intestine of pigs, cause acute enteritis, outbreaks are rare. In April 2019, Sweden and Denmark identified a cross-border outbreak of YE O3 and undertook an investigation to stop the outbreak.

Methods :

We recognized the outbreak by cross-border communication and identified cases (YE O3, ST18, 0-1SNP difference in cgMLST) using whole genome sequencing (WGS). Cases were interviewed concerning food consumption prior to disease. Both countries did matched case-control studies and trace-back investigations.

Results:

Fifty-seven cases were confirmed, 37 from Sweden. The median age was 26; 31 cases were female. Symptom onset peaked in both countries in early March 2019. All interviewed Danish cases (n=16) shopped in retail group X and 19/24 interviewed Swedish cases in retail chain C. Spinach was consumed more by Danish cases (16/16) compared to controls (4/45). Moving an exposed case to the unexposed group resulted in an OR of 98 (95%CI 10-4,200). The Swedish case-control study could not associate any food items with being a case. Spinach ranked among items consumed by most cases (20/29 (69%)). Trace-back of deliveries of fresh spinach sold in retail group X and retail chain C identified common batches from a single producer from a third EU country.

Conclusions:

Close cross-border collaboration guided the investigation, and combining evidence from both countries enabled identification of the likely vehicle, fresh spinach. Leafy greens have in recent years been implicated in several YE outbreaks, reinforcing that other vehicles than pork should be considered in outbreak investigations. To our knowledge, this is the first outbreak of YE investigated using WGS, which clearly facilitated swift data sharing and recognition of a cross-border outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: food-borne infections, yersiniosis, Disease Outbreaks, Yersinia Infections, Epidemiology, Intersectoral Collaboration, Whole Genome Sequencing

ABSTRACT ID: 828

PRESENTED BY: Laura Espenhain / laes@ssi.dk

11.2. A case control study investigating food exposures and the subseqent risk for developing hepatitis E infection in blood donors in England, April 2018-2019

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Background:

Hepatitis E virus (HEV) is the most common cause of acute hepatitis in the world. In high-income countries, acute HEV infections have been transmitted via blood transfusion. Due to this risk, universal blood donation screening for HEV was initiated in England in April 2017. This study used the blood screening programme to determine which food exposures were associated with HEV infection within the blood donor population.

Methods:

A case was defined as a blood donor, residing in England, who tested positive for HEV RNA on routine donation between April 2018-April 2019. A control was a blood donor, who donated within the same period but was not HEV positive. Participants completed questionnaires providing information on travel, food consumption, purchasing preferences, animal exposures, environmental exposures, alcohol intake, medication and co-morbidities. Data was processed using univariate and multivariable logistic regression.

Results:

In total, 119 cases and 565 controls, with no travel history outside the United Kingdom (UK) in the nine weeks prior to donation of blood, were included in the analysis. By univariate analysis eight of 19 food items, were associated with HEV infection. After including these exposures in a multivariable model the consumption of bacon and other cured pork meats were significantly ($p < 0.001$) associated with being a case.

Conclusions:

This study is the first to investigate potential risk factors for UK-acquired HEV infections in blood donors in England. As infected donors are more likely to be asymptomatic, compared to acute cases, they may be more representative of infection in the general population in England than acute cases. HEV infection is endemic in pigs and the main route of transmission for non-travel-related HEV infections in high-income countries is foodborne.

Subject: Surveillance

Keywords: Hepatitis E, Zoonosis,Pork products

ABSTRACT ID: 825

PRESENTED BY: Iona Smith / Iona.Smith@phe.gov.uk

Parallel Session 12
DAY 2, Thursday, 28. November 2019
14:30-15:30

Influenza: vaccination and intervention (2)

Moderator

Jim McMenamin

Abstracts

12.1. Impact of national influenza vaccination strategy among the high-risk Portuguese population in severe influenza outcomes

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Background:

All aged individuals with a chronic condition and those with 65 and more years are at increased risk of severe influenza post-infection complications. There is limited research on cases averted by the yearly vaccination programmes in high- risk individuals. The objective was to estimate the impact of trivalent seasonal influenza vaccination on averted hospitalizations and death among the high-risk population in Portugal.

Methods:

The impact of trivalent seasonal influenza vaccination was estimated using vaccine coverage, vaccine effectiveness and number of influenza-related hospitalizations and deaths. The number of averted events (NAE), prevented fraction (PF) and number needed to vaccinate (NVN) were estimated for seasons 2014/15 to 2016/17. Estimates of 2.5 and 97.5

uncertainty percentiles of all impact parameters were obtained through Monte Carlo simulations.

Results:

The vaccination strategy averted on average approximately 1833 hospitalizations and 231 deaths. Highest NAE were observed in the ≥65 years population (85% of hospitalizations and 95% deaths) and in 2016/17 season (1957 hospitalizations and 257 deaths). On average, seasonal vaccination prevented 21% of hospitalizations in the population aged 65 and more, and 18.5% in the population with chronic conditions. The vaccination also prevented 19.5% [11.8-25.4] of deaths in the high-risk population, including individuals ‹65 years with chronic conditions. It would be needed to vaccinate 3360 high-risk individuals, to prevent one hospitalization and 60874 high-risk individuals to prevent one death.

Conclusions:

The yearly influenza vaccination had a sustained positive benefit for the high-risk population, reducing hospitalizations and deaths. These results can support public health plans towards increase of vaccine coverage in high risk groups.

Subject: Burden of disease

Keywords: influenza, influenza vaccine, impact, high-risk, hospitalizations, deaths

ABSTRACT ID: 572

PRESENTED BY: Ausenda Machado / ausenda.machado@insa.min-saude.pt

12.2. Deaths, hospitalisations and GP visits attributable to influenza infection averted by the influenza vaccination programme in the Netherlands among persons aged 65 and older, seasons 2015/16–2017/18

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Background:

Compared to the traditional measure vaccine effectiveness (VE), number of cases averted may more intuitively demonstrate the value of influenza vaccination. We estimate number of deaths, hospitalisations and GP visits averted by the influenza vaccination programme in the Netherlands for seasons 2015/16–2017/18, among those aged 65 years and older.

Methods:

First, the observed number of cases attributable to influenza infection was estimated. For GP visits this was based on incidence of ILI from sentinel GP surveillance, influenza virus positivity rate, and sensitivity of virological testing. For mortality and hospitalisations the FluMomo model was applied to all-cause mortality data and to national hospital discharge data (unavailable for 2017/18). Secondly, the number of averted cases was calculated from the estimated observed cases, national vaccination coverage and VE. For GP visits and hospitalisations, VE was based on I- MOVE VEs, corrected for the proportion of subtypes circulating in the Netherlands; for mortality, a VE of 4.6% (95% confidence interval (CI): 0.7–8.3) was obtained from the literature. 95% CIs were derived through Monte Carlo simulation.

Results:

GP visits averted were estimated at 8,480 (95%CI: 3,400–16,300), 2,190 (95%CI: -2,140–7,520), and 8,690 (95%CI: 1,160–17,500), for seasons 2015/16, 2016/17, and 2017/18. During these seasons, 48 (95%CI: 7–92), 156 (95%CI: 24–296), and 198 (95%CI: 30–374) deaths were averted. For hospitalisations this was 767 (95%CI: 433–1,190) in 2015/16 and 794 (95%CI: 175–1,470) in 2016/17.

Conclusions:

These impact estimates are useful for public health communication, because absolute numbers are easier to understand than VE expressed as percentages. This might reinforce the message that influenza vaccination is important for prevention of severe disease and deaths, even with low to moderate VE.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza Vaccines,Human Influenza,Incidence,Mortality,Hospitalization

ABSTRACT ID: 335

PRESENTED BY: Frederika Dijkstra /frederika.dijkstra@rivm.nl

12.3. 2018/19 primary care influenza vaccine effectiveness against influenza A(H3N2) in Europe: no effectiveness among 15–64 year olds

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Background:

The often low vaccine effectiveness (VE) against influenza A(H3N2) was frequently attributed to mismatch between vaccine and circulating influenza strains and/or differing antibody landscapes in the host.

In 2018/19, interim reports of VE point estimates against influenza A(H3N2) among all ages in three European networks were <0%.

We used end-of-season European I-MOVE multicentre test-negative studies comparing 2011/12–2017/18 to 2018/19, seasons including vaccine and circulating virus mismatch, to better understand the VE against A(H3N2).

Methods:

Primary care practitioners swabbed patients presenting with influenza like illness, collecting information on demographics, vaccination and clinical characteristics. Cases were RT-PCR positive for influenza A(H3N2) and controls negative for any influenza. We calculated VE using logistic regression, adjusting for study site and potential confounders (age, sex, onset time, presence of chronic conditions). We stratified VE by age-group (0–14, 15–64, >=65 years).

Results:

I-MOVE 2018/19 end-of-season VE against influenza A(H3N2) was -4% (95%CI: -30 to 16) overall, and 52% (95%CI: 13–73), -38% (95%CI: -83 to -3) and 23% (95%CI: -19 to 50) among those aged 0–14, 15–64 and >=65 years, respectively.

VE against influenza A(H3N2) in 2011/12 to 2017/18 seasons among 15–64 year-olds ranged between 9–34%; average VE was 24%.

Conclusions:

The 2018/19 interim VE against influenza A(H3N2) of <0% among all ages was driven by a lack of VE among 15–64 year-olds. Such VE in this age-group is unprecedented even in mismatched post-pandemic A(H3N2) seasons.

This unusual season, with further research into interaction between population immune history and vaccine in context of circulating virus amino acid differences or egg-adapted vaccine strains, may provide us with an extra piece of the puzzle to understand age variation in immunologic responses among vaccinated.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza, Multicentre study, A(H3N2), Age/birth cohort-specific vaccine effectiveness, Vaccine effectiveness, 2018/19

ABSTRACT ID: 399

PRESENTED BY: Esther Kissling / e.kissling@epiconcept.fr

Parallel Session 13
DAY 2, Thursday, 28. November 2019
17:00-18:40

HIV and STI: prevalence and prevention

Moderator

Aura Andreasen

Abstracts

13.1. Prevalence of gonorrhea and chlamydia in a community clinic for Men who Have Sex with Men in Portugal

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Background:

Men who have sex with men (MSM) are at greater risk for sexually transmitted infections (STIs). Data on MSM chlamydia and gonorrhea prevalence estimates and associated risk factors is scarce. To our knowledge, this is the first study to describe the prevalence and the determinants of both chlamydia and gonorrhea infections in MSM in Portugal.

Methods:

We conducted a cross-sectional study using data from 1,832 visits to CheckpointLX, a community-based center for screening blood-borne viruses and other STIs in MSM.

Results:

Overall prevalence of chlamydia or gonorrhea in our sample was 16.05%, with 14.23% coinfection and 40.73% asymptomatic presentation among those testing positive. Anorectal infection was most common for chlamydia (67.26%), followed by urethral (24.78%) and oral (19.47%) infection. Oral infection was most common for gonorrhea (55.63%), followed by anal (51.25%) and urethral (17.50%) infection. In multivariate analyses, young age (U=94684, p=0.014), being foreign-born (x2=11.724, p=0.003), reporting STI symptoms (x2=5.316, p=0.021), inhaled drug use (x2=4.278, p=0.039) and having a higher number of concurrent (x2=18.769, p<0.001) or total (x2=5.988, p=0.050) sexual partners were each associated with higher rates of chlamydia or gonorrhea infection.

Conclusions:

Young and migrant MSM are a vulnerable population to STIs, as are those who use inhaled drugs and those with a higher number of concurrent or total sexual partners. Although Portugal has no guidelines on chlamydia and gonorrhea screening, our results point towards a need for greater awareness about the importance of high frequency screening for those at increased risk (i.e. every 3 to 6 months).

Subject: Burden of disease

Keywords: sexually transmitted infections; men who have sex with men; chlamydia; gonorrhea

ABSTRACT ID: 92

PRESENTED BY: Sofia Ribeiro / sofia.ribeiro@gatportugal.org

13.2. Does using pre-exposure prophylaxis for HIV increase the risk of acquiring other sexually transmitted infections?

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Background:

Whilst pre-exposure prophylaxis (PrEP) is effective in preventing new HIV infections in people at high risk, there is concern that it might result in a higher risk of acquiring other sexually transmitted infections (STI) via a shift in sexual behaviour.

Methods:

Using data from the Sexual Health in Wales Surveillance System, our study population included all attendees to sexual health clinics in Wales between 1/7/2017 and 30/6/2018 that were eligible for PrEP. We identified those that started PrEP and those that declined it and compared STI incidence rates before and after PrEP start or decline, respectively. We defined “before” as 1/7/2015 to start/decline date; and “after” as start/decline date to 30/9/2018, date of PrEP stop, or date of PrEP start for decliners starting after 30/06/2018. We used Poisson regression to obtain incidence rate ratios for PrEP users (IRRPrEP) and decliners (IRRDecline) in separate models. A third Poisson regression with an interaction term between period (before/after) and group (PrEP use/decline) was used to obtain the ratio of incidence rates.

Results:

In PrEP users (n=561), the STI incidence increased from 27.6/100-person-years “before” to 55.4/100-person-years “after” (IRR_{PrEP}=2; 95%-CI 1.7-2.4). Among decliners (n=300), it increased from 17.8/100-person-years to 27.9/100-person-years ($IRR_{Decline}$=1.6, 95%-CI 1.2-2.1). The IRR increase in the PrEP users was 1.3-times higher than in the decliners (95%-CI 0.90-1.81).

Conclusions:

Both PrEP users and decliners show a sharp increase in STI over this short time. We recommend further research to establish whether the slightly higher incidence increase in PrEP users is significant and surveying risk behaviours of people eligible for PrEP to better understand the increasing risk of STIs.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: PrEP, HIV, Wales, Intervention, STI

ABSTRACT ID: 394

PRESENTED BY: Laia Fina Homar / laia.fina@wales.nhs.uk

13.3. Estimating the infection time among people who inject drugs during an HIV-outbreak in Athens, Greece: Evidence that interventions significantly decreased the number of new transmissions

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Background:

New diagnoses of HIV-1 infections among people who inject drugs (PWID) increased significantly in 2011 in Athens, Greece. Our aim was to estimate the time of infection and to investigate for potential trend in time to diagnosis for PWID during August 2010-December 2014. A large seek-test-treat program (ARISTOTLE) targeting PWID, was carried out in Athens, during August 2012- December 2013. The prevalence of HIV among PWID in 2013 reached 16.5%.

Methods:

Analysis included sequences from 741 HIV(+) PWID, and 36 non-PWID infected within PWID-specific clusters sampled in Greece during 20/08/2010-02/12/2014. Diagnoses dates were known, and infection dates were based on molecular clock calculations.

Results:

The number of new infections and diagnoses were 3 and 0 for 2009, 46 and 1 for 2010, 201 and 136 for 2011, 366 and 282 for 2012, 159 and 264 for 2013, 4 and 94 for 2014, respectively. New infections declined significantly after 2012, whereas considerable change in new diagnoses was monitored after 2013. There was an increasing trend in the time interval between the date of infection and diagnosis during 2011-2014 (p<0.001). The median (IQR) time between infection and diagnosis was 0.24 years (0.15, 0.40) for 2011, 0.32 years (0.17, 0.60) for 2012, 0.54 years (0.28, 0.99) for 2013 and 0.96 (0.60, 1.51) for 2014.

Conclusions:

Our findings based on molecular methods with dense sampling, show that there was a steep decline in HIV infections after 2012 probably due to the intervention programs, including ARISTOLE, implemented as a response to the outbreak. The decline in the number of new transmissions was probably associated with an increase in the time interval between time of infection and diagnosis over time.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: HIV, people who inject drugs, outbreak, phylodynamics, infection dates

ABSTRACT ID: 757

PRESENTED BY: Evangelia-Georgia Kostaki / ekostakh@med.uoa.gr

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13.4. What is the optimal testing strategy for oropharyngeal Neisseria gonorrhoeae in women visiting STI clinics?

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Background:

Oropharyngeal Neisseria gonorrhoeae is not routinely tested for in women visiting Dutch STI clinics. It is hypothesized that many oropharyngeal infections remain undetected due to its asymptomatic nature, creating a reservoir for ongoing transmission and drug resistance. It is yet unknown what the optimal testing policy is for women, as data on universal testing are missing.

Methods:

Surveillance data 2008-2017 from all Dutch STI clinics were used (n=546,246 consultations). Oropharyngeal testing policy was defined as universal testing, that is ›85% of consultations included oropharyngeal testing per clinic per year or selective testing(‹85% tested). The proportion infections missed using selective testing was calculated by extrapolating N.gonorrhoeae positivity found by routine universal testing. Independent risk factors for oropharyngeal N.gonorrhoeae were assessed among women routinely universally screened between 2016-2017 using backward multivariable logistic regression analyses.

Results:

Routine universal testing was used in 11% (n=57,359) of consultations, selective testing in 81% (n=444,283). Positivity was comparable between routine and selective testing; 1.4%(95%CI1.3-1.5,n=703), and 1.4%(95%CI1.3-1.3,n=1858,P=0.68). Selective testing missed 70.1%(95%CI69%-71%,n=4,363) of infections. The proportion oropharyngeal-only was 47% in routine and 52% in selective testing. Independent risk factors were being notified for any STI (OR1.3,95%CI1.03-1.5), concurrent urogenital N.gonorrhoeae (OR80.0,95%CI59.0-108.4) and commercial sex work(OR4.1,95%CI2.8-5.9). When using the risk factors except urogenital N.gonorrhoeae as testing indicators, 27.8% (n=5,418) of all women would be tested, finding 55.6% (n=119) of infections.

Conclusions:

Selective testing potentially misses almost 70% of oropharyngeal N.gonorrhoeae in women, of which almost half were oropharyngeal-only infections. Using two risk factors as testing indicators, half of all oropharyngeal N.gonorrhoeae infections would be detected by testing almost one-third of women. This seems like a valid and minimal testing strategy for women, as is advocated in the Dutch STI-guidelines.

Subject: Surveillance

Keywords: Neisseria gonorrhoeae, Oropharyngeal, Women, STI, Testing policy, Oral

ABSTRACT ID: 205

PRESENTED BY: Christian Hoebe / genevieve.vanliere@ggdzl.nl

13.5. HIV in women in the EU/EEA: 25 years of surveillance data to inform prevention and control

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Background:

To inform improved HIV prevention and control for women in the EU/EEA, we estimate HIV incidence and describe socio-demographic, clinical and transmission group characteristics of women diagnosed with HIV from 1992-2017.

Methods:

New HIV diagnoses among women › 15 years reported by EU/EEA countries to the European Surveillance System were extracted and corrected for reporting delay. Age-specific rates per 100 000 population, proportions per transmission mode and region of origin, and median CD4 count were calculated for the period 1992 to 2017 (from 2000 for CD4 count). Incidence and the undiagnosed number of women living with HIV in the EU/EEA were estimated with the ECDC HIV Modelling Tool.

Results:

HIV incidence among women in the EU/EEA peaked in 2004 at 4.6 per 100 000 women and has declined steadily to 2.9 per 100 000 in 2017. Since 1992, rates were highest in women 25-39 years (13.3 in 2017), and declined in all age groups besides women ›50 years. Heterosexual transmission is the main mode of HIV transmission among women, increasing from 61.5% (1119/1820) of new diagnoses in 1992 to 94% (4175/4446) in 2017; transmission due to injecting drug use declined from 19% (348/1820) to 3.5% (155/4446). Since 2000, >50% of new HIV diagnoses in women were among foreign-born, most of whom originated from sub-Saharan Africa. Median CD4 count at diagnosis increased significantly from 290 (95% CI: 279-305) in 2000 to 333 (95% CI: 321-346) in 2017. About 9.6% (17 150/178 650) of women living with HIV in the EU/EEA remain undiagnosed.

Conclusions:

More effective prevention and control of HIV could be achieved by addressing heterosexual transmission and foreign-born women, while promoting earlier HIV diagnosis.

Subject: Surveillance

Keywords: HIV, women, surveillance, prevention

ABSTRACT ID: 445

PRESENTED BY: Anastasia Pharris / anastasia.pharris@ecdc.europa.eu

Parallel Session 14
DAY 2, Thursday, 28. November 2019
17:00-18:40

Respiratory disease: surveillance and modelling

Moderator

Angeliki Melidou

Abstracts

14.1. Non-influenza viruses associated with Severe Acute Respiratory Infections during influenza seasons 2015/2016 to 2017/2018, Belgium

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Background:

We describe here non-influenza virus detection rates and their association with severity in patients with severe acute respiratory infection (SARI).

Methods:

The Belgian SARI sentinel surveillance relies on data from six hospitals. SARI was defined as an infection requiring hospitalization with onset of fever and cough or dyspnea within the previous 10 days. We tested samples taken for the seasons 2015-2016 until 2017-2018 by multiplex RT-qPCRs for the detection of influenza viruses and 8 non-influenza respiratory viruses. We described detection rates and the affected population (N=3,200). We modelled the relationship with severity by age group using logistic regression adjusting for clustering within hospitals.

Results:

Twenty-eight per cent of the samples were negative for all viruses tested (n=892), 39% were positive for influenza only (n=1245) and 22% were positive for one single non-influenza respiratory virus (n=701), including human metapneumovirus (HMPV) (5.9%), respiratory syncytial virus (RSV) (4.7%), and picornaviruses (4.8%). We detected 11.3% co-infections (2 to 5 respiratory viruses) (n=362).

Complications (defined as death, admission to intensive care unit, development of acute respiratory distress syndrome, need of invasive mechanical ventilation, or need of extracorporeal membrane oxygenation) were reported in 15% of adults (292/2010, including 165 deaths) and 2.8% children (33/1190, including 2 deaths), respectively. Viral pneumonia was reported in 10.6% of adults and 6.8% of children, respectively.

Among adults, multivariable analysis identified a higher risk of viral pneumonia with HMPV infection versus influenza infection (OR 3.4, 95% CI 2.2-5.5).

Conclusions:

One third of the patients was positive for non-influenza viruses. The SARI surveillance also showed evidence of higher morbidity in adults associated to HMPV suggesting that early testing for non-influenza viruses could be beneficial for clinical management of SARI patients.

Subject: Surveillance

Keywords: human metapneumovirus, respiratory syncytial virus, rhinovirus, enterovirus, picornaviruses, surveillance, SARI, non-influenza

ABSTRACT ID: 265

PRESENTED BY: Lorenzo Subissi / lorenzo.subissi@sciensano.be

14.2. Surveillance of enterovirus types causing infection in Wales from 2015 to 2019

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Background:

Enteroviruses (EV), including Coxsackie viruses (CV) and ECHO viruses can cause severe respiratory and neurological infections. EV infections are under-diagnosed and limited surveillance is carried out across Europe. We present findings from EV surveillance and typing in Wales from 2015-2019.

Methods:

Passive EV laboratory surveillance began in Wales in 2015. Surveillance includes all samples from patients presenting with acute respiratory symptoms (using a Luminex RPP molecular assay and specific enterovirus assay with internal control) and all enterovirus detections from other sample types. Typing is carried out on all confirmed cases through a combination of EV-D68 specific RT PCR and partial VP1 gene sequencing.

Results:

Between 01/09/2015 and 15/04/2019, there were 1,370 confirmed EV infections, 82.3% were typed. More than 40 different virus types were detected: EV-D68, CV-A6 and ECHO-30 accounted for 50.1% of cases (21.3%, 17.1% and 12.1% respectively), ECHO-6 and ECHO-11 accounted for 7.4% and 6.0%. EV-D68 cases appeared in three seasons (December 2015 - February 2016, July 2016 - January 2017, July 2018 - December 2018). CV-A6 cases occurred throughout the period, with small annual peaks around October - November, similar to ECHO-11. ECHO-6 and ECHO-30 cases occurred predominantly in single waves from December 2016 - August 2017 and March 2017 - December 2017 respectively. ECHO-11 cases were youngest (median age 0.9y). CV-A6, EV-D68, ECHO-6 and ECHO-30 cases were all older ($P<0.05$), median ages 1.3y, 2.5y, 15.5y and 23.6y respectively. Intensive care (ICU) cases were most likely in EV-D68 infections (16.6% in ICU).

Conclusions:

These results add to limited evidence on circulation of clinically significant enteroviruses in Europe. Further developments, ongoing surveillance and international collaboration are required to better understand the distribution of these infections.

Subject: Surveillance

Keywords: Enterovirus, EVD68, Non-polio-enteroviruses, sequencing

ABSTRACT ID: 777

PRESENTED BY: Simon Cottrell / simon.cottrell@wales.nhs.uk

14.3. Identification of infection sources of Legionella using WGS, 2016-2018, Austria

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Background:

The Legionnares' Disease (LD) is caused by Legionella pneumophila (L.p.), mainly by serogroup (SG) 1. Whole genome sequencing (WGS) represents the ultimate tool to compare human isolates with water isolates. The aim of our study was to evaluate the usefulness of core genome multilocus sequence typing (cgMLST) in comparison with the conventional sequence based typing (SBT) for identifying the most likely sources(s) of infection.

Methods:

We characterized human isolates from 14 LD cases, occurring from 2016 to 2018 in Austria and 66 water isolates from epidemiologically related potable water systems (PWS) by SG, serotype (MAb-type) and cgMLST. On average three colonies per positive outlet sample were analysed. The SBT was extracted from the WGS data. We defined an epidemiologically related PWS as the likely source of infection, when the recovered water isolates differed from the corresponding human isolate by ≤4 alleles.

Results:

In 11 LD cases, the isolates matched with the water isolates from the related PWS by SG, Mab-type and SBT. Using cgMLST in three of these 11 SBT- based matches, the water isolates differed from the human isolate by five, 10 and 45 alleles. The water isolates from the eight cgMLST-based human-water matches originated from the PWS of a nursing home and a hotel, and from three hospitals and households, each.

Conclusions:

The cgMLST discarded one-third of the SBT based human-water isolate matches. Our findings may indicate that cgMLST is more reliable in identifying the infection source, compared with classical SBT. The probability of over- discrimination using a cgMLST cluster threshold of ≤4 allelic differences and selection of a small number of colonies per water outlet sample should be discussed.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: legionella pneumophila ,Whole Genome Sequencing,Legionnaire‘s Disease,Multilocus Sequence Typing

ABSTRACT ID: 376

PRESENTED BY: Ali Chakeri / ali@chakeri.at

14.4. Presentation and healthcare delays among people with tuberculosis in London, and the impact on treatment outcome

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Background:

Delay in diagnosis of pulmonary tuberculosis (TB) increases disease severity and the risk of transmission. A quarter of London's pulmonary TB patients have over four months of delay. We explore London data to classify delays, identify associated risk factors and assess treatment outcome.

Methods:

We conducted a retrospective cohort study using London surveillance data, 2012-2018 and included adults aged ≥18 years with pulmonary TB. We defined presentation delay (days from symptom onset to first healthcare visit) and healthcare delay (first healthcare visit to treatment commencement) as dichotomous variables; positive delay being days equal or greater than the 3rd quartile. We applied logistic regression models to identify risk factors associated with delays and treatment outcome at 12 months.

Results:

Of 7188 cases, 4539 reported presentation and 5193 healthcare delays. The 3rd quartiles for presentation and healthcare delay were 84 and 61 days, respectively. Presentation delay was associated with female sex (adjusted Odds Ratio (aOR)=1.21; (95%CI) 1.04-1.39), increasing age (aOR=1.004; 1.001-1.008), white compared to Asian ethnicity (aOR=1.35; 1.12-1.62), previous imprisonment (aOR=1.66; 1.22-2.26) and alcohol misuse (aOR=1.44; 1.08-1.89). Healthcare delay was associated with female sex (aOR=1.39; 1.21-1.59), increasing age (aOR=1.014; 1.009-1.018) and white compared to Asian ethnicity (aOR=1.41; 1.19-1.68).

Of 5678 cases with known outcome, 16% did not complete treatment. Neither delay (presentation/healthcare) was associated with non-completion ($p\text{-value}<0.05$).

Conclusions:

Female, white and older people with TB were more likely to experience both presentation and healthcare delays. In addition, social risk factors were associated with delays in first presenting. Despite not finding an association with non- completion, early diagnosis and treatment remains critical to reduce transmission. We recommend sharing results with stakeholders to inform strategies to reduce delays.

Subject: Surveillance

Keywords: tuberculosis, pulmonary, treatment outcome, epidemiology

ABSTRACT ID: 417

PRESENTED BY: Poppy Evenden / poppy.evenden@gmail.com

14.5. A school tuberculosis outbreak with a high rate of transmission, Italy, 2019 (LATE BREAKER)

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Background:

Italy has low tuberculosis incidence (6.5 cases/100,000 in 2017). We investigated a large tuberculosis outbreak in a north-eastern Italian school, detected in March 2019, when a school-aged child (index case) presented with a 5-week history of fever, asthenia, cough, weight loss and diffuse lymphadenopathy.

Methods:

A source-finding investigation was performed, followed by a contact investigation around the primary case, using the concentric circles approach. Screening was performed by clinical evaluation, tuberculin skin test (TST) and/or Chest X- Ray (CXR).

Results:

The primary case, an Italian-born schoolteacher of the index case, had non-resistant cavitary tuberculosis, positive microscopy and culture, and reported a positive TST as a child not followed by treatment. Based on symptom duration in the primary case and TST results among former students in the previous two years, it was determined that the schoolteacher was likely infectious since January 2018. Over 99% (691/695) of persons at risk were tested. Thirteen cases of active pulmonary disease were detected (11 asymptomatic schoolchildren and two staff) and 50 cases of latent infection (34 schoolchildren, ten staff, and six close contacts of the primary case). Attack rates were 1.9% for active tuberculosis and 7.2% for latent infection. Of the 13 active cases, only six were culture-positive and susceptible to first- line antibiotics, one had a positive PCR and the remaining six (all of whom children) were diagnosed by CXR.

Conclusions:

Prolonged exposure of contacts due to delayed diagnosis in the primary case was a key factor for this outbreak. To prevent school outbreaks, consideration should be given to administering a pre-employment health questionnaire to workers with sustained contact with children. The outbreak also highlights the difficulties in laboratory confirmation of tuberculosis in children.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Tuberculosis, Latent Tuberculosis, children, school, outbreak

ABSTRACT ID: 864

PRESENTED BY: Davide Gentili / davide.gentili@aulss2.veneto.it

Parallel Session 15
DAY 2, Thursday, 28. November 2019
17:00-18:30

Vaccine-preventable diseases: surveillance (2)

Moderator

Margaret Fitzgerald

Abstracts

15.1. Invasive Group B Streptococcus infections in adults in England, 2015-2016: analysis of population surveillance data

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Background:

Invasive group B streptococcal (iGBS) disease in adults is of growing clinical and public health concern following marked increases in incidence noted in many countries. The aim of this study was to characterize iGBS disease in adults in England to identify potential opportunities for future prevention.

Methods:

Episodes of iGBS disease in patients >=15 years old recorded in a national laboratory surveillance database between 01/01/2015 and 31/12/2016 were linked to hospital admissions (Hospital Episode Statistics, NHS Digital). Dates of death were obtained from NHS Digital's Demographic Batch Service.

Results:

There were 3,156 invasive iGBS episodes in adults recorded in England during 2015-2016, corresponding to an annual incidence rate of 3.48 per 100,000 population. In 87% of episodes GBS was isolated from a blood culture, followed by joint (5.6%), bone (2.7%) and lower respiratory tract (2.4%). The majority (97.6%) of patients had a single episode; 1.9% had two and 0.5% three or more episodes. iGBS incidence was highest in patients aged >=70 years and women aged 20-49 years. Most non-pregnancy iGBS diagnoses (93%) were from specimens taken within 48 hours of admission. Maternal infections accounted for 430/485 (89%) of episodes in women aged 20-39 years. iGBS disease was associated with the following co-morbidities: cardiovascular (64%), lung (38%), and kidney disease (38%) and diabetes (35%). Overall all-cause mortality (any setting) in the 12 months following an iGBS episode was 24%, with a median time to death of 45 days. No deaths following pregnancy-related iGBS episodes were identified.

Conclusions:

Although most iGBS cases in England occur among the elderly and in adults with co-morbidities, maternal cases contribute substantially to the overall burden of iGBS disease in England.

Subject: Burden of disease

Keywords: Streptococcus agalactiae, group B streptococcal disease, invasive infection, bacteraemia, adult

ABSTRACT ID: 655

PRESENTED BY: Simon Collin / simon.collin@phe.gov.uk

15.2. Clustering of susceptibility to measles in households: perspective for the next two decades

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Background:

As a result of the introduction period of the measles vaccine, the generation born between 1985 and 1995 in Belgium, has a relatively low immunity level. Over the next few decades, this level could potentially decline further due to the waning of vaccine-induced immunity. Moreover, as members of this generation are now becoming parents, and as vaccine hesitancy becomes an ever-growing concern, we face the risk of multiple generations of susceptible individuals living under the same roof, thus increasing the risk for measles outbreaks in the decades to come. Furthermore, administration of the first dose of vaccination against measles at 12 months puts an extra risk on newborns of susceptible parents.

Methods:

Based on projections of age-dependent immunity levels for 2020-2040, we assess the impact of household- based clustering of measles susceptibility on outbreak risks in Flanders, Belgium. We use Stride, an individual-based simulator for the transmission of infectious diseases, which can account for heterogeneities in contacts and immunity status based on age, context and household membership.

Results:

We expect household-based clustering to increase the risk for measles outbreaks in the following years. However, as time progresses, we expect to see the impact of household-based clustering decline again. As the generation born between 1985 and 1995 ages, they will no longer have susceptible children living in their households and these will thus contribute less to the transmission of the disease.

Conclusions:

To avoid outbreaks of measles in the coming years, attention should be given to immunizing the generation born between 1985-1995, as well as their young children. As such, we avoid the risk of measles spreading through the population by infecting several generations within the same household.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Measles,Computer simulation, Vaccination, Uncertainty, Disease Outbreaks, Belgium

ABSTRACT ID: 699

PRESENTED BY: Elise Kuylen / elise.kuylen@uantwerpen.be

15.3. National burden of measles complications in Italy during a large outbreak in 2017-2018

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Background: Measles can lead to complications in up to 30% of cases. We describe measles complications reported during a large outbreak in Italy.

Methods:

We analyzed measles cases reported to the national measles and rubella integrated surveillance system, with symptom onset from 1 January 2017 to 31 December 2018. Complications were analysed by age, sex, vaccinations status, and measles genotype.

Results:

Overall 8,088 cases were reported (79.6% laboratory confirmed, 13.3% epidemiologically linked and 7.1% clinically confirmed). Median age was 26 years, 50.4% were male, 91.8% were unvaccinated, 48% were hospitalised. B3 and D8 were the most common genotypes, identified respectively in 74.7% and 25.1% of 2,004 genotyped cases. Complications occurred in 37.9% of cases. Stomatitis (n=1363, 16.8%) and diarrhea (n=1318, 16.3%) were the most common complications across all ages, followed by keratoconjunctivitis (n=945, 11.7%) and hepatitis (n=739, 9.1%). Other complications included pneumonia (n=647, 8.0%), otitis (n=348, 4.3%) and seizures (n=27, 0.3%). Four encephalitis cases and thirteen deaths occurred (Case Fatality Rate 1.6/1,000). Complications were more frequent in cases ≥ 20 years of age compared to 5-19 years and <5 years (41.3% vs 30.7% and 30.9%, $p<0.01$), in unvaccinated compared to vaccinated with one or two doses (40.2% vs 31.2% and 21.8%, $p<0.01$), in genotype B3 compared to D8 (44.5% vs 29.6%, $p<0.01$). No gender differences were found. Pneumonia was more frequent among cases ≥ 20 years compared to younger cases.

Conclusions:

The proportion of complicated cases during this outbreak was greater than expected; this may be due to the high median age of cases. CFR was comparable to that reported in the literature. Further studies are needed to investigate correlation between genotypes and complications.

Subject: Surveillance

Keywords: measles; outbreak; complication; surveillance

ABSTRACT ID: 647

PRESENTED BY: Patrizio Pezzotti/ patrizio.pezzotti@iss.it

15.4. Measles in the EU/EEA in 2016-2019: where are cases imported from?

Benedetto Simone [1]

N. Bundle [2], C. Belledarde de Saint Lary [3], S. Bacci [4], L. Pastore Celentano [5]

[1] Ecdc

[2,3,4,5] Ecdc

Background:

The European Union / European Economic Area (EU/EEA) is experiencing a resurgence of measles, with 44,074 cases and 84 deaths reported between 01/01/2016 and 31/03/2019, despite 25/30 Member States (MS) meeting the measles elimination target in 2017. We described proportion and origin of imported cases in the EU/EEA to inform public health action in MS.

Methods:

We extracted data for cases reported to the European Centre for Disease Prevention and Control by MS between 01/01/2016 and 31/03/2019. We defined imported cases as cases with recorded exposure to measles outside of the reporting country 7–18 days prior to rash onset.

Results:

Of 39,173 cases with available information (89% of all reported cases), 1,599 (4.1%) were imported. Seventy-two percent of imported cases acquired their infection in Europe, more frequently in other EU/EEA countries (43%) than in non-EU/EEA countries (29%). Asia and Africa accounted for 19% and 8% of imported cases, respectively. One fourth of imported cases were from endemic MS (Romania: 253; Italy: 81; Germany: 36; France: 33). Several MS, despite having eliminated measles, exported a consistent number of cases to other MS (Poland: 160; Spain: 76; UK: 52).

Conclusions:

The main source of measles importation in EU/EEA MS are other EU/EEA MS. Movement of people to/from endemic countries poses a risk not only of sporadic importation, but also of sustained transmission in areas with suboptimal vaccination coverage, also in MS that achieved elimination. Complete epidemiological and laboratory investigation to distinguish separate chains of transmission may be challenging in the context of virus importations with the same genomic sequence. Measles vaccination should be offered, whenever possible, to all travellers, including those moving within the EU/EEA, following national recommendations.

Subject: Surveillance

Keywords: measles, vaccine-preventable disease, elimination, importation

ABSTRACT ID: 747

PRESENTED BY: Benedetto Simone / Benedetto.Simone@ecdc.europa.eu

Parallel Session 16
DAY 3, Friday, 29. NOVEMBER 2019
11:00-12:40

Vaccine-preventable diseases: epidemiology

Moderator

Piotr Kramarz

Abstracts

16.2. Lessons learned from the transmission chain of a measles outbreak in Stockholm County 2017

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[5] Department of Communicable Disease Prevention and Control, Stockholm Region|Division of Infectious diseases, Department of Medicine Solna, Karolinska Institutet

Background:

Measles is a notifiable disease in Sweden. The vaccination coverage in Sweden for measles is 97%.

In January 2017, a child travelling from Pakistan became the index case of a measles outbreak in Stockholm County with a transmission chain of three generations. The Stockholm County medical officer (SmSt) led the outbreak investigation. The present report describes the outbreak, the post outbreak analysis and the identification of control measure improvements that could have counteracted wider spread of the outbreak.

Methods:

Epidemiological data, outbreak control measures and documented interviews with patients/patient caregivers were extracted from the electronic surveillance system, SmiNet. Health-care visits by cases during the outbreak were sourced from the Common Healthcare Register, GVR. Data from GVR and interviews allowed backtracking to deduce and pinpoint the actual transmission events. Post outbreak analysis of control measures was applied on the transmission events. All outbreaks and interventions following the here described outbreak were subsequently analysed by data extraction from SmiNet.

Results:

Twelve cases of measles, of which 9 were children (≤3 years), all linked to the index case, were confirmed from January- March 2017. Both adult cases and two of the children had reported pre-event vaccination. All transmission occurrences were detected, and 13 control measure gaps were identified at different levels such as triage, delay to clinical diagnosis, contact tracing, language barriers, immunity of health-care personnel and health-care facility outline.

The post outbreak analysis led to an updated action plan, extended education efforts and the formation of local outbreak management teams.

Conclusions:

Post outbreak analysis is an important way to improve infectious disease control efforts. Later measles outbreaks in Stockholm county has not gone beyond first generation spread.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: outbreak, control measures, vaccine preventable disease, transmission chain

ABSTRACT ID: 772

PRESENTED BY: Joanna Nederby Öhd / joanna.nederby-ohd@sll.se

16.3. Age group-specific Rotavirus Infection and Acute Gastroenteritis five years after the introduction of rotavirus immunisation in the UK

Charlotte M. Gower [1]

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Background:

Rotavirus is the most common cause of diarrhoea in young children and is associated with considerable healthcare utilisation. A two-dose oral rotavirus vaccine (Rotarix®) was introduced into the UK infant immunisation programme in 2013. High vaccine uptake was rapidly achieved leading to a large decline in primary care attendance and hospitalisations for acute gastroenteritis (AGE) across all age groups in the first year following vaccine introduction.

This study aimed to assess the continued impact of the UK rotavirus immunisation programme in the five years since the programme was introduced.

Methods:

National level data on the number of laboratory confirmed rotavirus infections and hospital admission due to AGE were analysed from 2000 until 2018. Age-specific rate ratios and numbers of cases averted in each of the five post vaccination seasons compared to the pre-vaccination period were estimated using negative binomial models. Changes in the average age of infection and seasonality of rotavirus infections were also investigated.

Results:

Laboratory confirmed rotavirus infections were reduced by 69-83% overall and by 77-88% in the under 1 year age group in the five years of the post-vaccine period. There was evidence of herd protection in non-vaccinated groups. Hospital admissions due to AGE were reduced by 12-35% overall, and by 25-48% in the under 1 year olds. Average age of laboratory confirmed rotavirus infections increased from 1.36 years to 1.87 years in the under 5 age group. Seasonal changes occurred with peak incidence being less pronounced and seasons lasting longer.

Conclusions:

There was a large and sustained drop in both laboratory confirmed rotavirus infections and AGE hospital admissions in each of the five years since the introduction of the UK rotavirus immunisation programme.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: rotavirus, vaccination, impact, hospitalisations, rate ratio

ABSTRACT ID: 669

PRESENTED BY: Charlotte M. Gower / charlotte.gower@phe.gov.uk

16.4. Increased risk of varicella among pregnant immigrant women from temperate and tropical countries after arrival in Quebec, Canada

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Background:

Varicella is a relatively benign childhood disease but causes severe disease in adults, with pregnant women at highest risk. Childhood varicella vaccination decreases varicella rates in all age groups through herd immunity but may lead to the accumulation of susceptible adults. Childbearing women migrating from tropical countries may be varicella-susceptible (~15%) due to different viral transmission dynamics in their countries of origin and lack of varicella vaccination. This study aimed to describe the epidemiology of varicella among pregnant immigrants and non-immigrants before and after a childhood varicella vaccination program.

