

European Scientific Conference on Applied Infectious Disease Epidemiology

Online, 24-27 November 2020



www.ecdc.europa.eu

Foreword



I hope you found the first online edition of ESCAIDE stimulating and rewarding, and that you have had an enjoyable experience.

The original plan was to hold ESCAIDE in Warsaw, Poland, this year. Regrettably, one of the consequences of COVID-19 was the need to restrict travel and defer from holding mass gathering events, such as ESCAIDE, and so it was that we concluded that it was not possible to plan to hold ESCAIDE as a physical event in 2020, and instead we started planning, in April of this year, to hold the conference as a virtual event in 2020.

The decision to preserve the conference was founded on what we believe to be the invaluable benefit of offering a forum to share thinking and knowledge in such a challenging year for infectious disease prevention and control. Our hope is that by making content available online, everyone is able to access sessions after the conference finishes. I also strongly believe that this change in format provides a unique opportunity to reach a broader audience.

I would like to express my enormous appreciation to my Scientific committee colleagues, who have been able to attract some of the most eminent figures to address the conference and deliver a stimulating plenary programme. The conference began with a keynote session on the COVID-19 pandemic and its epidemiological, clinical and societal impacts (Plenary A). The challenges of pandemic preparedness planning and response in times of COVID-19 were debated in Plenary B. Plenary C discussed the role of behaviour change and new technologies such as drugs, diagnostic modalities, monitoring and infection control precautions in tacking Antimicrobial resistance. The conference concluded with Plenary D, a debate on the future of field-epidemiology training programmes, while reflecting on how those have helped to prepare a generation of public health workforce active today. It was particularly apposite that we held this debate in the year that sees EPIET celebrate its 25th anniversary.

As in every year, the ESCAIDE 2020 conference programme was also built around abstracts that have undergone a peer review process to assess the quality and public health relevance of each submission. This is made possible through the willingness of the many researchers and public health professionals to share their work by submitting abstracts, the large number of reviewers who guide abstract selection, the session moderators who steer the conference sessions, and finally the ESCAIDE scientific committee who oversee the scientific programme as a whole.

I would like to thank the authors who made the effort to submit an abstract to the conference. It is something we take for granted each year, but it is remarkable that in face of this year's extraordinary pressure for infectious disease professionals, you remain committed to writing scientific summaries of your work, so others have an opportunity to learn from your experiences.

The online environment might have discouraged networking and interactions, but I hope you took time to create new contacts that will be of real benefit in your daily work. I wish you all had a most enjoyable ESCAIDE 2020, and hope that you left the conference with useful contacts and renewed enthusiasm for your role in the fight to address communicable disease.

M. hr

Prof. Mike Catchpole Chair, ESCAIDE Scientific Committee

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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.



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.



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.



Scientific Committee



Frode Forland

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

Frode Forland is the Director of Infectious Disease Prevention and Control at the Norwegian Institute of Public Health. He initiated and led the 'Global Health Preparedness Program' under the 'Global Health Security Agenda', supporting Malawi, Palestine, Moldova and Ghana in building capacity for health security and implementing the International Health Regulations. He has worked at the Royal Tropical Institute in Amsterdam to establish the 'Collaboration for Evidence Based Healthcare in Africa' and at the European Center for Disease Prevention and Control in Stockholm with Development of methods for Evidence Based Public Health in Europe. Previously he was the Director of the Division for Primary Health Care at the Norwegian Directorate of Health and the Department for Guidelines, Prioritization and Quality improvement. He has worked several years in Africa and was a Board Member of Guidelines International Network for four years. He is the Vice Chair of the Norwegian Forum for Global Health Research. Frode has a keen interest in Global Health, Public Health and Evidence Based Healthcare. By profession, he is a Medical Doctor with specialty degrees in General Practice and Public Health.



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.