Methods:

All medically-attended varicella cases during pregnancy in Quebec, 1996-2014, were identified in administrative health databases linked to immigration data. Varicella rates and comparative rate ratios (RRI-NI) and 95% CI for pregnant immigrants vs. non-immigrants overall and for each vaccination period: pre (1996-1998), private (1999-2005), and public (2006-2014) were estimated.

Results:

Among 216,614 varicella cases, 1285 occurred during pregnancy; 20% occurred among immigrants (n=259) and 10% required hospitalization (N=132). Varicella rates decreased overall from 10.1 to 0.9/100,000 childbearing women over the study period. Pregnant immigrants however, had higher rates of varicella for all visit types during the study period; outpatient visits [RR_{I-NI}=2.33; 95%CI=1.98-2.74], emergency room visits [1.76; 1.38-2.25], and attributable hospitalizations [3.72; 2.56-5.40]. This disparity increased after the introduction of childhood vaccination as immigrants accounted for 14% and 36% of pregnant varicella cases in the pre vs public-vaccination periods, respectively. Immigrants from South Asia [RR_{I-NI}=7.8; CI:3.8-16.0], Sub-Saharan Africa [5.1; 2.2-11.6] and Latin America/Caribbean [4.9; 2.9-8.1] were at highest risk.

Conclusions:

Pregnant immigrant women had higher varicella rates during all vaccination periods compared to non- immigrants. These data highlight the need to provide targeted varicella vaccination for susceptible childbearing immigrant women.

Subject: International health and migration

Keywords: chickenpox, pregnancy, immigrants, childhood vaccine, varicella

ABSTRACT ID: 447

PRESENTED BY: Elisa Llorente Pastor / elisallp7@gmail.com

Parallel Session Abstracts

Parallel Session 17
DAY 3, Friday, 29. November 2019
11:00-12:40

Hepatitis B and C: surveillance and disease burden

Moderator

Isabel Oliver

Abstracts

17.1. Developing and piloting a standardised European protocol for hepatitis C prevalence surveys in the general population (2016-2019)

Stine Nielsen [1]

I. Sperle [2], M. Gassowski [3], A. Ciccaglione [4], H. Brummer-Korvenkontio [5], S. Toikkanen [6], Z. Naneva [7], A. Amato-Gauci [8], E. Duffel [9], R. Zimmermann [10]

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Background:

Robust estimates of the number of people with chronic hepatitis C (HCV) are essential for an appropriate public health response and for monitoring progress towards the WHO goal of eliminating viral hepatitis. Existing HCV prevalence studies in the EU/EEA countries are heterogeneous and often of poor quality due to non-probability based sampling methods, small sample sizes and lack of standardisation leading to poor national representativeness. This project aimed to develop and pilot standardised protocols for undertaking nationally representative HCV serosurveys in the general adult population.

Methods:

Between 08/2016-06/2019, a team from the Robert Koch-Institute contracted by the European Centre for Disease Prevention and Control (ECDC) synthesised evidence on existing HCV prevalence surveys and survey methodology and drafted a protocol. The methodological elements of the protocol were piloted in Bulgaria, Finland and Italy. An international multidisciplinary expert group was consulted regularly.

Results:

The protocol includes three alternative study designs: a stand-alone; a ‘nested’ within an existing health survey; and a retrospective testing survey design. A decision algorithm advising which design to use was developed. The protocol was piloted and finalised covering minimum and gold standards for all aspects from sampling, data protection and ethical issues, recruitment, specimen collection and laboratory testing options, staff training, data management and budget considerations. Through piloting all survey designs were found useful for estimating HCV prevalence in the general adult population.

Conclusions:

An evidence-based protocol for undertaking HCV prevalence serosurveys in the general population reflecting the different needs, resources and epidemiological situations across Europe has been developed and found useful through piloting. This technical guidance will help support EU/EEA countries in estimating their national viral hepatitis burden as part of a wider ECDC toolkit.

Subject: Burden of disease

Keywords: Hepatitis C, Prevalence, Cross-Sectional Studies, Epidemiologic Methods, Pilot Projects, Guideline [Publication Type]

ABSTRACT ID: 261

PRESENTED BY: Stine Nielsen / stine.nielsen12@gmail.com

17.2. Get Tested LeEDs: Estimating bloodborne virus prevalence through routine opt-out emergency department testing

Elizabeth Smout [1]

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Background:

Routine testing for blood-borne viruses (BBVs) within hospital emergency departments (EDs) has the potential to provide access to testing for individuals who do not routinely access health services, allowing for earlier diagnosis and access to treatment and care. We evaluated the introduction of integrated, routine, opt-out testing for HIV, hepatitis B virus (HBV) and hepatitis C virus (HCV) infections in EDs at Leeds Teaching Hospitals NHS Trust, UK.

Methods:

From October 2018, HIV antibody, HBV (HBV surface antigen [HBsAg]) and HCV (HCV antibody [anti-HCV] and HCV- RNA) testing were offered to all ED attendees aged 16–65 years at the time of attendance who had a blood test for urea and electrolytes. Testing uptake, BBV seropositivity and linkage to care were calculated from 22 weeks of testing data.

Results:

Testing uptake was 49.5% (10,054/20,301). We identified 45 HIV, 204 HCV-Ab, 90 HCV-RNA and 45 HBsAg-positive ED attendees. Overall HIV seroprevalence was 0.5%; HCV-Ab 2.1%; HCV-RNA 0.9% and HBsAg 0.5%. 20.0% (9/45) of HIV positive, 46.7% (42/90) of HCV-RNA positive and 51.1% (23/45) of HBsAg-positive individuals were new diagnoses. Of those eligible for linkage to care (newly diagnosed or previously diagnosed but lost to follow-up), 88.9% (8/9) HIV- positive, 24.1% (21/87) of HCV-RNA positive and 34.8% (8/23) HBsAg-positive individuals had been linked to care at the time of analysis.

Conclusions:

BBV testing within the ED was feasible and effective, with BBV seroprevalence higher than population estimates for Leeds. We recommend implementing BBV testing as part of routine care within ED settings in areas with a high BBV prevalence as a cost-effective method of detecting undiagnosed infections. Awareness of the programme should be increased among ED staff in order to maximise testing uptake.

Subject: Burden of disease

Keywords: Hepatitis B, Hepatitis C, HIV, Emergency department

ABSTRACT ID: 199

PRESENTED BY: Elizabeth Smout / elizabeth.smout@phe.gov.uk

17.3. More than 1,000 people infected by hepatitis C virus through blood transfusions before screening was implemented remain alive but undiagnosed: a nation-wide, retrospective cohort study, Sweden

Viktor Dahl [1]

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Background:

Screening of blood donors for hepatitis C virus (HCV) was introduced in Sweden in 1992. To estimate the number of individuals who are likely to have been infected with HCV before that and who remain alive but are still undiagnosed we conducted a nationwide retrospective cohort study.

Methods:

We linked a national database on blood transfusions, with data on blood donation and transfusions in Sweden since the 1970s, and the national database for notifiable infections, which contains all cases notified with HCV-infection since the 1990s. First, we tracked recipients of donors with confirmed viral hepatitis. Second, we computed a donor-specific risk score, defined as the difference between the observed and the expected number of HCV-infections among all prior recipients of each donor, where thresholds were determined using simulation.

Results :

In all we included 1,146,307 recipients of transfusions. Transfusion transmission only occurred before 1992 when donor screening had been completely implemented. We found 44 donors and 1180 recipients likely to be infected with HCV who were still alive and living in Sweden but remain undiagnosed.

Conclusions:

There is still a substantial number of individuals in Sweden likely infected with HCV through blood transfusion who are unaware of their infection. We recommend that a follow-up study should be conducted to validate the method we used by approaching these individuals and offer testing. This would also serve as an opportunity to offer treatment to those who remain infected.

Subject: Burden of disease

Keywords: virus, hepatitis c, Parenterally-Transmitted, Hepacivirus

ABSTRACT ID: 302

PRESENTED BY: Viktor Dahl / viktor.dahl@folkhalsomyndigheten.se

17.4. Are men who have sex with men (MSM) in Europe protected from hepatitis B? - Findings from the European MSM Internet Suey (EMIS-2010)

Michael Brandl [1]

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Background:

Hepatitis B (HepB) vaccination is recommended for men-who-have-sex-with-men (MSM) in many countries, but information on vaccine coverage is scarce. We studied HepB vaccination recommendations and coverage among MSM in 38 European countries to guide prevention.

Methods:

We reviewed existing and collected new information on national HepB vaccination guidelines. From a large (N=174,209) pan-European MSM survey (EMIS-2010), we used data on self-reported HepB vaccination, age, education, settlement size and disclosure of same-sex sexual orientation ('outness', a proxy for societies' homopositivity). We excluded participants with a history of HepB. In multilevel (participants, countries) logistic regression models, we calculated adjusted odds ratios (aOR) with 95% confidence intervals (95%CI).

Results:

We analysed data of 163,106 MSM in 38 European countries. Median age was 32 (interquartile range: 25–41), 49.8% had higher education, 54.9% lived in settlements with ‹500,000 inhabitants, 38.3% were out to all or almost all, and 56.7% reported ever being vaccinated against HepB. 65.5% of participants lived in 21 countries where HepB vaccination for MSM was recommended and free-of-charge, 12.6% were potentially reached by universal childhood HepB vaccination programmes. In a model including age, education, settlement size, outness, universal vaccination programmes, and MSM-specific vaccination recommendations, the odds for being vaccinated increased with outness ('out to all or almost all': aOR=1.76, 95%CI: 1.69–1.82 vs. 'not out'), and if living in countries, where HepB vaccination was recommended and free-of-charge for MSM (aOR=2.22, 95%CI: 1.48–3.32 vs. 'no recommendation').

Conclusions:

In 2010, across Europe, large proportions of MSM were vulnerable to HepB, despite available vaccinations. To increase HepB vaccination coverage among MSM, implementation of MSM-specific recommendations and improvement of the societal climate for MSM is needed. Further measures to facilitate vaccine uptake should be investigated.

Subject: Burden of disease

Keywords: Hepatitis B, Vaccination, Sexual and Gender Minorities, Europe

ABSTRACT ID: 508

PRESENTED BY: Michael Brandl / brandlm@rki.de

Parallel Session Abstracts

Parallel Session 18
DAY 3, Friday, 29. November 2019
11:00-12:40

Food- and waterborne diseases and zoonoses: outbreaks (2)

Moderator

Chris Williams

Abstracts

18.1. Outbreak of Salmonella Agbeni with severe clinical presentation linked to exotic dried fruit mix, Norway, 2019

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Background:

On 12 February 2019, the Norwegian Institute of Public Health (NIPH) identified a cluster of four Salmonella Agbeni cases, identical by whole genome sequencing (WGS). We investigated to identify the outbreak source and implement control measures.

Methods:

Cases were defined as individuals with laboratory confirmed S. Agbeni infection sequence type ST2009 (MLST) and cluster type CT2489 (core genome MLST, 3002 loci). We interviewed all cases using trawling questionnaires or targeted questionnaires with photographs, and collected food samples from selected cases. We performed a case-control study, matching three controls per case by age, sex and geography. Odd ratios (ORs) with 95% confidence intervals (95%CI) for common exposure were calculated in STATA.

Results:

We identified 56 cases (<3 allelic differences), 59% female with median age 50 (range 2-91). Symptom onset was between 31 December 2018 and 16 March 2019. Twenty-one cases were hospitalized, seven had invasive infections and ten had urinary tract infections. Forty-six cases (82%) confirmed consumption of a specific dried exotic fruit mix. Cases were more likely to have consumed the fruit mix than controls (cases= 8, controls =31, OR 68, 95% CI 4-3298). S. Agbeni CT2489 was isolated from the fruit mix, resulting in withdrawal of the product from the market on 6 March 2019.

Conclusions:

Epidemiological and microbiological investigations confirmed the fruit mix as the source of this outbreak, which was characterised by severe clinical presentation. As dried exotic fruits may serve as vehicles for Salmonella, the Norwegian Food Safety Authority has instituted sampling of dried fruits in the salmonella surveillance program for 2019. We recommend reinforcing hygiene and safe food handling for dried fruit at all steps in the food production chain.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella, exotic dried fruit, outbreak, whole genome sequencing

ABSTRACT ID: 201

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18.2. Large waterborne gastroenteritis outbreak of mixed origin in Western Macedonia, Greece, January – February 2019

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Background:

In January 2019, a large gastroenteritis outbreak in Western Macedonia, Greece, caused extended media attention. We investigated to identify the possible mode and vehicle of transmission and implement control measures.

Methods:

We recorded cases who visited health care services (HCSs) with diarrhoea and/or vomiting between 25/01-03/02/2019 and conducted a 1:1 case-control study (CCS) selecting HCSs' visitors ≥18 years between 25-28/01/2019. We additionally conducted a retrospective cohort study (CS) among town's pupils aged 6-12 years. We calculated odds ratios (OR), relative risks (RR) and 95% confidence intervals (95% CI) for CCS and CS, respectively. Clinical and water samples were tested by conventional and molecular methods, and water supply system was inspected.

Results:

We recorded 476 cases; 52% female. Median age was 47 years (range 0-93). Main symptoms were diarrhoea (88.7%) and vomiting (86.2%). Cases peaked on 26/01/2019 and subsided on 04/02/2019, compatible with a point-source outbreak followed by secondary cases.

Forty-eight cases and 52 controls participated in CCS and 236 students in CS. Both studies indicated tap water as likely vehicle of transmission (CCS: OR=10, 95% CI: 2.1-93, explaining 96% of cases, CS: RR=2.2, 95% CI: 1.4-3.5).

Norovirus, Campylobacter jejuni, EHEC and EPEC were detected in 11 of 13 stool specimens; two or more pathogens were detected in seven. Water samples were collected after chlorination and tested negative. Technical failures were identified (i.e. disintegration of the tanks' walls and openings on their roof), possibly leading to water contamination.

Conclusions:

Results were consistent with a waterborne outbreak. Chlorination before samples' collection hampered confirmation of the outbreak's source. We recommended better co-ordination of water sampling, increased awareness for early detection, and remediation of technical failures of the water supply system.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: waterborne diseases, outbreak, investigation, case-control study, environmental

ABSTRACT ID: 122

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18.3. An outbreak of Salmonella monophasic Typhimurium associated with several pork products, Denmark, 2018-19

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Background:

In Denmark, large outbreaks of Salmonella with more than 20 cases have become rare in recent years. In October 2018, we identified a Salmonella outbreak through surveillance and initiated an investigation with the aim of identifying the source and controlling the outbreak.

Methods:

In Denmark, isolates from cases of Salmonella are whole-genome sequenced and analyzed by core genome multilocus sequence typing. We defined an outbreak case as a laboratory-confirmed case of Salmonella monophasic Typhimurium sequence type 5296 cluster 1 with symptom onset between October 2018 and January 2019. We conducted hypothesis-generating interviews and a matched case-control study. Controls were extracted from the Danish civil registration system and matched on sex, age and municipality. We also conducted food sampling and trace-back investigations.

Results:

Forty-nine cases were identified. The median age was 65 years (range 0-97) and 53% were male. Sixty-one percent of cases were hospitalized, but no deaths were reported. Initial interviews suggested a classical form of raw Danish pork sausage (medister sausage) as the outbreak vehicle. Medister sausage, pork chops and ground veal/pork meat showed mORs of 26 (95%-CI: 3-210), 4 (95%-CI: 1-13) and 4 (95%-CI: 1-10), respectively. In a multivariable analysis, only medister sausage remained significant. Several patients described eating the sausage raw or undercooked. Samples of medister sausage analyzed were negative for Salmonella and investigations at the production site did not reveal the mechanism of contamination.

Conclusions:

This outbreak was likely caused by consumption of several pork products. We identified medister sausage, a popular product in Denmark as a particular risk product that requires proper preparation, recommending it to be both boiled and fried thoroughly before consumption.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: outbreak investigation, Salmonella monophasic Typhimurium

ABSTRACT ID: 203

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18.4. Consumption of black sausage is associated with a large listeriosis outbreak in Germany, 2018-2019

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Background:

Between August 2018 and February 2019, 11/16 federal states in Germany reported 110 cases of Listeria monocytogenes (LM) infections, belonging to one core genome MLST cluster. The outbreak was investigated to identify the source and prevent further infection.

Methods:

For a case-control study we defined a case as a German resident with acute and invasive listeriosis, onset of symptoms since August 2018, and pathogen isolate belonging to core genome (cg) MLST types CT4465/CT7353. Population- based controls were telephone recruited and frequency-matched by age, sex and residence distribution to cases. Both were interviewed with a standardized questionnaire on purchase and consumption of food items and compared using logistic regression adjusted for matching variables (STATA, 15.1). We tested food items for LM and sequenced isolates using whole genome sequencing.

Results:

The case-control study compared 41 cases to 155 controls and showed a strong association with food purchase at supermarket chain A (adjusted OR: 23; 95%CI: 2.9- 170). Univariate analysis showed significant association for 29 food items. Multivariable analysis resulted in an association for minced meat (aOR: 42; 95%CI: 4.3-420), black sausage (aOR: 23, 95%CI: 4.3-120), cold cuts of roast pork (aOR: 15; 95%CI: 2.9-82) and edam cheese (aOR: 7.3; 95%CI: 1.6-33). Sequences of LM isolates from black sausage from a diseased case and from supermarket chain A were genetically identical with the outbreak strain according to cgMLST.

Conclusions:

Epidemiological and microbiological analysis point towards black sausage purchased at supermarket chain A as the outbreak vehicle. To stop outbreaks quickly, we recommend timely molecular surveillance and subsequent investigations of outbreak clusters jointly by stakeholders as common practice in Germany, in order to identify and withdraw vehicles.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Listeria monocytogenes, Outbreak investigation, Food safety, Case-control study, Whole-genome sequencing

ABSTRACT ID: 341

PRESENTED BY: Amrei Krings / kringsa@rki.de

18.5. A whole genome sequencing defined national outbreak of Salmonella Enteritidis associated with the consumption of a raw liquid egg white product

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Background:

In September 2018, a local authority was alerted to two cases of salmonellosis who had consumed a raw ready-to-eat liquid egg white product. Product supplied by one case was found to be highly contaminated with S. Enteritidis. We investigated with the aim of identifying additional cases and implementing appropriate control measures.

Methods:

Food chain traceback was undertaken and product was sampled from suppliers and distributors. All Salmonella isolates were sequenced, and a phylogenetic tree constructed. Routinely sequenced isolates from all cases of salmonellosis in England were compared against product isolates to identify closely genetically-related cases. Cases were interviewed, using an outbreak-specific questionnaire, to identify egg product exposures in the week before onset.

Results:

Two contaminated batches of liquid egg white product were identified and promptly recalled. All case and food isolates fell within a 5-single nucleotide polymorphism (SNP) cluster of S. Enteritidis (t5.360), linked to an ongoing European- wide outbreak. A total of nine cases from across England were identified with onset dates between 17 August and 3 September, all within 1 SNP difference of at least one food isolate. Exposure information was available for seven cases. All seven cases reported drinking liquid egg white, and five specifically reported drinking the outbreak-associated brand. Food chain traceback investigations established that the product was heat treated and bottled in France, where a bottling machine disinfection issue was subsequently identified.

Conclusions:

This outbreak was caused by nationally distributed Salmonella contaminated batches of a liquid egg white product sold as a shelf-stable product. Routine whole genome sequencing enabled the ascertainment of widely geographically distributed cases and provided clear evidence that the rapid recall of product had been an effective control measure.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella, Whole Genome Sequencing, Infectious Disease Outbreak, Phylogeny

ABSTRACT ID: 506

PRESENTED BY: Lara Utsi / lara.utsi@phe.gov.uk

Parallel Session 19
DAY 3, Friday, 29. November 2019
14:30-15:30

Vaccine-preventable diseases: surveillance (3)

Moderator

Benedetto Simone

Abstracts

19.1. Anti-PT IgA and anti-ACT IgG are valuable tools for the serodiagnosis of Bordetella pertussis infection in recently vaccinated subjects

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Background:

Measuring IgG antibody titers to pertussis toxin (PT) is the most specific and sensitive method to serodiagnose a Bordetella pertussis infection. However, this does not distinguish infection from recent vaccination, as anti-PT IgG are stimulated by the acellular pertussis vaccine. We aim to identify additional B. pertussis-specific serological markers that can discriminate between infection and recent vaccination, to improve pertussis serodiagnosis in symptomatic subjects with a recent vaccination history and elevated anti-PT IgG titers or for use in seroprevalence studies.

Methods:

The utility of measuring IgA directed to vaccine antigen PT, and IgG directed to non-vaccine antigens (Fim2/3, LPS, ACT and CatACT) was evaluated comparing subjects groups with known vaccination and infection status, aged 10-89 years (n=390). Serological responses were monitored using commercial ELISAs (PT, Fim2/3, LPS, ACT) or an in house immunoblot assay (CatACT). Comparing pertussis-infected symptomatic subjects (n=140) with recently vaccinated, non- infected subjects (n=100), revealed the optimal cut-off, accuracy, sensitivity and specificity for each single parameter.

Results:

For diagnosis of pertussis infection, the measurement of anti-PT IgA (cut-off 15 IU/mL) and anti-ACT IgG (cut-off 15 U/mL) resulted in accuracies of 95% and 87.5%, sensitivities of 92.9% and 83.6% and specificities of 98% and 93%, respectively. Screening using anti-PT IgA testing followed by confirmation with anti-ACT IgG testing increased the specificity to 100% (95% CI 96.3-100%) at the cost of sensitivity (77.1%, 95% CI 69.5-83.3%).

Conclusions:

The use of both Anti-PT IgA and anti-ACT IgG markers can discriminate between recent vaccination and infection. When such distinction is needed, the use of these markers can be recommended in the context of both routine pertussis serodiagnostics and pertussis seroprevalence studies.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: pertussis, bordetella, immunology, serology, antigen, vaccine, diagnosis, woophing cough

ABSTRACT ID: 279

PRESENTED BY: Lorenzo Subissi / lorenzo.subissi@sciensano.be

19.2. Incidence and severity of pertussis hospitalisations in infants aged less than one year, results of PERTINENT sentinel system, 2016-2018

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Background:

Pertussis surveillance systems are heterogenous across Europe. Since 2015, ECDC has commissioned PERTINENT, a hospital-based active pertussis surveillance system of infants in six EU/EEA countries (37 hospitals, 7 sites). We aimed to measure pertussis incidence and describe its severity.

Methods:

We developed a generic protocol and laboratory guidelines. We organised site-visits and a laboratory workshop to ensure harmonisation of practices and allow pooling of sites' data. Cases were hospitalised infants testing positive for B.pertussis by PCR or culture. Very severe cases were deceased patients or those in need of ECMO or ICU admission. Sites collected demographic, clinical, laboratory data, vaccination status, risk/protective factors. We estimated annual incidences by site by dividing the number of cases by the estimated catchment population.

Results:

From December 2015 to December 2018, we identified 442 B.pertussis cases including one B.parapertussis co-infection. The median age, birthweight and gestational age were 2.5 months, 3290g and 39 weeks, respectively. The highest number of reported cases was in August 2016 (N=29) and June 2017 (N=28). Fifteen cases (3%) had atypical presentation either with cough or cyanosis only or without pertussis-like symptoms. Seventy-five cases (24%) were very severe including five deceased infants too young to be vaccinated. The median age was 1.4 months in very severe cases and 2.8 months in less severe cases ($p<0.001$). Six of seven sites had lower hospitalisation incidences in 2018 (range 0-84.5/100,000 infants) than in 2017 (range 10.3-207.4/100,000 infants).

Conclusions:

Our results suggest a decrease of incidence in all but one site. Active surveillance allowed the identification of atypical and very severe cases. Enhanced surveillance of hospitalised pertussis in Europe is essential to measure the burden of disease and monitor its evolving epidemiology.

Subject: Surveillance

Keywords: Whooping cough,Public Health Surveillance,Burden of Disease

ABSTRACT ID: 120

PRESENTED BY: Sabrina Bacci / l.merdrignac@epiconcept.fr

Parallel Session Abstracts

19.3. Impact of vaccination programmes with 10 and 13-valent pneumococcal conjugate vaccines on invasive pneumococcal disease incidence by age group in SpIDnet/I-MOVE+ countries

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Background:

SpIDnet/I-MOVE+ projects conduct enhanced population-based invasive pneumococcal disease (IPD) surveillance in 10 European countries: six use 13-valent pneumococcal conjugate vaccine (PCV13), two the 10-valent (PCV10) and two use both vaccines. We measured the impact of pneumococcal vaccines on IPD incidence.

Methods:

We calculated country-specific IPD incidence rate ratios (IRR) by age group and serotype category (all types, PCV7, PCV10nonPCV7, PCV13nonPCV10, nonPCV13) comparing IPD incidence in the seventh PCV10/13 year (2017) to the average incidence in the PCV7 period. We computed pooled IRR using random-effects meta-analysis, and impact as (1-IRR)*100.

Results:

In 2017, participating sites reported 884 IPD cases in children <5 years of age, 6333 in 5-64 year-olds and 9319 in those aged 65+ years. The incidence of IPD caused by PCV7, PCV10nonPCV7, PCV13nonPCV10 decreased by 90%, 97%, 50%, respectively in those <5 years of age, by 85%, 91%, 25%, respectively in 5-64 year-olds and by 83%, 92%, 5%, respectively in 65+ year-olds. In sites using PCV13 only, PCV13nonPCV10 IPD incidence decreased by 22% in 65+ year-olds. NonPCV13 IPD incidence increased by 92% in those aged <5 years, 84% in 5-64 year-olds and 89% in those aged 65+ year-olds. All type IPD incidence decreased by 47% in those aged <5 years, 23% in 5-64 year-olds, and 6% in those aged 65+ years

Conclusions:

A substantial decrease in the IPD incidence caused by PCV7 and PCV10nonPCV7 serotypes and a marked increase in nonPCV13 IPD incidence were consistent across age groups. PCV13nonPCV10 and overall IPD incidence decline were higher in children than the other age groups. Enhanced surveillance in all age groups is important for monitoring the effect of childhood pneumococcal vaccination programmes before the introduction of extended PCV formulations.

Subject: Surveillance

Keywords: Invasive pneumococcal disease, pneumococcal conjugate vaccine, surveillance, Streptococcus pneumoniae

ABSTRACT ID: 299

PRESENTED BY: Camelia Savulescu / c.savulescu@epiconcept.fr

Parallel Session 20
DAY 3, Friday, 29. November 2019
14:30-15:30

Food- and waterborne diseases and zoonoses: surveillance

Moderator

Vicky Lefevre

Abstracts

20.1. Prevalence and correlates of Q fever among abattoir workers in central South Africa: a serological study

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Background:

Q fever (QF) is a ubiquitous zoonotic disease, originating from livestock, affecting persons working with animals/animal products. Infection usually occurs following inhalation of the bacterial spore-like forms. Severity of clinical disease varies, but large community outbreaks and serious long-term complications occur. Prevalence in abattoir workers, who are a sentinel for QF, is unknown in South Africa. Our objectives were to estimate QF seroprevalence and correlates in sampled abattoir workers in the Free State and Northern Cape region.

Methods:

This study analysed secondary data from a cross-sectional zoonotic disease survey of abattoir workers in 2018. Previous exposure was determined using an enzyme-linked immunosorbent assay for IgG antibodies against C. burnetii phase II antigen. Logistic regression methods were employed to estimate QF seroprevalence and correlates of seropositivity in this sample.

Results:

We sampled 382 abattoir workers from 16 abattoir facilities. Abattoir seroprevalence ranged from 8 to 62% and was 30% overall (95% confidence interval [25-35%]). Logistic regression models suggest that age (adjusted odds ratio (AOR) 0.97 [0.95-0.99]), livestock ownership (AOR 0.3 [0.1-0.6]) and longer establishment of abattoirs (AOR 0.6 [0.4-0.9]) were protective against previous QF exposure. In contrast, for every increase in the level of contact with carcasses/meat products, the odds of exposure doubled (AOR 2.1 [1.2-3.8]).

Conclusions:

We recommend increased precautions for personnel spending extended periods in contact with carcasses/meat products and QF health education at abattoirs, prioritising newly established facilities. Perhaps early exposure to C. burnetii protects people in this group but cohort studies are needed to better elucidate risk factors. Vaccination of people and/or animals, as done in other countries, could be considered but randomised controlled trials in South Africa would be needed to establish vaccine efficacy.

Subject: Burden of disease

Keywords: Q fever, Coxiella burnetii, abattoirs, occupational disease, prevalence

ABSTRACT ID: 134

PRESENTED BY: Liesl De Boni / liesl.deboni@gmail.com

20.2. Hepatitis A seroprevalence estimates in Belgium

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Background:

The incidence of hepatitis A virus (HAV) infection in Belgium has decreased over time due to improved living and hygienic conditions. Since 1992 a vaccine is available and is recommended for high-risk groups such as men who have sex with men, patients with liver diseases and people travelling to endemic countries. There is limited, outdated, and no nation-wide knowledge on the current immunization status in Belgium. We therefore estimated the seroprevalence of HAV immunoglobulin G (IgG) antibodies in the general Belgian population.

Methods:

The study was conducted using residual samples collected in the three Belgian regions, in 2013-2015. Anti-HAV IgG levels were measured to determine whether the patient had protective antibodies against the virus. Results were adjusted for cluster sampling and standardized for age, sex and district population according to the Belgian population structure in 2013. Prevalence and 95% confidence intervals (CI) were calculated.

Results:

Twenty-eight laboratories from 42/43 national districts, with specimens from 3,164 patients, were included. The adjusted standardized 2013-2015 seroprevalence of HAV in Belgium was 49.5%, (CI 45.3-53.7%), slightly but not significantly higher in women than men (52.0% vs. 46.9%), and significantly higher in the Brussels region when compared to Flanders and Wallonia (64.5% vs 46.7% and 49.7% respectively, p=0.02). We found an age-dependent trend with 2 patterns: a mean 20% increase per 10-years age group up to age 40, and a mean 10% increase above age 40.

Conclusions:

This study presents updated overall and age-specific estimates of HAV seroprevalence in Belgium and by region. Comparison with a 1993 study conducted in Flanders revealed a 10% decrease in seroprevalence in that region. These results provide essential information to inform future vaccination strategies in Belgium.

Subject: Surveillance

Keywords: Hepatitis A, Seroprevalence, Belgium

ABSTRACT ID: 211

PRESENTED BY: Ana Hoxha / ana.hoxha@sciensano.be

20.3. Effects of changes in diagnostics and notification criteria on Shiga toxin-producing Escherichia coli surveillance in the Netherlands, 1999-2018

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Background:

Surveillance is an important tool for monitoring incidence, occurrence of outbreaks and trends. Especially trends are sensitive to changes in diagnostics and notification criteria. In the Netherlands, the STEC surveillance was expanded in 2007 from O157 to all STEC, concurrent with the introduction of PCR techniques besides the existing cultures. In July 2016, the notification criteria were narrowed to acute, more severe, STEC infections. The impact of these changes were investigated.

Methods:

Laboratories and physicians have to report STEC infections to their regional public health service, who notify to the national level. Laboratories can send STEC isolates to the RIVM-laboratory, where the isolates are tested for the presence of virulence genes, including shigatoxin genes, and O- an H-typing is performed. The effect of the changes on the STEC notifications were examined over the years 1999-2018.

Results:

Per year, 32-57 STEC O157 cases were notified over 1999-2006. Extension of the surveillance to all STEC in 2007 lead to a large increase in reported STEC infections with a peak of 1175 reports in 2013. In 40% of the cases the infection was acute, in 18% there was no clear recent onset and in 42% this was unknown. After narrowing the surveillance to acute infections, 392-488 cases were notified in 2017-2018 with less than 5% of the reports without basic data.

Conclusions:

The introduction of new diagnostic techniques led to the possibility of surveilling all STEC infections. Nevertheless, it also polluted the surveillance with cases who are hardly relevant for the public health. The focus on acute, more severe, infections improved the relevance and accuracy of the STEC surveillance, although outbreaks with mainly mild infections could be missed.

Subject: Surveillance

Keywords: Shiga-Toxigenic Escherichia coli, epidemiology, public health, incidence, trends

ABSTRACT ID: 490

PRESENTED BY: Ingrid Friesema / ingrid.friesema@rivm.nl

Parallel Session 21
DAY 3, Friday, 29. November 2019
14:30-15:30

Late breakers

Moderator

Alain Moren

Abstracts

21.1. Resurgence of an international Hepatitis A outbreak linked to a strain from imported frozen strawberries, Germany, 2018/2019

Claudia Ruscher [1]

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Background:

Following the investigation and control of foodborne Hepatitis A outbreaks linked to frozen strawberries in Sweden and Austria in 2018, Germany is currently affected by an ongoing resurgence of the same strain (EPIS UI-487)). The outbreak is characterized by two waves starting in late 2018 and July 2019. We initiated epidemiologic investigations, including case-control studies (ccs), to investigate an association with food-items containing frozen strawberries.

Methods:

An outbreak case was a person with laboratory-confirmed, symptomatic hepatitis A, notified between 09/2018 and 08/2019 and a sequence identical to the outbreak strain. Case-control studies were conducted during both waves using as controls employees of the Robert Koch-Institute (ccs1) and the SOHSA (ccs2).

Results :

Overall, 56 cases were ascertained, 30 in the first wave and 26 in the second. In univariable logistic regression, cases in ccs1 (n=21) more frequently reported consumption of frozen strawberry cake (n=14; OR 43, 95% CI 9.1-221), especially from brand A (n=12; OR 32, 95% CI 6.9-163) than controls. Likewise, cases in ccs2 (n=11) more frequently reported consumption of frozen cake (n=8; OR 16; 95%CI 2.3-125) and frozen strawberry cake (n=5; OR 6.9; 95%CI 0.97- 54.6) than controls. Ongoing trace back investigations revealed that the producer involved in the previous outbreaks in Sweden and Austria had received frozen strawberries originating from Egypt via a wholesaler that also delivered frozen strawberries to manufacturer of brand A.

Conclusions:

Epidemiological investigations provide consistent and strong evidence for frozen strawberry cake from brand A as a vehicle in this ongoing outbreak and suggest a connection to previous outbreaks in Sweden and Austria. Further international trace back and food investigations, triggered by epidemiologic evidence are urgently needed to ultimately control the outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Hepatitis A, Germany , Foodborne diseases, Genotype, Disease outbreaks

ABSTRACT ID: 876

PRESENTED BY: Claudia Ruscher / claudia.ruscher@lageso.berlin.de

21.2. Large outbreak of Campylobacter jejuni infections following contamination of municipal water supply, June 2019, Norway

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Background:

On 6 June 2019, the municipal health officer and the Norwegian Institute of Public Health were notified of ‹ 50 cases of gastroenteritis in Municipality A. Due to the acute onset and geographical distribution of cases, we suspected drinking water contamination. We investigated the outbreak to confirm the source and to ensure that appropriate control measures were implemented.

Methods:

A case was defined as a person in a household served by Water Supply System A (WSS-A) with gastroenteritis with duration › 24 hours from 1-19 June 2019. We conducted a survey of illness in childcare centers to rapidly confirm affected areas, and an SMS-based cohort study of all residents served by WSS-A to calculate attack rates by water supply zone. We conducted inspections and collected samples from WSS-A. We performed whole genome sequencing (WGS) on human and environmental isolates.

Results:

We estimated that over 2000 people became ill from 6-11 June 2019. The attack rate was highest in childcare centers supplied with drinking water from Reservoir X. Respondents from 2,526 households representing 7,652 people participated in the cohort study. The attack rate was 42-55% in water supply zones supplied by Reservoir X compared to ≤ 20% in other zones (RR = 4.6). Campylobacter jejuni isolated from cases (n=24) and water samples (n=4) were identical by WGS. Environmental contamination through cracks in Reservoir X most likely occurred during heavy rainfall following an extended dry period.

Conclusions:

Boil advisories were sent out and Reservoir X was removed from service after which no subsequent cases were reported. This outbreak is a reminder that water distribution networks are susceptible to contamination, highlighting that outdated reservoirs should be continuously reassessed.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Disease Outbreaks; Campylobacter; Water Supply; Drinking; Norway

ABSTRACT ID: 877

PRESENTED BY: Susanne Hyllestad / susanne.hyllestad@fhi.no

21.3. Reoccurring zoonotic cryptosporidiosis outbreaks in veterinary students in Denmark, a combined epidemiological and microbiological study during the full academic year 2018- 2019

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Background:

In several countries, including Denmark, Cryptosporidium parvum outbreaks are common in veterinary students in relation to handling calves. In September 2018, after an outbreak related to fetotomy training, we initiated a one-year cohort study to identify risk factors and provide guidance for preventing these outbreaks.

Methods:

The cohort included all veterinary students participating in a fetotomy exercise between September 2018 and June 2019 at University of Copenhagen. The students completed an online questionnaire about symptoms and potential risk actions during the exercise. Cases were those reporting gastrointestinal symptoms within incubation period, 2-12 days. Risk ratios (RR) with 95% confidence intervals (CI) were calculated. Real-time PCR was used to detect C. parvum DNA in stool samples from students and to quantify faecal parasite load in all calves used. Positive samples were genotyped.

Results:

119 students, divided in 16 groups, attended the exercise and 97/119(81.5%) completed the questionnaire. Eleven cases (9.2%) were identified, of which 5/11(45%) were laboratory-confirmed. Cases clustered in two outbreaks, with attack rates 4/10 in September and 7/9 in January. No cases reported other contact with calves. Main risk factors identified were visible faecal contamination on clothes (RR:11.4; 95%CI:1.5-85.6), experiencing problems with personal protective equipment (PPE) (RR:4.6; 95%CI:1.1-20.2), and not washing hands with soap (RR:5.74; 95%CI:1.6-20.5). C. parvum was detected in 28/49(57%) calves, and the quantitative results showed a dose-response relationship: presence of a calf with high faecal parasite load in the training room was a specific risk for the students (RR:18.6; 95%CI:2.5-138.4). Type IIaA15G2R1 was detected in all typed samples, from both students and calves.

Conclusions:

To prevent zoonotic cryptosporidiosis outbreaks among veterinary students, we recommend 1)improving PPE use, 2)increasing adherence to hygiene, 3)using non-infected calves.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Outbreak, Microbiology, Zoonosis, Occupational hazard, One Health

ABSTRACT ID: 851

PRESENTED BY: Daniel Thomas-Lopez / dthlopez@hotmail.com

Poster Abstracts

This abstract book has been produced using author's 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

MODERATED POSTER SESSION A
DAY 1, Wednesday 27. November 2019
15:40-16:40

Track 1: Antimicrobial resistance

Moderator:
Outi Lyytikäinen

Abstracts

1.1. Antimicrobial resistance in Saxony-Anhalt: data from a national surveillance system shows increase in vancomycin- resistant Enterococcus faecium, 2015-2017

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Background:

In Germany, vancomycin resistance among enterococci (VRE) as well as carbapenem-resistance has increased in the past years with differences between regions but only few analyses at state level exist for Saxony-Anhalt (ST). We aim to describe trends in antimicrobial resistance (AMR) in ST to inform local stakeholders for any need to adapt current hygiene measures.

Methods:

We extracted data from the national laboratory sentinel surveillance system for antimicrobial resistance (ARS), which includes data from five hospitals in ST during 2015-2017. For the first isolate from blood cultures per patient per year, we calculated proportions of non-susceptible isolates for selected pathogens and antibiotic groups. We calculated 95% confidence intervals (95% CI) and compared proportions over time using the Chi-square test for trend.

Results:

We included 4,606 isolates. Non-susceptibility to carbapenems was found in 0/834 Escherichia (E.) coli, 0/163 Klebsiella (K.) pneumoniae and 18/93 (19%, 95%CI: 12-30) Pseudomonas aeruginosa isolates and to 3rd generation cephalosporins for E. coli in 91/834 (11%, 95%CI: 8.7-14) and for K. pneumoniae in 22/163 (14%, 95%CI: 8.5-21) isolates with no significant trend for any antibiotic group over time. The overall proportion for MRSA among S. aureus was 34/547 (6.2%, 95%CI: 3.9-9.7) with also no trend. Non-susceptible isolates of VRE significantly increased from 0 /49 to 6/44(14%) (95%CI: 5-32) (p-value for trend <0.001).

Conclusions:

The regional AMR situation corresponds with national data showing an increase in VRE, while carbapenem non- susceptibility remained low. Therefore, particularly, VRE should be monitored closely, adherence to hygienic measures should be reinforced and antibiotic stewardship programmes implemented to avoid further spread of VRE at state and national level.

Subject: Surveillance

Keywords: surveillance, antimicrobial resistance, vancomycin-resistant Enterococcus faecium, epidemiology

ABSTRACT ID: 500

PRESENTED BY: Inessa Markus / markusi@rki.de

Poster Abstracts

1.3. Anthropogenic pollution and impact on detection of carbapenemase-producing Enterobacterales in recreational waters

Brigid Hooban [1]

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Background:

It is increasingly recognised that the environment plays an important role in the transmission and persistence of antimicrobial resistant bacteria (ARB). The aim of this study was to assess the impact of anthropogenic pollution on the presence of carbapenemase-producing Enterobacterales (CPE) in recreational waters.

Methods:

Geographical information systems were used to identify sampling locations by generating maps combining sources of anthropogenic pollution and aquatic transmission routes. Sampling points included polluted seawater (3 urban, 5 rural), rivers (3 urban, 2 rural) and lakes (2 rural). Samples were also collected at unpolluted locations (1 urban river, 1 urban and 2 rural seawaters). Pollution sources included raw sewage discharges, storm water overflows (SWOs) and waste water treatment plant (WWTP) discharges. Samples were filtered using the CapE method. CHROMagar mSuperCARBA™ was used for the detection of carbapenem resistant Enterobacterales (CRE). Bacterial species were identified using MALDI-TOF. Disk diffusion testing in accordance with EUCAST criteria was performed on CRE isolates. Confirmed CREs were screened for carbapenemase genes by real-time PCR: bla$_{VIM}$, bla$_{IMP}$, bla$_{OXA-48}$, bla$_{NDM-1}$, and bla$_{KPC}$.

Results:

CPE detection was confined to polluted areas. An OXA-48-producing Klebsiella pneumoniae was detected in 1 urban seawater and 1 urban river, both receiving WWTP discharges and SWOs. An OXA-48-producing Escherichia coli was detected in an urban seawater near a WWTP. A NDM-1-producing Escherichia coli was detected in a rural lake receiving discharges from a WWTP and SWO.

Conclusions:

These findings indicate that human activity has a major impact on detection of CPE in waters. Increased surveillance of ARB in the environment is warranted to better understand and identify measures to mitigate transmission and persistence of antimicrobial resistance.

Subject: Microbiology

Keywords: Carbapenemase, aquatic environments, seawater, freshwater.

ABSTRACT ID: 652

PRESENTED BY: Brigid Hooban / b.hooban1@nuigalway.ie

1.4. Carbapenem non-susceptibility is widespread amongst enterobacteriaceae and Acinetobacter spp. in Baden- Württemberg, Germany: results from the first 2.5 years of national surveillance, May 2016 to 2018

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Background:

Carbapenem-resistance has been increasing EU-wide, posing a serious public health threat to many countries. We analysed surveillance data of carbapenem non-susceptible enterobacteriaceae (CNE) and Acinetobacter spp. (CNA) for Baden-Württemberg, Germany, for the first time to assess public health relevance and guide prevention strategies.

Methods:

Laboratory notification of cases of CNE and CNA infection or colonisation was introduced to the national surveillance system in May 2016. We used descriptive statistics to calculate incidences for Baden-Württemberg, Germany.

Results:

Between May 2016 and December 2018, 657 CNE (median age 65 years [0-94 years]; 58% male) and 134 CNA cases (median age 68 years [0-88 years]; 65% male) were notified. Annual number of CNE infections and colonisations increased from 62/137 in 2017 to 105/224 in 2018 ($p<0.001$). Outbreaks accounted for 3% and 2% of cases, respectively. The notified incidences of CNA (3.2/100,000) and CNE (22/100,000) were highest in patients ≥70 years. Infections accounted for 32% of CNE and for 37% of CNA cases; 4 CNE- (2%) and 6 CNA-infections (16%) were fatal. CNE and CNA were notified in 93% and 82% of districts; incidences [0.6-24/100,000 and 0.4-4.9/100,000] varied considerably between districts. CPE sub-species were determined in 95%; Klebsiella pneumoniae (39%) and Escherichia coli (22%) were the most frequent. Carbapenemase-gene(s) were identified for 31% of CNE and CNA; most frequently OXA-48 (37%) with CNE and OXA-23 (66%) with CNA.

Conclusions:

Our analysis of the surveillance data highlights the public health relevance of carbapenem non- susceptibility in Southwest Germany. Hygiene measures and antibiotic stewardship programmes must be strengthened. Additional information on screening practices in hospitals and risk factors are essential for further understanding the geographic variation and the increase of CNE notifications in 2018.

Subject: Surveillance

Keywords: antimicrobial resistance, carbapenemases, carbapenem-resistance, surveillance

Poster Abstracts

ABSTRACT ID: 532

PRESENTED BY: Maylin Meincke / maylin.meincke@rps.bwl.de

1.5. The prevalence and risk factors for rectal carriage of antimicrobial resistance in Dutch and Flemish children attending day care centres: a point prevalence study (i-4-1- Health project)

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[14] The i-4-1-Health Study Group

Background:
Microorganisms (MO) can easily be transmitted between children attending day care centres (DCCs). Children are at higher risk for infections and are therefore more likely to receive antimicrobial treatment, which might increase the risk for carrying resistant MO. However, little is known about the prevalence of and risk factors for rectal carriage of resistant MO in children. We aimed to assess the prevalence of antimicrobial resistance (AMR) and antibiotic use, and risk factors for AMR carrier status among DCCs children in the Dutch-Belgian cross-border region.
Methods:
DCCs from the Dutch-Belgian cross-border region were included. Stool samples (Fecal Swab, Copan Diagnostics) were selectively cultured (ChromID ESBL/CARBA/OXA-48/VRE, bioMérieux; in-house McC ciprofloxacin) after non-selective pre-enrichment (TSB, Copan Diagnostics) to identify vancomycin-resistant enterococci (VRE), extended-spectrum beta- lactamase producing Enterobacteriaceae (ESBL-E), ciprofloxacin-resistant Enterobacteriaceae (CipR-E) and carbapenemase-producing Enterobacteriaceae (CPE). Risk factors for AMR carriage were assessed using a questionnaire. We calculated AMR prevalences and conducted multivariate logistic regressions to assess risk factors.
Results:
46 DCCs were included comprising 945 children. Preliminary findings show ESBL-E prevalence of 6.0% (n=30) and 15.8% (n=71), and CipR-E prevalence of 7.6% (n=38) and 17.4% (n=78) among Dutch and Flemish children respectively. No VRE or CPE cases were found. Antibiotic use (<6 months) and hospital admissions (<6 months) were significantly higher in Flanders than in the Netherlands. No animal contact was the only predictor for ESBL-E (OR:1.67; 95%CI: 1.04-2.67) and living in Flanders the only predictor for CipR-E (OR: 2.53; 95%CI: 1.38 – 4.64).
Conclusions:
Rectal carriage of ESBL-E and CipR-E prevalence is higher for Flemish than for Dutch DCCs children. This study could not find a relationship between antibiotic use within the past 6 months and the AMR carrier status.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Child Day Care Centres, Infection Control, Drug Resistance Bacterial, Risk Factors, Netherlands, Belgium

ABSTRACT ID: 608

PRESENTED BY: Sara Dequeker / sara.dequeker@sciensano.be

1.6. The impact of medical training on the level of antibiotic knowledge and behaviour of medical nurses students

Cosmin Dumitru [1]

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Background:
Attitudes and knowledge regarding the use of antimicrobials in the general population can be influenced by healthcare workers, like medical nurses. In order to offer the proper support for education and information campaigns, we should first have a better understanding of the information and practices of the medical nurses and their attitudes regarding antimicrobial use.
Methods:
In 2018 we designed a cross-sectional study including students from the Faculty of Medical Nurses from first to last year of study. The knowledge and attitudes regarding antimicrobial use were evaluated using a questionnaire, divided in four sections, general data about the participant, antibiotic knowledge, antimicrobial resistance knowledge and antibiotic usage.
Results:
The study included 300 participants with a median age of 21 years-old. 48.57% of first-year and 63.33% of last-year students specified that antibiotics work against bacteria. Regarding the use of antimicrobials, 68.57% of the first-year students take antibiotics without prescription, while in the last-year the percent decreases to 43.33%. A percentage 58.57% of the first-year students think antibiotics are efficient in treating cold or flu, while only 35% of the final-year students responded affirmative to the same question.
Conclusions:
Although the knowledge of the students improves during their education and training, they do not apply them accordingly and continue to use antibiotics without medical prescription with more than a third of them thinking that antibiotics are appropriate in treating cold or flu. Medical nurses play an important role in giving antimicrobial information to patients making it very important to take measures to improve their knowledge regarding the subject and the way they apply it.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: medical nurses, antibiotic use, antibiotic knowledge, medical training, attitude of health personnel

ABSTRACT ID: 773

PRESENTED BY: Cosmin Dumitru / dumitrucosmingeorge23@gmail.com

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Poster Abstracts

Track 2: Emerging and vector- borne diseases, and international health (1)

Moderator:

Barbara Schimmer

Abstracts

2.1. Infectious disease screening of refugees and asylum seekers arriving to Malta (2015-2019), the shifting paradigm of a humanitarian crisis in the EU, (LATE BREAKER)

Raquel Medialdea-Carrera [1]

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Background:

Increased arrivals of asylum seekers to the EU has prompted the implementation of public health screening for detection of infectious diseases among newly arrived humanitarian migrants. We aimed to document demographic characteristics and prevalence of infectious diseases in asylum seekers arriving in Malta and understand the challenges among healthcare workers to delivery.

Methods:

We describe a case series including all asylum seekers arriving in Malta from January 2015 to July 2019. We conducted face-to-face interviews and examinations, offered Tuberculosis screening and provided linkage to care when needed. Qualitative semi-structured interviews were conducted to examine the challenges faced by healthcare workers conducting the screening(n=8).

Results:

A total of 9,411 asylum seekers arrived in Malta from 78 different countries of origin including 7,543 (80%) male and 1,805 (20%) minors(<18 years). At arrival, 8% of females were pregnant. Chest-X-Ray abnormalities were reported in 3.6% of arrivals with 77 (0.8%) diagnosed with active Tuberculosis. During Jan-July 2019, 10% of migrants presented with symptoms suggestive of infectious disease including fever, cough, vomit and/or diarrhea, 13% had scabies and 1.8% required further secondary referral such as dentistry or ophthalmology. Healthcare workers reported multiple challenges including diverse cultural and language differences, limited institutional infrastructure capacity, insufficient human resources and specialist training and contradiction between professional ethics and local policy.

Conclusions :

The screening contributed to early detection of infectious diseases among asylum seekers. Healthcare workers involved face multiple challenges. We recommend ensuring the support of cultural mediators, providing adequate training and improving the infrastructures in migrant reception centers. This data supports the need for asylum seekers to have access to a comprehensive post-arrival medical assessment to safeguard the health of both individual refugees and the community.

Subject: International health and migration

Keywords: Migrants Health, Refugees, Screening, Tuberculosis, Scabies, Healthcare workers

ABSTRACT ID: 834

PRESENTED BY: Raquel Medialdea-Carrera /

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2.2. An outbreak of scabies in a nursing home: the potential use of PCR on bed linens for diagnosis

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[8] Public Health Service of the region of Rotterdam-Rijnmond (GGD Rotterdam-Rijnmond), Rotterdam, the Netherlands

Background:

In October 2018, a public health service in The Hague was notified of a scabies outbreak by the management of a nursing home. This was the fifth outbreak since March 2015. In this context of repetitive outbreaks, we described the extent of this outbreak and investigated risk factors for scabies.

Methods:

For a retrospective cohort study among residents and staff, we obtained data on demographics, symptoms and predisposing factors (contacts with possible sources of scabies inside/outside the nursing home) through medical records for residents and questionnaires for staff. We defined cases as: possible (reported symptoms), probable (scabies-like lesions) and confirmed (PCR or microscopy in skin-flakes). Experimentally for case finding, we included skin-flakes from bed-linens of possible cases.

Results:

All residents (41) and 37/44 staff were included. We identified 20 possible, four probable and six confirmed cases. The overall attack rate for probable/confirmed cases was 10/78 (13%); 8/41 (20%) among residents. Three cases were confirmed by PCR and four by microscopy.

Of these, two bed-linen specimens were PCR-positive. The attack rate was higher for staff with pre-existing skin conditions (RR 3.0;95%CI:1.9–4.9) and contacts in the family with scabies-like symptoms (RR 3.2;95%CI:1.9–5.3). Staff with physical contact with residents were less likely to develop disease (RR0.39;95%CI:0.25–0.62). No significant risk factors were found for residents.

Conclusions:

We found significant risk factors for staff, but not for residents. Due to the repetitive outbreaks staff dealing with patients might have taken more protective measures. In a scabies outbreak, we recommend to include screening staff with pre- existing skin conditions and with household members who have scabies-like symptoms. We recommend evaluating the potential of scabies-PCR on bed-linens to contribute to case finding.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: scabies, outbreak investigation

ABSTRACT ID: 442

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2.3. Epidemiological situation of visceral leishmaniasis in humans, Greece 2004-2018. Future challenges

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Background:

Visceral leishmaniasis (VL) is a parasitic disease transmitted by sandflies. Dogs are considered the main reservoir hosts in the Mediterranean basin. We describe the epidemiological situation of VL in Greece during 2004-2018 and identify risk areas/populations in order to reassess the public health priority of the disease in the country and support developing an action plan for its control.

Methods:

We extracted VL data from the mandatory notification system where a case is an individual with compatible clinical manifestations and laboratory confirmation. We calculated incidence rates by reporting year and month, region of residence, sex and age. We calculated hospitalisation rates, proportions of clinical signs/symptoms, positive diagnostic tests, immunosuppression, country of origin, travel history and dog-ownership.

Results:

Overall, 872 cases were notified with no clear trend or seasonality; mean annual incidence rate was 0.5/100,000 (range: 0.3/100,000-0.8/100,000); 0.7/100,000 in males and 0.4/100,000 in females, with the highest incidence in age-group 0-4 years (1.4/100,000). Cases were recorded in all 13 regions of Greece, with Thessaly presenting the highest mean annual incidence rate (0.7/100,000). Among cases, 763 (96.5%) were Greeks, 78 (10.7%) reported recent travel abroad, 274 (36.6%) owned a dog, and 154 (23.4%) reported underlying immunosuppression. In total, 652 (75%) cases presented persistent fever, 627 (72%) hepatosplenomegaly, and 822 (94.3%) were hospitalised. Among 872 cases, positive serology, microscopy and PCR was reported in 64.8%, 40% and 37.8%, respectively.

Conclusions:

In Greece VL is endemic and should be considered a public health priority, as it poses a considerable burden and young children are the most affected. A sustainable action plan in the context of One Health approach should be developed, including enhanced surveillance, reservoir and vector control, and health education.

Subject: Surveillance

Keywords: Leishmaniasis, Visceral, Phlebotomine sand flies, Public Health Surveillance, canine leishmaniasis

ABSTRACT ID: 121

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2.4. Population attributable fraction of stomach cancer related to Helicobacter pylori among Koreans

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Background:

Infection with Helicobacter pylori (H. pylori) has been recognized as the most significant risk factor for the incidence of stomach cancer. Stomach cancer is the most common cancer in Korea reporting 13.3% of all cancers in the year of 2016. Especially in men, stomach cancer ranks the top with 50.9 per 100,000 of age-standardised incidence rate (ASR), whereas it is ranked as the fourth with 22.0 per 100,000 of ASR in women. The objective of this study was to compare the attributable fraction of H. pylori as a risk factor in occurrence of stomach cancer, in which it tends to differ between genders.

Methods:

The population attributable fraction (PAF) was calculated as a function of the relative risk of stomach cancer associated with H. pylori infection. To estimate PAF due to H. pylori to development of stomach cancer, the prevalence of H. pylori infection was extrapolated for the year of 1990 and the pooled relative risk (RR) was obtained by conducting a meta-analysis of eleven Korean studies recently published.

Results:

The estimated prevalence of H. pylori were 83.1% for men and 75.5% for women. The RR (95% confidence interval) pooled from 11 case-control studies by random effect model was 1.72 (1.23-2.40, I2=85.7%). The PAFs due to H. pylori was calculated by using Levin's formula, and the results were 37.4% in men and 35.2% in women that was not much different.

Conclusions:

The occurrence of stomach cancer in Korean may be affected by not only H. pylori infection but also other distinctive risk factors that may differ between genders, e.g., smoking or alcohol drinking. Further studies are required to compare the PAFs due to other risk factors.

Subject: Burden of disease

Keywords: Stomach Neoplasms,Helicobacter pylori,Infection,Korea

ABSTRACT ID: 394

PRESENTED BY: Yoon Park / ypark@ncc.re.kr

2.5. Factors related to the practice of cervical cancer screening in the Joal Health District in Senegal November, 2018

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Background:

In Senegal, cervical cancer (CR) ranks first among cancers diagnosed with an incidence of 1197 cases in 2010 and a specific mortality of 66%. It can be prevented by early detection and vaccination which was introduced in October 2018 in Senegal. However, the practice of screening is weak. The objective was to study factors related to the practice of cervical cancer screening (CCS) in the Joal Health District in November, 2018.

Methods:

A cross-sectional study was conducted from a stratified cluster survey using the Schwartz formula in the district population. Data were collected during individual interviews at home with a questionnaire; data focused on CR's knowledge, attitudes, practices and provision of care. Proportions of these indicators (marital status, occupation, income and education level) and Prevalence Odds Ratio (POR) were calculated. Data were analyzed using Epi Info 7.

Results:

A total of 600 women responded. Median age of women was 41 years (35-65 years). Practice of screening was 28.3%. The study showed that the practice of screening was higher among school-going women (64.12%), POR [1.76 (CI: 1.22-2.55)] p = 0.002; married women did more testing (91.76%), POR [1.97 (CI: 1.07-3.63)] p = 0.02; it was higher among women with income-generating activities (33.82), POR [1.51(CI: 1.04-2.18)] p = 0.02.Women with known risk factors for cervical cancer were 6.27 times more likely to be screened. The probability of being tested was 7.25 times higher when women knew where to go for screening.

Conclusions:

Education level, socioeconomic status, knowledge of risk factors, and provision of care could influence the practice of CCS. We recommend networking a mass information, to make screening services available and training Health workers in CCS.

Subject: Burden of disease

Keywords: Cervical cancer, Diagnosis, Screening, Senegal

ABSTRACT ID: 780

PRESENTED BY: Ibou GUEYE / gueyeibou@hotmail.com

2.6. Shiga toxin–producing Escherichia coli (STEC) O55:H7: a severe infection with an unknown source, England 2014-2018

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Background:

In 2014, STEC O55:H7 first emerged in England, with cases typified by severe morbidity. We describe STEC O55:H7 cases, compare clinical characteristics with cases of STEC O157, and summarise findings from outbreak investigations to improve understanding of this emergent pathogen.

Methods:

We compared demographic, clinical and exposure data from questionnaires from STEC O55:H7 cases with STEC O157 cases (STEC culture or serology positive) reported to national surveillance between 2014-2018 in a case-case study, calculating odds ratios (OR) and 95% confidence intervals (CI). Investigations, including case finding, whole genome sequencing (WGS), and environmental and animal sampling, were reviewed.

Results:

We included 44 STEC O55:H7 and 3,310 STEC O157 cases. The median age of STEC O55:H7 cases was 5 years (range 6 months–69 years) versus 24 years for O157 cases (1 month–99 years). Compared to STEC O157 cases, O55:H7 cases were just as likely to have bloody diarrhoea (OR:1.1, CI:0.6-2.0), but more likely be hospitalised (OR:4.1, CI:2.1–8.2), have haemolytic ureamic syndrome (OR:28.8, CI:14.7–56.1), to die (OR:22.5, CI:2.2–122.2) and to be linked to an outbreak (OR:96.0, CI: 24.8–819.6).

Forty-two (93%) STEC O55:H7 cases were within a WGS 10 single nucleotide polymorphism linkage cluster. STEC O55:H7 cases were clustered seasonally (May-November), and spatially (five geographic locations). Primary cases reported exposures suggesting a zoonotic or environmental reservoir and the only non-human STEC O55:H7 positive specimen was isolated from cat faeces. Extended screening of 4200 faecal specimens from bloody diarrhoea cases identified one additional case.

Conclusions:

In England, STEC O55:H7 has emerged as a highly pathogenic clonal group, with tight spatio-temporal clustering. We recommend enhanced epidemiological, microbiological and environmental investigations for newly emerging, severe, non-O157 STEC clusters.

Poster Abstracts

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Non-O157 STEC, Field Epidemiology, Outbreak

ABSTRACT ID: 678

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Track 3: Food- and waterborne diseases and zoonoses (1): outbreaks (I)

Moderator:

Steen Ethelberg

Abstracts

3.1. Outbreak of STEC O26 paediatric HUS cases associated with the consumption of soft raw cow's milk cheeses, France, March-May 2019

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Background:

From 25 March-27 April 2019, an excess of paediatric haemolytic uraemic syndrome (HUS) cases (19 cases, 13 confirmed STEC O26) was notified to Santé publique France, versus 5-10 over the same period historically. Investigations aimed to identify a common exposure and guide control measures.

Methods:

The outbreak period was defined from 1 March-12 May. Confirmed cases had infection with STEC O26 belonging to the outbreak cluster defined by whole genome sequencing. Possible cases were pediatric HUS with no microbiological confirmation, but an epidemiological link to the incriminated food source. Case caretakers were interviewed using a trawling questionnaire. Stool samples and isolates were sent to the French National Reference Center for strain characterization and phylogenetic analysis (cgMSLT and SNP). Traceback investigations were conducted using supermarket loyalty cards.

Results:

We identified 19 outbreak cases (18 confirmed, one possible). 17 cases had HUS. Median age was 22 months, 53% were female. Symptom onset was 31 March-12 May. Eight cases had neurological complications. Caretakers for 17 cases reported consumption of a specific soft raw cow's milk cheese. Traceback identified a common producer of these cheeses for 16 of 17 cases. All food and environmental samples from the producer were negative. The cheeses were internationally distributed, but no additional cases were reported.

Conclusions:

On 27 April, the complete production of the incriminated producer was recalled, on the basis of initial results of epidemiological and traceback investigations, while cgMLST and microbiological analysis of the cheeses were pending. This is the third HUS outbreak linked to raw milk cheese in France in the past year. Increasing awareness of the risk of consuming raw milk cheese for certain populations, notably young children, should be prioritized.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Shiga-toxin producing Escherichia coli, hemolytic and uremic syndrome, Raw milk cheese

ABSTRACT ID: 436

PRESENTED BY: Gabrielle Jones /

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3.2. Explosive foodborne outbreak of an enterotoxin-producing Staphylococcus aureus in a tourist vessel moored in Denmark 2018 with simultaneous isolation of the strain in patients and food

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Background:

On August 7, 2018, the Danish authorities were informed about an outbreak of acute gastroenteritis onboard a tourist vessel. Several ambulances transported 16 patients to three hospitals and fire department were summoned to clean up. The objective of this study was to identify the source of the outbreak and characterize the pathogen.

Methods:

Electronic questionnaires regarding illness and food consumption were sent to crewmembers and passengers. A case was defined as a person consuming dinner onboard the vessel on August 7, 2018 and subsequently developing vomiting and/or diarrhea. Remaining food items and patient stool samples were analyzed for pathogens. Isolated Staphylococcus aureus were spa typed and whole genome sequenced.

Single-nucleotide polymorphism (SNP) analysis was performed to determine relatedness of the strains.

Results:

Of the 23 answered questionnaires, fifteen reported illness with vomiting, diarrhea and nausea, with an average incubation period of 21/2 hours. Analytical epidemiology identified consumption of potato salad was significantly associated with illness. The potatoes were cooked, peeled and mixed with broth twenty-four hours prior to consumption and stored in the galley after preparation without cooling. S. aureus was found in potato salad (>1,000,000 colony forming units/g) and in two human faecal samples. The S. aureus with spa type t127 from food and human varied only with 1-2 SNP difference and carried genes for enterotoxins: sea, seb, seh and sek.

Conclusions:

The patients were infected by consumption of temperature violated potato salad on the vessel. The primary source of contamination was not found, nevertheless it highlights the importance of complying with good manufacturing practices to avoid contamination and ensure sufficient cooling to prevent excessive growth of pathogens, especially in settings where cooling facilities are limited.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: countrywide outbreak,Salmonella serovar Bareilly,PFGE,WGS

ABSTRACT ID: 466

PRESENTED BY: Susanne Schjørring / SSC@ssi.dk

3.3. Hepatitis A-outbreak in Germany linked to consumption of dates purchased in Morocco, 2018

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Background:

In April 2018, six cases of hepatitis A (HAV) with recent travel to Morocco were reported during two consecutive weeks to the Robert Koch-Institute, Germany. We investigated the outbreak to describe its extent and determine its source.

Methods:

We defined confirmed cases as individuals infected with subgenotype IB strain V18–16428, regardless of travel history; probable cases were those who travelled to Morocco after 1.3.2018 and possible cases were those who consumed food from Morocco after 1.3.2018 in Germany. We interviewed cases to identify exposures and conducted a case-control study including cases with Morocco-travel history. Controls were notified cases of campylobacter-infections who travelled to Morocco in the same time period. We estimated the association between exposure and illness using univariable logistic regression and calculating odds ratios (OR) and 95% confidence intervals (95% CI). We described reasons for travelling without prior vaccination.

Results:

We identified 39 cases (64% female, median age: 40 years, range: 8-77 years), 30 (77%) with recent travel history to Morocco and 9 without. For the case-control study we recruited 22 cases (10 confirmed) and 16 controls. Cases were more likely to have eaten dates than controls (OR 18, 95% CI 2.5-200), no other significant exposure was identified. The most frequently stated reasons for non-vaccination were unawareness of HAV-risk in Morocco (n=29 (85%)) and unawareness of an HAV-vaccine (n=10 (29%)). All 5 of the interviewed autochthonous cases, reported eating dates brought from Morocco by returning travelers.

Conclusions:

The likely cause of this HAV outbreak was consumption of dates purchased in Morocco. Existing HAV-vaccination recommendations were often unknown by unvaccinated travelers. New communication strategies for vaccination recommendations are needed. Feasibility of involving travel agencies should be explored.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: HAV, Outbreak

ABSTRACT ID: 684

PRESENTED BY: Martyna Gassowski / gassowskim@rki.de

3.4. Cracking the case: how local public health professionals unravel a foodborne norovirus outbreak in less than a week using a web-survey, Germany 2018

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Background:

On 17 December 2018, a company reported to the health authorities of Lower Saxony, in Germany, a gastroenteritis outbreak among 190 employees that attended a Christmas dinner two days before. We initiated an investigation to describe the outbreak, identify the pathogen and determine risk factors.

Methods:

In a retrospective cohort study among diners, we defined cases as diners with acute onset of diarrhoea or vomiting 6–50 hours after starting eating. We collected information from diners on demographics, disease and exposures via a web- based questionnaire sent to work email addresses, and from restaurant staff on food preparation and storage. We calculated adjusted odds ratios (aOR) with 95% confidence intervals for factors associated with illness. Faecal samples of cases and restaurant staff were tested for pathogenic bacteria and viruses. We typed Norovirus strains via sequence analysis.

Results:

From 190 diners, 111 participated (58%) and 89/111 (80%) answered within 3 days. Participants were aged 18-77 years (median 50), 58% were males. Overall, 83/111 met the case definition (attack rate 74%). Consumption of cheeses (aOR=4.2 [1.4-13]), roastbeef (aOR=4.7 [1.4-18]) and ham (aOR=5.0 [1.5-20]), and toilet use (aOR=4.9 [1.0-26]) were associated with the disease. Norovirus GII.P16-GII.4.2012 was detected from 2/4 cases, 1/3 asymptomatic and 5/6 symptomatic staff members (disease onset after dinner). Food served was mostly ready-to-eat; all staff participated in the service. Control measures comprised exclusion of norovirus-positive restaurant staff from work and disinfection of the restaurant kitchen.

Conclusions:

This common source norovirus outbreak was likely caused by person-to-food-to-person transmission. Guests and staff should comply with hygiene recommendations; furthermore, symptomatic food handlers must adhere to work exclusion rules. Using an online survey tool allowed to timely and efficiently resolve the outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Retrospective cohort study, Norovirus, outbreak, food-borne infection, epidemiology, acute gastrointestinal disease

ABSTRACT ID: 270

PRESENTED BY: Delphine Perriat / delphine.perriat@gmail.com

3.5. Investigation of a recurring Norovirus outbreak on a cruise ship, Malta, August-September 2018

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Background:

Norovirus is highly contagious and often responsible for protracted outbreaks in closed settings such as cruise ships; rapid response and control measures are fundamental to stop them. In September 2018, the report of a suspected norovirus outbreak on a cruise ship prompted an investigation to control the outbreak.

Methods:

Food, water and surface samples as well as stool samples from passengers and staff were tested for norovirus and other enteric pathogens by real time quantitative PCR (RT-qPCR). Clinical information was collected by the medical service onboard. We conducted interviews with staff and reviewed and advised health and hygiene management plans. A case was defined as any person onboard who had developed ≥3 diarrhea episodes or ≥1 vomiting episode accompanied by at least one of the following: diarrhea, abdominal cramps or fever.

Results:

In total, 104 cases were reported affecting three consecutive cruises (31/08 to 20/09/2018): 86 passengers, 18 staff (three food handlers). The attack rate among passengers was 4.3% and among staff 8.9%. Median symptom duration was 2 days (range: 1-6 days). Norovirus was detected by PCR in 9/11 stool samples (82%). No pathogen was detected in the environmental samples (0/20). Improved sanitation and control measures were implemented such as isolation of symptomatic cases until 48h without symptoms, disinfection of public areas and cabins, and health communication with passengers and staff.

Conclusions:

The outbreak was controlled before the fourth consecutive cruise started following the enforcement of isolation of cases. The epidemiological curve suggested person-to-person transmission with crew members possibly carrying the virus over between cruises. Adherence to existing international guidelines including the isolation of cases is needed for preventing, investigating, and controlling such outbreaks on cruise ships.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Norovirus, Gastroenteritis Infection, Malta, Cruise, Travel Health, Outbreak

ABSTRACT ID: 720

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3.6. Panic can spread faster than pathogens: communication pitfalls during a foodborne outbreak in Denmark in 2019

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Background:

On February 27th 2019, the Danish Veterinary and Food Administration (DVFA) and Statens Serum Institut (SSI) learnt from Danish media about the evacuation and closure of a graduate school following an “extremely contagious, airborne viral infection”. Seemingly, more than 100 people had fallen ill. Consequently, DVFA and SSI investigated the outbreak. We describe the communication flow behind the school closure and the investigation findings to capitalize lessons learnt.

Methods:

We uncovered the communication flow by interviewing school representatives and public health authorities. We then compared it with the routine roles of involved parties during local foodborne outbreaks. We conducted a cohort study among people present at school on February 24th-27th, using an online questionnaire. Cases were defined as having diarrhoea and/or vomiting on February 26th-27th. We calculated risk ratios (RR) for exposures to food from the school canteen using Quasi-Poisson regression. Stool samples were collected.

Results:

The school ricocheted through a web of authorities who failed to provide clear guidance. This rushed the school to evacuation and closure and generated panic. The outbreak was arbitrarily considered non-foodborne, and DVFA was involved too late to collect food samples. Our study included 169 people, 46 were cases, 40 occurring over 18 hours. People consuming a vegetarian sandwich had six times higher risk of illness (RR=5.9, 95%CI 3.5-10). Norovirus GII.P7-GII.14 was confirmed in seven stool samples.

Conclusions:

Communication pitfalls among authorities led to questionable control measures and hampered a thorough investigation. Field investigation, epidemiological and laboratory findings suggested that this was a point source foodborne norovirus outbreak. To avoid similar scenarios, we recommend strengthening the communication flow and clarifying responsibilities between food and health authorities at local and national level.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Communication; Disease Outbreaks; Foodborne Diseases; Norovirus

ABSTRACT ID: 300

PRESENTED BY: Guido Benedetti / gube@ssi.dk

Track 4: Food- and waterborne diseases and zoonoses (2): surveillance

Moderator:

Harold Noël

Abstracts

4.1. Investigating the occurrence of Verotoxigenic Escherichia coli (VTEC) in Irish private drinking water wells

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Background:

A collection of E. coli isolated from private wells in the Mid-West and South of Ireland were retrospectively analysed for the presence of the VTEC associated virulence factors vtx1, vtx2 and eae by real time PCR of the National VTEC laboratory. Further real time PCR assays were used to identify if VTEC isolates belonged to clinically important serotypes O157, O26, O153, O145, O111 and O104.

Methods:

Three of the 42 isolates (7.1%) tested so far were positive for vtx2. No isolates were vtx1 or eae positive. VTEC isolates did not belong to the 6 most clinically important serotypes and were phenotypically susceptible to a panel of 16 antimicrobials.

Results:

From 611 respondents (response rate 22%) to the survey, 327 (54%) were women; median age 53 (range 16-86). The awareness rate of the notice was 67% since 412 reported remembering having received a notice. From those 412, 273 (67%) reported remembering the advice of storing water in advance and 269 (66%) the boil water advise. Compliance rate to either of those two recommendations was 85%, but when the lower awareness rate was factored in, the effective compliance rate was calculated to be 57%. The respondent's compliance and awareness with the advices was independent of age, education, household type. Awareness of the notice was independent of sex but compliance was lower among men (OR 0.53, 95%CI 0.29-0.96).

Conclusions:

Private wells in Ireland are at increased risk of contamination with pathogenic strains of E. coli capable of causing human disease. This is preliminary data from the ongoing DESIGN (Detection of Environmental Sources of Infectious diseases in Groundwater Networks) study, which will identify the extent of VTEC contamination of Irish wells, thereby informing the development of policy to protect private well users.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: VTEC,E. coli,private wells,groundwater,waterborne zoonosis

ABSTRACT ID: 509

PRESENTED BY: Liam P Burke / liam.burke@nuigalway.ie

4.2. Spatiotemporal approaches to explore the environmental connection between cattle farms and sporadic cases of human infections of Shiga toxin/verocytotoxin-producing Escherichia coli in Sweden

Hyeyoung Kim [1]

S. Widgren [2], S. Kühlmann-Berenzon [3], E. Löf [4], U. Emanuelson [5],

Poster Abstracts

A. Lindberg [6]

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Background:

Sweden has recently experienced an increase in the number of cases of Shiga toxin/verocytotoxin- producing Escherichia coli (STEC/VTEC) infections. STEC/VTEC is known to be primarily transmitted from an animal reservoir to humans through food, water, and the environment. Identifying these transmission routes is essential and significant for improving public health. Several studies have revealed that living close to cattle farms can be a significant factor for STEC/VTEC infection. There is, however, a lack of literature providing a comprehensive understanding of environmental risk factors associated with the disease. We present spatiotemporal approaches to investigate environmental risk factors that affect STEC/VTEC infection at a regional scale.

Methods:

We obtained the human sporadic cases data during 2009-2013 and environmental, social and weather data in various formats, such as text and remote sensing imagery. We mapped the presence of the pathogen to describe spatial and temporal patterns. Then we employed Moran's I and local indicators of spatial association tests to identify statistically significant spatial clusters. Lastly, we carried out ordinary linear regression and spatiotemporal regression analyses to understand the connection among cattle farms, human STEC/VTEC cases, and environments.

Results:

As preliminary results, we detected a disease pattern in which positive clusters of STEC/VTEC spread from southwest to north in Sweden over time. Cattle farm density was statistically associated with the presence of the pathogen from 2009 to 2013 (p-values: 0.001-0.02). Annual precipitation was also statistically significant in 2010, 2011 and 2013 (p-values: 0.003-0.01).

Conclusions:

Our approaches will be of considerable benefit to model the association between the sporadic STEC/VTEC cases and the environment to understand the phenomenon better. Applied on real-time data they are also able to contribute to disease surveillance and control.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: STEC, VTEC, spatiotemporal analysis, spatial cluster

ABSTRACT ID: 534

PRESENTED BY: Hyeyoung Kim / hyeyoung.kim@sva.se

4.3. Are food exposures obtained through commercial market panels representative of the general population? Implications for epidemiological studies

Charlotte Andersen [1]

D. Curtis [2], P. Crook [3], R. Vivancos [4], D. Gardiner [5], N. McCarthy [6], P. Mook [7]

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Background:

Current methods of control recruitment for case-control studies can be slow (a particular issue for outbreak investigations), resource-intensive and subject to a range of biases. Commercial market panels are a potential source of rapidly recruited controls and have been used with apparent success in 5 instances when investigating GI pathogen outbreaks in the UK. Our study aimed to investigate inherent biases of this approach by evaluating food exposure data from these panel controls against an established, randomly sampled, population-based reference dataset.

Methods:

Market panel data were collected from two companies using retrospective internet-based surveys; these were compared to reference data from the National Diet and Nutrition Survey, which was collected prospectively using a paper-based diary. We collected exposure information for 71 foods. We used logistic regression to calculate adjusted Odds Ratios (aOR) to compare exposure to each food item between market panel and NDNS participants.

Results:

We compared 2,103 panel controls to 2,696 reference dataset participants. Adjusted for socio-demographic factors, exposure to 90% of foods was statistically different between both panels and the reference data. However, these differences were likely to be of limited practical importance (0.3

Conclusions:

Market panel food exposures were comparable to reference data for common food exposures but more likely to be different for uncommon exposures. This approach should be considered for outbreak investigation, in conjunction with other considerations such as population at risk, timeliness of response and study resources.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: epidemiological study design,gastrointestinal infection, outbreaks, Case-control studies

ABSTRACT ID: 518

PRESENTED BY: Charlotte Andersen / piers.mook@phe.gov.uk

4.4. Evaluation of surveillance system for entero-haemorrhagic E. coli 2013-2017, Czech Republic

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Background:

The Czech national enterohaemorrhagic E.coli (EHEC) surveillance is laboratory based. Faecal specimens from children <2 years with gastrointestinal infections are screened for EHEC. Suspected isolates (particularly of “top5” serogroups O157, O26, O103, O111, O145) are sent to the National reference laboratory for E. coli and Shigellae (NRL) for Shiga toxin genes detection/confirmation. Stools from haemolytic-uraemic syndrome (HUS) patients are sent directly to NRL. Case-based data are reported to national electronic system (EpiDat). Due to planned changes in legislation and EpiDat, we evaluated the surveillance system for data completeness including compliance with NRL and timeliness of reporting.

Methods:

Data reported to EpiDat during 2013-2017 containing the information on E. coli serogroup were analysed for completeness of information on Shiga toxin production and HUS. Data from EpiDat and NRL were linked to identify cases with missing confirmation in NRL. Timeliness of reporting was analysed as delay between dates of onset and notification.

Results:

Out of 10,003 E. coli infections with serogroup information, 22% were associated with “top5” serogroups.

Out of the “top5” serogroup cases reported, the compliance with referring to NLR was 46%, information on Shiga toxin production (reported on voluntary basis) was available in 71% of EHEC cases. From 113 EHEC cases with “top5” serogroups, 90% were tested in NRL. From 7 HUS cases, 86% were confirmed in NRL. The median delay between onset of symptoms and notification was 7 days.

Conclusions:

The evaluation revealed gaps in compliance in referring the “top5” E. coli serogroup strains to NRL. Reminders to local laboratories that confirmation in NRL is mandatory and technical enhancement of new electronic reporting system could contribute to better data completeness.

Subject: Surveillance

Keywords: entero-haemorrhagic E. coli, Shiga toxin, surveillance

ABSTRACT ID: 752

PRESENTED BY: Klara Labska / klara.labska@szu.cz

4.5. Typhoid in the woods – implementation and impact of genomics for typing Salmonella enterica serotype Typhi in a National Reference Centre

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Background:

Salmonella Typhi is a globally spread, potentially fatal food- and water-borne pathogen. In Europe, about 600, mostly travel-associated cases are reported annually. In late summer 2017, an outbreak of S. Typhi occurred in north-eastern Italy. The event took place in a remote mountainous area during an international mass gathering with nearly 3000 participants. An outbreak investigation was initiated after linked cases were reported by other Member States in the ECDC Epidemic Intelligence Surveillance System. We supported the outbreak investigation by applying whole genome sequencing and a simplified genomics tool to link Italian cases retrospectively.

Methods:

Five probable cases were reported by authorities in three regions in Italy, but for only three cases bacterial isolates were sent to the national reference laboratory. An additional sample from a time-linked case was also obtained. We retrieved whole-genome sequences from these four samples using Illumina MiSeq and ran de novo assemblies and SNP based phylogenetic analyses within the ARIES public Galaxy server (https://w3.iss. it/site/aries). For genotyping, a whole genome-based method adapted from a highly comprehensive genotyping framework published by Wong and colleagues was used (Nature Communications 7:12827, 2016).

Results:

Our simplified S. Typhi phylogeny accurately mimicked the original global phylogenetic tree. Implementing the genomic approach, the identified index case, one probable case and one secondary case were assigned to the same rare genotype, clade 2.2, while the time-linked S. Typhi case was shown to belong to clade 4.3 and not to the outbreak.

Conclusions:

We ran a streamline genomic investigation to complement the epidemiological investigation and successfully linked the cases. Simplifying high-resolution genomic analyses improves their utility and timeliness, increasing their value as tools in public health microbiology laboratories.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: S. Typhi, outbreak, genomics, public health

ABSTRACT ID: 763

PRESENTED BY: Erika Lindh / erika.lindh@helsinki.fi

4.6. Creation and evaluation of an algorithm for automated hepatitis A outbreak detection using Bulgarian surveillance data

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Background:

In Bulgaria, hepatitis A (HAV) causes community-wide outbreaks. Automated HAV outbreak detection can be useful, but is complicated as HAV reporting is monthly. Each Monday the National Center of Infectious and Parasitic Diseases recieves regional weekly suspected hepatitis (WSH) numbers (without specified aetiology), and spikes in WSH are often attributed to HAV. We developed a HAV outbreak detection algorithm using WSH data.

Methods:

We created a weekly variable (WSH_lagsum) by adding up WSH numbers from the previous 4 weeks (average HAV incubation time). We modelled non-epidemic WSH_lagsum baseline levels in 6/28 Bulgarian regions for 2013-2017, by removing the 15% highest WSH_lagsum values from the 10 years preceding each year and fitting a negative binomial regression model, including trend and seasonality terms. A signal was generated each time in 2013-2017 when WSH_lagsum crossed and remained over baseline for three consecutive weeks. To estimate algorithm sensitivity/specificity, a signal was classified as "true positive" if there was a substantial increase in monthly HAV numbers in at least two monthly reports, received directly after the signal.

Results:

Between 2013-2017, 21 substantial increases in HAV case numbers were identified in the 6 regions. The model generated 20 true positives, with overall sensitivity of 95% (regional range 67-100%) and specificity of 90% (regional range 83-98%). Depending on region, true positive signals were generated on average 1.2 to 6 weeks before the corresponding monthly HAV reports were received.

Conclusions:

Estimated sensitivity/specificity is similar to those of algorithms already introduced in other countries. Historical outbreak reports could not be used to evaluate sensitivity/specificity, as they often lacked essential temporal data. The model will now be piloted and evaluated in real time in several Bulgarian regions.

Subject: Surveillance

Keywords: Hepatitis A, epidemiology, surveillance, outbreak

ABSTRACT ID: 795

PRESENTED BY: Savina Stoitsova / stoitsova@ncipd.org

Track 5: Influenza and other respiratory viruses (1)

Moderator:

John Paget

Abstracts

5.1. Influenza season 2018/2019 completely dominated by Influenza A; findings from a sentinel surveillance in Bavaria, Germany

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Background:

Seasonal influenza constitutes an important public health burden in Europe. In Bavaria, Germany, sentinel surveillance for acute respiratory infections signals the start and end of the influenza season, describes circulating influenza viruses, and identifies groups at higher risk for severe disease. We describe Bavarian Influenza Sentinel (BIS) results from the 2018/2019 season.