Bruno Coignard

Director, Infectious Diseases Division, Santé publique France



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. Medical epidemiologist specialised in the epidemiology of healthcare-associated infections (HAI) and antimicrobial resistance (AMR), I work at Santé publique France (the French National Public Health Agency) in Paris, France since 2001. I first was involved in international activities (2001-2002) of our agency, then developed and coordinated from 2002 to 2013 HAI and AMR early warning and surveillance activities through the national Healthcare-Associated Infections Early Warning, Investigation and Surveillance Network (Raisin). I previously was trained as an Epidemic Intelligence Officer (EIS) at the Centers for Disease Control and Prevention (CDC, Atlanta, USA), Hospital Infections Program (1999-2001). My areas of work include the development, implementation and assessment of surveillance systems; early warning and outbreak investigation; management of collaborative surveillance programs; linkage with multiple partners at regional, national, European and international level; scientific expertise in relevant national and European bodies, including ECDC. From 2013 to 2016, I was Deputy Director of the Infectious Diseases Division of Santé publique France, particularly in charge of coordinating, at division level, alert and investigation activities (Chikungunya, Ebola, etc.), European/international affairs and our National Reference Laboratory (NRL) network. I now am Director of the Infectious Diseases Division at Santé publique France. I have authored/co-authored >90 publications in national/international peer-reviewed journals, >40 publications in the French Weekly Epidemiological Bulletin and 9 book chapters in the field of infectious diseases surveillance.

Scientific Committee



Vicky Lefevre

Head of Unit, Public Health Functions Unit, European Centre for Disease Prevention and Control (ECDC), Sweden

Vicky Lefevre joined the European Centre for Disease Prevention and Control in April 2018, as Acting Head of Unit for Surveillance and Response Support. Since January 2020, she has taken up the position of Acting Head of the Public Health Functions Unit and as of 1 June 2020, Vicky has been appointed the Head of Unit Public Health Functions at ECDC. She is a veterinarian by training and started her career as policy officer with the Belgian Food Safety Agency in 2003, where she was responsible for the implementation of European and national legislation in the area of food safety. Since then, she has been professionally involved in food safety and public health from different angles. Between 2009 and 2012, she was a research programme officer with the European Commission, DG Research, responsible for the management of EU funded research projects in the area of public health, food safety and quality. In 2012, she returned to the Belgian Food Safety Agency as Director responsible for Control Policy in the area of Food Safety. She became the Director General responsible for Control Policy in the area of Plant Health, Animal Health and Food Safety in that same Agency in 2015.



Magdalena Rosińska

National Institute of Public Health-National Institute of Hygiene (NIPH-NIH), Poland

Dr Magdalena Rosińska, professor of the National Institute of Public Health – National Institute of Hygiene (NIPH-NIH). She works for the Institute since 2002. In her role as a researcher and public health specialist, she has been studying epidemiology of blood-born and sexually transmitted infections, particularly HIV and HCV. She authored over 100 scientific publications in this field. She firstly graduated as Medical Doctor (2000) at the Medical University of Warsaw, then obtained a Master of Science in Biostatistics (2002) at the State University of New York at Albany, USA and a Master of Science in Mathematics (2003), at the University of Warsaw. She obtained her PhD in HIV epidemiology in 2008 and her Public Health Specialist Diploma in 2015 in the National Institute of Public in Warsaw.



Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2020.

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European Centre of Disease Prevention and Control (ECDC)

The European Centre of Disease Prevention and Control (ECDC) was established in 2005. It is an EU agency which aims to strengthen Europe's defences against infectious diseases. It is seated in Stockholm, Sweden.

In order to achieve this mission, ECDC works in partnership with national health protection bodies across Europe to strengthen and develop continent-wide disease surveillance and early warning systems. By working with experts throughout Europe, ECDC pools Europe's health knowledge to develop authoritative scientific opinions about the risks posed by current and emerging infectious diseases.

Within the field of its mission, the Centre shall:

- search for, collect, collate, evaluate and disseminate relevant scientific and technical data;
- provide scientific opinions and scientific and technical assistance including training;
- provide timely information to the Commission, the Member States, Community agencies and international organisations active within the field of public health;
- coordinate the European networking of bodies operating inthe fields within the Centre's mission, including networksthat emerge from public health activities supported by theCommission and operating the dedicated surveillance networks;
- exchange information, expertise and best practices, and facilitate the development and implementation of joint actions.

www.ecdc.europa.eu



Public Health Training Section (ECDC)

The ECDC Fellowship Programme is a two-year competency based training with two paths: the field epidemiology path (EPIET) and the public health microbiology path (EUPHEM).