Methods:

BIS comprises 75 physicians, both paediatricians and GPs, who submit specimens weekly from two randomly-chosen patients presenting with acute respiratory symptoms, from week 40 to week 16, to the state health authority (LGL). Specimens are tested with RT-PCR to identify the influenza virus type. Physicians use a standardized questionnaire to collect information about symptoms and vaccination status.

Results:

Of 1761 specimens tested for influenza, 35% were positive. Positivity rate, weighted by age (children, adults) was 36% (95%CI 33-38%). The majority of specimens were influenza A virus-positive (99.7%), (58% Influenza A(H1N1) and 37% A(H3N2)). The season started in week 2 and peaked over weeks 7–10 in 2019, with a positivity rate of more than 60%. The highest average positivity rates (38%) were among children aged 6-18 years. Vaccination coverage among people 60 and older, recommended to receive flu vaccine, was 33% among those with confirmed influenza infection, and 44% among those without.

Conclusions:

Results from this sentinel system, illustrated that season 2018-2019 was dominated by influenza type A, and virus circulation exhibited a month-long peak. The dominance of influenza A has been observed elsewhere in Germany and Europe, and is remarkable given the dominance of lineage B in season 2017/2018. Early detection of seasonal influenza provides valuable information for clinical decision-making; and characterization of circulating viruses informs future vaccine formulation.

Subject: Burden of disease

Keywords: influenza, sentinel system, surveillance, seasonal influenza

ABSTRACT ID: 725

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5.2. Genetic and antigenic characteristics of circulating influenza A viruses, WHO European Region, 2018/2019

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Background:

The 2018/2019 influenza season in the WHO European Region was dominated by type A viruses. A(H1N1)pdm09 and A(H3N2) viruses co-circulated widely with a greater proportion of A(H1N1)pdm09 detections. Very few influenza type B viruses were reported.

Methods:

National Influenza Centres (NICs) of the WHO European Region report genetic and antigenic virus characterisation data to The European Surveillance System operated by ECDC. Reports covering weeks 40/2018 to 16/2019 were analysed to compare circulating viruses with the respective vaccine virus components.

Results:

All 1732 A(H1N1)pdm09 viruses fell in a subclade of 6B.1, 6B.1A, defined by HA1 amino acid substitutions S74R, S164T and I295V, and a number of subgroups have emerged within the subclade defined by additional amino acid substitutions. Available antigenic data (n=2152) showed no evidence of changes in A(H1N1)pdm09 subclade 6B.1A viruses compared to the clade 6B.1 vaccine virus A/Michigan/45/2015.

Of 1736 A(H3N2) viruses, 1313 fell in clade 3C.2a (1145 in subclade 3C.2a1b, 66 in 3C.2a2, 57 in 3C.2a1, 32 in 3C.2a3 and nine in 3C.2a1a) and 423 in clade 3C.3a. Antigenic data reported for A(H3N2) viruses (n=570) indicated that those in clade 3C.2a were similar to the vaccine virus A/Singapore/INFIMH-16-0019/2016 (subclade 3C.2a1), while clade 3C.3a viruses were antigenically distinct. Clade 3C.3a viruses were detected in eight European countries and their proportion among A(H3N2) viruses increased from 0 to 33% during the season.

Conclusions:

The genetic diversity observed among A(H1N1)pdm09 subclade 6B.1A viruses and A(H3N2) clade 3C.2a viruses appeared not to cause antigenic dissimilarity compared to their respective vaccine viruses. However, antigenically distinct A(H3N2) clade 3C.3a viruses were increasingly detected in the Region. Simultaneous circulation of genetically and antigenically diverse A(H3N2) strains poses a challenge to vaccine strain selection.

Subject: Surveillance

Keywords: Human Influenza, Public Health Surveillance, Europe, Sentinel Surveillance

ABSTRACT ID: 358

PRESENTED BY: Angeliki Melidou / angeliki.melidou@ecdc.europa.eu

5.3. Risk factor analysis of Highly Pathogenic Avian Influenza in Greece

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[3,4,5,6] --

Background:

This is the first epidemiological investigation of Highly Pathogenic Avian Influenza (HPAI) outbreaks in Greece and aims to investigate the disease epidemiology of HPAI cases in Greece, taking into consideration the spatial pattern of HPAI occurrence and the low scale of the HPAI problem in Greece, and examine the key environmental risk factors associated with the HPAI occurrence.

Methods:

Based on „case“ definition (positive identification of HPAI H5/H7 infection via Real-Time RT-PCR diagnostic panel by proper laboratory), spatial (ArcGIS 10.6,ESRI Inc., Redland, CA) and statistical (SPSS 25.0, IBM) tools have been applied in order to explore the role of each risk factor responsible for the spread of HPAI in Greece. The following risk factors: specific wild species (orders Anseriformes and Charadriiformes), precipitation, temperature, poultry/human population density, distance to the closest highway, distance to the closest water collection and number of water bird mid-winter census counts (WMC) were investigated, upon HPAI occurrences,in both wild and poultry species, by applying uni- and multi-variable models through logistic regression method.

Results:

The final models are formulated as below: Logit ($p_{\text{wild bird}}$) = 7.8530 -0.6565*Coexist_mammal + 0.2852*Anseriformes + 0.2287*WMC – 0.5114*Charadriformes, Logit (p poultry) = 9.5917 + 0.6134*Human density -0.9009*Temperature + 0.4042*Anseriformes + 0.2118*WMC -0.7515*Charadriformes. Upon logistic regression, wild birds‘ probability of infection is positively determined by WMC and Anseriformes counts and negatively associated with coexistence with mammals and Charadriiformes counts. Concerning the poultry species, the HPAI occurrence is positively related to human population density, Anseriformes counts and WMC and negatively with temperature and Charadriiformes counts.

Conclusions:

Anthropogenic and environmental factors are implicated to disease epidemiology and this is considered as important for the implementation of risk-based surveillance and control of HPAI.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: risk analysis, HPAI,Greece,avian influenza,epidemiology

ABSTRACT ID: 293

PRESENTED BY: Ioanna Chatziprodromidou / ioannachatzi@msn.com

5.4. Predicted efficacy of cell-derived and egg-derived influenza vaccine against A(H3N2) strains circulating during the 2018/2019 season

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Background:

Influenza A(H3N2) virus evolves rapidly affecting seasonal vaccine efficacy (VE). In recent times, the low VE against A(H3N2) has also been attributed to substitutions acquired during the isolation of candidate vaccine virus (CVV) in eggs. Recently, CVV propagation in cell cultures has been implemented to limit this occurrence.

This study aimed at predicting VE against A(H3N2) strains circulated in Lombardy (Northern Italy) during the 2018/2019 influenza season by sequence analysis of the hemagglutinin (HA) gene and comparison with egg- and cell-derived CVVs.

Methods:

106 full-length (1778 bps) HA gene sequences were obtained directly from respiratory specimens and phylogenetically analysed. HA sequences of field strains were compared with 2018/2019 seasonal egg-CVV [A/Singapore/INFIMH-16-0019/2016(H3N2)] and cell-CVV [A/North Carolina/04/2016(H3N2)]. VE of egg-/cell-CVV against 2018/2019 field A(H3N2) viruses was quantified by Pepitope model (Bonomo&Deem, CID,2018:67).

Results:

3C.3a. Clade 3C.2a included both egg- and cell-CVV, with field strains sharing higher nucleotide similarity with cell-CVV (range: 98.4-99.0%) than with egg-CVV (range: 97.8-98.7%). None field strains had egg-adaptive mutations K160 and P194; the predicted VE against field viruses was 50% for egg-CVV and 75% for cell-CVV.

A(H3N2) strains in 3C.3a clade were drifted HA variants with 2 amino acid substitutions (Y159S and F193S) in the major antigenic sites; the predicted VE (both egg-/cell-CVV) against these field viruses was -1%.

Conclusions:

Half of A(H3N2) viruses circulating in 2018/2019 season clustered in 3C.2a clade, sharing higher similarity with cell-CVV than egg-CVV. The predicted VE against these strains was higher for cell-CVV than egg-CVV. The circulation of drifted HA variants (3C.3a) late in the season significantly affected VE.

Subject: Surveillance

Keywords: influenza A(H3N2) virus, hemagglutinin, molecular characterisation, phylogenetic analysis, egg-derived vaccine, predicted vaccine efficacy

ABSTRACT ID: 267

PRESENTED BY: Cristina Galli / cristina.galli@unimi.it

5.5. High influenza morbidity in children in Ireland, 2009-2019, supports the need for improved/alternative vaccination strategies

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Background:

In Ireland, influenza places a substantial burden on the health system, with the highest disease occurrence in children and the elderly. Influenza vaccines are recommended for use in risk groups (e.g. chronic health conditions and age ≥65 years), with trivalent vaccines mainly used. There is no universal paediatric influenza vaccination programme. We aim to provide evidence to support decisions regarding alternative influenza vaccination strategies.

Methods:

We described the burden of influenza among children aged 0-14 years in Ireland over ten seasons (2009/2010-2018/2019). We calculated clinical influenza-like illness (ILI) GP consultation rates and laboratory confirmed influenza hospitalisation and intensive care unit (ICU) admission rates. Data sources included Ireland's sentinel GP, Computerised Infectious Disease Reporting and ICU surveillance systems.

Results:

The highest GP ILI consultation rates were during seasons when influenza A(H1N1)pdm09 predominated (460/100,000 in 2009/2010; 206/100,000 in 2010/2011) and B/lineage vaccine mismatched viruses (co)predominated (112/100,000 in 2015/2016; 118/100,000 in 2017/2018). Since 2009, over 4,700 hospitalisations, 180 ICU admissions and 40 deaths were reported in children with laboratory-confirmed influenza. Hospitalisation rates were highest when influenza A(H1N1) pdm09 or a B/lineage mismatched virus (co)predominated (110/100,000 in 2017/2018 and 120/100,000 in 2018/2019). Low GP ILI consultation rates, hospital and ICU rates were observed in children during A(H3N2) predominant seasons. Over the study period, 68% of hospitalised influenza cases had no underlying medical conditions. In hospitalised children in risk groups, vaccine uptake ranged from 5-20% each season.

Conclusions:

Considerable paediatric morbidity and mortality was observed due to influenza, particularly when A(H1N1)pdm09 or B/lineage mismatched viruses (co)predominated. Strategies are needed to improve vaccine uptake in at-risk children and to protect healthy children. Quadrivalent vaccines and/or universal childhood vaccination should be considered.

Subject: Burden of disease

Keywords: Influenza,Burden of disease, Paediatric, Universal vaccination, Quadrivalent, Influenza A(H1N1)pdm09, Influenza B

ABSTRACT ID: 407

PRESENTED BY: Lisa Domegan / lisa.domegan@hse.ie

5.6. Influenza vaccine effectiveness against hospitalization with laboratory-confirmed influenza in Greece: a pooled analysis across five seasons, 2013/14 to 2017/18

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Background:

Estimating influenza vaccine effectiveness (IVE) across multiple seasons increases the sample size, allowing for subgroup analysis. To our knowledge, no previous study in Greece has reported pooled IVE estimates.

We aimed to estimate overall and viral subtype-specific IVE over the last five seasons, both annually and pooled, in order to provide information on vaccine benefits and support uptake.

Methods:

We used routine surveillance data on hospitalized patients for five influenza seasons, from 2013/14 to 2017/18. Swab samples from inpatients were tested for influenza by RT-PCR in three laboratories, covering the entire country. We used a test-negative study design to estimate IVE; cases were patients with a positive RT-PCR test for influenza, while patients testing negative were classified as controls. Vaccine effectiveness was calculated as one minus the odds ratio (OR) for influenza vaccination, estimated via logistic regression and adjusted for age, sex, hospitalization in intensive care unit (ICU) and calendar time.

Results:

We included 2889 patients with influenza as cases, and 4850 patients as controls. Across all seasons, adjusted IVE was 40% (95%CI: 18% to 56%) against all influenza, 65% against A(H1N1)pdm09 (95%CI: 20% to 85%), 17% against A(H3N2) (95%CI: 11% to 23%) and 47% against influenza B (95%CI: 31% to 59%). IVE against subtype A(H1N1)pdm09 was significantly higher for patients hospitalized in an ICU compared to patients in regular wards (72% vs 60%, p for interaction < 0.01).

Conclusions:

Over the study period, seasonal influenza vaccination has provided substantially higher protection against subtype A(H1N1)pdm09, but lower against A(H3N2), which is consistent with existing evidence. The National Public Health Organization can contribute to systematically monitoring seasonal IVE, providing evidence to promote vaccination, sustain uptake and inform vaccine development.

Subject: Surveillance

Keywords: influenza surveillance, vaccine effectiveness, viral subtypes, epidemiology

ABSTRACT ID: 269

PRESENTED BY: Elisavet Mouratidou / elsamouratidou@gmail.com

Track 6: HIV, sexually transmitted infections and viral hepatitis (1): surveillance and burden of disease

Moderator:

Anastasia Pharris

Abstracts

6.1. Drug use during sex among Dutch swingers and associated sexual risk behaviour: a hidden phenomenon?

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Background:

Drug use while swinging was reported by 44% (443/1005); 51%(n=292) in women, 44%(n=311) in bisexual men, and 39%(n=402) in heterosexual men (p=0.007). Among drug-using swingers, XTC (92%), GHB (76%), and laughing gas (69%) were mostly used; 69% used four or more different drugs. Condomless vaginal sex was reported by 46% in drug-using swingers (vs. 35% in non-drug-using swingers; p<0.001) and condomless anal sex by 30% in drug- using swingers (vs. 21% in non-drug-using swingers; p=0.012). Being a female swinger (aOR:2.10; 95%CI:1.36-3.09) and condomless vaginal sex (aOR:1.71; 95%CI:1.24-2.35) were independently associated with drug use.

Methods:

In 2018, 1005 participants completed an online questionnaire that was advertised at Dutch swinger-websites. Inclusion criteria were: recent swinging (<12 months) and being aged >18 years. Drug use during sex was assessed and compared between heterosexual male, bisexual male, and female swingers using chi-square tests. Multivariable logistic regression analysis was used to assess factors (sociodemographic characteristics, alcohol, and condomless sex with swing partners) associated with drug use.

Results:

Drug use while swinging was reported by 44% (443/1005); 51%(n=292) in women, 44%(n=311) in bisexual men, and 39%(n=402) in heterosexual men (p=0.007). Among drug-using swingers, XTC (92%), GHB (76%), and laughing gas (69%) were mostly used; 69% used four or more different drugs. Condomless vaginal sex was reported by 46% in drug-using swingers (vs. 35% in non-drug-using swingers; p<0.001) and condomless anal sex by 30% in drug- using swingers (vs. 21% in non-drug-using swingers; p=0.012). Being a female swinger (aOR:2.10; 95%CI:1.36-3.09) and condomless vaginal sex (aOR:1.71; 95%CI:1.24-2.35) were independently associated with drug use.

Conclusions:

This study among a large group of swingers in the Netherlands shows that drug use during sex was highly prevalent and associated with condomless vaginal sex. This suggests that it could be informative for STI healthcare workers to include questions on drug use during sex as part of the sexual history for swingers.

Subject: Surveillance

Keywords: Drug use during sex, swingers, sexual risk behaviour, online survey

ABSTRACT ID: 179

PRESENTED BY: Ymke Evers / ymke.evers@ggdzl.nl

Poster Abstracts

6.2. Modelling the incidence and prevalence of HIV in 2018 in a country without CD4 count data: The Norwegian experience with the ECDC HIV modelling tool

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Background:

Norway aims for ≥90% of people living with HIV (PLHIV) to know their HIV-status by 2020, following the first UNAIDS 90-90-90 target. We estimated HIV incidence, number of PLHIV and proportion of undiagnosed persons (PUP) among HIV-1-positive ≥15-year-olds in Norway.

Methods:

We used the ECDC HIV modelling tool incidence method (version 1.3.0), inputting national surveillance data on new HIV diagnoses, HIV diagnoses with a concurrent AIDS diagnosis, and HIV mortality from 1984-2018. We excluded cases reported as infected before immigration to Norway. We used national Danish CD4 count data as a proxy for Norwegian data, and ran the model with and without these data. We modelled different populations (Norwegians and migrants) and transmission groups (men who have sex with men (MSM), heterosexuals and people who inject drugs (PWID)), using Poisson regression.

Results:

An estimated 45 new HIV infections occurred in 2018 [95%CI: 19-169]. There were 3331 PLHIV [95%CI: 3156–3618] by the end of 2018, of which 325 were undiagnosed [95%CI: 248–521]. The PUP decreased consistently from 2005 (27.2% [95%CI: 24.8%-29.2%]), to 9.7% [95%CI: 7.6–14.7%] in 2018. The PUP was similar among Norwegians (9.3%) and migrants (11.7%). The PUP was 8.5% among MSM, 18.2% among heterosexuals, and 15.4% among PWID. Excluding Danish CD4 count data resulted in lower estimates for all outcomes, although confidence intervals overlapped with the original model.

Conclusions:

Norway is on target to achieve the first 90-90-90 target. Collecting Norwegian data on CD4 counts, outward migration, and all-cause mortality among HIV cases would refine the estimate. Norway will continue to work to reduce new HIV infections and the PUP, particularly through pre-exposure prophylaxis and increased testing among risk groups, and rapid treatment initiation.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: HIV, statistical models, incidence, prevalence

ABSTRACT ID: 183

PRESENTED BY: Robert Whittaker / robneilwhittaker@gmail.com

6.3. Sustainable Development Goal 3: Ensure healthy lives and promote well-being for all at all ages – can the EU/EEA measure up on tuberculosis, viral hepatitis and HIV?

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Background:

Sustainable Development Goal (SDG) 3.3 aims to end the epidemics of AIDS and tuberculosis (TB), and combat hepatitis by 2030. Specific targets include: i) 80% incidence reduction for TB, 90% for chronic hepatitis B and C, and 100% for HIV; and ii) reduction in number of deaths of 90% (TB), 65% (viral hepatitis), and 100% (HIV).

Methods:

For each target and infection, we identified appropriate data sources for the EU/EEA, described progress made, and reflected on data challenges. For incidence, we used the European Surveillance System (TESSy) notification rate as a proxy for TB, model estimates based on TESSy data for HIV, and World Health Organization prevalence survey data and mathematical modelling for hepatitis B/C. For TB deaths we used Eurostat data, and for hepatitis, liver disease deaths from Eurostat, applying the estimated fraction attributable to hepatitis B/C. For HIV, Global Burden of Disease estimates provided AIDS deaths.

Results:

For TB, the 2017 notification rate was 10.7 per 100 000 population, and the 2030 target is 2.4 per 100 000; 2015 number of deaths: 4 437, 2030 target: 444. For hepatitis B/C, EU/EEA incidence estimates are pending. The estimated number of deaths in 2015 was 68 062, 2030 target: 23 821. For HIV, the 2017 incidence estimate was 5.0 per 100 000 and number of deaths 4 003, with the 2030 target being elimination of both.

Conclusions:

Despite limited data availability and quality, EU/EEA progress can be monitored for several SDG sub- targets using routinely collected surveillance and vital statistics data, combined with survey data and modelling. Results indicate that the EU/EEA will struggle to meet the 2030 SDG for TB, viral hepatitis and HIV.

Subject: Burden of disease

Keywords: HIV, Hepatitis C, Hepatitis B, Tuberculosi

ABSTRACT ID: 409

PRESENTED BY: Lina Nerlander/ lina.nerlander@ecdc.europa.eu

6.4. Evidence-based prioritisation of infectious diseases for surveillance and public health action in Belgium

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Background:

National public health agencies struggle to prioritise infectious diseases for prevention and control. We aimed to apply the ECDC recommended prioritization methodology to rank infectious diseases according to their relative importance, in order to inform future surveillance and public health action in Belgium.

Methods:

We applied the multi-criteria decision analysis (MCDA) approach. A balanced set of 18 criteria, structured in five hierarchical criteria groups, was composed by a working group of epidemiologists and statisticians. Subsequently, the criteria were weighted according to perceived impact, by a panel of experts (n=80; median weights calculated) in an online survey. In a second survey, 37 experts scored each disease against the 18 criteria, guided by surveillance and background data concerning the period 2010-2016. These values were averaged among all experts. The weighted sum of the 18 criteria's score composed the total score per disease, on which the ranking was based.

Results:

The diseases ranked highest were: pertussis, human immunodeficiency virus infection, hepatitis C and hepatitis B. Among the five criteria groups, the highest weights were assigned to 'impact on the patient', followed by 'impact on public health'. Differences in perception were identified between clinicians, microbiologists and public health workers, with physicians prioritising impact on the patient higher. Among the 18 individual criteria, the highest weights were assigned to 'case fatality ratio', 'spreading potential' and 'existing multi drugs resistance'.

Conclusions:

This project effectively ranked infectious diseases. The diseases ranked highest are included in current public health programs, but additional programs among risk groups might be valuable. Further cross-reference of the obtained ranking with current programs is recommended. We recommend to implement this method in a recurrent evaluation cycle of national public health priorities.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Priority setting, Program evaluations, MCDA, Public health priorities, Resource mapping

ABSTRACT ID: 502

PRESENTED BY: Sofieke Klamer / sofieke.klamer@sciensano.be

6.5. Number of people living with hepatitis B and C in Germany

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Background:

Germany is a low prevalence country for hepatitis B (HepB) and C (HepC), but prevalence is higher among vulnerable groups like first-generation migrants (migrants) or people who inject drugs (PWID). We estimated for the first time the number of people living with HepB and HepC in Germany under consideration of populations with low and increased prevalence of infection, in order to understand burden of disease and guide prevention.

Methods:

We applied a modified workbook method to estimate the total number of people living with HepB (HBsAg-seropositive) and HepC (anti-HCV-seropositive) in Germany, 2013. Population size and prevalence estimates from studies in the general population and subgroups with increased risk of HepB and HepC, like PWID, migrants and HIV infected men who have sex with men (HIV+MSM) were used for the calculations. We report averages together with low and high estimates per population group.

Results:

We estimated 343,000 (245,000-489,000) people living with HepB. From those 6.7% (23,000; 11,000-33,000) were <18 years of age, 54% (185,000; 89,000-323,200) adults in the general population, 39% (134,000; 131,000-137,000) migrants, 0.4% (1300; 350-3,000) PWID and 0.2% (750; 700-800) HIV+MSM. We estimated 331,000 (200,000-510,000) people being anti-HCV positive. Of them, 55% (181,000; 92,000–334,000) were adults in the general population, 22% (74,000; 43,000-87,000) PWID, 22% (74,000; 63,000-87,000) migrants and 0.5% HIV+MSM (1,800; 1,700-2,000).

Conclusions:

We provide first estimates of people living with HepB and being anti-HepC positive in Germany, that serve as a basis for further monitoring. Considerable share of people living with HepB is among migrants and with HepC among PWID, who should be targeted for prevention and control. Populations with low and increased prevalence must be included in nationwide estimates and continuous monitoring.

Subject: Burden of disease

Keywords: Hepatitis B, Hepatitis C, estimation, migrants, people who inject drugs

ABSTRACT ID: 563

PRESENTED BY: Katrin Kremer / kremerk@rki.de

Track 7: Vaccine-preventable diseases (1): measles

Moderator:

Marion Muehlen

Abstracts

7.1. Measles outbreak in a public hospital, Szczecin, Poland, January 2019

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Background:

In January 2019, a measles infection in an employee in a 168-bed hospital was reported to the local sanitary station (PSSE) in Szczecin, Poland. Further transmission occurred in the hospital and more cases were reported in the community. We investigated to identify transmission routes and implement control measures.

Methods:

An outbreak case was any hospital staff, visitor, or patient, or any person in contact with them, meeting clinical criteria, from 3rd January. Cases were interviewed by PSSE to identify contacts and verify vaccination status. Susceptible contacts were offered post exposure vaccination (PEV). Clinical specimens were sent to the National Reference Laboratory for RT-PCR and serology confirmation. We collected vaccination status, geographical location and queried hospital authorities about control measures.

Results:

The index case, the hospital employee, returned from Ukraine one day before onset of symptoms. We identified 17 (8 confirmed, 7 probable, 2 suspect) outbreak cases including 11 hospital personnel. Four of the personnel provided vaccine documentation (36%), of which three had received 2 doses. Contacts identified as susceptible (130) received PEV. Eight cases were contacts of the index case but were not promptly identified and did not receive PEV. The hospital refused new admissions for 19 days.

Another 16 cases were identified in the community, with exposure information not sufficient to establish an epidemiologic link with the outbreak.

Conclusions:

The introduction of measles into a susceptible population and missing contacts for PEV led to a hospital-associated outbreak. For the community cases, exposure may have occurred in multiple public spaces around the hospital.

Most of the hospital staff who developed measles lacked vaccination records. The PSSE has recommended MMR vaccination for all hospital personnel without such documentation.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: measles, Outbreaks, vaccines and immunisation, Healthcare workers, Poland

ABSTRACT ID: 55

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7.3. Measles outbreak, Lebanon, 2018

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Background:

Despite the availability of free and safe vaccine in Lebanon, measles outbreaks continue to occur in periodic trend of 4-5 years. The last outbreak was in 2018. Here we describe the epidemiological features of 2018 Measles outbreak in Lebanon.

Methods:

Measles is an immediately notifiable diseases using case-based approach. A suspected patient is any person presenting rash and fever, while confirmed is when tested positive for measles IgM or PCR. Patient is epi-linked if direct contact with another laboratory confirmed case occurred within the last 28 days. Upon notification, investigation is initiated including data collection, clinical sample collection and referral to National Measles Laboratory for IgM and/or PCR testing. Data are entered in national database using Epidata and analyzed using Stata. Weekly measles bulletin is posted on MOPH website.

Results:

From January to December 2018, 938 patients were classified as measles with 54% lab confirmed, 3% epi- linked and 43% clinical cases. The attack rate reached 16/10000. The most affected provinces were Baalbeck–Hermel (73/100000), Beqaa (52/100000) and Mount-Lebanon (11/100000). The circulating genotype was D8. 82% were Lebanese, and 18% Syrian. High risk groups were children under 5 years (93/100000) and children aged 5-9 years old (28/100000). 26% of children aged 1-9 years did receive at least one dose of measles containing vaccine. No death was reported. Patients were mainly reported by hospitals (69%).

Conclusions:

The high attack rate among children less 10 years indicates the need to enhance routine vaccination. Accelerated immunization activities were initiated in localities reporting measles cases.

Subject: Surveillance

Keywords: measles , outbreak, surveillance

ABSTRACT ID: 416

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7.4. Just another brick in the wall? School-based clustering of measles susceptibility

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Background:

Global elimination of measles is an important WHO-goal. To reach this goal, the target for vaccination coverage is set at 95% in 2020, both at the national and district level. In many places, the vaccination coverage exceeds, or is close to, this threshold. Nevertheless, outbreaks of measles still occur - indicating that we need to look beyond the district level. Susceptible individuals can be clustered based on more than geographical location alone. For example, in schools many susceptible individuals may gather. As like-minded parents often send their children to the same schools, multiple children within the same class group may not be immunized due to their parents‘ beliefs regarding vaccination (e.g. anthroposophic schools). Moreover, many school-aged children have yet to receive the second dose of a measles-containing vaccine. These children are thus not fully protected against the disease.

Methods:

To assess the impact of school-based clustering of measles susceptibility on outbreak risks, we conduct a case-study for Flanders, Belgium. We use Stride, an individual-based simulator for the transmission of infectious diseases. An individual-based model can account for heterogeneities in contacts and immunity status.

Results:

We find that, as clustering levels increase, the risk for measles outbreaks increases, even though the initial number of susceptible individuals is the same in all scenarios. The closer the overall immunity level of the population is to the theorized herd immunity threshold, the stronger these effects.

Conclusions:

To make the final push towards measles elimination, heterogeneities, such as school-based clustering, should be taken into account. Furthermore, the usefulness of administering the second dose of the vaccine at an earlier age, or the organization of catch-up campaigns in under-immunized schools, should be examined.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Measles, Computer simulation, Vaccination, Disease outbreaks, Uncertainty, Belgium

ABSTRACT ID: 712

PRESENTED BY: Elise Kuylen / elise.kuylen@uantwerpen.be

7.5. Who is at risk of measles in EU/EEA?

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Background:

Measles is targeted for elimination in the WHO European Region yet outbreaks are still occurring in several EU/ EEA Member States (MS). Vaccination coverage (VC) of at least 95% with two doses of measles-containing vaccine (MCV) is recommended to interrupt transmission.

We describe the epidemiology of measles cases, VC and estimate the proportion of unimmunised individuals born in the EU/EEA between 1999 and 2019 in order to inform the prioritization of interventions to reach elimination.

Methods:

We analysed measles cases reported to the European Centre for Disease Prevention and Control by 30 EU/EEA countries between 1 April 2009 and 31 March 2019 and assessed WHO/UNICEF VC data. To estimate the number and proportion of people in birth cohorts 1999 to 2019 that were unimmunised, we multiplied the population (source: Eurostat 2018) by the proportion unimmunised two years later (source: WHO/UNICEF), subtracting the number of cases reported (source: ECDC) among that birth cohort.

Results :

The median age of cases increased from 10 years in 2009/10 (IQR: 2-18 years) to 17 years in 2018/19 (IQR 3-31 years). In 25 of 30 countries with most cases in adults, the median age increased from 12 to 22 years. The number of MS achieving 95% VC for two doses of MCV fell from 14 in 2007 to four in 2017. An estimated 5,153,548 (4.9%) of individuals born in 1999-2019 are unimmunised to measles.

Conclusions :

Older age groups affected, suboptimal vaccination coverage and a large pool of unimmunised individuals accumulated over time pose challenges to reach and sustain elimination. In addition to high quality routine vaccination programmes, interventions to identify and close immunity gaps and opportunities for vaccination checks should be introduced as appropriate.

Subject: Surveillance

Keywords: measles, vaccine-preventable diseases, elimination, adults, susceptible

ABSTRACT ID: 769

PRESENTED BY: Nick Bundle / nick.bundle@ecdc.europa.eu

7.6. Investigation of measles cases in the Kouibly health district, Cote d'Ivoire, March 2019

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Background:

In 2018, Côte d'Ivoire introduced the measles and rubella vaccine at the age of 9months. Mortality rate is 2% annually. Vaccination coverage rate in the district in 2018 was 71%. Analysis of the biological results from January to March 2019 of measles identified outbreak in Kouibly district. We investigated to identify risks factors and recommended control measures.

Methods:

A case-control study was conducted. The confirmed case was any suspected case who resulted positive to measles Immunoglobulin M (IgM).We selected 1 case for 2 Controls. A control was a person sharing same characteristics with the case but without measles symptoms. A total of 32 cases and 64 controls were included. We did an active search through the Health centers and a house-to-house for additional cases. The attack rate and Odds ratio (OR) were calculated for risk factors. Biological tests were obtained from the laboratory. Data were analyzed using Epi Info 7.

Results:

A total of 32 confirmed cases were found, attack rate 14.7 per 100,000. Median age was 5 years (5months to 38 years).19 cases (65.62%) were from Flansobly health center. Sex ratio Female/Male was 3.6. The most affected age group was 5-14 years. Zero death was notified. 21 cases (59.37%) were unvaccinated. OR for vaccine status was associated to measles and statistically significant [6.09(CI:2.3-15.6)p=0.001], promiscuity [1.03(CI:0.17-5.97)p=1] and displacement [2.04(CI:0.61-6.81) p=0.36] were associated but not statistically significant. Seven samples were positive for measles IgM.

Conclusions:

Measles outbreak occurred in Kouibly health district possibly due to unvaccinated people. Promiscuity and displacement were associated but not statistically significant. We recommended proper case management, population sensitization and reactive vaccination as response to the outbreak.

Subject: International health and migration

Keywords: Measles, Health, Côte d'Ivoire, Investigation

ABSTRACT ID: 801

PRESENTED BY: BONZOU Adjoua Jeanne / jadjoua571@gmail.com

Track 8: Vaccine-preventable diseases (2): surveillance

Moderator:

Jussi Sane

Abstracts

8.1. Impact and effectiveness of the 10-valent pneumococcal conjugate vaccine on invasive pneumococcal disease among children under 5 years of age in the Netherlands

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Background:

In 2011, the 7-valent pneumococcal conjugate vaccine (PCV7) was replaced by a ten-valent vaccine (PCV10) in the Netherlands. Studies assessing the effect of PCV10 are limited. We report the effect of switching from PCV7 to PCV10 by estimating both impact and effectiveness against invasive pneumococcal disease (IPD) in children aged <5 years.

Methods:

We included IPD cases reported between 2009-2018 via the national surveillance system. To assess the overall effect of the PCV10 vaccination program, we compared IPD incidence 6-7 years after PCV10 introduction (2017-2018) to the two years just before the switch to PCV10 (2009-2010). We estimated vaccine effectiveness (VE) using the indirect cohort method, comparing vaccination status (at least two vaccine doses) in IPD-cases caused by PCV10 serotypes (cases) to non-PCV10 IPD-cases (controls), in children eligible for PCV10 (born after March 2011 and at least five months old).

Results:

The incidence of IPD decreased from 8.5 (n=157) in 2009-2010 to 7.1 per 100,000 (n=124) in 2017-2018 (Incidence rate ratio (IRR) 0.84, 95%CI: 0.67-1.07). IPD caused by the additional serotypes included in PCV10 reduced by 92% (IRR 0.08, 95%CI: 0.02-0.26). There was a non-significant increase of non-PCV10 IPD (IRR 1.19, 95%CI: 0.91-1.55). Among 228 children IPD-cases eligible for PCV10, the overall VE was 90% (95%CI: 63-97) and did not differ by sex or age at diagnosis.

Conclusions:

Six years after switching from PCV7 to PCV10, we observed high effectiveness of PCV10 and a decline in the overall incidence of IPD cases with a large decrease of IPD due to additional PCV10 serotypes. The slight increase of non-PCV10 IPD suggests serotype replacement over time warranting continued monitoring to assess the sustained impact of PCV10 on IPD epidemiology.

Subject: Burden of disease

Keywords: Invasive pneumococcal disease, impact of vaccination, vaccine effectiveness, pneumococcal conjugate vaccination

ABSTRACT ID: 156

PRESENTED BY: Laurene Peckeu / l.peckeu.mcj@gmail.com

8.2. Parallel change of pneumococcal serotype distribution in childhood carriage and invasive disease following a pcv13-to- pcv10 vaccination programme switch

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Background:

Since the pneumococcal conjugate vaccination (PCV-)programme switch (PCV13-to-PCV10 in 2015/2016), a prospective nasopharyngeal carriage study complements the Belgian invasive pneumococcal disease (IPD-) surveillance to monitor the serotype distribution of Streptococcus pneumoniae (Sp) in children under two years of age.

Methods:

From January 2016 until April/December 2018 (carriage/IPD), Sp isolated from single nasopharyngeal swabs (carriage- isolates) from healthy children and Sp cultured from blood, cerebrospinal, pleural or joint fluid (IPD-isolates) were investigated in parallel. Nurses yearly collected 751-1100 swabs in 85-112 randomly selected day-care centres and 91-94 hospital laboratories participated in the IPD-surveillance. Sp-strains were serotyped by Quellung-reaction. The proportion of age-appropriate PCV10-vaccinated children in the carriage study increased from 0.0% in 2016 to 82.1% in 2018. Reported changes were significant ($p<0.05$) in Chi^2 analysis.

Results:

In total, 1961 carriage-strains and 352 IPD-strains were analysed. The proportion of PCV13-vaccine serotypes increased (2016 vs 2018) from 6.0% to 9.9% in carriage and from 13.5% to 35.8% in IPD, mainly due to an increase in 19A (carriage: 0.3%-7.0%, IPD: 2.1%-27.0%). Other consistent changes in carriage were noted for 6C (1.0%-6.6%) and 15A (7.0%-3.4%). The overall dominating IPD-serotypes during this three year period, were 19A (16%), 12F (11%), 33F (8%), 10A (7%) and 24F (7%). These serotypes accounted for only 14.0% of Sp-strains in carriage, in which serotypes 23B (14.3%), 23A (8.5%), 15B (8.0%), 11A (7.9%), 21 (7.5%), 10A (5.9%) were dominating.

Conclusions:

PCV10-induced cross-protection against serotype 19A was not confirmed in the current study, that revealed a quick re- emergence of serotype 19A in both carriage and IPD in children below two years of age as their PCV10-vaccinated proportion enlarged. By combining carriage-assessment with IPD-surveillance we provide further basis for policy-making on PCV-programme options.

Subject: Surveillance

Keywords: Streptococcus pneumoniae,Nasopharyngeal carriage, Day-care, Invasive pneumococcal disease, Surveillance, Pneumococcal conjugate vaccines

ABSTRACT ID: 3

PRESENTED BY: Ine Wouters / ine.wouters@uantwerpen.be

8.3. Host factor associated mortality following invasive pneumococcal disease in adults in France

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Background:

Concurrent comorbidities may increase mortality following invasive pneumococcal disease (IPD). In France, anti-pneumococcal vaccination in adults is recommended for risk groups (immunosuppressed or with at-risk conditions/diseases). During 2014-2017, we conducted a hospital-based study of IPD in adults to identify factors associated with fatality.

Methods:

We included IPD cases, excluding meningitis, in adults from 25 acute-care hospitals in six French regions (7% of population). Deaths were those occurring among IPD cases during the first 30 days of hospitalization. Infectious disease specialists collected clinical/microbiological data on all cases. We calculated adjusted Hazard ratios (aHR) using parametric survival analysis.

Results:

During 2014-2017, 908 cases (median age 71 (range 18-101) years) and 188 (21%) deaths were recorded; 74% had pneumonia, 84% belonged to a risk group and 31% had >2 chronic diseases/conditions; 10% of immunocompromised or at-risk cases and 9% of those who sought healthcare in the previous year received a pneumococcal vaccine. Case-fatality increased with increasing age (aHR per year 1.04, 95%CI:1.0-1.1) and was higher among cases with >2 chronic conditions (aHR 1.9; 95%CI:1.2-3.0) compared with others. Fatality was also higher among cases with shock (aHR 7.6; 95%CI:4.6-12) or malignant solid tumor (aHR 2.6; 95%CI:1.7-3.8), but lower among cases admitted to an ICU (aHR 0.22; 95%CI:0.13-0.36), and those who had received at least one dose of anti- pneumococcal vaccine (aHR 0.22; 95%CI:0.09-0.56). Two emerging serotypes (10A and 23A) were independently associated with fatality.

Conclusions:

Concurrent comorbidities increased mortality following IPD. The low proportion of cases vaccinated even among those who had previously sought healthcare suggests missed opportunities for vaccination and low vaccination coverage among risk groups. We recommend enhancing efforts to improve vaccination coverage in risk groups

Subject: Surveillance

Keywords: Invasive pneumococcal disease,pneumococcal conjugate vaccine, surveillance, Streptococcus pneumoniae, mortality

ABSTRACT ID: 425

PRESENTED BY: Kostas Danis / costas.danis@santepubliquefrance.fr

8.4. Indirect effects of Paediatric Conjugate Vaccines on Invasive Pneumococcal Disease in Older Adults

Pilar Ciruela [1]

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Poster Abstracts

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Background:

To assess the indirect effect of paediatric PCV13 vaccination on people aged 65 years and over with IPD in Catalonia (Spain) and determine predictive factors of the case fatality rate (CFR) in this age group.

Methods:

IPD cases in people aged 65 years and over reported to the Microbiological Reporting System of Catalonia during 2009-2016 were analysed. The indirect effect of PCV13 vaccination was calculated comparing the incidence rate (IR) in 2009 and 2014-2016. Predictors of mortality were determined using multivariate logistic regression.

Results:

During 2009-2016, 3,439 IPD cases were reported. The IR decreased (22%) in 2014-2016 vs 2009 (40.2 and 31.5 per 100,000 persons-year, respectively; p<0.001). The IR of PCV13 serotypes decreased (53%) and PPV23non13 serotypes increased (47%). Patients with chronic cardiovascular condition (19.1% vs. 12.5%; p=0.004) and immunodeficiency (14.5% vs 7.1%; p=0.013) declined in 2014-2016, while patients with 1 or more high-risk condition increased (20.7% vs 28.1%; p=0.009). In 2014-2016, there were 219/1,253 deaths (17.5%). The CFR was associated with age (85 years and over: aOR 2.91; 95%CI 1.89–4.48), meningitis (aOR 2.29; 95%CI 1.25–4.19), non-focal bacteraemia (aOR 3.73; 95%CI 2.00–6.94) and high risk comorbidities (aOR 1.89 95%CI 1.08-3.32). PPV23non13 serotypes were associated with lower mortality than PCV13 serotypes (aOR 0.54; 95%CI 0.34-0.86).

Conclusions:

The incidence of IPD decreased in people aged 65 years and over due to a reduction in PCV13 serotypes, although an increase in PPV23non13 serotypes was detected. The CFR was associated with age, meningitis, non-focal bacteraemia, high risk conditions and PCV13 serotypes.

Subject: Surveillance

Keywords: Streptococcus pneumoniae; IPD; PCV13; adults; case fatality rate; comorbidities

ABSTRACT ID: 611

PRESENTED BY: Pilar Ciruela / pilar.ciruela@gencat.cat

8.5. A comprehensive evaluation of the invasive meningococcal disease surveillance system in Ireland, 2012-2017

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Background:

National enhanced surveillance of invasive meningococcal disease (IMD) in Ireland aims to promptly identify and manage cases and monitor trends in the burden of disease, but it has never been evaluated. We assessed completeness of data, timeliness of notifications, sensitivity of mortality data, simplicity, usefulness, and flexibility of the surveillance system.

Methods:

We extracted IMD cases reported in the electronic surveillance system (CIDR), between 2012-2017 to evaluate completeness of selected variables, notification delay (time between onset and notification), laboratory reporting delay (time between specimen collection and laboratory notification), and sensitivity of mortality through probabilistic record linkage with the national death register. We conducted an online survey among stakeholders evaluating, on a 5-point scale, simplicity, usefulness, and flexibility of the system.

Results:

In 2012-2017, 467 cases were reported. Completeness of age, serogroup, vaccination status and outcome was 100%, 97%, 87%, and 82%, respectively. Completeness of vaccination status increased from 2012-2014 (57%) to 2015-2017 (90%). Overall, 47% of cases were notified within three days and laboratories reported 32% of results within seven days, although proportion of timely laboratory reporting increased from 25% in 2012-2014 to 38% in 2015-2017. Sensitivity of CIDR for mortality outcome was 89%.

Respondents' agreement on simplicity, usefulness, and flexibility was 62%, 46% and 6%, respectively. Users asked for more training, suggested automatic updating of laboratory fields and timely inclusion of enhanced variables on CIDR.

Conclusions:

Data completeness and sensitivity of the system is very high, however, timeliness of electronic laboratory notifications is sub-optimal. We recommend additional resources to reduce delays in laboratory notifications and to identify technical solutions to improve CIDR flexibility in order for the electronic system to support a timely public health response.

Subject: Surveillance

Keywords: Neisseria meningitidis, surveillance, evaluation, Ireland

ABSTRACT ID: 234

PRESENTED BY: Annalisa Quattrocchi / annalisaquattrocchi@hotmail.com

8.6. Impact of level of completeness of contact details on processing time of notifications in the German Surveillance System for infectious diseases

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Background:

Notifications of infectious diseases need to contain complete information to implement timely measures and prevent further transmission. Incomplete contact details may require additional investigations by local health offices before implementation of measures is possible. We analyzed completeness of contact details on notifications to determine its impact on duration of overall case processing.

Methods:

We randomly selected >300 notifications evenly distributed over the year 2017 and type of notifier from five local health offices. Contact details were defined complete if name, address and telephone number of the case were available and valid on the incoming notification. We defined duration of case processing as period between date of notification receipt until date of closure, corresponding to the date when investigations and measures were completed. We analyzed the impact of complete contact details on duration of case processing using Kruskal-Wallis test stratifying by mode of investigation (telephone or mail). We limited the analysis to notifications of vaccine-preventable and gastrointestinal diseases usually requiring investigations and implementation of measures.

Results:

We analyzed 2,051 notifications; 1,532/2,051 (75%) from local health offices preferring telephone and 519/2,051 (25%) preferring mail for investigations. Contact details were complete on 161 (8%) incoming notifications. Median duration of case processing increased from 1 (range 0-49) to 3 (range 0-264) days when contact details were incomplete in offices preferring telephone for investigation (p<0.001) and from 5 (range 0-65) to 6 (range 0-179) days in offices preferring mail for investigation (p=0.05).

Conclusions:

Completeness of contact details has a considerable impact on duration of case processing irrespective of the mode of investigation. Increasing the level of completeness of contact details on notifications may reduce duration of case processing including timely implementation of measures.

Subject: Surveillance

Keywords: Surveillance, data completeness,timeliness of case processing

ABSTRACT ID: 559

PRESENTED BY: Adine Marquis / marquisa@rki.de

MODERATED POSTER SESSION B
DAY 2: Thursday, 28 November 2019
15:40-16:40

Track 9: Healthcare-associated infections

Moderator:

Jan Walter

Abstracts

9.1. Non-invasive group A Streptococcal infections and the risk of puerperal fever: a case-control study following an outbreak in the Netherlands, July-August 2018

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Background:

We observed an increase in notifications of puerperal group A streptococcal (GAS) infections in July-August 2018 throughout the Netherlands without evidence for common sources. General practitioners reported a simultaneous increase in consultations for impetigo. We tested the hypothesis that the outbreak of puerperal GAS infections resulted from increased exposure to GAS via impetigo in the community.

Methods:

We conducted a population-based case-control study in October 2018 to assess peripartum exposure to possible GAS infections (impetigo, pharyngitis and scarlet fever) and childbirth-related risk factors using an online questionnaire. To be included, cases and controls had to have given birth in July-August 2018. Confirmed (notified and microbiologically positive) cases were recruited through municipal public health services, and probable (self-reported) cases and controls through social media. We calculated odds ratios (OR) and 95% confidence intervals (95% CI) with logistic regression analysis.

Results:

We enrolled 22 confirmed and 23 probable cases and 2,400 population controls. Contact with persons (80% household contacts) with impetigo was reported by 8% of cases and 2% of controls (OR 3.26, 95% CI 0.98-10.88) and contact with impetigo, pharyngitis or scarlet fever by 28% and 9% respectively (OR 4.12, 95% CI 1.95-8.68). The population attributable fraction for contact with possible GAS infections was 22%. In multivariable analysis, contact with possible GAS infections remained an independent risk factor (OR 4.28, 95% CI 2.02-9.09).

Conclusions:

We found an increased risk of puerperal fever after community contact with possible GAS infections. Further study of this association, including laboratory confirmation of non-invasive GAS infections, is warranted. We recommend advising peripartum women to avoid close contact with persons with possible GAS infections and to seek diagnosis and treatment for these contacts where feasible.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Puerperal fever, Group A Streptococcal infections, Impetigo, Case-control study, The Netherlands, Outbreak investigation

ABSTRACT ID: 89

PRESENTED BY: Jossy Van den Boogaard / jossy.van.den.boogaard@rivm.nl

Poster Abstracts

9.2. Hospital-acquired infections in adult intensive care units in Ireland: Comparison between two national point prevalence surveys

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Background:

In the absence of a national surveillance of hospital-acquired infections (HAI) in intensive care units (ICU) in Ireland, we compared the prevalence of HAI from Irish adult ICUs participating in two national point prevalence surveys (PPS) undertaken in May 2012 and 2017, respectively.

Methods:

We performed descriptive analysis of patient characteristics and HAI data gathered from ICUs participating in both surveys, using a common European protocol. We estimated HAI prevalence and 95% confidence intervals (CI), and performed logistic regression analyses, adjusting for age, gender, disease prognosis, surgery since admission, length of admission, and hospital type.

Results:

There were 25 hospitals and 28 adult ICUs (>90% national coverage) that performed both PPS (2012; n=153 patients and 2017; n=162). Age, gender and risk factor prevalence was similar between PPS. In 2017, fewer patients were categorised with severe underlying conditions, compared with 2012 (36% versus 48%; p=0.035). In 2017, the HAI prevalence was lower than 2012 (25%; 95%CI:19%-32% and 27%; 95%CI:20%-34%, respectively), although not significant after adjusting for differences in patient case mix. However, factors associated with higher HAI prevalence differed between the two surveys.

Pneumonia was the most prevalent HAI in both PPS (42% and 52%), followed by surgical site infections in 2012 (15%) and bloodstream infections in 2017 (13%). Enterobacteriaceae were the most frequent microorganisms in both PPS (27% and 30%).

Conclusions:

HAI remain an important target for improvement. Although differences in point prevalence of HAIs and patient characteristics was observed between the two surveys, more accurate information on HAI burden and variation over time is lacking. We recommend resourcing and implementing a routine HAI-ICU surveillance programme, to estimate incidence and monitor trends of HAI in ICUs.

Subject: Surveillance

Keywords: Intensive care units ,Healthcare-associated infections, prevalence, Ireland

ABSTRACT ID: 240

PRESENTED BY: Annalisa Quattrocchi /

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9.3. Intensified surveillance and extended hygiene measures to control a hospital outbreak of Clostridioides (Clostridium) difficile ribotype 027 (RT027) in Germany 2018

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Background:

A 400-bed hospital in Central Germany reported an outbreak of Clostridioides (C.) difficile infections (CDI) in February 2018. Within one month 14 CDI patients on three wards were identified. We describe interventions from February to December 2018 to confirm and control the outbreak. A major goal was raising awareness of stakeholders for implementing measures to prevent nosocomial transmission.

Methods:

We implemented an intensified CDI surveillance. All C. difficile isolates were collected for ribotyping and core genome Multi Locus Sequence Typing (cgMLST). Medical records of all CDI cases were used for descriptive epidemiology. We defined probable cases as CDI in- or outpatients diagnosed at the hospital laboratory in 2018 with an epidemiological link to a confirmed case before cgMLST. Cases were confirmed by cgMLST. Extended hygiene and preventive measures were implemented stepwise during the progression of the outbreak.

Results:

Between January 24 and December 31 2018, 110 CDI patients were reported in three hospital sites and isolates from 85 patients were available for cgMLST. Of 52 (61%) isolates of ribotype (RT) 027, 39 isolates (75%) belonged to 2 different clusters using cgMLST. Twenty eight confirmed and five probable cases were linked to cluster 1 (February-December) and the second cluster comprised 11 confirmed cases (April). Infection control measures included strict isolation of CDI patients, additional hand washing, intensified environmental cleaning with sporicidal disinfectants, final disinfection with additional hydrogen peroxide nebulization and temporary ward closures.

Conclusions:

Rigorous infection control measures including sporicidal surface disinfection, and in this case also ward closures were necessary to limit the spread of C. difficile RT027. Molecular typing allowed justifying these measures to stakeholders by the ability to clearly differentiate between outbreak cases and non-cases.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Clostridium difficile, PCR ribotype 027,Outbreak, Multilocus Sequence Typing,Infection Control,Hospitals

ABSTRACT ID: 281

PRESENTED BY: Matthias Holfeld / matthias.holfeld@sachsen-anhalt.de

Poster Abstracts

9.4. Identified barriers and facilitating factors for infection control implementation within long term care facilities - A systematic literature review

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Background:

Healthcare-associated infections (HAIs) form a risk for patients and a burden for health care institutions and health care systems. Besides hospitals, this burden is high in Long Term Care Facilities (LTCFs). To prevent infections, staff needs to adhere to hygiene measures and regulations. In order to improve infection control in LTCFs, it is essential to identify barriers and facilitating factors for the implementation of these hygiene measures and regulations. This systematic literature review aims to make an updated inventory of barriers and facilitating factors for infection control within LTCFs.

Methods:

This study was performed according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. Pubmed, MEDLINE, and Cochrane Central Register of Controlled Trials and Cochrane Database of Systematic Reviews were searched for studies published in English between January 1998 up to July 2018. Barriers and facilitators for infection control were categorized according to the theory of planned behaviour and environmental theories used in intervention mapping.

Results:

Barriers and facilitating factors for professionals on the work floor differed for professionals in a management role. Most barriers occur on the organizational level. Few facilitating factors and barriers were identified on a societal and interpersonal level. Staff often lack materials, training, time, manpower, and cooperation from residents and visitors to perform (new) infection control measures. Management should be convinced of the measure's effectiveness and should acquire the trust of staff for successful implementation of infection control measures.

Conclusions:

To improve infection control in LTCFs, barriers and facilitating factors for working staff and management should be tackled equally. Acquiring buy-in from management and supplying staff with the necessary materials, time, and manpower appear to be most important.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Mycoplasma pneumoniae,Macrolide-resistant Mycoplasma pneumoniae,community-acquired pneumonia

ABSTRACT ID: 396

PRESENTED BY: Mitch van Hensbergen / Mitch.vanhensbergen@ggdzl.nl

9.5. Experience of surveillance of SSI in a teaching hospital in Ghana, a prospective cohort study

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Background:

Surgical site infections (SSI) impacts on the clinical, financial and social aspects of a patient, from an increased hospital stay to increased morbidity and mortality. Implementing a surveillance system for SSI helps institutions device strategies to reduce or prevent them. No surveillance systems exist to monitor SSI in Ghana.This study contributes to the knowledge of how to develop a surveillance system for control of SSI in hospitals in Ghana.

Methods:

A prospective active surveillance for SSI was undertaken at the general surgical unit of the Korle Bu Teaching Hospital from 1st July 2017 to 31st December 2018, with quarterly feedback of results to surgeons. it involved a daily surveillance of patients who had a surgical procedure, followed by a post discharge surveillance using both a healthcare personnel-based survey using a wound card and a patient-based telephone survey.

Results:

3267 patients had active surveillance and showed a 10% incidence risk of SSI, with an increased morbidity for patients who developed an SSI including spending an average of seven extra days in hospital and a relative mortality risk of 2.6. 48.3% of SSI were diagnosed in the post discharge setting using the post discharge healthcare personnel- based survey which showed a response rate of 48%. The SSI incidence risk reduced from 13.5% in the first quarter to 8.1% in the last quarter of the study period.

Conclusions:

This study highlights the high burden of SSI in terms of morbidity and mortality in a lower-middle-income country and reiterates the importance of a surveillance system with feedback for monitoring SSI. Post discharge surveillance is important and using a healthcare personnel-based survey may be an effective means of monitoring SSIs in that setting.

Poster Abstracts

Subject: Surveillance

Keywords: Surveillance, Monitoring, Surveillance system, Surgical site infections, Ghana

ABSTRACT ID: 567

PRESENTED BY: A. A. A. Antoinette Bediako-Bowan / abediako-bowan@ug.edu.gh

9.6. Outbreak of carbapenem-resistant Klebsiella pneumoniae, in Italy, 2018–2019: the role of patient transfers between hospitals in facilitating transmission (LATE BREAKER)

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Background:

A large outbreak of New Delhi metallo-beta-lactamase (NDM)-producing K. pneumoniae with 708 cases including bloodstream infections (BSI) involving 17 hospitals between November 2018 and August 2019, was reported in Tuscany, Italy. We hypothesized that hospitals that share more patients are more likely to be involved in the same outbreak. We therefore explored the effect of patient transfers between hospitals on the spread of the outbreak at national level.

Methods:

We mapped all cases of hospital-acquired confirmed NDM or metallo-beta lactamase positive K. pneumoniae (NDM/MDL KP) bloodstream infections (BSI), reported between January 2017 and August 2019 to the national surveillance for carbapenem-resistant Enterobacteriaceae. We recreated the Italian hospital network based on the 2017 hospital discharge records and used this: (i) as a proxy for patient transfers between the hospitals that reported at least one case in July-December 2018 and January-June 2019 ("outbreak hospitals"), and (ii) to compare the patient transfers between the "outbreak hospitals" with the frequency distribution of transfers obtained by 1000 random networks.

Results:

Sixty-six cases were reported within the study period. The number of reported cases increased over time (2017: n=14; 2018: n=23). Seven regions reported 29 cases between January and August 2019, of which most were reported from Tuscany (n=20). The 12 hospitals reporting cases in January-June 2019, shared 699 patients in the reconstructed network, while only 0.7% of the random networks of 12 hospitals had more transfers between them.

Conclusions:

This is the first large NDM/MBL KP outbreak in Italy, which mostly affected Tuscany. The outbreak spread more extensively in hospitals that exchange high number of patients. The structure of the hospital network should be considered when designing infection prevention and control strategies.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: antimicrobial resistance,Italy,hospital networks

ABSTRACT ID: 888

PRESENTED BY: Xanthi Andrianou / xanthi.andrianou@iss.it

Track 10: Emerging and vector-borne diseases, and International health (2): vector-borne diseases

Moderator:

Ines Steffens

Abstracts

10.2. Detection of West Nile Virus (WNV) in mosquito pools collected during 2017-2018 from the East Macedonia-Thrace region in Greece

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Background:

West Nile virus disease is a mosquito-borne and a major public threat in Europe. In Greece, it is mainly transmitted by Culex pipiens mosquitoes. The aim of the project is to investigate WNV presence in mosquito pools, as an early warning system for WNV circulation in the entomological surveillance program.

Methods:

Mosquito samples were collected by CO_2 traps in representative sites of Xanthi and Drama Regional Units (R.U.) in Northern Greece -69 and 15 respectively, during 2017-2018 (April-October). Samples were sent to the National School of Public Health (NSPH) for morphological identification. Culex pipiens were grouped in 84 pools of 1-200 adults. RNA extraction was performed and samples were analyzed by Real-Time PCR for WNV lineages 1 and 2. Positive samples were subjected to conventional PCR and purification for sequencing targeting the WNV E-region.

Results:

Eleven among 84 mosquito pools were positive for WNV presence. Positive pools were isolated from Xanthi R.U. (five from traps in July 2017- four in May, July, September and October 2018) and Drama R.U. (two from traps in August 2018). Two WNV disease cases were recorded in Xanthi R.U. (September/October 2018). Conventional PCR and sequencing will follow.

Conclusions:

Although no human cases were diagnosed in 2017, WNV was detected in mosquito pools. The virus re- emerged in 2018 and results concur with epidemiological data, as WNV circulation in the area has been noted in dates preceding human cases' detection. This highlights the importance of a stable early warning system, regarding mosquito monitoring and WNV circulation in areas/countries with high endemicity rates, reinforcing a crucial type of integrated surveillance (human/bird/insects/horse).

Subject: Surveillance

Keywords: West Nile Virus (WNV), entomoligical surveillance,mosquito poools,early warning system

ABSTRACT ID: 455

PRESENTED BY: Anastasia Flountzi /fanastasia@hotmail.com

10.3. Epidemiological Determinants Associated with the Spread of Dengue Fever in Mangu town Bara Kahu, Islamabad -October 2017

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Background:

Dengue has emerged as a vector-borne disease with an increase in number of cases with multiple outbreaks throughout Pakistan and hospitalization each passing year. It is one of the important public health emergencies of international concern as per International Health Regulations (IHR). In recent years number of cases in peri urban areas of Islamabad has increased significantly in post monsoon season

Objectives:To identify epidemiological determinants of Dengue for preventing future outbreaks in the study area i.e. Mangu Town Bara Kahu Islamabad

Methods:

A case control study was conducted in September 2017 to identify the epidemiological determinants for spread of Dengue Fever. Cases were those confirmed with IgM/IgG positive (n=59) living in Mangu Town Bara Kahu Islamabad and controls (n=200) were selected from the same area who were suspected cases with laboratory negative results. A standardized questionnaire was developed to collect data. A line list of cases was developed, and data was analyzed using Epi Info version 7.0

Results:

The presence of indoor stagnant water (OR 3.7), indoor larvae (OR 3.1), not using repellent (OR 2.7), and older age (OR 1.2) were independent determinants of dengue infection ($P<0.01$ for all). Male gender being more exposed to vector were predominant.

Conclusions:

Dengue has emerged in the poor peri-urban areas of Islamabad typically in post-monsoon seasons reaching peak during the months of September, gradually declining and waning off in the month of December. Health education campaigns for improved water storage practices. Indoor residual sprays in peri-urban high-risk areas 1 month before the transmission period, Community based environmental management were recommended.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Peri urban Areas. vector-borne diseases. Community based environmental management

ABSTRACT ID: 140

PRESENTED BY: Nadia Noreen / nadia.jamil3@gmail.com

10.6. Unprecedented increase in hantavirus infections in Slovenia from January to September 2019 calls for higher awareness on preventive measures (LATE BREAKER)

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Background:

Human hantavirus infection occurs mostly via aerosol inhalation of virus-contaminated rodent excreta. In Slovenia, notification of laboratory confirmed cases of hantavirus infection is compulsory. Between January and March 2019, Slovenia observed a 2,5-fold increase in case notifications compared to peak year 2012. We performed an epidemiological investigation to identify risk factors in order to implement prevention and control measures.

Methods:

We collected data on notified hantavirus infection cases from notification forms sent by clinicians/laboratories to the National Institute of Public Health (NIJZ). We invited all cases to be interviewed using a national approved questionnaire form. We collected data on demographics, environmental and behavioural risk factors.

Results:

Between January 1st and September 12th, 229 cases were notified to the NIJZ (11/100,000 population) peaking in May (n=57). Median age was 45 (range 10-91 years) with 69% males. Overall, 98% of infections were Puumala virus and 2% Dobrava virus. Hospitalization proportion was 86%, no deaths were reported. Three regions reported majority of cases (80%): Maribor, Ljubljana and Novo mesto. The case interview response rate was 51%. Six cases reported needing dialysis because of renal failure. The most frequent recognised risk factors were contact with rodent or their excreta (57%) during farm/woods work (54%) or during holiday cottage stay (44%).

Conclusions:

With the highest reported incidence of hantavirus infections to date in Slovenia, population awareness should be raised on the human-environmental aspects and rodent control with the implementation of countrywide promotion activities prioritising the most affected risk groups and regions. Studies on the impact of awareness raising communication strategies and preventive measures are needed.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Hantavirus infection, risk factors, preventive measures, awareness, Slovenia

ABSTRACT ID: 897

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Track 11: Food- and waterborne diseases (3): epidemiology and burden of disease

Moderator:

Werner Ruppitsch

Abstracts

11.1. Increased burden of disease associated with domestic campylobacteriosis in Sweden during the 2016/17 outbreak

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Background:

In 2016-2017, a large outbreak of domestic campylobacteriosis occurred in Sweden, with over 5000 more cases than expected, and apparently unusual severity. We compared cases during the outbreak with the preceding endemic period in terms of hospitalization, mortality, Disability-Adjusted-Life-Years (DALYs), and cost of illness.

Methods :

We defined the outbreak period as August 2016-May 2017 and the endemic period as March 2009-February 2014. For each period, we calculated: 1) the percentage of campylobacteriosis cases hospitalized with 95% Confidence Interval (CI), directly standardized by age and sex based on national hospitalizations for infectious diseases; 2) median and interquartile range (IQR) of hospitalization duration; and 3) case-fatality rates, compared with Fisher's exact test. Based on the number of cases above expected and its CI, we calculated the outbreak-attributable DALYs and cost-of-illness of the outbreak period, and associated ranges. DALYs and cost-of-illness for the endemic period were divided by 6, to obtain the equivalent of a 10-month comparison period.

Results:

The standardized hospitalization rate was 28% [95% CI: 25-30] during the outbreak and 25% [95% CI: 23-27] in the endemic period. The median duration of hospitalization was 3 days [IQR= 3] for both. The case-fatality rate was 0.16% during the outbreak and 0.13% in the endemic period (p=0.58). The outbreak-attributable DALYs were 4056 [range: 3339-4772] compared to an expected 1989. The outbreak-attributable cost of illness was 7.3 [range: 6.0-8.6] compared to an expected 3.3 million euros.

Conclusions:

Although severity was not greater, DALYs and cost of illness associated with Campylobacter tripled during the outbreak, due to the large number of cases. Quantifying the economic and public health impact of foodborne outbreaks provides additional evidence for the value of preventive measures.

Subject: Burden of disease

Keywords: Campylobacter, Cost of Illness, Global Burden of Disease, Disease Outbreaks

ABSTRACT ID: 69

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11.2. Hepatitis E virus among patients on haemodialysis in Croatia

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Background:

Hepatitis E virus (HEV) infection is an emerging infectious disease in many European countries. Previous studies in Europe indicate that HEV seroprevalence among patients on maintenance haemodialysis (HD) ranges from 1% to 37%. Risk factors for HEV infection among HD recipients are not fully understood. The aim of this study was to determine the prevalence and risk factors for HEV infection among HD recipients in Croatia, to propose recommendations for preventive measures.

Methods:

We implemented a cross-sectional study, inviting 515 individuals on HD from 6 medical facilities in 5 Croatian cities. Three facilities are in the continental region (Zagreb sites 1 and 2, and Osijek) and 3 in the coastal region (Sibenik, Dubrovnik and Pula). A self-administered questionnaire elicited risk factors for HEV infection: age, gender, food and water consumption, travel, household composition, animal contact, transfusion history and hemodialysis duration. Blood samples were tested for IgG HEV antibody using an enzyme immunoassay.

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Results:

A total of 392 HD recipients (76%) participated; their median age was 70.5 years (range 21-92 years) and 145 (37%) were female. IgG HEV antibodies were detected in 125 (32%) of participants. Multiple logistic regression indicated that age (OR=1.03; 95%CI=1.01-1.05) and living in the continental region (OR=3.55; 95%CI=2.12-5.96) were risk factors for HEV seropositivity.

Conclusions:

Almost 1/3 of HD recipients in Croatia had been exposed to HEV, which is among the highest seroprevalence rates reported in Europe. As HEV infection has been documented among pigs in the continental region of Croatia, we hypothesize that traditional pork-based food consumption could be an important risk factor, and should be investigated further. Routine HEV screening among HD recipients is recommended in this part of Croatia.

Subject: Burden of disease

Keywords: hepatitis E virus, haemodialysis, Croatia

ABSTRACT ID: 95

PRESENTED BY: Morana Tomljenovic/ tomljenovicmorana@gmail.com

11.3. Estimation of toxoplasmosis incidence in Germany from healthcare claims data, 2011 – 2016

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Background:

Toxoplasma gondii causes zoonotic infections contracted by contaminated food or infested cat faeces. Seroprevalence in Germany ranges from 20% (18-29 years) to 77% (70-79 years); however, incidence estimates regarding disease manifestation are lacking. This study aims to investigate disease incidence in order to provide prevention recommendations.

Methods:

We used healthcare claims data covering approx. 6 million insured inhabitants in Germany from 2011 – 2016. We considered patients incident if continuously negative for eight quarters baseline before infection and distinguished from chronic cases, which were excluded from the analysis. Cases were defined based on International Classification of Diseases codes (ICD-10) and Anatomical-Therapeutic-Chemical (ATC) Classification System. We calculated the estimated number of cases by adjusting counted cases to the general population based on age, sex and federal state distribution and analyzed by demographics and region.

Results:

We estimated between 6,700 cases of toxoplasmosis in 2016 (95%CI: 5,900-7,800) and 8.600 cases in 2011 (95%CI: 7,600-10,000). Incidence was lowest in 2016 with 8.1/100,000 and highest in 2011 with 11/100,000, respectively. Estimations resulted in the following number of cases for ocular (n=1,200; 95%CI: 940-1,900), cerebral (n=200, 95%CI: 74-880) and congenital (n=65, 95%CI: 25-750) toxoplasmosis in 2016. The majority of cases (n=5,200; 95%CI: 4,500-6,300) were unspecified toxoplasmosis. Highest incidence of ocular toxoplasmosis cases in 2016 was among women (1.7/100,000 women; 95%CI: 1.2-3.3/100,000), people aged 51-60 years (2.7/100,000 inhabitants; 95%CI: 1.6-5.1/100,000), living in the federal state of Hessen (2.5/100,000 inhabitants; 95%CI: 1.1-4.9/100,000).

Conclusions:

Although healthcare claims data collect information for purposes other than epidemiological surveillance, the clinical information contained in this large dataset demonstrates substantial number of toxoplasmosis cases in Germany. Public health and food safety authorities should start implementing toxoplasmosis specific prevention programs.

Subject: Burden of disease

Keywords: Toxoplasmosis, Healthcare claims data, Incidence estimates

ABSTRACT ID: 324

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11.4. Epidemiological patterns of tularemia in Slovenia in the last decade

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Background:

There is a lack of robust epidemiological data on tularemia in Slovenia. In this research, we describe the socio-demographic distribution, risk factors and incidence of identified tularemia cases in Slovenia to help drive further research in the area and help shape preventive strategies.

Methods:

Descriptive analyses of socio-demographic, exposure and clinical factors were conducted for identified tularemia cases using notifiable disease surveillance data. Likelihood ratio chi-square or Fisher's exact tests were computed to test for associations between the patients' characteristics and self-reported at-risk exposures in the studied period. Logistic regression analysis was conducted with the intent to adjust for confounding. We set the level of statistical significance at 5%.

Results:

The estimated annual incidence rate was 0.05/100,000 inhabitants. Of the 17 incidence cases, males predominated (ratio: 1.7:1) and were on average 49 years old (range: 6–88 years). The median time between the onset of the symptoms and diagnosis was two weeks. The predominant clinical signs were fever (92%) and lymphadenitis (92%). The median symptom duration was 30 days (range: 11–65 days). Exposures correlated with infection were ixode bites and lawn-mowing. Cases presented with the ulceroglandular form were more likely to have reported a tick bite as a source of infection.

Conclusions:

There is an increasing incidence over the study period. The lay public should be aware of protective measures against tularemia on lawn mowers and arthropod bites in risk areas. Clinicians must suspect tularemia in patients with ulcers and enlarged lymph nodes also after the tick bite.

Subject: Surveillance

Keywords: Epidemiology; Slovenia; surveillance; tularemia; zoonoses

ABSTRACT ID: 356

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11.5. Current hepatitis A epidemiology in Bulgaria: encouraging trends and need for more efforts

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Background:

Bulgaria has hepatitis A (HAV) incidence higher than the average in the European Union/European Economic Area. HAV vaccination is recommended, but coverage is negligible. This study aims to characterize current HAV epidemiology in Bulgaria.

Methods:

We included clinically manifested HAV cases by region and age group (2003-2017), and sex (2008-2017), notified in aggregate form to the National Center of Infectious and Parasitic Diseases. We compared incidence by sex (chi2 test) and age group (Wilcoxon rank-sum test). Temporal trends were assessed by negative binomial regression, calculating incidence rate ratios (IRR), and 95% confidence intervals (95%CI). The relationship between regional median hepatitis A incidence and 16 regional socioeconomic indicators, obtained from the National Statistical Institute, was assessed by Spearman correlation.

Results:

Average annual national incidence (2003-2017) was 39 cases/100000 (range 8.3-95/100000), with cyclic regional increases every 4-6 years. Four regions reached >300/100000 in peak years. Average annual incidence (2010-2017) was intermediate (20-199/100000) in 16/28 and low (2-19/100000) in 12/28 regions. A negative temporal trend in case numbers was detected in 11 regions (strongest in Ruse - IRR 0.77, 95%CI 0.69-0.87). Incidence was consistently higher among males (male/female ratio 1.2), and 1-14-year-olds (lowering in older age-groups) ($p < 0.05$). Four socioeconomic factors correlated positively with incidence, with strongest correlation (Spearman's rho 0.60, $p < 0.05$) for "% of population in 1-4 grade" and "% of population under the poverty line".

Conclusions:

The cyclic pattern is likely driven by fluctuations in herd immunity (natural infection/accumulation of susceptible children). Trends in some regions are encouraging, but additional work is needed in the identified higher-risk regions and population groups. For this epidemiological context, the World Health Organization recommends large-scale HAV vaccination as an effective approach.

Subject: Surveillance

Keywords: hepatitis A, epidemiology, prevention and control, socioeconomic factors

ABSTRACT ID: 429

PRESENTED BY: Savina Stoitsova / stoitsova@ncipd.org

11.6. Persisting physical and mental exhaustion is frequent after Q-Fever infection: results from a cohort study in Baden- Württemberg, Germany, 2014-2015

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Background:

Chronic Q-fever (QF) and persisting fatigue symptoms (FS) can develop after QF-infection with detrimental effects on patients' quality of life. We aimed at determining frequency and risk factors of FS and detecting chronic QF in a large QF-outbreak in Baden-Württemberg, Germany, in July 2014, providing evidence for clinicians and public health policy makers.

Methods:

For the cohort study among outbreak-cases, we defined FS as persisting physical and/or mental exhaustion one year after QF-infection; a possible chronic QF case as having phase-1 IgG titer >1:1024 longer than 3 months; a symptomatic case as having had fever and/or pneumonia during acute QF. Blood samples were taken at months 3, 6 and 12 after QF outbreak and analysed using indirect immunofluorescence assay. We collected information on FS via a questionnaire at month 12. We performed multivariable analysis calculating relative risks adjusted by age (aRR).

Results:

We included 74/299 outbreak cases. Median age was 51 years [IQR: 41-59 years]; 51% were male. 19% were hospitalised and 85% symptomatic. FS was reported by 41% of respondents; i.e. 40% (25/63) of symptomatic and 45% (5/11) of asymptomatic cases experienced FS. For symptomatic cases, both dyspnoea (aRR 2.2, 95%CI: 1.4-3.6) and pneumonia (aRR 2.0, 95%CI: 1.0-3.9) resulted in a twofold higher FS risk. The phase-1 IgG titer of one asymptomatic case indicated possible chronic QF establishment.

Conclusions:

Our study indicates frequent FS in symptomatic and in asymptomatic cases. Clinicians should consider undiagnosed previous QF when patients from QF-endemic regions present with FS. Serological-follow-up-testing for at least a year is needed to ensure timely chronic QF treatment. Due to these possible QF long-term health impacts, prevention of QF-infection, such as animal QF-vaccination, is highly recommended.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Q fever, long-term effects, zoonosis, cohort study, serology

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ABSTRACT ID: 536

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Track 12: Food- and waterborne diseases and zoonoses (4): public health microbiology

Moderator:

Saara Kotila

Abstracts

12.1. Genetic polymorphism and antimicrobial resistance of Salmonella enterica serovar Enteritidis isolates from veterinary and food sources in Bulgaria

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Background:

Salmonellosis is one of the most frequent food-borne infections. It is caused by contaminated food mainly of animal origin, although human to human transmission and numerous environmental contaminations may also be inflicted. Between 30 and 60% of the reported food-borne outbreaks in the EU are caused by Salmonella and this is the second most commonly reported food-borne infection causing gastroenteritis. Salmonella enterica serovar Enteritidis (S. Enteritidis) is the most widespread serovar in Europe and other parts of the world.

Methods:

In this study we analysed forty-nine S. Enteritidis isolates from veterinary and food sources in Bulgaria obtained during the period of eight years. We used multiple-locus variable-number of tandem repeats analysis (MLVA) genotyping and the classical antimicrobial resistance (AMR) disc diffusion method to test the diversity of the isolates.

Results:

Results showed that isolates were divided into twenty-four MLVA and nine AMR profiles. The calculated Simpsons diversity index was 0.956 for MLVA and 0.754 for AMR, respectively. The AMR testing revealed that 47% of the isolates were resistant to one and 4% to ≥4 antimicrobials. The most frequent resistotypes were resistance to sulphonamides (n=21) and sensitive to all compounds (n=9). The most frequent MLVA profiles were 3-5-3-3-11 (n=6); 5-13-2-3-11 (n=5); 5-9-2-3-8 (n=5); 6-12-2-3-11 (n=4); 5-10-2-3-11 (n=3); 4-5-3-3-9 (n=3). MLVA profiles are presented according to the order of the loci sequenced: SE1, SE2, SE9, SE3 and SE5.

We searched for similar S. Enteritidis MLVA profiles in published data. A partial match was found for some profiles only.

Conclusions:

It could be concluded that the MLVA profiles of S. Enteritidis obtained in this study (the first ones for Bulgaria) have not been frequently isolated in other counties.

Subject: Microbiology

Keywords: Salmonellosis; S. Enteritidis; Zoonoses; Genetic testing

ABSTRACT ID: 320

PRESENTED BY: Gergana Mateva / gerymat@abv.bg

12.3. Contribution of E. coli O111 pathotypes to the aetiology of gastrointestinal disorders in children under 2 years of age in the Czech Republic (2013-2017)

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Background:

Escherichia coli O111 serogroup consists of enteropathogenic (EPEC), enterohaemorrhagic (EHEC) and enteroaggregative E. coli (EAEC) pathotypes. The Czech national EHEC surveillance in children <2 years with gastrointestinal infections is laboratory based. Suspected EHEC isolates are sent to the National reference laboratory for E. coli and Shigella (NRL) for detection/confirmation of Shiga toxin genes. Stools from HUS patients are sent directly to NRL. The aim of this study was to determine pathotypes of E. coli O111 isolates collected from the national surveillance system in 2013-2017, in order to identify other pathotypes than EHEC which are of public health importance.

Methods:

During the study period, O111 strains from individual cases were tested by PCR for pathotype-specific virulence genes (stx1, stx2, stx subtypes, eae, estIA, estIB, elt, ipaD, aggR, aatA, aaiC). HEp-2 adherence assay was performed in case of inconsistent PCR results for EAEC. EAEC strains were tested for antimicrobial resistance by a broth microdilution method. Minimum inhibitory concentrations were determined according to the EUCAST breakpoints.

Results:

Of 198 collected O111 isolates, 96 (49%) were EAEC, 76 (38%) EPEC, six (3%) EHEC, and 20 (10%) did not belong to any of tested pathotypes. 82 (88%) of EAEC strains were resistant to broad-spectrum cephalosporins (AmpC beta-lactamase producers), identified in all five studied years.

Conclusions:

EHEC accounted for 3% of O111 strains. EAEC was the most frequent pathotype in symptomatic children <2 years with identified E. coli O111 serogroup. High proportions of O111 EAEC AmpC beta-lactamase producers were found through the whole study period. Further study is needed to identify the origin of EAEC O111-associated AmpC genes in order to reduce their dissemination.

Subject: Microbiology

Keywords: E. coli O111,Enteroaggregative E. coli, Antibiotic Resistance, Surveillance, Gastrointestinal Disorders

ABSTRACT ID: 400

PRESENTED BY: Petra Bohuslavova / petra.bohuslavova@szu.cz

12.4. Implementation of Prospective Whole Genome Sequencing for E. coli and Shigella: The Ongoing Canadian Experience

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Background:

The Public Health Agency of Canada implemented prospective whole genome sequencing (WGS) for E. coli and Shigella in June 2018, providing increased resolution compared to previous subtyping methods (pulsed field gel electrophoresis (PFGE), multiple-locus variable number tandem repeat analysis (MLVA)). We describe the impact of this change on multi-jurisdictional cluster detection and investigation in Canada.

Methods:

The National Microbiology Laboratory identifies multi-jurisdictional clusters of E. coli (using both MLVA and WGS) and Shigella (WGS). The results of E. coli MLVA and WGS cluster analysis were compared. Characteristics and trends of multi-jurisdictional E. coli and Shigella clusters and outbreaks identified in the two years pre-WGS implementation were examined and compared to those identified post-WGS implementation. Epidemiologic information was obtained to determine possible sources of illness.

Results:

The number of multi-jurisdictional E. coli O157 clusters detected and investigated was similar pre and post-WGS implementation (10 vs. 13). MLVA for E. coli was more timely than WGS for cluster detection and outbreak response. The number of Shigella clusters detected and investigated increased (10 vs. 34): international travel and sexual contact have emerged as common risk factors.

Conclusions:

The first year of prospective WGS for E. coli suggests the impact is less substantial than for other pathogens (e.g., Salmonella, Listeria). While national investigations for Shigella are rare, the increased number of WGS clusters identified has required the development of cluster assessment criteria and consideration of roles and responsibilities (e.g., in sexual transmission clusters). WGS continues to improve the detection of and response to foodborne outbreaks in Canada. Next steps toward full implementation include possible discontinuation of MLVA for E. coli, and decentralization of WGS analysis to provincial laboratories.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: E. coli, Shigella, whole genome sequencing, cluster detection, investigation

ABSTRACT ID: 433

PRESENTED BY: Philippe Bélanger / jennifer.cutler@canada.ca

12.5. Real-time Bacillus anthracis spores field detection from aerosol samples based on magnetoresistive sensor technology

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Background:

Bioterrorism is a subject of worldwide concern.One of the most dangerous bioterrorism agents is Bacillus anthracis,which causes fatal pulmonary infections.This agent produces spores,resistant to physico-chemical stress,easy to produce and disperse in aerosols.In such an event,fast public health measures must be taken to minimize casualties,which demand tools for real-time field detection.We propose a compact model biosensor for real-time detection of aerosolized B.anthracis spores.

Methods:

Known spore quantities(104) of a B.anthracis simulant(Bacillus cereus)were transferred from aerosols to an acqueous medium using a portable aerosol collector.Sampling efficiency was assessed by performing plate counts before and after aerosol collection.Samples were injected into a microfluidic system,where spores were conjugated with specific antibodies,which were after conjugated with magnetic nanoparticles(MNPs).MNP coverage of spores was assessed by Scanning Electron Microscopy(SEM) and Atomic Force Microscopy.Labeled spores were flowed over magnetoresistive spin-valve sensors,which detect the presence of magnetic fields.The sensors' output signals were sent to an electronic interface,recorded by an acquisition setup and post-processed in a proprietary software.

Results:

Plate counts showed 70-80% of spores were collected from 30 aerosolized samples.SEM and AFM showed uniform MNP coverage,with an average of 400 MNPs per spore.The sensors detected the presence of labeled spores in all of the 30 samples tested.

Conclusions:

Our prototype system was able to successfully detect B.cereus spores in all the samples tested in 30 minutes.We present a cost-effective and rapid diagnostic tool with public health applications.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: Bacillus anthracis,Biosensing Techniques,Nanotechnology,Microfluidics,real-time pathogen detection,field pathogen detection

ABSTRACT ID: 453

PRESENTED BY: Pedro Fonseca / pedrodobroes@gmail.com

12.6. Molecular epidemiology of Echovirus 30 in Europe, 2016-2018

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Background:

In 2018, five European countries reported an increase in echovirus 30 (E30) infections. We explored the genetic characteristics and evolution of the virus strains detected prior and during the outbreak.

Methods:

The EU/EEA countries were invited by ECDC to submit E30 VP1 sequences (>200 bp) from years 2016-2018. Sequences were analysed using Simple Sequence Editor and phylogenetic trees built using Molecular Evolutionary Genetics Analysis 7.0.

Results:

1688 E30 VP1 sequences were reported by 22 European countries. 1182 sequences were of acceptable quality and length for phylogenetic analysis, most of these obtained from cerebrospinal fluid samples (809/1182; 68%). Sequences were divided into eight phylogenetic groups (G1-G8) based on 5% nucleotide divergence. Most sequences belonged to G1 (n=687) followed by G6 (n=263), G2 (n=166), G4 (n=56), G8 (n=4), G3 (n=3), G5 (n=2) and G7 (n=1). G2 viruses dominated in 2016 (128/250; 51%), whereas most sequences obtained in 2017 and 2018 belonged to G1 (279/456; 61% and 330/476; 69%, respectively). Country variation was observed: G1 was identified as the most prominent genetic lineage in the United Kingdom, Ireland, Norway and Germany already in 2016 and 2017. In 2018, G1 viruses continued to circulate elsewhere in Europe but were replaced by G6 viruses in the United Kingdom (92/142;65%).

Conclusions:

This study describes genetic diversity of E30 outbreak strains and the temporal and geographical dynamics of individual phylogenetic groups. These are important to monitor to understand causes of the outbreak as well as outcomes of it. Further analysis will illuminate the relationship of recombination events in genotype replacements.

Subject: Microbiology

Keywords: Human Enterovirus B, echovirus, epidemics, genetic evolution, Europe

ABSTRACT ID: 686

PRESENTED BY: Eeva Broberg / Eeva.Broberg@ecdc.europa.eu

Poster Abstracts

Track 13: HIV, sexually transmitted infections and viral hepatitis (2): intervention

Moderator:
Erika Duffell

Abstracts

13.1. Piloting an algorithm to guide clinical treatment decisions among notified partners of men having sex with men (MSM) with syphilis in Rotterdam, the Netherlands

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Background:

The Sexual Health Centre (SHC) Rotterdam introduced a decision guide for presumptive partner treatment (PPT) for syphilis. It aimed to identify partners at lower risk for infectious syphilis in order to avoid overtreatment. Those partners were offered standard testing, and treatment or follow-up consultation; partners at higher risk would be treated presumptively (without awaiting laboratory confirmation).