After the two-year training, EPIET and EUPHEM graduates are considered experts in applying epidemiological or microbiological methods to provide evidence to guide public health interventions for communicable disease prevention and control.

Both curriculum paths provide training and practical experience using the 'learning by doing' approach in acknowledged training sites across European Union (EU) and European Economic Area (EEA) Member States.

https://ecdc.europa.eu/en/epiet-euphem



Continuous Professional Development Programme (CPDP) – ECDC

Public Health Training (PHT), ECDC

ECDC has the mandate of supporting and coordinating training programmes in order to assist Member States and European Commission to have sufficient number of trained specialists in epidemiological surveillance and field investigations, and to have capabilities to define measures to control disease outbreaks. (ECDC Founding Regulation, 851/2004).

The ECDC Fellowship Program is a two-year competency based training with two paths: field epidemiology (EPIET) and public health microbiology (EUPHEM). This in-service programme is possible thanks to acknowledged training sites, public health institutes and laboratories across the EU/EEA Member States, where EPIET and EUPHEM fellows conduct surveillance, outbreak investigations and epidemiological studies, and produce scientific evidence to guide public health interventions for communicable disease prevention and control.

ECDC coordinates the Continuous Professional Development Program (CPDP), promoting a spirit of lifelong learning among public health professionals working in communicable disease prevention and control in the European Union (EU) and European Economic Area (EEA) Member States. The annual core CPD offer comprises: a Summer School, a Winter Workshop, short courses in blended formats and senior exchange visits, targeted to members of the Coordinating Competent Bodies network. Online courses, webinars, communities of practice, and access to training materials in the ECDC Virtual Academy (EVA) complement the training offer.

www.ecdc.europa.eu



Eurosurveillance (ECDC)

Eurosurveillance is a European peer-reviewed scientific journal devoted to the epidemiology, surveillance, prevention and control of communicable diseases, with a focus on such topics that are of relevance to Europe. It is a weekly online journal, with 50 issues per year published on Thursdays, and features short rapid communications, longer in-depth research articles, surveillance and outbreak reports, reviews and perspective papers, as well as short news items. Timely publication of short authoritative papers on ongoing outbreaks or other relevant public health events is one of the major assets of the journal. Under special circumstances when current events need to be urgently communicated to readers for rapid public health action, e-alerts can be released outside of the regular publishing schedule. Topical compilations of selected articles and special issues are also published in print with a limited number of copies. The entire content is open access, free of charge for both readers and authors. All articles are indexed in the PubMed/MEDLINE, PubMed Central (PMC), Scopus, EMBASE, EBSCO and Science Central databases. Eurosurveillance is listed in the Directory of Open Access Journals (DOAJ) as green open access. Furthermore, it is listed the Sherpa/Romeo database as a journal that allows pre- and postprint archiving. It thus complies with the open access standards required by international and national funders such as the European Commission (FP7 and Horizon 2020), the World Health Organization, the World Bank and the Wellcome Trust. The journal has been selected for coverage by Thomson Reuters and is indexed and abstracted in the Science Citation Index Expanded and in the Journal Citation Reports/Science Edition beginning with volume 14(1) 2009. The most recent impact factor, for the year 2018, is 7.4 (Journal Citation Reports, Thomson Reuters, 2019). This places Eurosurveillance at rank 4 among the 89 journals in the category Infectious Diseases. The Scopus-based SCImago Journal Rank (SJR) for 2018 ranks Eurosurveillance 58 of 2,863 journals in the category Medicine (miscellaneous). The journal is also in the first quarter (Q1) in the categories Epidemiology, Public Health, Environmental and Occupational Health and Virology. Google Scholar metrics in 2018 listed Eurosurveillance at ranks 3 and 10 among journals in the categories Epidemiology and Communicable Diseases, respectively.

www.eurosurveillance.org





EPIET Alumni Network (EAN)