Methods:

To assess the PPT algorithm performance, we reviewed all consultations with notified partners of men who have sex with men (MSM) diagnosed with syphilis in the SHC from 1 February to 31 December 2017. The algorithm is a 12-parameter binary decision tree with two possible outcomes: 'presumptive treatment' or 'await lab results'. We calculated sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) to evaluate the algorithm against clinical outcomes.

Results:

Among all consultations, 12% (16/135) had syphilis. In 35 consultations, the algorithm indicated 'await lab results'; 6% (2/35) subsequently tested positive. 'Presumptive treatment' was indicated in 74% (100/135). Among those, 86% (86/100) tested negative, all of whom reported their last sexual contact within the previous eight weeks. The algorithm sensitivity and specificity were 88% (14/16) and 28% (33/119), respectively, with a PPV of 14% (14/100) and NPV of 94% (33/35). The algorithm indication was followed in 81% (110/135).

Conclusions:

While PPT can prevent further transmission, it may lead to overtreatment. This algorithm avoided overtreatment of nearly a quarter of consultations and identified most MSM with infectious syphilis. Potential overtreatment of some partners is warranted, given the large proportion who were within 8 weeks of last sexual contact, when tests may not yet be able to detect syphilis. We recommend inclusion of this algorithm into routine sexual health practice.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Syphilis, Partner treatment, MSM, The Netherlands

ABSTRACT ID: 19

PRESENTED BY: Anna Loenenbach / aloenenbach@gmail.com

13.2. Need for tailored counselling by STI health care providers among the high-risk MSM engaging in chemsex

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Background:

Men who have sex with men (MSM) are increasingly using drugs during sex ('chemsex') and this has been associated with several health harms, including an increased risk for sexually transmitted infections (STI). Little evidence exists on the need for professional counselling among MSM engaging in chemsex.

Methods:

In 2018, 785 MSM were recruited at eight Dutch STI clinics, of which 511 MSM (65%) completed an online questionnaire about chemsex and needs for professional counselling. Questionnaire data were linked to patients' most recent STI laboratory test results. Chemsex was defined as using cocaine, crystal meth, designer drugs, GHB/GBL, ketamine, speed or XTC/MDMA during sex in the past six months.

Results:

Chemsex was reported by 41% (209/511). Among chemsex-MSM, 36% had a recent STI diagnosis and 26% was known HIV-positive. The need for professional counselling was reported by 23% (48/209). This was similar for MSM with and without a recent STI diagnosis (23% vs. 21%, p=0.68), and similar for MSM who were known HIV-positive and MSM who were HIV-negative (26% vs. 21%, p=0.61). STI health care providers (56%) and experts on drugs (46%) were the most reported sources for counselling. Increasing self-control (52%), safer use of drugs (44%) and reducing the risk of acquiring HIV (31%), bacterial STI (31%) and hepatitis C (29%) were the most mentioned topics to discuss.

Conclusions:

Our study shows that one in four MSM who visited the STI clinic and engaged in chemsex report a need for professional counselling. MSM report STI health care providers to be the trusted source to counsel on chemsex issues. STI clinics might be most suitable to discuss self-control and safer use of drugs alongside regular STI prevention and care.

Subject: Surveillance

Keywords: chemsex, men who have sex with men, counselling, sexually transmitted infections, human immunodeficiency virus

ABSTRACT ID: 182

PRESENTED BY: Ymke Evers / ymke.evers@ggdzl.nl

13.3. Seroprevalence and risk factors of hepatitis B and C infection using opt-out testing in a London emergency department

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Background:

UK policy promotes innovative strategies to diagnose viral hepatitis. Previous studies observed low uptake of hepatitis testing in London. Emergency department (ED) is considered as a potential setting for reaching under-served populations. We describe seroprevalence and risk factors from opt-out hepatitis B (HBV) and hepatitis C (HCV) testing of patients attending a London ED

Methods:

The study was done in two funding phases 12 Oct 2016 – 15 Feb 2017 and 12 Dec 2017 – 31 May 2018. ED attendees aged +16 years having blood tests were tested for HBV surface antigen (HBsAg) and HCV Antibody (Ab) using an electronic preselected blood test order set; followed by reflex HCV-Ag testing if positive for HCV-Ab. Duplicate ED attendances were removed from the dataset. We applied Poisson regression to identify risk factors and estimate the prevalence ratio (PR).

Results:

Hepatitis testing uptake for HBV and/or HCV was 76% (27,933/ 36,865). The overall seroprevalence of HBsAg and HCV- Ag were (0.8%, 95% confidence interval [CI] 0.7%-0.9%) and (0.9%, 95%CI 0.8-1.0%) respectively. In the adjusted model, risk factors for HBsAg positivity were being male (PR: 1.6, 95%CI 1.2-2.1), non-White British ethnicity (PR›4; particularly Black (PR: 14.4, 95%CI 8.3-24.8) or Asian (PR 13.4, 95% CI 7.1-25.0), being homeless (PR: 1.9, 95% CI 1.0-3.5) and being HIV positive (PR: 4.1, 95%CI 1.9-8.9). For HCV-Ag positivity, risk factors were identified as male (PR:2.5, 95% CI 1.7-3.5), age 30-49 years (PR:3.6, 95% CI 2.2-6.0), homeless (PR:17, 95%CI 13-22), and HIV positive (PR:2.8, 95% CI 1.5-5.1).

Conclusions:

Opt-out testing using preselected ordering at ED enables high uptake of hepatitis testing in under-served groups. Our findings encourage consideration of strategies for hepatitis diagnosis and linkage to care in ED.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: hepatitis B, hepatitis C,Emergency department,electronic preselected blood testing,opt-out testing

ABSTRACT ID: 210

PRESENTED BY: Basel Karo / baselkaro@gmail.com

13.4. Exploring knowledge and information needs regarding chronic hepatitis B screening using respondent-driven sampling: an online randomized recruitment method

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Poster Abstracts

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Background:

The Dutch Health Council recommended chronic hepatitis B (HBV) screening for first-generation immigrants originating from intermediate/high HBV endemic countries. Our aim was to explore knowledge and information needs regarding chronic HBV and its screening among Moroccan immigrants, and to explore how to recruit this population using respondent-driven sampling (RDS) optimally. This provides Dutch Municipal Health Services useful insights on how to reach and inform immigrants.

Methods:

We used RDS in combination with randomized recruitment strategies. First- and second-generation Moroccan immigrants were asked to fill in an online questionnaire and forward this to four Moroccans. Collected data included knowledge of disease and screening, and willingness to receive information and screen. Participants were randomized to one of three recruitment strategies: no incentive for filling in the questionnaire nor for successfully recruiting each contact, an incentive for filling in the questionnaire and for successfully recruiting each contact, and a gamified element as non-monetary incentive to stimulate peer-recruitment.

Results:

Preliminary analyses show a sample of 59 Moroccans (17-59 years), of which 63% was second-generation and 76% was female. Of these, 46% would like to have information about chronic HBV, while average knowledge score was 5.02 (0-10). Over 60% of participants intends to participate in chronic HBV screening, and would also recommend this to their (grand)parents. Using a monetary incentive seemed to be the most promising strategy in terms of number of recruitment waves (max:3). A gamified non-monetary incentive was least effective in stimulating peer-recruitment (max:0).

Conclusions:

Despite the limited level of knowledge and information needs, the majority of Moroccan immigrants had a positive screening intention. The next step is to determine whether online RDS can be applied to reach other immigrant groups.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: chronic hepatitis B, online respondent-driven sampling, digital health, immigrants, Moroccan, Netherlands

ABSTRACT ID: 319

PRESENTED BY: Nora Hamdiui / nora.hamdiui@rivm.nl

13.5. Can nail salon operators keep you safe? Research leading to municipal regulation in the Wellington region, New Zealand

Annette Nesdale [1]

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Background:

People having pedicures or other nail services risk infection (viral hepatitis, HIV, bacteria, or fungi) if their skin is cut or broken and infection control measures are inadequate. In New Zealand, salons offering nail services are unregulated with no enforceable standards or training requirements unless through municipal bylaws. The Wellington region (population ~473,000) has no bylaws and an increasing number of nail salons. This study aimed to:

- assess knowledge and infection control practices of nail salon operators
- provide local Councils with data on the health risks from nail salons

Methods:

Regional Public Health surveyed nail salons in the Wellington region. Operators were interviewed on-site using a questionnaire focused on knowledge of health risks, salon and equipment cleaning, staff qualifications, and attitudes towards regulation. Infection control advice was provided if issues were identified. Data analysis utilized Epi Info7 with proportional significance assessed by Chi square and a two-tail Mantel-Haenszel.

Results:

Fifty seven of the region‘s 127 nail salons participated. Lack of knowledge and inadequate infection control was common, with only 12% reporting adequate disinfection, sterilisation and storage of equipment. Nineteen percent of operators could not name any health risks associated with nail treatment, while 46% of salons did not ask customers about any pre-existing health conditions. Salons without adequate trained staff were three times less likely (p= 0.007) to have a written cleaning schedule and six times more likely (p=0.02) to cut away thick heel skin with a blade. Overall, 93% operators supported regulation.

Conclusions:

Infection control knowledge and practices in nail salons in the Wellington region are poor. This research and subsequent media coverage directly led to two Councils consulting with their communities about nail salon regulation.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Blood Borne Pathogens, Nails, Infection Control , Policy, Knowledge

ABSTRACT ID: 15

PRESENTED BY: Annette Nesdale / annette.nesdale@huttvalleydhb.org.nz

Track 14: Tuberculosis and other respiratory diseases (excluding viruses) (1): surveillance and modelling

Moderator:

Daniel Thomas

Abstracts

Poster Abstracts

14.1. Using Bayesian spatial models to map and to identify geographical hotspots of multidrug-resistant tuberculosis in Portugal

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Background:

Multidrug-resistant tuberculosis (MDR-TB) is increasing worldwide and it represents a major threat against tuberculosis eradication. In 2017, in Europe, 3.7% of all TB cases were MDR-TB, ranging from 0–25.4%. In Portugal, this proportion was 1%, however incidence is not homogeneous across the country. Control strategies need to be adjusted in potentially high risk areas, with hypothetical active transmission of MDR-strains. To identify such areas, we investigated if MDR-cases are overrepresented in some municipalities. Spatial distribution of MDR-TB and non-MDR-TB notification rates were compared throughout the country.

Methods:

Notifications of MDR-TB and non-MDR-TB cases according to municipality (n=278), year, age group, and sex were obtained from the national TB Surveillance System (SVIG-TB) for the period 2000-2016. Hierarchical Bayesian spatial models were fitted to obtain smoothed standardized notification ratios and corresponding 95% Credible Internals (95% CrI) and to identify high and low risk areas. The Pearson correlation coefficient (ρ) was computed to quantify the overlap between MDR-TB and non- MDR-TB.

Results:

In the study period 53 417 TB cases were notified, 583 of them were MDR-TB. Thirty-six municipalities were identified as areas of significantly elevated rates of non-MDR-TB, but only eight of them had also significantly elevated rates of MDR-TB. We found a moderate correlation (ρ= 0.653; 95% CrI 0.457-0.728) between non-MDR-TB and MDR-TB standardized notification ratios.

Conclusions:

The estimated moderate correlation suggests that in addition to MDR-TB development, transmission of resistant strains occurs in specific areas of Portugal. An assessment of the factors and epidemiological characteristics of population in these areas will allow us to adjust local control strategies and focus resources in order to prevent and reduce MDR-TB in Portugal.

Subject: Surveillance

Keywords: Tuberculosis, Multidrug-resistant tuberculosis, Spatial patterns, Hotspots, Factors associated

ABSTRACT ID: 141

PRESENTED BY: Olena Oliveira / id7080@alunos.uminho.pt

14.2. Longitudinal modeling of Tuberculosis in mainland Portugal, 2009-2016

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Background:

Despite the observed decline in tuberculosis incidence rate in the past 10 years in Portugal, it was estimated to be 17,1/100.000 population in 2017, thus remaining a public health issue. Seasonal variation of tuberculosis incidence in Portugal has already been suggested, however, recent epidemiological changes may have altered this pattern. We aimed to characterize and model seasonal variation of tuberculosis monthly incidence rates in Portugal and to assess the longitudinal effect of climate factors in tuberculosis seasonality.

Methods:

Monthly diagnosed tuberculosis cases from 2009 to 2016 in 18 mainland Portugal districts were obtained from the Portuguese Tuberculosis Surveillance System. Climate data (temperature, humidity and rainfall) were obtained from the Portuguese Institute of the Sea and the Atmosphere. We performed a longitudinal analysis using Generalized Additive Mixed Models.

Results:

A total of 19.192 tuberculosis cases were included and the average monthly count was 199,9+/-27,0 [SD]. The observed month-specific counts of tuberculosis cases suggested a cyclical pattern every year with a peak between April and July, and a trough in December. The final model included time as the explanatory variable (R-square adjusted=0.951; $p<0.001$), a cyclic spline as the smoothing term (df=7.584) and random effects of districts (df=16.581). Climate variables (with a lag of 0 to 6 months) weren't included in the final model, since their effect on tuberculosis incidence was absorbed by the passage of time.

Conclusions:

An annual seasonal pattern of tuberculosis in Portugal was shown, in line with findings from previous studies. Unfortunately, it was not possible to explain this pattern based on the changes of climate variables throughout the year. Other explanatory factors should be assessed by further research, in order to optimize disease control and intervention.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: seasonality, tuberculosis, temperature, rainfall, humidity

Poster Abstracts

ABSTRACT ID: 250

PRESENTED BY: Ana Lucia Ferreira Figueiredo / figueiredo.analucia@gmail.com

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14.3. Decline of tuberculosis notification rate in different population groups and regions in Portugal, 2010-2017

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Background:

Tuberculosis (TB) incidence has declined in Portugal in recent decades, but trends appear to differ between regions and population groups. We investigated these differences in order to inform prevention and control programmes.

Methods:

In Portugal, cases of active TB are notified to the national tuberculosis surveillance system. We performed a time series analysis of TB notification rates between 2010-2017 in different population groups and Portuguese regions. Interannual decline percentages and respective 95% confidence interval (95%CI) were estimated using poisson and binomial negative regression models.

Results:

The overall TB notification rate decreased from 25.7/100.000 population in 2010 to 17.5/100.000 in 2017 (5.3%/year). The range of the interannual decline percentages in the continental Portuguese regions was between -4.4% (95%CI:-8.2%, -0.5%, for Alentejo) and -5.4% (95%CI:-6.4%, 4.4%, for Northern region). The interannual decline in notification rate was smaller in non-Portuguese nationals (-1.57%, 95%CI:-4.79%, 1.75%) versus Portuguese (-5.85%, 95%CI:-6.98%, -4.70%); children under five years (+1.77%, 95%CI: -4.61%, 8.58%) versus other ages (-5.38%, 95%CI:-6.33%,-4.42%); and HIV-negative people (-6.48%, 95%CI: -9.54%, -3.31%) vs HIV-positive (-13.12%, 95%CI; -14.81%,-11.40%).

Conclusions:

The declines in TB notification rates were smaller in children under five years old and non-Portuguese nationals, although numbers were very small for children. No significant differences were observed between Portuguese regions. The steeper decline of TB notification rates in HIV-positive may be due to more intensive screening and preventive treatment in the last decades. We recommend focusing opportunistic screening of TB in non-Portuguese and ensuring that newborns with specific risk factors are timely offered BCG vaccination.

Subject: Surveillance

Keywords: time series analysis, vulnerable population groups, tuberculosis, non-nationals ,HIV positives

ABSTRACT ID: 423

PRESENTED BY: Alexis Sentís / alexissentis@gmail.com

14.4. Introducing whole genome sequencing for TB relatedness surveillance in London

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[1] PHE

[2,3,4,5,6,7,8,9,10] PHE

Background:

In January 2018 Public Health England began using whole genome sequencing (WGS) for routine tuberculosis (TB) speciation, resistance predictions and relatedness in London. We implemented a process to systematically collect and review TB relatedness information in London to identify where public health action is required to interrupt transmission. We report results from the first year.

Methods:

Newly clustered London residents were identified each month from a prototype system that uses a 12-single nucleotide polymorphism (SNP) cut-off to assign isolates of 2 or more individuals to clusters. These were added to cluster records that recorded summary details of the clustered patients and phylogenetic tree and used for cluster review. From April we restricted review to new patients within 5 SNPs of another due to increasing numbers of patients. In May we began notifying London TB clinics if their patients were part of such clusters.

Results:

Between February 2018 and January 2019 233 patients were reported, a median of 18 per month. Of these, 176 were within 5 SNPs and featured in 94 clusters. The majority (63) increased by 1 patient, 18 by 2, 3 by 3 and 10 by 4 or more (with a maximum of 12). These top 10 clusters were characterised by combinations of: isoniazid resistance (three), family members (four), social risk factors (two), particular ethnic groups (four) and geographically clustered (five).

Conclusions:

These initial results demonstrate potential for this surveillance system to identify venues and groups with very recent TB transmission. This allows local services to focus efforts to intervene to prevent further transmission and active disease. Monitoring clusters will also inform understanding of transmission patterns of TB in London by describing groups experiencing ongoing exposure.

Subject: Surveillance

Keywords: TB surveillance whole genome sequencing

ABSTRACT ID: 683

PRESENTED BY: Neil Macdonald / neil.macdonald@phe.gov.uk

Poster Abstracts

14.5. TB and A&E: use of acute services by people with TB in London 2012-17

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Background:

In England, when people are unwell, most are expected to attend primary care services such as GPs. However, those seriously ill, or unable to access primary care, may use acute services, such as A&E. We aim to describe where adults with TB in London first present to healthcare services, and to describe those attending acute services.

Methods:

We analysed cohort review data from the London Tuberculosis Register and included 7,059 adults from 2012-2017. Services were classed as "acute" or "primary" and logistic regression used to identify associations with first presenting at acute services.

Results:

A third (37%, 2,645) of people initially presented at acute services. People experiencing social risk factors were more likely to present at acute services - particularly those reporting alcohol misuse (adjusted odds ratio, aOR, 2.7, CI: 2.1– 3.6), homelessness (aOR 1.9, CI: 1.5 – 2.5), and mental health issues (aOR 1.5, CI: 1.2– 1.8). Increased odds were also seen for males (aOR 1.2, CI: 1.1 – 1.4), people of black-Caribbean (aOR 1.6, CI: 1.2– 2.1) or black-African (aOR 1.6, CI: 1.4– 1.9) ethnicity (compared to Indian ethnicity) and with pulmonary disease (aOR 1.2, CI: 1.1– 1.3).

Conclusions:

We found one in three people with TB in London first presented at acute services, and was more likely for those with social risk factors. Potentially because they are more unwell, possibly due to delays in seeking healthcare, or, as a marginalised group, have difficulties accessing primary services. We recommend TB services use cohort reviews to identify barriers to access of primary care. Understanding where people with TB access healthcare may identify opportunities for earlier diagnosis and earlier starts to treatment, key elements of TB control.

Subject: Burden of disease

Keywords: Tuberculosis, Service Use, Surveillance

ABSTRACT ID: 689

PRESENTED BY: Clare Sawyer /clare.sawyer@phe.gov.uk

Track 15: Influenza and other respiratory viruses (2): vaccination and interventions

Moderator:

Peter Kriedl

Abstracts

15.1. «Skewed to the centre»: what is behind the geographical imbalance of the influenza vaccination coverage among the elderly in Denmark?

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Background:

The elderly (aged ≥65 years) are at risk of influenza and its consequences. Currently, the influenza vaccination coverage (VC) in Europe misses the recommended 75% target. In Denmark, 50% of elderly were vaccinated during the 2017/2018 season, with higher VCs in urban municipalities. Literature suggests that wide-ranging health determinants (HDs) impact influenza VC. We explored the relationship between elderly influenza VC in 2017/2018 and HD-related indicators across the 98 Danish municipalities.

Methods:

We extracted influenza VCs among elderly and geography- and HD-related indicators from publicly available databases. HDs covered demographic (e.g. resident elderly/kilometer2 ratio), societal (e.g. family wealth, proportional education attainment) and health system indicators (e.g. medical practices/elderly ratio, per-capita health care expenditure). We estimated median [interquartile range] VCs (overall, and stratified by urban and rural municipalities). We explored relationships between VCs and HDs using Quasi-Poisson regression models for rates.

Results:

Median VC in Danish municipalities was 48% [46%-51%]. Stratified by urban and rural municipalities it was 51% [48%-55%] and 46% [44%-48%], respectively. Municipalities with higher per-capita health care expenditures ($p=0.01$), family wealth ($p<0.01$) and education attainments ($p<0.01$) were associated with higher VCs. In urban municipalities, higher medical practices/elderly ratios ($p=0.03$), family wealth ($p<0.01$) and education attainments ($p<0.01$) were associated with higher VCs. In rural municipalities, higher resident elderly/kilometer2 ratios were associated with higher VCs ($p<0.01$).

Conclusions:

As shown elsewhere, we found that wider society- and health system-related factors (e.g. health care expenditure and the availability of medical practices) contribute to the influenza VC and the related urban-rural gradient among the elderly in Denmark. We recommend such evidence to contribute tailoring future campaigns e.g. by prioritising less served areas. Further individual-level analysis will contribute to identifying vulnerable groups.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza, Human; Vaccination Coverage; Aged; Social Determinants of Health

ABSTRACT ID: 306

PRESENTED BY: Guido Benedetti / gube@ssi.dk

15.2. Moderate influenza vaccine effectiveness in Ireland during the 2018/2019 season

Lisa Domegan [1]

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Background:

In Ireland, influenza vaccines are recommended for use in risk groups each season. A single brand trivalent inactivated sub-unit vaccine represented the main vaccine used during the 2018/2019 season. We aimed to estimate influenza vaccine effectiveness (VE) in primary care in Ireland during the 2018/2019 season.

Methods:

We undertook a test-negative design (TND) case-control study, as part of the I-MOVE network. We compared vaccination status of laboratory confirmed influenza cases with laboratory-negative patients among those meeting the EU influenza-like illness (ILI) case definition presenting to primary care. We used logistic regression to calculate influenza VE, adjusting for potential confounders. A random sample of influenza virus positive specimens was selected for sequencing.

Results:

We included 183 cases and 151 controls in the analysis (October-April), with vaccine uptake at 15%. Adjusted influenza VE estimates were 52% [95% CI: -3-78] against all medically attended laboratory confirmed influenza and 71% [95% CI: 28-88] against influenza A(H1N1)pdm09. Among target groups for vaccination, adjusted VE was 58% [95% CI: -14-85] against all influenza and 77% [95% CI: 22-93] against A(H1N1)pdm09. Age specific estimates against all influenza were 51% [95% CI: -23-80] for those aged 15-64 years and 39% [95% CI: -187-87] for those ≥65 years. Further subset analysis was not possible, due to small sample size. Of sequenced viruses the majority were influenza A(H1N1)pdm09 clade 6B.1 (vaccine strain A/Michigan/45/2015), including three emerging subgroups, all containing the HA1 amino acid substitution S183P.

Conclusions:

Moderate influenza vaccine effectiveness against A(H1N1)pdm09 was observed in Ireland during the 2018/2019 season. Increasing genetic diversity of A(H1N1)pdm09 viruses did not affect VE, however further monitoring of variants and the potential impact on VE is necessary.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza, Vaccine Effectiveness, Influenza A(H1N1)pdm09, Case Control Study

ABSTRACT ID: 414

PRESENTED BY: Lisa Domegan / lisa.domegan@hse.ie

15.3. Tailoring the National influenza vaccination strategy using a bottom-up approach, Slovenia, 2018

Mario Fafangel [1]

K. Orozen [2], T. Petras [3], N. Sinkovec [4], S. Vuzem [5], M. Vrdelja [6], M. Lamovsek [7], T. Medved [8], K. Borsic [9], M. Socan [10]

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Background:

Bottom-up approaches could help develop user-sensitive solutions. In Slovenia primary care physicians (family doctors and paediatricians) are key providers of influenza vaccination. In 2017/2018 vaccination coverage among adults aged 65 years and older was 12%. For groups with higher risk influenza vaccination is partially publicly reimbursed. To account for obstacles at the healthcare delivery point we conducted a nationwide cross-sectional survey among vaccination providers as part of the National influenza vaccination strategy development in year 2018.

Methods:

Participants were included from comprehensive e-mail lists of family doctors (N=352) and paediatricians (N=255). From January-February 2018, using an online survey, we collected data on their influenza vaccination status, knowledge, practices and perceived obstacles/needs to improve coverage.

Results:

We received 139/607 compiled surveys. Unvaccinated physicians (21/129 in 2016/2017) expressed fear of side effects and belief that vaccination causes disease (7/17). Vaccination was not recommended to children aged <2 years (36/70) and pregnant women (22/36). Main identified obstacles were staff overburdening (75/115) and patient refusal (56/114). Providers expressed the need for nationwide health education (95/95), promotion materials (105/115), free vaccination for groups with higher risk (83/114) and standing orders enabling non-physician medical personnel to vaccinate without direct physician involvement (72/112).

Conclusions:

We identified knowledge and practices gaps to be addressed with education of providers. The main obstacles/needs were included in the National strategy proposal which is under revision/staggered implementation by the Ministry of Health. In 2019/2020 influenza vaccination for groups with higher risk will be fully publicly reimbursed. Implementation of a bottom-up approach enabled a strategy development that accounts for frontline obstacles hindering access to vaccination. Dynamic vaccination environment supports seasonal evaluation and revision of the strategy.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: influenza, vaccination coverage, Slovenia, survey, health planning guidelines

ABSTRACT ID: 501

PRESENTED BY: Mario Fafangel / mario.fafangel@nijz.si

Poster Abstracts

15.4. The effect of individual reminders and communication of herd immunity on influenza immunization

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Background:

Vaccination is considered to be one of the most effective and successful means of preventive medicine. However, increasing levels of vaccine hesitancy pose a serious threat to the success of vaccination programs. We test the impact of sending a reminder and communicating the concept of herd immunity on influenza vaccine uptake among elderly using a large-scale natural field experiment (n = 48125).

Methods:

We randomized the messages of printed letters that were mailed to individuals eligible for free influenza vaccines in Finland during the influenza season 2018-2019. We assigned three treatment groups: (1) No letter, (2) Standard letter, and (3) Herd immunity letter. We implemented our experiment in two geographic areas with different historical vaccination uptake rates. The main outcome was the percentage of vaccine uptake among the eligible population.

Results:

We found that receiving any type of letter increased influenza vaccine uptake by 6 percentage points (95% CI: 4.1–8.8 pp). This effect was substantially larger (9 percentage points, 95% CI: 6.7 – 11.0 pp) among individuals with no previous history of influenza vaccines. Our results showed that communicating the concept of herd immunity and highlighting the associated social benefits of vaccination using postal letters did not significantly affect vaccine uptake. From the confidence intervals, we can rule out effects larger than 1–1.5 percentage point increase in vaccination uptake

Conclusions:

Our results highlight the effectiveness of simple individual reminders on influenza immunization, but question the impact of subtle contextual changes on immunization rates. Our results call for more randomized field trials to understand the potential and limits of simple nudges in vaccination communication and advocacy.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza, vaccination, public health, herd immunity, health behavior

ABSTRACT ID: 579

PRESENTED BY: Lauri Sääksvuori / lauri.saaksvuori@thl.fi

15.5. Which hospitalised patients with influenza are treated with neuraminidase inhibitors? Data from eleven EU countries, 2010–2019

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Background:

Treatment with neuraminidase inhibitors (NAI) reduces the impact of severe influenza disease. We analysed surveillance data on hospitalised influenza patients in EU countries from the 2010/11 to 2018/19 influenza seasons to better understand who receives treatment with NAI.

Methods:

The European Surveillance System collects weekly case-based data on hospitalised laboratory-confirmed influenza cases. For this study, we included cases with known NAI treatment data, virus (sub)type, hospital unit type (intensive care unit (ICU)/non-ICU), age, sex and vaccination status. We excluded cases with hospitalisation date before or >10days after illness onset and treatment initiation before or >22days after onset. Poisson regression models were used to estimate the incidence rate ratio (IRR) for NAI treatment (versus non-treatment) for patient demographics, virus (sub)type, timing of hospitalisation, influenza vaccination, ICU admission and reporting country.

Results:

Eleven countries reported 16,979 cases; 5,045 (30%) were admitted to ICUs. Oseltamivir was given to 13,922 patients (82%), 45 (0.3%) received zanamivir and 20 (0.2%) received both. ICU patients were more likely than non-ICU patients to receive NAI treatment (1.08, 95%CI 1.06-1.09). So were patients with unsubtyped influenza A (IRR 1.14, 95%CI: 1.12-1.17) or A(H1N1)pdm09 (IRR 1.13, 95%CI 1.10-1.16) compared to influenza B patients. A(H3N2) infection was not significantly associated with treatment (IRR 1.0, 95%CI 0.98-1.04). Older people were more likely to be treated with NAIs than 0-19 years olds (20-39 years: IRR 1.43, 95%CI 1.37-1.49; 40-64 years: IRR 1.44, 05%CI 1.38-1.50; >65 years: IRR 1.68, 95%CI 1.32-1.43). Vaccination against influenza was not associated with NAI treatment (IRR 0.99, 95%CI 0.98-1.01).

Conclusions:

NAI use was common in hospitalised patients, but less frequently given to younger people (<20 years), not in ICU or those infected with influenza B virus.

Poster Abstracts

Subject: Surveillance

Keywords: influenza, hospital, surveillance, EU/EEA, antiviral treatment

ABSTRACT ID: 316

PRESENTED BY: Cornelia Adlhoch/ cornelia.adlhoch@ecdc.europa.eu

15.6. Evaluating the impact of influenza vaccination on respiratory antibiotic prescribing in England: A preliminary, multi-level mixed effects analysis of a national patient database, 2010 11 to 2017 18

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Background:

Resistance to antibiotics is an issue of great importance, with inappropriate prescription of antibiotics in primary care identified as a contributor. Influenza vaccination may reduce such use. Our aim was to establish if influenza vaccination has any effect on use of antibiotics in GP surgeries to treat patients with chest infections.

Methods:

We extracted patient and prescribing data for five GP practices from the Royal College of General Practitioners (RCGP) Research and Surveillance Centre (RSC) database for influenza seasons 2015-16 and 2016-17. We conducted descriptive, univariate and stratified analyses to assess potential confounders and effect modifiers. We constructed a multi-level, mixed-effects Poisson regression model with time-dependent covariates to calculate adjusted rate ratios (aRR) for respiratory antibiotic prescriptions by influenza vaccination status. Antibiotic prescribing rates for urinary tract infections (UTI) were calculated as a benchmark for residual confounding.

Results:

Data for 87,849 patient-influenza seasons were included. The multivariable model, adjusting for age, sex, deprivation, comorbidities, propensity to consult, vaccination/prescribing history, location, GP practice and month, showed that compared to being unvaccinated, vaccination with inactivated influenza vaccine was associated with an increase in prescribing of both respiratory antibiotics (aRR:1.09, p=<0.01) and UTI antibiotics (aRR:1.14, p=<0.01). Vaccination with live-attenuated vaccine was also associated with an increase (Respiratory - aRR:1.11, p=0.14; UTI - aRR:1.34, p=0.09).

Conclusions:

The higher prescribing rates for respiratory antibiotics observed in individuals receiving influenza vaccine in this preliminary analysis is unexpected and requires further investigation. The risk of prescribing UTI antibiotics, which should not be affected by influenza vaccination, indicates there is considerable residual confounding/bias. The analysis is being extended to all sentinel practices to rule out that influenza vaccination could still contribute to a reduction in prescribing.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Antimicrobial Stewardship, Influenza Vaccines, Primary Health Care, Respiratory Tract Diseases

ABSTRACT ID: 667

PRESENTED BY: Matt Edmunds / matt.edmunds@phe.gov.uk

Track 16: Vaccine-preventable diseases (2)

Moderator:

Sabrina Bacci

Abstracts

16.1. Genomic surveillance of B. pertussis: a pilot study for an Austrian province

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Background:

Bordetella pertussis causes respiratory disease pertussis, reemerging worldwide during recent years. Evasion of the vaccine-induced immunity is a possible reason for the reemergence. The aim of the study was to characterize and compare from May 2018 onwards, the circulating strains in an Austrian province where the incidence of pertussis increased from 26 cases/100,000 inhabitants in 2017 to 56 in 2018 to the vaccine strain.

Methods:

We collected 41 B. pertussis isolates from 41 cases within our pilot isolate-based B. pertussis surveillance system. Isolates were whole genome (WG)-sequenced and typed using a new cgMLST scheme comprising 2.938 genes and a virulence gene (VGs) scheme encoding for vaccine targets including pertussis toxin (ptxP, ptxS1), pertactin (prn), filamentous hemagglutinin (fhaB) and fimbriae (fim2, fim3) genes. The sequence type (ST) was extracted from the WGS data and the genetic relatedness between the isolates assessed.

Results:

Nineteen cases were males and 22 females with an age range of 0-71 years. 17 cases belonged to the same district and 19 cases had been vaccinated. Based on a preliminary cluster threshold of ≤6 alleles, we identified five clusters of isolates, some originating from members of the same household. All isolates were ST2 and 34 (83%) presented VGs types ptxP-3, ptxS1-A, prn-2, fim2-1, fim3-1 and fhaB-1, differing genetically from the vaccine strain.

Conclusions:

Our results show that the circulating strains in the Austrian province differed from the vaccine strain. Therefore, expansion of the surveillance system at national level is recommended to assess the impact on vaccine effectiveness. We recommend the use of cgMLST in conjunction with epidemiological data to detect B. pertussis transmission chains.

Subject: Surveillance

Keywords: Bordetella pertussis,Genomic surveillance, Austria, transmission chains, cgMLST, vaccine antigens

ABSTRACT ID: 72

PRESENTED BY: Adriana Cabal Rosel / adriana@cabalrosel.com

16.2. Effectiveness of maternal pertussis vaccine during pregnancy in protecting infants in the region of Lisbon and Tagus Valley in 2017: a case-control study

Sara Gomes Raposo [1]

B. Nunes [2]

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Background:

A pattern indicating the resurgence of whooping cough in Portugal has been registered since 2004. Most of the notified cases happened in children aged less than 6 months of age, without priming vaccination initiated or completed. After the last outbreak in 2016, maternal vaccine during pregnancy was included in the National Vaccination Plan on January 1st, 2017 has a preventive measure. This study aims to estimate the effectiveness of the maternal vaccine during pregnancy in the region of Lisbon and Tagus Valley.

Methods:

A longitudinal, retrospective, observational, matched case-control study was performed having included the notified cases of pertussis in children aged less than 6 months, without priming vaccination started or completed, residents in the Lisbon and Tagus Valley region, between 01.01.2017 and 31.12.2017. The cases were obtained from the regional records of SINAVE. Two controls without pertussis diagnosis with the same age and followed in the same health care center were selected to pair with each case. A multiple conditional logistic regression was used to calculate the adjusted Odds Ratio. Vaccine effectiveness was estimated using the formula: 1-Odds Ratio.

Results:

A total of 32 cases and 64 controls were obtained. 84,3% of the cases had a confirmed hospital admission to treat complications. The unadjusted vaccine effectiveness estimate was 79% (95% CI, 35-93%), while adjusted was 95% (95% CI, 65-99%).

Conclusions:

The findings indicate the existence of high vaccine effectiveness, adding evidence favoring the implementation of this public health measure. The results raise the question if the vaccine is more effective in preventing the disease itself or the severe forms of the disease.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Vaccination, Pertussis Vaccine, Whooping Cough, Public Health, Matched Case-Control Studies

ABSTRACT ID: 664

PRESENTED BY: Sara Gomes Raposo / saragomesraposo@gmail.com

16.3. Increase of pertussis in Finland 2015-2018: possible artifact due to seroresponse to vaccination?

Timothee Dub [1]

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Background:

In Finland, from 2015 to 2018, pertussis incidence increased from three to nine cases per 100 000. A large proportion of cases during this period occurred among 0-4 and 10-14 year olds, age groups eligible for pertussis vaccination in the national immunisation programme. We investigated whether the increase in reported cases was real or could potentially be explained by false positives.

Methods:

We extracted laboratory confirmed cases data from the National Infectious Diseases Registry (NIDR) and linked them to individual records from the National Vaccine Register (NVR) which was implemented since 2009. We described microbiological diagnosis methods (MDM) to identify potential false positive cases, i.e. patients diagnosed using IgG serology within a year of immunisation.

Results:

During 2015-2018, out of 1467 pertussis cases notified to NIDR, 326 were born from 2009 onwards. Overall, 141/1467 (10%) cases had received pertussis containing vaccine within a year prior to diagnosis confirmed with IgG serology, including 103/326 (32%) cases born since 2009. Additionally, among 0-4 year olds, as many as four in ten cases (94/225) might have been due to serological response following routine immunisation. The proportion of potential false positives remained stable over time, ranging from 12/165 (7%) initially to 46/469 (10%) in 2018.

Conclusions:

False positives contribute to the amount of pertussis cases seen in Finland, but cannot wholly account for the recent increase. PCR should be considered as preferred MDM in children aged 0-4 years, likely to have been immunized recently. Additionally, in the future, clinical data from recently vaccinated cases should be reviewed in order to confirm pertussis diagnosis and improve the quality of the routine surveillance.

Subject: Surveillance

Keywords: Pertussis,Microbiological Diagnosis Methods, Surveillance, Bordetella pertussis ,False positives

ABSTRACT ID: 238

PRESENTED BY: Timothee Dub / timothee.dub@thl.fi

16.4. Socioeconomic and demographic factors associated with uptake of the first pertussis booster vaccination in the federal state of Brandenburg 2007 – 2016

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Background:

A first pertussis booster has been recommended in preschool children in Germany since 2006 with known low booster uptake (PBU) in most federal states. We looked at the association of PBU with individual socio-economic and demographic factors and MMR-vaccination in Brandenburg to identify targeted interventions.

Methods:

We used data collected during mandatory school entry medical examinations (SEE) in Brandenburg between 2007 and 2016 describing PBU in all 18 districts. For 2016 we analysed PBU by district, vicinity to Berlin (metropolitan area) age, sex, parental employment and education, mother tongue, number of siblings, single parents and complete MMR uptake (2 doses). To control for district variation, we implemented a mixed-effect logistic regression model treating districts as random and calculated adjusted odds ratios (aOR) and 95% confidence intervals (95%CI).

Results:

On average 22,240 children underwent SEE yearly with 53% aged 5 years and 47% >5 years. The PBU increased over time from 30% in 2007 to 35% in 2016 (mean 34%) with a marked variability among districts (2016: range 22% to 57%). In 2016, children aged >5 years (aOR:2.02; 95%CI 1.90-2.17) having a complete MMR uptake (7.90; 95%CI 6.67-11.01) with <2 siblings (1.17; 95%CI 1.07-1.28) and living outside the metropolitan area (1.20; 95%CI 1.10-1.32) were more likely to receive booster vaccination. We could not find an association with the education status of parents or other socioeconomic factors.

Conclusions:

PBU needs to be improved in all districts in Brandenburg. Individual socioeconomic factors fail to be suitable predictors for PBU in Brandenburg. Pediatricians should be encouraged to check their patients' vaccinations status at each visit and advocate booster vaccination, especially in the metropolitan area.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Child, Preschool , Odds Ratio , Single Parent , Whooping Cough , Logistic Models , Siblings , Confidence Intervals , Brandenburg, Parents , Secondary Immunization, Socioeconomic Factors , Pediatricians , Vaccination , Employment , Germany

ABSTRACT ID: 615

PRESENTED BY: Benjamin Tittmann / benjamin.tittmann@lavg.brandenburg.de

16.5 Impact of an accelerated measles-mumps-rubella (MMR) vaccine schedule on vaccine coverage: an ecological study among London children, 2012-2018

Joanne Lacy [1]

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Background:

Vaccine coverage in London is the lowest in the UK and MMR dose 2 coverage (MMR2) is below the World Health Organisation's 95% recommended target. Prior to 2012, in response to increased measles activity at the time, 7 out of the 33 London Local Authorities (LAs) introduced early MMR2 vaccination from as early as 15 months onwards instead of the nationally recommended 3 years and 4 months. We evaluated the effect of early vaccination on coverage of MMR vaccination over 6 years.

Methods:

We compared London LAs implementing MMR2 early with those following the existing schedule in terms of vaccine coverage measured at 5 years between 2012 to 2018, using generalised estimating equations (GEE) regressions adjusted for year and DTaP/IPV/Hib coverage measured at 2 years as a proxy for baseline local vaccination programme performance.

Results:

Average MMR2 coverage was higher among early implementing LAs from 2012/13 onwards. Coverage difference was highest in 2017/18 (9.2 percentage points, 95% CI 4.8, 13.5, $p<0.001$). On average, compared to London LAs on the existing schedule, MMR2 coverage among early implementing LAs was 3.3 percentage points higher (95% CI 1.4, 5.3, $p=0.01$) over the 6 years after adjusting for DTaP/IPV/Hib coverage and year.

Conclusions:

Our findings indicate that vaccinating children earlier with MMR2 results in significantly higher vaccine coverage and therefore LAs should consider offering an accelerated MMR schedule to help achieve the 95% recommended target. Further research is needed to assess the association at a more granular level, but our findings underline a potential opportunity to increase MMR coverage.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Vaccination coverage, Vaccination, Measles-Mumps-Rubella Vaccine, London, Measles

ABSTRACT ID: 570

PRESENTED BY: Joanne Lacy / joanne.lacy@phe.gov.uk

16.6. Positive impact of the 2018 mandatory vaccinations' extension in France

Laure Fonteneau [1]

D. Lévy-Bruhl [2], C. Ménard [3], S. Vaux [4], A. Barret [5], I. Bonmarin [6], B. Coignard [7], S. Quelet [8]

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Background:

In France, the number of mandatory vaccinations up to 2 years of age increased by law from 3 to 11, for children born since 1st January 2018. We assessed the impact of this law by measuring vaccination coverage (VC) of children born in 2018 and by assessing in February 2019 the opinion on vaccination of parents of children <2 years old.

Methods:

We used vaccine reimbursement data, extracted on 28 March 2019, to compare VC at 7 months of age for children born from January to May in 2017 and 2018, for the first doses of hexavalent, pneumococcal and meningococcal C (MenC) vaccines. Parents' opinions were collected through a representative sample of 1002 parents.

Results:

Between 2017 and 2018, the use of hexavalent vaccine increased from 93.3% to 98.6% (+5.5 points). Pneumococcal VC increased from 98.0% to 99.4% (+1.4 points) and MenC VC from 39.3% to 75.7% (+36.4 points). MenC incidence in infants decreased from a yearly average of 17 cases in 2012-2016 to only 4 in 2018. In 2019, 67% of the parents are favorable to mandatory vaccinations; 91% declared that vaccination is important for children's health and 87% for the collective protection (+5 points each, compared to a similar survey conducted in 2018). Data for vaccination beyond the first year of age also show an increase, although children were not concerned by the new law.

Conclusions:

These results suggest a positive impact of the law but also of the active promotion of the vaccination that accompanied the law (social marketing, television campaign, website on vaccination....). Data for MMR first dose and MenC second dose at 12 months of age VC will be available in September.

Subject: Surveillance

Keywords: Mandatory vaccination. Vaccination coverage. Reimbursement data. France.

ABSTRACT ID: 123

PRESENTED BY: Laure Fonteneau / laure.fonteneau@santepubliquefrance.fr

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MODERATED POSTER SESSION C
DAY 3: Friday, 29 November 2018
15:40-16:40

Track 17: Food- and waterborne diseases and zoonoses (5): outbreaks (II)

Moderator:

Gerhard Falkenhorst

Abstracts

17.1. Outbreak of listeriosis caused by consumption of raw fermented trout, Norway, 2018 to 2019: a need to raise awareness of risk groups

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Background:

In December 2018, the Norwegian Institute of Public Health (NIPH) detected a cluster of five cases of a previously unseen strain of Listeria monocytogenes. We investigated the outbreak to identify its source and implement control measures.

Methods:

Listeriosis cases are routinely notified to the NIPH. We performed whole genome sequencing (WGS) of L. monocytogenes isolates and identified their serogroup, sequence type and cluster type. We defined cases as people with laboratory-confirmed listeriosis with the outbreak strain. We inquired if national public health institutes in other European Union countries had outbreak cases. We gathered information on cases through notifications, and exposures through trawling questionnaires. We sampled leftovers of common exposures from cases and, if listeria-positive, compared WGS sequences to the outbreak strain.

Results:

We identified thirteen cases; 77% male, median age 74 years (range 53-90). Twelve cases were diagnosed in five municipalities in Norway, and one in Sweden. The index case was sampled in February 2018. All other cases were sampled between November 2018 and January 2019. Twelve cases reported eating raw fermented trout ("rakfisk") prior to illness; the only common exposure identified. Rakfisk-leftovers from a single Norwegian producer (farmed/slaughtered in Sweden, packaged in Norway) provided by four cases were positive for the outbreak strain.

Conclusions:

Results indicate the source of the outbreak was rakfisk. The product was recalled in January 2019; no cases were reported thereafter. L. monocytogenes was likely introduced into the production line before February 2018. All cases belonged to known listeriosis risk groups, despite targeted advice from health authorities and package warnings. There is a need to further raise awareness of risk groups for Listeria infection, and that rakfisk is a risk product.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Listeria, outbreak, foodborne disease, whole genome sequencing

ABSTRACT ID: 181

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17.2. Deploying an online access panel as a control group for case-control studies in the investigation of gastrointestinal outbreaks: early experiences from Germany

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Background:

In outbreaks, established methods of recruiting population controls for case-control studies can be time consuming, and often such studies are not conducted, though indicated. We explored the feasibility and reliability of using an online panel as a control group in case-control studies to investigate foodborne outbreaks, in Lower Saxony, Germany.

Methods:

We deployed a web-survey by email to all 277 members of a non-probabilistic access panel from Lower Saxony in 2019. We investigated the representativeness of the panel for Lower Saxony concerning basic socio-demographic characteristics. We compared responses of the panel members with responses of controls from four case-control studies that investigated foodborne outbreaks in Germany between 2003 and 2017. We tested hypotheses of identifying the same food items associated with the outbreak disease using odds ratios (ORs).

Results:

Overall 203/277 (73%) panel members answered the survey, 132/203 (65%) within a week. There were statistically significant differences in the distribution of socio-demographic characteristics between the panel members and the population of Lower Saxony. In three studies, the ORs of the food items associated with the diseases in the historical case-control studies were similar to the ORs when using the panel as a control group. In the fourth study, the source of the outbreak was related to a specific time and geographical location.

Conclusions:

Using a non-probabilistic panel as a control group in case-control studies gave similar results as using randomly selected controls. It successfully identified the likely source of three historical outbreaks, despite the lack of representativeness. Public health professionals should be encouraged to consider recruiting controls in access panels for future investigations. We recommend the further evaluation of this approach in parallel case-control and case-panel studies.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Online-survey, access panel, case-control studies, epidemiology research design, outbreaks, gastrointestinal disease

ABSTRACT ID: 272

PRESENTED BY: Delphine Perriat / delphine.perriat@gmail.com

17.3. Large and prolonged outbreak of Salmonella Typhimurium affecting 51 schools, Belgium 2018

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Background:

On May 22nd, the Flemish infection control team was notified of 15 gastroenteritis cases in two schools. By May 25th, cases were reported in 30 schools, all supplied by caterer A, that distributed ~10,000 meals daily among 83 schools. We investigated the extent and source of this outbreak to limit further spread.

Methods:

We carried out a cohort study of children attending five affected schools using online questionnaires completed by parents. Probable cases: students with gastroenteritis symptom(s) of between 18 May and 9 June. Confirmed cases: probable cases with lab-confirmed Salmonella. We calculated exposure-specific attack rates (AR) and risk ratios (RR) with 95%-confidence intervals (CI). Case finding was performed among 83 schools and the incremental risk difference in school ARs per kilometre from the caterer's premises was estimated using linear regression. 207 environmental/food samples were analysed.

Results:

423 responses (29%) were captured in the cohort study, including 157 cases with a median age of 6.8 years, 50% reporting fever and 33% vomiting. Eating food from caterer A (RR=8.1, 95%CI 3.1-21.2) and eating salad and turkey on 17th May (RR=3.2, 95%CI 1.5-6.7) were associated with illness. Cases (n=546) were identified in 51/83 schools, including 399 confirmed cases, over 21 days. School ARs ranged between 0-25%, with a 1.3% increase in AR per 10km from the caterer's premises (p=0.001). All non-human microbiological analyses were negative.

Conclusions:

The meal on May 17th was the likely source of infection. Food distributions of caterer A were halted between 25 May and 9 June. Higher ARs among distant schools suggest transport of unrefrigerated food may contributed to the outbreak's extent. We recommend strengthening food safety regulations for caterers supplying schools or public services.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Foodborne outbreak, Salmonella Typhimurium, Cohort study, Unrefrigerated transport, School-level analysis

ABSTRACT ID: 527

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17.4. Epidemiological characteristics of Haemorrhagic fever with renal syndrome cases during the 2017 outbreak in Croatia

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Background:

Background : Hemorrhagic fever with renal syndrome (HFRS) is endemic in Croatia; five outbreaks have been documented since 1995. Exposure occurs when people inhale aerosol or dust contaminated by excreta of infected rodents. In 2017, during the largest outbreak in Croatia, we collected additional information to better understand how cases may have been exposed to infection in different counties.

Methods:

We interviewed cases using a structured questionnaire and collected information on risk activities before disease onset, hospitalization and disease severity. Risk activities were grouped in five categories: hiking/picnicking, forestry/farm work, cleaning house or surroundings, multiple activities, and unknown. We defined severe cases as those resulting in death or requiring intensive care. We calculated odds ratios for different risk activities for severe cases.

Results:

In 2017, 389 HFRS cases from 15/21 Croatian counties were reported to the Croatian Institute of Public Health. 340 questionnaires were completed: 99 from Zagreb and 241 from other counties. 79% of all cases were male; 51% were aged 25-44 years. The largest proportion (55/99, 56%) of cases from Zagreb reported hiking in recreational areas as the main risk activity. In other counties, 48% (115/241) cases reported farm/forestry work, and 26% (64/241) cleaning house or surroundings. There was no difference in hospitalization between Zagreb and other counties. The odds of being exposed through forestry/farm work was 2.09 (95%CI:0.82-5.3) among severe cases.

Conclusions:

Risk activities varied between Zagreb and other counties. Continued national surveillance is required to inform specific prevention strategies for people living and working in, or travelling to endemic areas. Prevention strategies in Zagreb should include communication to the general population, while in other Croatian counties, prevention activities should focus on forestry and farm workers.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: haemorrhagic fever with renal syndrome, Croatia, outbreak, zoonoses

ABSTRACT ID: 549

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17.5. Tularaemia outbreak after a hare hunt in Bavaria, Germany, 2018 – lacking awareness about the disease and its potential transmission routes?

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Background:

A tularaemia outbreak occurred after a hare hunt in Bavaria. Tularaemia is a rare disease in Germany with hunters being one of the main risk groups. We investigated the outbreak to identify the most likely transmission routes and activities associated with infection.

Methods:

We conducted a retrospective cohort study among hunting participants (n=35) and interviewed four butchery employees who handled the hunted hares. We used a questionnaire asking about potential risk factors including hare handling. All 39 persons and several hunted hares were tested. Cases had IgM antibodies against Francisella tularensis. We calculated relative risks (RR) with 95%-confidence intervals (CI).

Results:

We identified 11 cases (nine hunting participants, two employees; attack rate 28%). Cases were aged 11–62 years and nine were male (82%). Ten cases reported mainly flu-like symptoms, but none reported ulcers or lymphadenopathy. All ten received early antibiotic treatment. Nine cases reported direct hare contact. Among all 39, one non-case reported using any personal protection. Hunters who were involved in the processing of hares (RR=7.6 [95%-CI 1.9–31]), including those who rinsed hares (RR=4.80 [95%-CI 1.9–12], and who were <2 meters from the hares while they were processed (RR=9.5 [95%-CI 1.3–68]) had a significantly higher risk of infection. One hare was positive for tularaemia.

Poster Abstracts

Conclusions:

In this outbreak, only nonspecific symptoms occurred that were not indicative of a specific transmission route. This might be explained by early treatment. However, as cases did not use personal protection we conclude that transmission could have occurred by inhalation of infectious aerosols and/or direct skin contact. People who process hunted hares should be better informed about tularaemia risks and the importance of using personal protection.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Tularaemia, Francisella tularensis, zoonoses, hare hunting, risk factors, disease outbreak

ABSTRACT ID: 605

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17.6. Outbreak of Salmonella Enteritidis linked to an unusual vehicle in southern Germany, November 2018

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Background:

In November 2018, several cases of Salmonella Enteritidis, linked to a private event, were reported to a local health authority in Bavaria. We investigated to identify the vehicle of the outbreak and prevent further illness.

Methods:

All 86 guests received a questionnaire, to ascertain food consumed at the event. We assessed associations between food items and illness to identify the vehicle of infection. Salmonella stool and food samples were serotyped at local laboratories. Whole genome sequencing and cgMLST (EnteroBase scheme) was conducted at RKI or the Bavarian Health and Food Safety Authority. Food safety authorities conducted trace-back of suspected food items.

Results:

Among 78 guests who answered the questionnaire (response rate 90%), 26 reported gastrointestinal symptoms. Six of the 26 provided a stool sample and all had laboratory-confirmed S. Enteritidis infection. Four food items were significantly associated with SE infection; spätzle had the highest risk ratio (RR 8, 95%CI: 2-30). Spätzle is pasta made with raw whole eggs, cooked briefly in boiling water. Frozen pre-cooked spätzle from the implicated batch tested positive for S. Enteritidis. Eggs from the source farm tested negative. The spätzle isolate was identical (0-1 alleles difference in cgMLST) to the cases' isolates (n=5). All belonged to complex type (CT)1892: CT-1892 cases outside this outbreak have been reported in other states, dating back to 2015.

Conclusions:

Epidemiological data suggested that spätzle was the vehicle of infection. The food trace-back and microbiological investigation confirmed that spätzle, apparently contaminated during the production process, caused the outbreak. The distribution of identical CT-1892 isolates over several years and locations illustrates that more epidemiological context, through for example cohort studies, are required to identify the origin of CT-1892.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: salmonella, outbreak investigation, Salmonella Enteritidis, Whole Genome Sequencing

ABSTRACT ID: 743

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Track 18: Tuberculosis and other respiratory diseases (excluding viruses) (2): epidemiology

Moderator:

Senia Rosales-Klintz

Abstracts

18.1. Multidisciplinary investigation of a Legionella pneumophila outbreak due to novel subtype 2733 in South West England, January 2019

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Background:

Five cases of Legionella pneumophila were identified within a 6km radius in South West England between August 2018 and January 2019. A multidisciplinary investigation was conducted to describe the cases and generate hypotheses for potential sources, to guide appropriate public health response

Methods:

Demographic information and case histories (locations visited and routes travelled) were retrieved from standard surveillance and bespoke trawling questionnaires and mapped in ArcGIS 10.2. A Legionella Cluster Detection (LCD) Tool was run to assess the likelihood of cases occurring sporadically. A Source Zone Inference Model (SZIM) was used to predict a potential location for the source, along with weighted wind roses to illustrate prevailing wind direction(s) during each case's incubation period. Clinical isolates were whole genome sequenced; samples were tested from the households of four cases and thirteen other sites selected on the basis of epidemiological and/ or environmental risk of harbouring Legionella.

Results:

Between 08 August 2018 and 13 January 2019, five cases of Legionella pneumophila were identified as part of this cluster. The LCD found it statistically unlikely that these cases were sporadic. Three respiratory samples were confirmed as serogroup 1, subtype 2733 and an outbreak declared. All cases were local residents and epidemiological investigations and SZIM identified the same area of interest. Weighted wind roses indicated that cases were unlikely to have been exposed to plumes from active cooling towers. Environmental samples were not positive for Legionella pneumophila.

Conclusions:

Outbreak control teams need to be aware of data requirements for new tools and technologies, and approaches to synthesis and interpretation of diverse outputs, to inform risk assessment and optimise timeliness of Legionaire's outbreak response.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Legionnaires' disease, Legionella pneumophila, field epidemiology, outbreak, meterological data

ABSTRACT ID: 102

PRESENTED BY: Ranya Mulchandani / ranya.mulchandani@phe.gov.uk

18.2. Epidemiology of Legionnaire's disease in Greece during 2008-2018: focus on foreign travellers

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Background:

Studies on the epidemiology of Legionnaires' disease (LD) in Greece are limited. We aimed to explore the epidemiology of LD in Greece from January 2008 to September 2018 in order to plan prevention activities.

Methods:

Using the 2012 EU/EEA case definition we analyzed all LD cases reported to the National Public Health Organization through the Mandatory Notifiable Diseases system (MND), the European Legionnaires' disease Surveillance Network (ELDSNet) and notifications by foreign public health authorities from 1/1/2008-30/9/2018. We described all cases and tested for differences in notification rates amongst tourists between calendar years, using the total nights spent by incoming and domestic tourists in Greece as denominator.

Results:

During the study period a total of 844 LD cases were reported, of which 795 (94%) confirmed and 49 (6%) probable. Among total cases, 558 (66%) were male and 693 (82%) were over 50 years old (median: 62, range: 6-92). Furthermore, 539 (64%) were travel-associated, 253 (30%) community-acquired, 29 (3%) hospital-acquired and 23 (3%) ship-associated. Among travel-associated cases: 494 (92%) were non-Greek travelers visiting Greece notified through ELDSNet and by foreign countries and 411 (76%) were located in three touristic island prefectures out of thirteen prefectures in Greece. We compared notification rates of travel-associated LD cases in 2017-2018 to 2008-2016 and observed a geographically dispersed increase (1.2/1,000,000 nights of stay versus 0.6/1,000,000, $p < 0.001$).

Conclusions:

We identified an increase in notification rates of LD mainly among non-Greek travelers in 2017-2018 not explained by any changes in the reporting system or large outbreaks and implemented public health measures including awareness activities in the areas with the highest case burden. Further environmental research is recommended to identify factors contributing to the increase.

Subject: Surveillance

Keywords: Legionnaires' disease, surveillance, epidemiology, Greece

ABSTRACT ID: 271

PRESENTED BY: Elisavet Mouratidou / elsamouratidou@gmail.com

18.4. Changing Epidemiology of Tuberculosis Among Children in South Korea: Notification rate (2001-2017) and Mortality (1997-2017)

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Background:

Our study aims to investigate the incidence/mortality rates and changing trends in tuberculosis in children in Korea.

Methods:

The age-standardised incidence/mortality rates and age-specific incidence/mortality rates (0-4 years, 5-9 years and 10-14 years old) for tuberculosis were estimated using the registry database of CDC in the year 2001-2017 and using the cause of death database of Korea Statistics in the year of 1997-2017. The trends in incidence/mortality rates for tuberculosis in children by subtype of tuberculosis were analyzed using Joinpoint regression model.

Results:

The incidence cases for tuberculosis was 581,264 during 2001-2017, of whom 5,448 (0.9%) was children≤14 years old. The age-standardised incidence rates per 100,000 persons have decreased annually by 8.8% from 73.9 in 2001 to 42.8 in 2017. During the same period, incidence rates for children have decreased for all age groups (3.6 to 0.7 for children aged 0-4, 2.9 to 0.3 for children aged 5-9, 10.4 to 3.2 for children aged 10-14). The number of death from tuberculosis was 57,053 during 1997-2017, of whom 91 (0.002%) was children aged≤14 years old. 47 children (51.5%) died from pulmonary tuberculosis, 9 (9.9%) died from extrapulmonary tuberculosis, and 35 (38.5%) died from disseminated tuberculosis. The age-standardised mortality rates per 100,000 persons have declined annually by 4.7% from 9.5 in 1997 to 7.8 in 2002 and decreased annually by 8.0% from 7.8 in 2002 to 1.9 in 2017.

Conclusions:

The incidence of tuberculosis among children has steadily decreased since 2001 in Korea, and the decreasing slope has been accelerating in recent years, especially for the children aged 5-14 years. Similarly, the trends of mortality rate for tuberculosis has decreased more rapidly since 2002.

Subject: Burden of disease

Keywords: Tuberculosis, children, incidence, mortality, trend

ABSTRACT ID: 493

PRESENTED BY: Byung-Woo Kim / bero@ncc.re.kr

18.5. Trends of pulmonary and extrapulmonary tuberculosis in Malta over 29 years (1990-2018) and the impact of screening newly arrived migrants to Malta,

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Background:

During the last 30 years, the Maltese population has increased due to migration from EU and non-EU countries. Since 2002, new migrants arriving in Malta from high tuberculosis (TB) incidence areas are screened on entry using chest X- ray (CXR) and/or Mantoux test. We analysed TB surveillance data from Malta to inform the strategy for TB elimination.

Methods:

We describe demographics, clinical characteristics and trends of pulmonary and extra-pulmonary TB in Malta from 1990 to 2018. We also analysed data from the national migrant and asylum seekers screening database from 2002 to 2018 and assessed the contribution of the migrant screening programme to case detection.

Results:

In total, 864 TB cases were reported with 71% diagnosed as active pulmonary TB and 29% as extra- pulmonary TB. The mean annual incidence rate was 7.3/100,000. The incidence peaked at 13/100,000 in 2008, continued to be high and was 11.4/100,000 in 2018. Since 2002, 90% of asylum seekers arriving in Malta (26,407/29,341) have been screened on entry. Approximately 1.2% of them were diagnosed and treated for active TB: 72% (232) pulmonary TB; 28% (91) extrapulmonary TB. Among all TB-positive cases diagnosed since 2010 (n=339), 11% were HIV co-infected. A total of 892 (3.4%) minors(<18years) were diagnosed with latent TB infection and received preventive treatment.

Conclusions:

TB incidence increased in Malta during the last 29 years. TB screening among migrants on entry has been effective in identifying active and latent TB and, thus, enabling early treatment and reduced transmission. Its continuation will be crucial to control and drive towards TB elimination in the coming years. Active surveillance and diagnostic testing of TB- HIV coinfection continues to be relevant for both clinical and public health purposes.

Subject: International health and migration

Keywords: Tuberculosis, Malta, Migration, HIV, Tuberculosis screening, Pulmonary Tuberculosis, Extra-pulmonary Tuberculosis

ABSTRACT ID: 723

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18.6. Avian Influenza surveillance among wild birds in Asian part of Russia (2018-2019) (LATE BREAKER)

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Background :

Wild birds of aquatic ecosystems considered to be the natural reservoir of influenza viruses. Due to essential aspects of genetic structure, replication and reassortation of different IAVs, novel

strains with new antigenic properties can emerge leading to outbreaks among poultry, wild birds and mammals including human. Main migration routes of wild aquatic birds cross territories of

Asian part of Russia making these territories urgent for surveillance. During previous surveillance different subtypes was detected. Crucial role in understanding of recent presence and dynamics of spreading is given to regular surveillance.

Methods:

Cloacal swabs from 1330 wild aquatic birds were collected during influenza virus surveillance in Autumn in 2018-2019. Sampling sites were located in Western Siberia (Novosibirsk region, msk region, Tyva region), Northern East of Siberia (Yakutia region), south-central region of Siberia (Buryatia) and Russian Far East (Primorye region). Viruses were isolated using cultivation in serum pathogen-free chicken eggs. Type and subtypes of viruses were established both using Real Time PCR and Next generation sequencing.

Results:

In total, more than 43 LPAI viruses were isolated predominantly from birds of Anseriformes order. No high pathogenic avian influenza (HPAI) viruses were isolated. The low pathogenic avian influenza (LPAI) viruses were further subtyped as H1N1, H3N8, H4N6, H5N3, H8N4, H11N9, H12N5, H13N6, H16N3. Some of them were found to be intra- and intercontinental reassortants.

Conclusions:

Broad variety of LPAI viruses were revealed. However, previously outbreaks in Uvs-Nuur Lake (Tyva region) were reported in 2016 further caused poultry outbreaks in Central Russia in 2017. This study demonstrates the demand for continuing surveillance to detect new variants of influenza viruses and contribute prevention of outbreaks. This work was supported by Russian Science Foundation (grant #17-44-07001).

Subject: Surveillance

Keywords: influenza virus,surveillance,Russia,avian influenza,wild birds

ABSTRACT ID: 871

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Track 19: Emerging and vector-borne diseases and International health (3): surveillance approaches

Moderator:

Teija Korhonen

Abstracts

19.1. Countries at risk of importation of chikungunya virus cases from Southern Thailand: a modeling study

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Background:

Southern Thailand has been experiencing a large chikungunya virus (CHIKV) outbreak since October 2018. Given the magnitude and duration of the outbreak and its location in a popular tourist destination, we sought to determine international case exportation risk and identify countries at greatest risk of receiving travel-associated imported CHIKV cases.

Methods:

We used a stochastic model to estimate the expected number of exported cases from Southern Thailand between October 2018 and March 2019. The model incorporated data on CHIKV natural history, infection rates in Southern Thailand, average length of stay for tourists, and international outbound air passenger numbers from the outbreak area. For countries highly connected to Southern Thailand by air travel, we ran 1000 simulations to estimate the expected number of imported cases. We also identified destination countries with conditions suitable for autochthonous CHIKV transmission.

Results:

Over the outbreak period, we estimated that an average of 98 (95% credible interval (CrI): 79-119) cases would be exported from Southern Thailand to international destinations via air travel. China was projected to receive the most cases (28, 95% CrI: 18-39), followed by Singapore (7, 95% CrI: 2-12) and Malaysia (5, 95% CrI: 1-10). Twenty-two countries were projected to receive at least one imported case, and 63% of these countries had one or more regions that could potentially support autochthonous CHIKV transmission.

Conclusions:

The overall risk of international exportation of CHIKV cases associated with the outbreak is Southern Thailand is high. Our model projections are consistent with recent reports of CHIKV in travelers returning from the region. Countries should be alert to the possibility of CHIKV infection in returning travelers, particularly in regions where autochthonous transmission is possible.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Chikungunya virus, arboviruses, travel-related diseases, disease outbreaks ,air travel

ABSTRACT ID: 161

PRESENTED BY: Ashleigh Tuite / ashleigh.tuite@utoronto.ca

19.2. An early-warning system of West Nile Virus risk in northern Greece

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Background:

West Nile Virus (WNV) is listed among the main vector-borne diseases that pose a severe public health threat in Europe. Recent outbreaks have revealed the urgent necessity for a field, data-driven early-warning system, that would serve as a decision support tool for vector control operations.

Methods:

The multifaceted nature of WNV transmission calls for a holistic approach that incorporates systematic sampling and monitoring of vectors and sentinels, timely pathogen detection and an integrated modeling approach that simulates the environmental and meteorological impact on all aforementioned compartments. In the current analysis, bi-weekly sampled mosquito data are used, in conjunction with numerical weather forecast data and a suit of environmental/geographic covariates, in order to assess the bi-weekly potential distribution of the Culex mosquito species in northern Greece. Data on infected vectors and/or sentinels are further incorporated into the modeling process and contribute towards the forecasting of WNV risk.

Results:

The aforementioned methodology applied for the WNV outbreak of 2018 in the same study area displayed reliable capacity to identify the spatial distribution of Culex mosquitoes and to further identify the areas of increased WNV risk. The same approach will be applied for the 2019 season in a fully-operational mode, yielding bi-weekly WNV risk maps.

Conclusions:

An integrated approach of assessing WNV risk is applied in northern Greece, with the purpose to support vector control actions, with a bi-weekly temporal resolution.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: West-Nile Virus, Ecological niche modeling, Early-warning system

ABSTRACT ID: 724

PRESENTED BY: Maria Chara Karypidou / karypidou@geo.auth.gr

19.3. Evaluation of an event-based surveillance system for detection of infectious disease outbreaks in Nigeria 2016-18

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Background:

Event-based surveillance (EBS) is the organised, rapid capture of unstructured information on events of public health concern to supplement traditional indicator-based surveillance. EBS was established at the Nigeria CDC in 2016. We aimed to describe and evaluate the system according to attributes: usefulness, simplicity, acceptability, timeliness and data quality to make recommendations to maximise utility.

Methods:

We described the system according to its components and data flows and performed descriptive analysis of signals received between September 2017 and June 2018. We collected information from staff involved in EBS, from junior to director level, via questionnaires, semi-structured interviews, and observation of practices by system users.

Results:

The system comprised an automated internet-based data mining tool and a call centre receiving communications from the public and healthcare staff. Information indicative of health events (signals) were prioritised and escalated for investigation. Amongst 43,631 signals detected, 138 (0.3%) were escalated as suspected events. 63 (46%) were verified as true events. Records of prioritisation, escalation and investigation were available for 57 (41%), 103 (75%) and 4 (6%) suspected events respectively. Verified events included outbreaks of Lassa fever (25, 40%), cholera (13, 21%) and meningitis (6, 10%). Median interval from detection to escalation was one day. Signal prioritisation and escalation logging mechanisms were applied inconsistently. Interviewees provided multiple examples of major outbreaks detected earlier than using traditional sources. Users were satisfied with processes though suggested alerts and reports be better targeted for action.

Conclusions:

EBS proved effective in supplementing routine surveillance sources in detecting outbreaks. However, the lack of robust procedures may underestimate impact. We recommend optimising the system through standardisation of processes to improve efficiency and translation to public health action.

Subject: Surveillance

Keywords: event based surveillance, nigeria

ABSTRACT ID: 528

PRESENTED BY: Kazim Beebeejaun / kazim.beebeejaun@phe.gov.uk

19.4. EpiCore, a novel approach crowdsourcing verification to enable epidemic intelligence

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Background:

Significant efforts have been made to improve early detection within epidemic intelligence. Several novel event-based surveillance processes have emerged resulting in increased signal volume. EpiCore is a network of human and animal health professionals crowdsourced to contribute to verification of these signals. EpiCore does not aim to replace any official mechanism and is meant to be a complementary information source. Created in 2014, it is currently used by GeoSentinel, HealthMap, ProMED and MSF-Spain to enhance their Epidemic Intelligence workflows

Poster Abstracts

Methods:

Epicore data from January 2018 to April 2019 have been analyzed to characterize the utility provided to the different organisations sending out requests for information (RFI) to the EpiCore network.

Results:

230 RFI were sent during the observed period (ProMED 74.3%, HealthMap 19.1 %, MSF-Spain 6.1% and Geosentinel <1%) with a response rate of 61% and a median response time of 4 hours. ProMED and HealthMap primarily collected early stages details on events reported by media to improve the quality of their online posts and rule out false alarms; MSF-Spain predominantly followed up on rumors detected directly from the field to implement local response activities; GeoSentinel used EpiCore to verify events detected through travel-related surveillance in countries of suspected transmission. All organisations were able to see the same information in real time, this way EpiCore contributed to lessening information silos and reducing duplication efforts during verification.

Conclusions:

EpiCore is changing the event verification landscape by providing EI organizations access to a network of professionals to provide ground truths during a potential event. In the future, EpiCore may also play a role in assisting national and subnational authorities on verification activities, particularly in remote areas.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Epidemic Intelligence, Verification, Event-Based Surveillance, Community-based surveillance

ABSTRACT ID: 486

PRESENTED BY: Jas Mantero / jasmantero@gmail.com

19.5. Development and validation of good epidemiological practice (GEP) guidelines for global health

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Background:

Widely endorsed guidelines for good epidemiological practice (GEP) in global health are not available. Yet, a number of documents have laid the foundations for their development. Based on this existing body of work, we developed a set of GEP guidelines specifically tailored to the idiosyncrasies of global health epidemiology.The aim of this study was to validate the guidelines and reach consensus among of wide representation of stakeholders involved in the commissioning, conduct, appraisal and publication of global health research.

Methods:

We conducted a Delphi study, consisting of two rounds of online consultation. The first round included open-ended questions to encourage qualitative input from experts while the second was a quantitative scoring round. Online consultation was followed by a face-to-face meeting to resolve issues that remained thorny despite two rounds of consultation.

Results:

Sixty-six experts participated the first round of consultation, and fourty in the second round. Respondents covered a range of organisations (universities, national public health institutes NGOs, funding organisations, technical multi-lateanl agencies, pharmaceutical companies; peer-reviewed journals) from countries around the world (first round Europe: 27; Africa: 14; Asia: 11; North America: 8; South-America: 3; Austalia: 1). Eight key experts were invited for a face-to-face meeting. The outcome of the study consists of a final set of 6 standards and accompanying criteria covering the following steps in the study process: 1) Study preparation; 2) Study protocol and ethical review; 3) Data collection; 4) Data management; 5) Analysis; 6) Reporting and dissemination.

Conclusions:

GEP guidelines for global health are now available. While they will not by themselves guard global health from questionable research practices, they are certainly part of a concerted effort to ensure rigour and transparency.

Subject: Toolkits

Keywords: guidelines reproducibility transparency, good practice

ABSTRACT ID: 42

PRESENTED BY: Daniel Jeannetot / s.alba@kit.nl

Track 20: HIV, sexually transmitted infections and viral hepatitis (III): surveillance & epidemiology

Moderator:

Lisa Hansen

Abstracts

20.1. Molecular surveillance is needed for hepatitis A outbreak case detection, Sweden, 2009 to 2018

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Background:

The Public Health Agency of Sweden (PHAS) has a national hepatitis A (HAV) molecular surveillance program; however, submitting samples for sequencing is not mandatory. We evaluated the contribution of sequence-based typing (2009-2018) for outbreak detection in order to improve surveillance and risk mitigation.

Methods:

We analysed Sanger sequencing derived HAV sequences and identified Sequence-Based Clusters (SBC, ≥459nt/460nt similarity). We defined cases as part of an outbreak if connected to an SBC and ≥1 sequence matched an European outbreak strain or ≥3 sequences belonged to cases (i) less than 8 weeks apart and/or (ii) sharing an epidemiological link. Epidemiologically linkable un-sequenced cases were added to the outbreaks. We evaluated the contribution of sequence-based typing to identify an outbreak by defining each case as linked by sequence, epidemiological or both information.

Results:

During the study period, 47% (450/957) of the notified HAV cases were sequenced. We identified 67 SBCs. Analysis of the SBCs revealed 24 outbreaks (179 cases) including all 14 previously confirmed. To these, additional 23 non- sequenced cases with an epidemiological link were attributed. Of the then total 202 outbreak cases, 59% (119/202) were linked by sequence, 11% (23/202) by epidemiological and 30% (60/202) by both types of information. Without sequencing, 16 of the 24 outbreaks (67%) would not have been detected.

Conclusions:

Molecular HAV surveillance added substantial value for detection of outbreaks and outbreak cases in Sweden. Implementing routine sequencing would enable PHAS to detect outbreaks more comprehensively, initiate targeted control measures and synchronize efforts with European investigations.

Subject: Surveillance

Keywords: Hepatitis A virus, Sequence Analysis, Molecular Surveillance, Sweden

ABSTRACT ID: 219

PRESENTED BY: Maximilian Riess / max.riess@live.de

20.2. Neisseria gonorrhoeae antimicrobial resistance among cases imported to the EU/EEA

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Background:

During 2018-2019, increasing numbers of multidrug-resistant and extensively drug-resistant Neisseria gonorrhoeae strains were reported globally, mainly linked to travel to South-East Asia. Travel-related gonorrhoea cases could lead to importation of such strains to the EU/EEA. We analysed data from the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP) to describe antimicrobial resistance (AMR) patterns among imported cases.

Methods:

Using Euro-GASP data from 2011-2017, geometric mean minimum inhibitory concentrations (MIC) of isolates tested for ciprofloxacin, azithromycin, cefixime and ceftriaxone were calculated by region of infection (United Nations grouping). Regional risk for resistance was analysed for each antimicrobial adjusting for year, gender and sexual orientation using logistic regression.

Results:

Of 16,250 isolates reported from 28 EU/EEA countries during this time, the probable country of infection was known for 9,042 (56%) cases. Of these, 448 (5.0%) were imported; of which 51% were likely acquired in another EU/EEA country and 23% in South Asia. Geometric mean MICs were highest for azithromycin, cefixime and ceftriaxone among persons infected in the East-Asia and Pacific region (0.584, 0.04 and 0.011 mg/l, respectively) and for ciprofloxacin in Latin America (2.4 mg/l). Among cases acquired outside the EU/EEA, azithromycin resistance was associated with infection in Latin America (aOR: 8.0 p=0.04) and ciprofloxacin resistance with infection in Latin America (aOR: 8.5 p=0.046) and South Asia (aOR: 6.2 p=0.02).

Conclusions:

Although imported cases from outside the EU/EEA were small in number, there were significant differences in AMR depending on region of infection highlighting the risks of AMR importation. Clinicians need to be aware of the risk of importation of AMR strains. Better quality data may allow Euro-GASP to provide an indication of N. gonorrhoeae AMR in regions without established surveillance.

Subject: Surveillance

Keywords: Gonorrhoea, Antimicrobial Resistance,surveillance,STI

ABSTRACT ID: 247

PRESENTED BY: Gianfranco Spiteri / gianfranco.spiteri@ecdc.europa.eu

20.3. Human Immunodeficiency Virus cascade of care in Poland: improving, but still not on target

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Background:

Timely diagnosis, treatment and achieving viral suppression is key to control human immunodeficiency virus (HIV) epidemic. We aimed at estimating trends in the basic elements of the cascade of care: the number of people living with HIV (PLHIV), the number of diagnosed (PLHIV-D), the number treated (PLHIV-T) and the number of virally supressed (PLHIV-S) in Poland.

Methods:

We used: 1) case-based surveillance data adjusted for reporting delay to estimate, with ECDC Modelling Tool, the proportion diagnosed; 2) National Health Fund data linked with vital registry to estimate PLHIV-D, excluding deaths and emigrants (people not in contact with health care for ≥3 years); 3) HIV treatment programme data for PLHIV–T; 4) published survey results to estimate PLHIV-S. The undiagnosed fraction was applied to the estimated PLHIV-D to obtain the estimate of PLHIV. Due to data availability the estimations were limited to 2011 – 2017.

Results:

In 2017 there were 15,166 (95%CI 13,859 – 16,938) PLHIV, of whom 12,385 were diagnosed, proportion diagnosed - 82% (95%CI 73%-89%). This proportion increased steadily from 72% in 2011, by 1.7% per year. There were 10,496 PLHIV-T by the end of 2017, 85% of the estimated PLHIV-D. The proportion treated raised from 65% in 2011, by 2.9% annually. Published survey data on proportion virally suppressed indicated that 96% of PLHIV-T were suppressed in 2016. Applying this proportion to 2017 data would result in 10,052 PLHIV-S.

Conclusions:

The improvement in the cascade of care in Poland is insufficient to meet the 2020 target of 90% of PLHIV diagnosed, but achieving the goal of 90% of PLHIV-D on treatment, by 2020, is likely. Lack of diagnosis may hamper the control of the HIV epidemic in Poland.

Subject: Surveillance

Keywords: HIV; prevalence; undiagnosed fraction; prevalence; cascade of care, Poland

ABSTRACT ID: 363

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20.4. Surveillance of transmitted HIV drug resistance in Hungary

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Background:

Transmitted HIV-1 drug resistance (TDR) may affect the success of first-line antiretroviral treatment. The aim of this study was to monitor the presence of HIV-1 strains carrying transmitted drug resistance-associated mutations (TDRMs) in newly diagnosed, treatment-naïve patients in Hungary. Extensive implementation of integrase inhibitors into the medical care initiated to investigate TDR of this drug class as well.

Methods:

274 HIV-infected individuals diagnosed between 2013 and 2018 were included in the study; most of them belonged to the MSM (men who have sex with men) group. HIV-1 subtypes and TDRMs were determined by sequencing partial protease, reverse transcriptase and integrase coding regions of the pol gene. The sequences were analysed using the Stanford HIV Drug Resistance Database algorithm. Transmission clusters among patients were identified using phylogenetic analysis.

Results:

Although subtype B HIV-1 strains were predominant (84.7%) in the study, non-B subtypes including A, F, CRF01_AE, CRF02_AG, C, D and G were also recorded. The overall prevalence of TDR was 9.1% (25/274; 95% CI: 6.3-13.1%). Most of TDRMs were detected in subtype B HIV-1 strains. Nucleoside reverse transcriptase inhibitor (NRTI)-associated mutations were the most frequent indicators of TDR (21/274; 7.7%; 95% CI: 5.1-11.4%), followed by mutations conferring resistance to protease inhibitors (PIs) (3/274, 1.1%; 95% CI: 0.4-3.2%) and non-nucleoside reverse transcriptase inhibitors (NNRTIs) (2/274; 0.7%; 95% CI: 0.2-2.6%). Drug resistance of integrase inhibitors were tested in 136 newly diagnosed, untreated patients. Major integrase resistance mutation (T66A) was detected in 1 case (1/136; 0.7%; 95% CI: 0.1-4.1). Cluster analysis revealed potential transmission clusters with TDRM carrying samples.

Conclusions:

Onward transmission of drug resistant subtype B HIV-1 strains accounted for the majority of TDRs observed among treatment-naïve HIV-infected individuals in Hungary.

Subject: Surveillance

Keywords: HIV-1, transmitted drug resistance, Hungary, transmission cluster, ongoing transmission

ABSTRACT ID: 488

PRESENTED BY: Éva Áy / ayeva.pj@gmail.com

20.5. Three approaches to estimate Mycoplasma genitalium seroprevalence in the general German population

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Poster Abstracts

Background:

Multiplex serology of population-based survey samples would be cost-effective and feasible in estimating Mycoplasma genitalium (MG) seroprevalence in the general German population. However, a reliable gold standard is lacking and defining thresholds for seropositivity is challenging. To assess uncertainty of MG seroprevalence estimates, we present three methods.

Methods:

We analysed sera from the population-based "German National Health Interview and Examination Survey 1998" for MG antibodies using a pre-validated, multiplex, fluorescent bead-based assay. MG seropositivity was defined as concomitant seropositivity for antigens MgPaN and rMgPa. (1) We set thresholds for seropositivity by visual inspection of inflection points (VIP) of percentile plots. (2) We conducted a sensitivity analysis for lowest and highest prevalence from literature (1% and 15%). Therefore, we aimed for thresholds yielding the same number of false positives as false negatives in reference sera. For (1) and (2), we applied survey weights to calculate prevalences and 95%-confidence intervals (95%CI). (3) We implemented a Bayesian model using a Gibbs sampler including prior knowledge on prevalence, sensitivity and specificity based on reference sera testing and expert opinion.

Results:

Sera of 6,038 participants aged 17-79 years (median 44 years) were analysed. VIP resulted in thresholds of 1,000 median fluorescence intensity (MFI) units with weighted seroprevalence of 6.5% (95%CI: 5.7-7.3%). Thresholds for sensitivity analyses were set at 700 and 1,200 MFI which resulted in seroprevalences of 8.7% (95%CI: 7.8-9.7%) and 5.4% (95%CI: 4.7-6.2%), respectively. The Bayesian model estimated a seroprevalence of 4.3% (95%-credible interval: 1.5-7.5%).

Conclusions:

In the absence of clearly defined thresholds, MG seroprevalence estimates ranged between 4.3% and 8.7%. To allow for more accurate estimates, MG serology should be validated prospectively on patients with confirmed infection.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)
Keywords: Mycoplasma genitalium, seroprevalence, Germany, sensitivity analysis, uncertainty quantification, Bayesian approach

ABSTRACT ID: 560

PRESENTED BY: Felix Reichert / reichertf@rki.de

20.6. Ongoing syphilis outbreak in the European Union and European Economic Area (EU/EEA) – populations at risk, determinants of transmission and options for response (LATE BREAKER)

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Background:

Syphilis notification rates have been increasing the EU/EEA since 2010, with an accelerated trend observed in recent years predominantly among men who have sex with men (MSM). By request of Member States, the European Centre for Diseases Prevention and Control (ECDC) engaged in comprehensively describe the epidemic and formulate evidence-based options for response.