The EPIET Alumni Network (EAN) was founded in 2000 to help develop, maintain and fortify a network of European public health epidemiologists that have participated in the European Programme for Intervention Epidemiology Training (EPIET). Later this also included fellows and alumni from the European Programme for Public Health Microbiology Training (EUPHEM) and the EU/EFTA/EEA Field Epidemiology Training Programmes (FETP). As well as alumni of training programmes, the EAN also has a limited number of 'external' members who, through their work, meet similar objectives to the EAN. The EAN is an association, run by an elected voluntary advisory board of six elected members.

www.epietalumni.net



European Respiratory Society (ERS)

ERS is an international organisation that brings together physicians, healthcare professionals, scientists and other experts working in respiratory medicine. It is one of the leading medical organisations in the respiratory field, with a growing membership representing over 140 countries worldwide. Its mission is to promote lung health in order to alleviate suffering from disease and drive standards for respiratory medicine globally.

www.ersnet.org



European Society for Clinical Virology (ESCV)

The European Society for Clinical Virology (ESCV) was formed from the European Group for Rapid Viral Diagnosis and the European Society against Virus Diseases which merged on 1 January 1997. aims are to promote knowledge in the field of basic and clinical virology, including aspects of Public Health virology. This is achieved through the organisation of educational meetings and workshops, as well as providing travel grants to attend meetings and the ECDC Observership programme. It also provides awards for work in the fields of basic and clinical virology.

The ESCV is registered as a "Company Limited by Guarantee" and listed in the Central Register of Charities in England and Wales (No 1099537).

www.escv.org

www.escmid.org



European Society of Clinical Microbiology and Infectious Diseases (ESCMID)

Since its founding in 1983, ESCMID has evolved to become Europe's leading society in clinical microbiology and infectious diseases with members from all over the world. For more than 35 years, ESCMID has been influential in the areas of microbiology and infectious disease, and currently reaches more than 33,000 individual and affiliated members with news, scientific opportunities and guidelines. ESCMID runs and supports many conferences and educational events, and its flagship congress, ECCMID was attended by over 13,000 delegates this year.



Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET)

First incorporated in 1997, Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET) is a global network of field epidemiology training programs (FETPs), trainees, and graduates. Currently, TEPHINET comprises 71 programs actively training field epidemiologists in more than 100 countries. TEPHINET member programs include those with laboratory and veterinary education components. Overall, TEPHINET comprises more than 12,000 FETP graduates who play a critical role in improving global health security by strengthening country capacity to detect and respond to disease outbreaks. With a secretariat based in Atlanta, Georgia, USA, and a global Advisory Board, TEPHINET is the only global network of FETPs and spans multiple regional FETP networks, sub-regional programs, and national programs.

Mission

To empower and mobilize a competent field epidemiology workforce for all people through standardized training, experiential learning, training program quality improvement, mentoring, and knowledge exchanges in order to connect epidemiologists better, faster, and with quality across the globe.

Vision

All people are protected by a field epidemiology workforce capable of detecting and responding to health threats.

Contact: Tina Rezvani Email: trezvani@tephinet.org

www.tephinet.org



Global Outbreak Alert and Response Network (GOARN)

The Global Outbreak Alert and Response Network (GOARN) was established in 2000 to provide a much-needed coordination solution to all countries to harness international expertise and resources in service of infectious disease epidemics that threaten the health and wellbeing of their populations. With the Secretariat hosted by the World Health Organization (WHO), today GOARN comprises of over 250 technical institutions and network across the globe. Our partners include UN organizations, International NGOs professional networks, and national public health institutions- all with the ability to provide resources rapidly to support affected countries in controlling disease outbreaks.