Methods:

A non-systematic literature review (PubMed, Embase, Scopus; 2007-2018) was combined with an analysis of EU/EEA surveillance data (2007-2017) to describe trends, identify populations most at risk and determinants of transmission. A systematic literature review (PubMed, Embase, Scopus, Cochrane Database of Systematic Reviews, hand-and Google searches; 2007-2018) was conducted to identify interventions to respond to syphilis outbreaks and/or increased notifications. Both literature searches covered the EU/EEA, the EU candidate countries, Australia, Canada, Japan, New Zealand and the USA. 189 studies on syphilis epidemiology and 78 on response interventions met eligibility criteria.

Results:

During 2007-2017, 260,505 syphilis cases were reported from 30 EU/EEA countries with numbers of reported cases increasing from 19,898 in 2007 to 33,193 in 2017, notification rates from 4.6 to 7.1 and male-to-female-ratio from 3.0 to 8.5. Most (62%, 94,015/152,233) cases were MSM. During 2014-2017, cases among HIV-negative-MSM increased by 74% and among HIV-positive-MSM by 31%. Engagement in high-risk sexual practice and several social vulnerabilities were identified as drivers of intensified transmission, with some variations across risk groups.

Public health responses should combine enhanced screening of populations at risk, partner notification, case management and education. Response interventions should consider local epidemiology, main determinants of transmission and target populations most at risk.

Conclusions:

Syphilis epidemic in the EU/EEA is evolving, predominantly affecting MSM. A detailed technical advice document has been recently published by ECDC.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: syphilis, epidemic, EU/EEA, evidence-based interventions, response

ABSTRACT ID: 886

PRESENTED BY: Otilia Mardh / Otilia.Mardh@ecdc.europa.eu

Track 21: Influenza and other respiratory viruses (3): human respiratory syncytial virus

Moderator:

Eeva Broberg

Abstracts

21.1. Human respiratory syncytial type A and B viruses in Finland, 2010-2018

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Background:

We implemented typing of human respiratory syncytial virus (RSV) to describe the distribution of RSV types in Finland and provide information for RSV surveillance and future vaccination policy.

Methods:

The variable RSV nucleoprotein gene was chosen for RSVA and RSVB type differentiation in a PCR based assay using primers and probes courtesy of Statens Serum Institut, Denmark. Assay implementation was validated using five commercial RSV external quality assurance panels from 2014-2018 (n=44). After validation, all available RSV positive specimens (n=301) from 12/2010-05/2018 were typed. The collection consisted of influenza and other respiratory virus sentinel (outpatients) and non-sentinel (hospitalized and intensive care unit (ICU) patients) surveillance specimens.

Results:

Assay sensitivity for detecting RSVA was 82% (14/17 positive specimens), and for detecting RSVB, 100% (21/21). Assay specificity was 100% for both types (6/6 negative specimens). In the typed collection, 187 specimens (62%) contained RSVB, 99 (33%) – RSVA and 3 (1%) – both viruses. Twelve specimens (4%) were negative. RSVB was the main type during 3/4 investigated RSV epidemic seasons (2011-2012, 2015-2016 and 2017-2018). Overall, RSVB dominated in males (96/155, 62%) and females (68/98, 69%) as well as in children, especially in the risk group of under 2-year-olds (76/105, 72%) and age group 10-19-year-olds (40/55, 73%). RSVB was also a leading type in outpatients (156/238, 66%), hospitalized (26/39, 67%) and ICU (8/15, 53%) patients.

Conclusions:

The newly introduced RSV typing assay detects both RSV types. The typing results provide a first glance at baseline information for RSV surveillance in Finland with RSVB dominating in the screened collection. We recommend ongoing typing of RSV positive specimens to provide information on RSV type distribution for surveillance and a possible future vaccination programme.

Subject: Surveillance

Keywords: Respiratory Syncytial Viruses, PCR, surveillance, Finland

ABSTRACT ID: 47

PRESENTED BY: Marius Linkevicius / marius.linkevicius@thl.fi

21.2. Evaluation of the Respiratory Syncytial Virus laboratory-based surveillance system in Portugal, 2017-2018

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Background:

The Portuguese Laboratory Network for the Diagnosis of Influenza Infection (PLNDII) comprise fourteen hospital-based laboratories and might perform two tasks for respiratory syncytial virus (RSV) surveillance in Portugal in 2017-2018: (A) all reported the RSV-positive cases of every age weekly and, (B) all were invited to participate in the genetic characterization of RSV-positive cases from children <5 years and adults ≥65 years by sending RSV-positive samples and a form with epidemiological characteristics to the National Institute of Health (INSA). Three attributes were evaluated in order to improve RSV laboratory-based surveillance system in Portugal.

Methods:

RSV data analysis from the PLNDII during 2017–2018 was performed and on-line questionnaires were sent to the laboratories (n=14). Simplicity was rated according to the ease of operation in components A and B. Acceptability was evaluated through the case reporting rate and the perception of the RSV public health relevance. Data completeness was evaluated as data variables completeness.

Results:

Eleven of fourteen laboratories (78.6%) were involved in the genetic characterization of RSV and eight (57.1%) answered the questionnaire. All laboratories (8/8) perceived the public health relevance of the disease and 64.3% (9/14) reported cases for >90% weeks. The data collection form, devised by INSA, was reported as easy to fill in by five laboratories (62.5%, 5/8) for component A and by four (50%, 4/8) for component B. For genetic characterization, five laboratories (45.5%) completed all variables for 127 patients whereas six laboratories (54.5%) had >50% unknown or incomplete signs/symptoms for 188 patients.

Conclusions:

RSV laboratory-based surveillance system was evaluated as acceptable and simple. However, the format of the data collection form requires improvement while preserving the contents.

Subject: Surveillance

Keywords: Respiratory syncytial virus, evaluation, laboratory-based surveillance, Portugal

ABSTRACT ID: 361

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21.3. Establishment of a global surveillance network to assess differences in the epidemiology of RSV in primary and secondary care: the GERi project

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Background:

Respiratory syncytial virus (RSV) is the leading cause of acute lower respiratory infections in children. RSV is also recognized as a cause of illness in adults and high-risk adults, with a disease burden similar to that of seasonal influenza A. To support optimal immunization strategies to prevent and control RSV in the future, it is critically important to understand who develops symptoms leading to healthcare usage in the community and in hospitalized patients.

Methods:

National surveillance systems in 27 countries were contacted to join the GERi study from January to April 2019. All countries were asked to provide their RSV surveillance data since 2000, with data collected separately for primary care and hospitalized patients. Countries will also be asked to complete a survey on the main features of the country's RSV surveillance system, including questions on the methods used for the identification of the RSV virus, the definition of inpatient and outpatient care used and the representativeness of their data.

Results:

So far 16 countries have accepted to join GERi, with data already available for Ecuador, New Zealand, Russia, Singapore and South Africa. Data collection will be ongoing until the end of 2019. The focus of our analyses will be on the spatio-temporal characteristics of RSV epidemics (start, peak, length of epidemics) and age differences, and whether these are evolving over time. We will be able to present preliminary findings during the ESCAIDE conference.

Conclusions:

We are in the process of establishing a global RSV surveillance network that will provide valuable data to assess differences in the epidemiology of RSV in different settings and will provide support to future prevention and control measures.

Subject: Surveillance

Keywords: RSV, surveillance, epidemiology

ABSTRACT ID: 511

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21.4. Virological surveillance of respiratory syncytial virus (RSV) through a hospital-based surveillance network in Catalonia (2015-2018). Present, past and future

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Background:

Respiratory syncytial virus (RSV) is recognised as an important respiratory pathogen, particularly in the youngest population. The primary objectives of this hospital-based surveillance network, created in the 2015-2016 season, are to describe the RSV epidemiology and the genetic features of circulating RSV strains in our geographical area.

Methods:

The hospital-based surveillance network is currently composed by eight large paediatric hospitals in Catalonia (Spain). Since the 2015-2016 season, from October to May, the following information is gathered for every laboratory- confirmed RSV case attended in the participating hospitals: age, gender, and hospital and ICU admissions. The genetic features (genetic group and genotype) from a representative sampling of strains are further reported.

Results:

A total of 5,774 (17%) cases were laboratory-confirmed for RSV from 33,492 tested respiratory specimens, of which 4,370 (76%) were hospitalised. RSV epidemics started between epidemiological weeks 44-48, and ended between weeks 5-6 of the upcoming year. The epidemic peaks occurred between epidemiological weeks 49-53, when positivity rates of tested-specimens ranged 48-61%.

Among hospitalised patients, 87% (3,818/4,370) cases were <2 years-old (median age: 4.7 months; interquartile range: 1.60 – 13.9 months), 56% (2,435/4,370) were males, and 17% (731/4,370) required ICU admission.

Viruses belonging to both RSV genetic groups were co-detected. However, the predominant RSV genetic group shifted among the several seasons from RSV-A during the 2015-2016 (83%) to RSV-B during the 2016-2017 (56%), the 2017-2018 (74%) and the 2018-2019 (59%) seasons. Most of the characterised viruses belonged to ON1 (RSV-A) and BA9 (RSV-B) genotypes.

Conclusions:

The high burden of RSV disease in the most susceptible population (<2 years-old children) and its genetic diversity remark the need to maintain a hospital-based network for the clinical and virological surveillance.

Subject: Surveillance

Keywords: respiratory syncytial virus, respiratory infection, surveillance,

RSV

ABSTRACT ID: 552

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21.5. Human Respiratory Syncytial virus infection in pediatric population during four consecutive seasons in a tertiary care hospital in Barcelona (Spain)

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Background:

Human respiratory syncytial virus (HRSV) infection is the main cause of bronchiolitis among infants, increasing hospital and Pediatric Intensive Care Unit (PICU) admissions and respiratory support requirements. We describe clinical and microbiological characteristics of patients under 2 years of age admitted at a tertiary hospital in Barcelona (Spain) for HRSV bronchiolitis from epiweek 40/2014 to 20/2018.

Methods:

Clinical and microbiological data of hospitalized children under 2 years with HRSV bronchiolitis were retrospectively reviewed. HRSV laboratory-confirmation in respiratory samples was performed either by using antigen detection-based or molecular methods. The genetic group (HRSV-A or B) was determined by Seegene Allplex RT-PCR or by a nucleoprotein-specific real-time RT-PCR assay. Hospital and PICU lengths of stay and proportion of intubated patients were compared among HRSV subtypes.

Results:

A total of 727 patients met the inclusion criteria. The median age was 148 days. A total of 7.7% of the patients were born prematurely and 5,1% had other comorbidities. HRSV-B predominated in all but one season (2015-2016) when HRSV-A was detected in the 79.5% of patients. The mean hospital stay was 6.24 days (standard deviation [sd] 14.09), being slightly higher in those with HRSV-B infection (6,40 days; p=0,75). PICU admission was necessary in 132 (18.2%) patients. The mean PICU stay was 6,3 days (sd 4,5), being significantly higher for those with HRSV-A infection (6,9 days, p=0.04). A higher proportion of patients with HRSV-A infection required intubation (7,6%) compared with those with HRSV-B infection (2,9, p= 0.004).

Conclusions:

Patients under 2 years with HRSV-A bronchiolitis have more severe disease than those with HRSV-B infection, requiring longer stays in PICU and higher probability of intubation.

Subject: Burden of disease

Keywords: human respiratory syncytial virus, length of stay, Pediatric Intensive Care Unit, intubation, hospitalization

ABSTRACT ID: 716

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Track 22: Influenza and other respiratory viruses (4)

Moderator:

Flaviu Plata

Abstracts

22.1. Combining sentinel GP networks improves the surveillance of influenza in Flanders, Belgium

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Background:

Intensity and seasonality of influenza epidemics in Belgium are weekly monitored with actively reported data from a sentinel general practitioners (SGP) network. Another independent sentinel GP-based morbidity registration network exists in Flanders region, called Intego, which can provide additional information extracted from electronic health records such as drug prescriptions and underlying medical conditions. We compared data on influenza like illness (ILI) cases between both networks in order to evaluate the inclusion of Intego to complement influenza surveillance.

Methods:

The data sources were compared in terms of case definitions, coverage and information available. We conducted a retrospective analysis of data from both networks on ILI cases from 2015 to 2017. We compared weekly and annual incidence rates, overall and by age group, and estimated the annual number of ILI cases. Cross correlation factors were calculated up to lag 5, with each lag of one week

Results:

Trends of weekly incidence rates were similar between both networks, showing the same patterns in increase and decrease over the entire study period. Epidemic thresholds, estimated for SGP data, identified identical epidemic weeks when applied to Intego data. The cross correlation was highest at lag 0 (.98), with the three epidemic peaks reported on same weeks. However all three peaks were on average 30% lower for the Intego network. Trends by age group were in agreement with children <15 years presenting consistently higher incidences rates.

Conclusions:

Both networks measure ILI cases and are comparable in monitoring the intensity and seasonality of influenza epidemics over time. Beside incidences, they complement each other in the information provided and the inclusion of both networks in one integrated Influenza surveillance system would represent an added value.

Subject: Surveillance

Keywords: Influenza, Surveillance, General Practitioner, Belgium

ABSTRACT ID: 187

PRESENTED BY: Ana Hoxha / ana.hoxha@sciensano.be

22.3. The added value of applying genomic data for predicting the severity of influenza infection

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Background:

Severity of seasonal influenza depends on both the viral and host characteristics. Whole genome sequencing (WGS) enables the detection of mutations in the viral genome, resulting in high-dimensional datasets. This study aims to find the combination of predictors that best predicts a severe influenza infection among hospitalized patients, and to assess the relevance of incorporating genomic viral data in the predictive model.

Methods:

160 H3N2 influenza positive samples from the 2016-2017 season originating from the surveillance of severe acute respiratory infections in Belgium were selected for WGS using a case-control sampling approach. A severe influenza infection was defined as having at least one complication (stay in Intensive Care Unit, Acute Respiratory Distress Syndrome, Extracorporeal Membrane Oxygenation, invasive respiratory support, or death). Host characteristics were obtained from the clinical forms and consensus nucleotide mutations were identified by comparing the genomic sequences to a reference. A penalized Elastic Net logistic regression model was used to select predictor variables for severity from the combined dataset. The model combining host and genomic data was compared with the model that only included host data using a likelihood-ratio test and the area under the ROC curve (AUC).

Results:

Chronic respiratory condition, chronic cardiovascular condition, renal insufficiency, immunocompromised condition and 3 mutations, were selected in the sparse Elastic Net regression model. The model including mutations in addition to the host characteristics had an improved fit compared to the model with only host characteristics (X2= 12.03, df=3, p =0.007), and the optimism-adjusted AUC increased from 0.671 to 0.732.

Conclusions:

Adding genomic data (selected mutations in the viral genome) to the model containing host characteristics improved the prediction of a severe influenza infection.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: influenza, genomics, statistical methods, prediction model

ABSTRACT ID: 368

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22.4. Increasing trend of mortality and cost of infectious disease in Republic of Korea, 2010-2017

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Background:

Due to rapid economic growth and development of health care system, average life expectancy and overall mortality rate tended to improve in the Republic of Korea. However, the Republic of Korea is still endangered by the outbreak of infectious diseases that causes great burdens on health care system. This study identifies the trends of changes in mortality and economic burden of infectious diseases.

Methods:

Data from health care statistics of the Health Insurance Review and Assessment Service(2010-2017) and Korean Statistics Information Service(1997-2017) were used. The National Health Insurance System is mandatory insurance and all Korean citizens are enrolled. We selected 10 infectious disease groups (intestinal infections, tuberculosis, vaccine-preventable diseases, sepsis, viral hepatitis, HIV-related diseases, central nervous system infections, rheumatic heart diseases, respiratory tract infections, and arthropod-borne viral diseases).

Results:

The age-standardized mortality rate for infectious diseases increased from 26.9/100,000 population in 1997 to 38.3/100,000 population in 2017 and had an upward trend since 2004. It had significant increase in respiratory tract infections and among persons age≥65 years during the same period. The costs of infectious diseases increased to 4.6 billion USD in 2017 from 3.2 billion USD in 2010. The largest proportion of the costs was observed in respiratory tract infections as 828.2 million USD in 2017(25.6%). The annual cost per patient who visited hospital for infectious diseases increased from 46.2 USD in 2010 to 63.8 USD in 2017.

Conclusions:

The mortality rate among elderly persons and persons with respiratory tract infections tended to increase for recent 13 years. The economic burden of infectious diseases has consistently increased, especially respiratory tract infections. It is essential to establish an effective management policy considering particular infectious diseases and patients groups.

Subject: Burden of disease

Keywords: Communicable Diseases, Mortality, Health Care Costs, Republic of Korea

Poster Abstracts

ABSTRACT ID: 123

PRESENTED BY: Dahye Baik / dahye7602@ncc.re.kr

22.5. Molecular characterisation of influenza viruses by partial and whole-genome sequencing during the 2018-2019 season at a tertiary university hospital in Catalonia (Spain)

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Background:

Influenza viruses (FLUV) remain a major cause of morbidity and mortality. The aim of this study was to describe the genetic features of influenza A viruses (FLUAV) detected in patients who were admitted at a tertiary hospital during the 2018-2019 season.

Methods: Respiratory tract specimens were tested for influenza laboratory-confirmation. The sequencing of the complete coding haemagglutinin-1 (HA1) domain (from all detected viruses) and neuraminidase (NA) protein (from severe cases) was performed. Whole-genome sequencing (WGS) on Illumina Miseq platform of FLUV from severe and mild cases (1:1) was carried out in order to compare their genetic features.

Results:

A total of 6,978 samples (5,255 patients) were processed, of which 1,478 (21%) samples from 1,394 (27%) patients were influenza laboratory-confirmed. Most cases (1,392; 99.9%) were FLUAV-confirmed cases, of which 689 (49.6%) were A(H1N1)pdm09, 651 (46.8%) A(H3N2) and 50 (3.6%) unsubtyped. Phylogenetic analyses of HA1 sequences revealed that all (246) A(H1)pdm09 sequences belonged to subclade 6B.1. The D222G mutation in HA1 (virulence marker) was detected in a severe A(H1N1)pmd09-confirmed case. Among A(H3) viruses (218), different genetic subclades were observed: 156/218, 3C.2a1b; 47/218, 3C.3a; 9/218, 3C.2a3; and 6/218, 3C.2a2. No amino acid substitutions related to reduced antiviral susceptibility were found. Preliminary WGS data from 38 severe and 33 mild cases revealed no significant differences between their genetic features.

Conclusions:

There was a balanced co-circulation of both FLUAV subtypes throughout the season. The unique characterised virulence marker for A(H1N1) pdm09, which is related to lower respiratory tract tropism, was detected in just one severe case. Although no WGS differences could be found between severe and mild cases in this preliminary data, further strains must be fully sequenced.

Subject: Surveillance

Keywords: influenza viruses; surveillance; whole-genome sequencing; genetic characterisation; respiratory infections.

ABSTRACT ID: 562

PRESENTED BY: Andrés Antón / cristina.andres@vhir.org

22.6. Assessing Severity: Strengths and Limitations in use of laboratory confirmed fatal influenza cases reported through the German Notification System

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Background:

The number of fatal cases and the case fatality ratio (CFR) contribute to severity-assessment of an influenza epidemic – especially seriousness of disease. This is relevant for seasonal Influenza and also for a pandemic wave. As part of pandemic preparedness we aim to assess notified fatal influenza cases data of the two recent influenza seasons to detect their strength and limitations.

Methods:

In Germany every laboratory-confirmed influenza case must be notified to local health authorities (LHA). After investigating missing information supplementary to the laboratory confirmation the LHA transmit the data to the National Public Health Institute, where every fatal case is subject to a plausibility process. The data of fatal influenza cases were analyzed regarding age structure, being part of outbreaks and vaccination status for the 2017/18 and 2018/19 season.

Results:

For the 2017/18 season, there are approx. 1,700 fatal outcomes out of a total of approx. 330,000 influenza cases (CFR 0.5 %). Regarding the current season 2018/19, there are currently about 870 fatal cases of influenza out of a total of 180,000 influenza cases (CFR 0.48 %). The highest proportion is of the age group 65 years and over (approx. 85%, both seasons) and in particular of those 80 years and over (approx. 2017/18: 50%; 2018/19: 42%). Of the fatal cases, a proportion of 6% is associated with outbreaks in 2017/18, which increased to 12% in 2018/19.

Conclusions:

The data of the German Notification System is subject to limitations, with a missing denominator (number of being tested) being the most crucial one. However, the data offer important information on the most severely affected groups, thus providing a basis for recommendations for the prevention and control of influenza.

Subject: Surveillance

Keywords: Influenza [D007251],Public Health Surveillance [D062486],Epidemiological Monitoring [D062665],Disease Notification [D018563],Germany [D005858]

ABSTRACT ID: 569

PRESENTED BY: Julia Schilling / SchillingJ@rki.de

Poster Abstracts

Track 23: Vaccine-preventable diseases (4): vaccine coverage, uptake and response

Moderator:

Pavla Krizova

Abstracts

23.1. Immunisation of healthcare workers in the Nordic countries: Differences in policy and practice and a lack of surveillance

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Background:

Healthcare workers (HCWs) are at higher risk of both exposure to and transmission of infectious diseases. Two European Union (EU) directives (2010/32/EU and 2000/54/EC) state that employers are responsible for assessing employees' exposure to occupational infectious hazard and for offering immunisation, accordingly. Our aims were to assess: 1) current policy for immunisation of HCWs, and 2) the availability of vaccine coverage data for HCWs, in the Nordic countries.

Methods:

We surveyed national vaccination experts in Denmark, Finland, Iceland, Norway and Sweden, and Swedish county medical officers, due to decentralized organisation. We used a self-administered structured questionnaire on diseases and HCW categories covered by the recommendation and availability of coverage data. The surveyed experts validated these results.

Results:

All national experts (n=7) and 81% (17/21) of the Swedish county medical officers responded. EU member states had transposed the European directives into national law, while Norway and Iceland had similar legislation. There were national immunisation recommendations in Finland, Iceland and Norway, national guidelines in Denmark, and regional recommendations in 15 out of 17 responding Swedish counties. Hepatitis B and pertussis immunisation were recommended in all countries where national guidelines/recommendations existed and in 13 and 5 Swedish counties, respectively. Measles immunisation was recommended in Iceland, Norway and Finland and 14 Swedish counties. No coverage data were available for HCWs at a national or sub-national level except for two Swedish counties and ad-hoc hospital surveys elsewhere.

Conclusions:

Recommendations on HCWs immunisation differed across Nordic countries. No country systematically measured uptake of HCW immunisation programmes. This lack of data hampers assessment of the existing recommendations, and any future interventions to improve uptake in this group.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: healthcare workers, immunisation, recommendations, Nordic countries

ABSTRACT ID: 62

PRESENTED BY: Timothee Dub / timothee.dub@thl.fi

23.2. Is there an association between socioeconomic status and immune response to infant and childhood vaccination in the Netherlands?

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[3,4,5,6] --

Background:

Socioeconomic status (SES) is a well-known determinant of health, but its relationship with vaccine-induced immunity is less documented. We explored the association between SES and immunoglobulin G (IgG) levels against vaccine- preventable diseases in vaccinated children in the Dutch National Immunization Programme.

Methods:

Data from a population-wide cross-sectional serosurvey in the Netherlands (2006-2007) were used. We compared geometric mean IgG concentrations/titers (GMC/T) against measles, mumps, rubella, Haemophilus influenzae type b (Hib), Neisseria meningococcus type C, diphtheria, tetanus, poliovirus types 1,2,3 and pertussis in children of high versus low SES by linear regression analysis, calculating GMC/T ratios. We included 894 children (0-12 years) at one of two timeframes: 1 month to 1 year, or 1-3 years after vaccination. Mother's educational level and net household income served as binary indicators of SES.

Results:

No consistent patterns between and within pathogens at either timeframe were observed by income and educational level. The GMC/T ratio favoured high educational level at 1m-1y for Hib (2.99, 95%CI 1.42-6.30) and for polio 2 after second booster vaccination (1.14, 1.01-1.27). The GMC/T ratio favoured low income for polio 1, 2 and 3 1m-1y after primary vaccination (respectively: 0.74, 0.58-0.94; 0.79, 0.64-0.97;

0.72, 0.55-0.95), polio 3 and pertussis 1-3y after primary vaccination (0.70, 0.56-0.88; 0.66, 0.47-0.95), mumps and rubella 1-3y after first vaccination (0.73, 0.55-0.97; 0.70, 0.55-0.90), and rubella 1m-1y after second vaccination (0.83, 0.55-0.90). There was no association between SES and the proportion of protective IgG levels

Conclusions:

We found no consistent association between SES and immune response to vaccination in the Netherlands. We recommend confirming these results with the next nationwide serosurvey. Meanwhile, no additional public health action is needed in tailoring vaccination-schemes according to SES.

Subject: Burden of disease

Keywords: Socioeconomic status, Vaccine-preventable diseases, Immune response, Vaccination

ABSTRACT ID: 86

PRESENTED BY: Jossy Van den Boogaard /

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23.3. Sociodemographic determinants of not being registered with the 5-year booster for children born in 2010 living in Copenhagen

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Background:

Childhood vaccination coverage in Denmark differs between vaccines and municipalities. Copenhagen municipality has one of the lowest coverages. The objective of this study was to assess sociodemographic determinants for not being registered in the Danish vaccination register (DDV) with the 5-year diphtheria-tetanus-pertussis and polio booster for children in Copenhagen.

Methods:

In the Danish civil registration system we identified children born in 2010 and living in Copenhagen as of July 2018, and extracted sociodemographic factors for each child. In DDV, we identified children not registered with the 5-year booster. In the Danish National Health Service Register, we identified which general practitioner each child was registered with. Data were linked using a unique personal identifier assigned to all residents. We applied a multivariable logistic regression model and estimated odds ratios and 95% confidence intervals.

Results:

In total 6039 children were born in 2010 and living in Copenhagen in July 2018. The recorded vaccination coverage for the 5-year booster was 89%. The following factors were associated with not being registered with the 5-year booster: being born from a young mother <25 years of age, having at least two older siblings, not living with both parents sharing custody or being registered with a general practitioner working alone. The highest odds were found for immigrants to Denmark (OR 11, 95% CI: 8-15).

Conclusions:

Non-registration of the 5-year booster could be due to non-vaccination or underreporting and children with any of the identified risk factors should have their vaccination status checked and updated in the DDV by their general practitioner. We also recommend providing targeted communication to immigrants to Denmark about the Danish vaccination schedule.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: The Danish Vaccination Register, Determinants of vaccination, logistic regression

ABSTRACT ID: 130

PRESENTED BY: Ida Glode Helmuth /idgk@ssi.dk

23.4. Introducing a local health facility-level vaccination coverage monitoring system into the national vaccination coverage surveillance in England

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Background: In England, childhood immunisation coverage is collected from local child health records at ages 12 months, 24 months and 5 years through a national surveillance system called COVER (Cover of Vaccination Evaluated Rapidly). Data are published quarterly for each of the 152 districts. High-quality coverage data at the local health facility-level would improve local public health intelligence and programme performance. We designed and implemented a validation process for the newly-collected facility-level data to ensure that COVER data outputs remain high quality and fit for purpose.

Methods:

We evaluated facility-level data collected between September 2017 and August 2018 for data completeness (proportion of health facilities reporting per quarter), data concurrence (<10% difference between facility-level vaccine coverage aggregated to district-level and vaccine coverage at district-level) and consistency (<10% difference between facility- level vaccine coverage aggregated to district-level and average vaccine coverage for the previous three quarters).

Results:

All facilities reported data in all quarters. In the 152 England districts, aggregated facility-level data and district-level data were concurrent in 146 (96%), 143 (94%) and 141 (93%) districts for the 12 month, 24 month and 5 year data, respectively. For consistency, 95% (145/152) of aggregated facility-level data were within the 10% threshold for the 12 month vaccinations, 95% (24 month) and 94% (5 year).

Conclusions:

In most districts, facility-level data was complete, consistent and concurrent with district-level data. Facility-level data can be used to improve intelligence on inequalities in vaccine coverage and support immunisation policy decision- making. The validation process identified facilities outside the thresholds that require further investigation. The process has now been implemented by the COVER team in Public Health England.

Poster Abstracts

Subject: Surveillance

Keywords: vaccination coverage, local health facility

ABSTRACT ID: 561

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23.5. Implementation of a national digital vaccination reminder service in Denmark

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Background:

In Denmark the vaccination coverage rates for the second measles-mumps-rubella vaccination and the diphtheria-tetanus-pertussis-polio booster are below 95%. Parents forgetting the vaccination is one of the most frequent causes of non-vaccination. In 2019 a national vaccination reminder system will be implemented within the Danish Immunization Information System (IIS). We describe the reminder system and the estimated costs for its maintenance.

Methods:

From 1st August 2019 all vaccines in the national childhood vaccination programme will automatically be added to the electronic vaccination record of newborn children as a list of recommended vaccinations with specific due dates. 14 days before a vaccination due date a reminder is sent to both parents or caregivers digital mailbox, which is used by all public authorities. If the vaccination is not registered in the IIS within 30 days after the due date a recall reminder will be sent to both parents. Parents who have exemption for receival of digital mail will receive a printed reminder by mail. In order to catch-up on previous birth cohorts, the later vaccinations in the vaccination programme will be added to children turning four or 12 years of age.

Results:

Each birth cohort is approximately 62,000 children. When the reminder system is rolled out to all children below 13 years it is estimated to generate app. 1.1 million pre-vaccination reminders to parents of 560,000 children and 112,000 post-vaccination recall reminders pr. year. The costs for the maintenance of the system has been estimated to approximately 400.000 Euro pr. year.

Conclusions:

It is feasible to use an IIS to develop large scale electronic reminder services with the aim to optimize timing of vaccination and overall coverage.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: mmunisation Information System, Vaccination, Reminder service, Vaccination Coverage

ABSTRACT ID: 693

PRESENTED BY: Tyra Grove Krause / tgv@ssi.dk

23.6. Inequalities in uptake of routine childhood immunisations, analysis of coverage data from 2009-2019; Wales UK

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Background:

The European Vaccine Action Plan 2015-2020 highlights the importance of identifying and reducing inequities in vaccination uptake. However, there are few published reports on equity of immunisation uptake in children.

Methods:

Individual immunisation records for all children resident in Wales, aged one to 15 years, from April 2009 to March 2019, were extracted from the National Child Health Database. Data included residency at Lower Super Output Area (LSOA) level. The proportion of children up to date with routine immunisations reaching first, fourth and fifteenth birthday were calculated. LSOA of residence were allocated into quintiles of deprivation, using overall Welsh Index of Multiple Deprivation rankings.

Results:

During 2018-19, uptake in children resident in the most deprived compared to the least deprived areas (inequity gap) was: 93.0% versus 96.0% in one-year olds, 88.0% versus 93.0% in five-year olds and 79.0% versus 73.0% in 15-year olds. The odds of being unimmunised were significantly higher in the most deprived compared to the least deprived areas at all ages, with odds ratios of 1.8 (CI 95% 1.5 – 2.1), 1.8 (CI 95% 1.6 – 2.0) and 1.4 (CI 95% 1.3 – 1.5) in one, five and fifteen year olds respectively. From 2009 to 2019, the immunisation inequity gap has remained stable in one year olds and five year olds and decreased in fifteen year olds (from 12.0% to 6.0%).

Conclusions:

Socioeconomic inequities in immunisation uptake are smallest in infants and increase in older children and teenagers. Progress has been made in reducing inequities in teenagers. Further work is needed in identifying specific barriers to immunisation in deprived areas and targeting interventions to reduce inequalities evident over the past ten years.

Subject: Surveillance

Keywords: Child, Adolescent, Immunization, Vaccine preventable diseases, Socioeconomic Factors

ABSTRACT ID: 749

PRESENTED BY: Malorie Perry / Malorie.Perry@wales.nhs.uk

Poster Abstracts

Track 24: Late breakers

Moderator:

Sooria Balasegaram

Abstracts

24.1. Making a splash: large Norovirus outbreak associated with an outdoor theme park splash area, July 2019,

Rachel Glass [1]

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Background:

In July 2019, Public Health England was alerted of a gastroenteritis outbreak among visitors to a theme park. 151 cases self-reported including members of large groups. We aimed to identify the source of infection to inform prevention and control measures.

Methods:

A retrospective cohort study was undertaken among members of three groups who attended on Wednesday 24th July. Cases were defined as any person visiting that day with diarrhoea or vomiting <72 hours afterwards. Data were collected using a secure electronic questionnaire. We undertook descriptive, univariable and multivariable analyses with odds ratios (OR), adjusted OR and 95% confidence intervals (CI) for exposures calculated. Clinical and environmental samples were tested and a site risk assessment undertaken.

Results:

Among the 362 group members, 105 (29% response rate) completed the questionnaire; 69 (66%) provided sufficient information for analysis. There were 35 cases (attack rate 51%). All cases visited the splash park and independent associations were identified between the splash park (aOR: 23.9, 95% CI: 1.2-472.6) and age <20 years (aOR: 12.2, 95% CI: 3.24-46.0) with becoming ill. The site assessment revealed a child vomited adjacent to the splash park that day with inadequate cleaning procedures. Norovirus was identified in five clinical samples and water samples indicated faecal contamination. Water quality parameters were outside the recommended range.

Conclusions:

This is the second UK outbreak of Norovirus associated with an outdoor water park. The UK urgently needs guidance for outdoor water parks, which are becoming increasingly popular in recent years due to warmer weather. We recommend the same standards as leisure pools should apply regarding water regulations and sanitary facilities and that regular monitoring of splash parks is ensured.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Outbreak investigation,Outdoor water parks,Gastrointestinal disease,Norovirus,Infectious disease

ABSTRACT ID: 856

PRESENTED BY: Rachel Glass / rachel.glass@phe.gov.uk

24.2. Drivers of a summer influenza epidemic – New South Wales, Australia, 2018-2019

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Background:

Influenza rates in New South Wales (NSW), Australia typically follow a seasonal pattern with a winter epidemic peak (June-August) and low transmission otherwise. However, incidence rates were unusually high in the summer of December 2018- March 2019, with almost double the notifications of the previous summer. We aimed to test the hypothesis that inter-seasonal influenza infection in NSW was associated with pre-illness travel and/or influenza vaccination status.

Methods:

We undertook a case-control study using the NSW notifiable diseases database; a 'case' was defined as laboratory- confirmed influenza with illness-onset between 1 December 2018 and 21 March 2019. Those notified with pertussis over the same time-frame served as the control group. Individuals with listed mobile numbers (n=3632) were sent an online survey via Short Message Service (SMS) in May, 2019. Multivariable logistic regression assessed associations between influenza illness and key exposures.

Results:

There were 7225 individuals who met the influenza case definition; respondents (cases=649, controls=260) were found to be representative of the source population (n=8,929) on key demographic factors. The odds of travel and/or contact with an ill overseas traveller amongst cases was seven times that for controls in early summer (Dec-Jan: AOR=7.09, p=<0.001) while the association was attenuated in latter months (Feb-Mar: AOR=1.69, p=0.152). There was no difference in influenza vaccination status between groups.

Conclusions:

The incidence of summer influenza appears to be increasing in Australia. Our study suggests that travel was an early driver in the development of the 2018/2019 summer epidemic in NSW and that local transmission continued despite "unfavourable" summer conditions. Results could prompt a re-evaluation of current recommendations for pre-travel vaccination or the timing for the seasonal influenza vaccine in NSW and other temperate zones.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Influenza,Travel,Seasons,Vaccination,Epidemics

ABSTRACT ID: 847

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24.3. Norovirus outbreak on a Douro River cruise ship in 2019: successful pathogen detection despite hampered epidemiological investigation

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Background:

No acute gastroenteritis outbreaks on cruise ships sailing along the Douro River have been recently reported to the Northern Public Health Department of Portugal. Notwithstanding, demand on Douro River cruises is growing considerably. At the end of August 2019, following an anonymous complaint, an investigation was conducted to determine the cause of an acute gastroenteritis outbreak on a Douro's cruise ship.

Methods:

Less than 48 hours from the report, the Public Health Authorities and the Authority for Economic and Food Safety inspected the ship. A joint investigation was then conducted through a cross-sectional study. A case was defined as a passenger or crew member of the ship who reported vomiting and/or diarrhea during the ongoing and previous 11-day tour. Epidemiological analysis was not feasible since the investigation was hampered by the cruise ship company. Samples were collected and tested for norovirus: 1 feces specimen, 5 surface swabs, 8 food samples, and 2 water samples.

Results:

A total of 251 people were exposed, of which at least 11 (29,7%) crew members and 24 (11,2%) passengers met the case definition. However, only 6 cases were interviewed. Two surface swab samples tested positive for norovirus GII, while food samples tested negative. The results of the remaining analyzes are pending. Immediate outbreak control measures were implemented.

Conclusions:

The investigation confirmed an acute gastroenteritis outbreak of norovirus GII on a cruise ship in the Douro River in 2019. The source and vehicle of the outbreak could not be identified. Detection of norovirus on surface swabs is usually difficult due to the low numbers of virus particles recovered by this method, despite evidence of its resistance in the environment.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: disease outbreaks,norovirus,ships,gastroenteritis

ABSTRACT ID: 890

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24.4. Supplementary measles immunization activities in Tyrol during the European Immunization Week, April 2019

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Background:

In Austria, twice as many measles cases (n=144) were notified during the first 8 months of 2019 compared to the entire year of 2018. Media coverage around measles outbreaks peaked in January and April/May. The European Immunization Week 2019, held during week 17, aimed "to raise awareness of the importance of immunization". In April, Tyrol launched a broad information campaign and offered measles-mumps-rubella vaccine (MMR) during a "long afternoon of vaccination" (LAV) free of charge. The objective of our study was to assess the impact of the campaign on MMR vaccine uptake.

Methods:

We compared the monthly MMR uptake obtained from the electronic vaccine registry for the first 6 months of 2019 with the same period of 2018. We analysed the weekly uptake between week 12 and 22 (18. March – 2 June) and stratified the results by district and age group.

Results:

During the first 6 months of 2019 the number of administered MMR doses increased by 52% compared to the same period of 2018 (from 8,305 doses in 2018 to 12,418 doses in 2019). Most MMR doses were administered in April and May, mainly during week 17, when the LAV took place (519 MMR doses within 3 hours). The uptake was highest in birth cohorts 1960-1987, followed by births cohorts prior to 1960. In birth cohorts 2017/18, the additional impact was lowest, although the routine uptake was the highest (around 300 doses per week). The increased uptake lasted for a four week period in all age groups.

Conclusions:

The 50% increase of MMR uptake was promising but cannot only be attributed to the awareness raising campaign. The intense media coverage probably also played an important role.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Measles, vaccination, health priorities, Europe

ABSTRACT ID: 835

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Poster Abstracts

24.5. A large outbreak of Cryptosporidium hominis associated with swimming pool use during a children's football tournament: evidence for persistent contamination

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Background:

In May 2019 Public Health England were alerted to a gastroenteritis outbreak in persons attending a football tournament and staying at a holiday park. We aimed to determine the source of infection and control the outbreak.

Methods:

A retrospective cohort study was undertaken among persons attending the tournament between 3-6 May 2019. Confirmed cases attended the tournament and reported symptoms of gastroenteritis with confirmed Cryptosporidium spp.. Probable cases reported symptoms without laboratory confirmation. Descriptive, univariable and multivariable analyses were undertaken with relative risk (RR) and odds ratios (OR) with 95% confidence intervals (CI) calculated for exposures. Clinical and environmental samples underwent microbiological testing.

Results:

Seven hundred persons attended the tournament and 177(25%) responded to the questionnaire. There were 86 cases (attack rate (AR):49%) of which 12 were confirmed as C.hominis. Swimming at the holiday park accounted for 97% of cases (AR 74%) and was significantly associated with illness (RR:14.0, 95% CI: 4.7-43.4). Odds of illness increased with pool usage (one-use OR:40.8, 95% CI: 11.5-144.9 and two OR:76.0, 95% CI: 18.3-315.9). Independent associations were found between visiting the pool on day one (OR:10.9, 95% CI: 1.7-70.6), day two (OR:8.5, 95% CI: 3.2-22.3) or day three (OR: 4.9, 95% CI: 1.8-13.6) and becoming ill. A pool water sample tested negative for bacterial indicator parameters (aerobic colony count, coliforms and Escherichia coli).

Conclusions:

We found strong evidence for a Cryptosporidium outbreak associated with use of the holiday park pool. The data suggest persistent contamination from day one or multiple separate contamination events. We recommend facilities with intensive pool usage follow current guidelines, fit appropriate pool filters and have sanitation procedures in place to prevent persistent contamination.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Outbreak investigation; gastrointestinal disease; Cryptosporidium ; Swimming Pool;

ABSTRACT ID: 880

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24.6. Implementation of a diagnostic screening program for chronic Q-fever in the Netherlands

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Background:

Chronic Q-fever causes potentially life-threatening complications and high mortality. Timely detection and treatment of patients with chronic Q-fever infection is important. Medical risk factors for chronic Q-fever after acute infection are well described. A recent study has shown that targeted screening of patients with risk factors, in regions with previous outbreaks, is cost-effective. We therefore started the implementation of targeted chronic Q-fever screening in general practices (GP) in the Netherlands, almost 10 years after a large Q-fever epidemic.

Methods:

GPs select and invite patients with specific heart valve or vascular disease or an immunocompromised status in their practice. Antibodies against Coxiella burnetii are tested with immunofluorescence assay (IFA). While an IgG II titre of ≥1:64 shows a past infection with Q-fever, an IgG I titre of ≥1:512 is considered suspect for chronic Q-fever. A definite diagnosis is made by medical examination and radiological imaging findings in clinical centres with expertise in chronic Q-fever.

Results :

In a first pilot phase, four GP practices (catchment area of 26,900 patients) were included to perform the screening with 939 eligible patients. Of these patients, 520 (55.4%) were tested of which 123 (23.7%) test results showed evidence of a past infection with C. burnetii and two (0.4%) were considered suspect for chronic Q-fever (1.6% of seropositive patients).

Conclusions:

Years after a large Q-fever epidemic, targeted screening in high-risk groups may still detect undiagnosed chronic infections. The proportion of patients with evidence of a past infection with C. burnetii was much higher than expected. Although not previously reported in the international literature, this might suggest that certain risk groups are more susceptible to acute infection after a certain exposure compared to the general population.

Poster Abstracts

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: chronic Q-fever; Coxiella burnetii; diagnostic screening program; infected aneurysm; heart valve; immunocompromised patients

ABSTRACT ID: 836

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