Over the past 2 years decades GOARN has conducted over 135 operations and deployed over 2900 experts to assist more than 90 countries worldwide. At the request of a Ministry of Health, we deliver support to augment the overall WHO response to the public health emergency. Based on the varied and evolving needs of an emergency, this support could include the deployment of technical experts to the affected countries, under the leadership of WHO, the provision of technical advice through expert committees establish during the emergency and the provision of resources for the response efforts, such as laboratory and operational logistics, tools and equipment to reinforce field teams, etc. Besides providing direct response assistance to public health emergencies our partners also host a comprehensive international outbreak response training programme to strengthen our response capacities, conduct operational research and develop of tools to support GOARN field teams in improving outbreak response interventions and share real-time information on outbreak alerts and risk assessments with WHO to identify outbreak response needs early.

https://extranet.who.int/goarn/

Plenary A: Keynote session on COVID-19



Dr. Andrea Ammon

Director, European Centre for Disease Prevention and Control (ECDC)

Dr. Andrea Ammon was formally appointed as the Director of the European Centre for Disease Prevention and Control in June 2017. Previously, Dr. Ammon was ECDC's Acting Director from May 2015.

Dr. Ammon joined ECDC as the Head of the Surveillance Unit in 2005. The unit was responsible for developing The European Surveillance System (TESSy), implementing a long-term surveillance strategy for the European Union (EU), evaluating the Dedicated Surveillance Networks (DSN), performing step-by-step transfer of DSN activities to ECDC, revising the EU case definitions and producing an Annual Epidemiological Report on infectious diseases in the EU.

From April 2011 to April 2015, Dr. Ammon was Deputy to the Director and Head of Unit for Resource Management and Coordination.

Prior to joining the ECDC, Dr Ammon served in several roles at the Robert Koch-Institute, in Berlin, Germany, most recently as Head of Department for Infectious Disease Epidemiology. In this capacity, she maintained and further developed the German national surveillance system; coordinated the national outbreak response team for current and emerging infections; coordinated emergency planning for influenza; directed the national Field Epidemiology Training Programme; coordinated epidemiological research programmes in infectious diseases and provided scientific advice for government Ministries, Members of Parliament, and the public.



Dr. Maria Van Kerkhove

COVID-19 Technical Lead, Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead, Health Emergency Program, High Threat Pathogens Unit, World Health Organization (WHO)

Dr 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.



Plenary A: Keynote session on COVID-19



Prof. George F. Gao

Director-General, China Center for Disease Control and Prevention (China CDC)

George F. Gao, DPhil (Oxon), MSc is Director-General of the Chinese Center for Disease Control and Prevention (China CDC), Vice President of the National Natural Science Foundation of China (NSFC), Director and Professor at CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, and Dean of the Medical School, University of Chinese Academy of Sciences.

George obtained his PhD (DPhil) degree from Oxford University, UK and did his postdoc work in both Oxford University and Harvard University. Using interdisciplinary methods, including virology, immunology and structural biology, Gao has made remarkable contributions to the study of interspecies pathogen transmission. His work revealed the origin and interspecies transmission mechanism of avian influenza virus including the virus entry mechanism and T-cell molecular recognition. He is a leading figure for the control of infectious diseases in China and a world advocate voice of global public health strategy. He led China Mobile Laboratory Testing Team in the fight against Ebola outbreak in Sierra Leone in 2014 and continued his leadership in China CDC's efforts supporting public health capacity strengthening in developing countries in Africa.

George is elected as the foreign associate or corresponding fellow/member of Chinese Academy of Sciences, the Third World Academy of Sciences, African Academy of Sciences, US National Academy of Sciences, American Academy of Microbiology, European Molecular Biology Organization, American Association for the Advancement of Science, Royal Society of Edinburgh, and the dean or professor of medical school/universities. He has published more than 600 peer-reviewws scientific papers in journals such as Cell, Nature, Science, The Lancet, New England Journal of Medicine, Proceedings of the National Academy of Sciences USA etc., 10 books or book chapters and holds more than 25 UK, US and Chinese patents.

George was awarded the TWAS Prize in Medical Science in 2012 and the Nikkei Asia Prize in 2014, and with numerous awards and prizes from China, including the recent National Award for the Distinguished Scientist in 2016, the National Science and Technology Award and National Innovation Award in 2017.

Plenary B: Pandemic preparedness in times of COVID-19: how have pandemic preparedness plans contributed to responding to this global public health threat?



Dr. Anders Tegnell

Deputy Director General and State epidemiologist, Public Health Agency of Sweden

Dr. Anders Tegnell is the Deputy Director General and State Epidemiologist of the Public Health Agency of Sweden. He has been the Swedish State Epidemiologist since 2013. He is a medical doctor with a PhD in infectious disease.

Dr. Tegnell has international experience, for example from Laos in 1990-1993 (WHO) and from DRC during the Ebola outbreak in 1995, and he has extensive experience of leading different Swedish government agencies at different levels in the field of public health and disease control.



Dr. Francesco Maraglino

Director, Unit for Prevention of Communicable Diseases, Italian Ministry of Health

Dr. Francesco Maraglino, Senior Medical Executive Officer, is the Director of the Unit for Prevention of Communicable Diseases in the Italian Ministry of Health. He was born in Taranto, Puglia, in the south of Italy.

Dr. Maraglino is a Medical Doctor (MD), specialist in Epidemiology and Healthcare Statistics. After working as a Medical Officer in the Navy, as Medical Consultant in the Hospital of Taranto (including the Division of Infectious Diseases) and in the Emergency Service of the local Fire Dpt., he started in 1994 his career in the Ministry of Health, during which Dr Maraglino has been appointed, during the years, as Director of the Port and Airport Health Offices of Rome-Fiumicino, Taranto and Genova and as Head of the Unit for the Nation Healthcare Planning.

He represents Italy in many European and international institutions and fora as ECDC (Member of the Management Board; National Coordinator of the CCB, NFP for Preparedness), European Commission – Health Security Committee, WHO, Global Health Security Initiative, Global Health Security Agenda.



Plenary B: Pandemic preparedness in times of COVID-19: how have pandemic preparedness plans contributed to responding to this global public health threat?



Prof. Devi Sridhar

Professor and Chair in Global Public Health, University of Edinburgh Medical School

Devi Sridhar is a Professor at the University of Edinburgh Medical School and holds a Personal Chair in Global Public Health.

She is the founding Director of the Global Health Governance Programme and holds a Wellcome Trust Investigator Award. She was previously Associate Professor in Global Health Politics and a Fellow at Wolfson College, Oxford University and a Postdoctoral Research Fellow at All Souls College, Oxford University. She was also a visiting Associate Professor at LMU-Munich and guest lecturer at the Harvard School of Public Health and the Public Health Foundation of India.

Her books include 'Governing Global Health: Who Runs the World and Why?' (OUP, 2017) and 'the Battle against Hunger: Choice, Circumstance and the World Bank' (OUP, 2007) and she has published in Nature, Science, the New England Journal of Medicine, the Lancet and the British Medical Journal. She served on the board of Save the Children UK, on the World Economic Forum Council on the Health Industry and co-chaired the Harvard/LSHTM Independent Panel on the Global Response to Ebola.

She holds a DPhil and MPhil from Oxford as a Rhodes Scholar and a B.S. from the University of Miami in the Honors Medical Program. Her work is concentrated in three areas: international health organizations, financing of global public health and developing better tools for priority-setting.



Dr. Gabrielle Breugelmans

Head of Epidemiology, Coalition for Epidemic Preparedness Innovations (CEPI)

Dr Gabrielle Breugelmans is the Head of Epidemiology at the Coalition for Epidemic Preparedness Innovations (CEPI), where she started in March of this year. Dr Breugelmans is an infectious disease epidemiologist with a large expertise in global health, poverty related diseases, access to medicine, and vaccinology in low- to middle-income countries. She holds a PhD and MPH in Epidemiology from the Johns Hopkins Bloomberg School of Public Health in the U.S and a Master of Science degree in Health Sciences from the University of Maastricht in the Netherlands.

Prior to joining CEPI, she held the position of Director of Research at the Access to Medicine Foundation where she was responsible for directing the Antimicrobial Resistance Benchmark and the Access to Medicine Index research activities. From 2012-2017, she was the North-North Cooperation manager at the European and Developing Countries Clinical Trials Partnership (EDCTP).

She has also held various other positions including at the Agence de Médecine Préventive, a French NGO specialised in field-based research in vaccinology and epidemiology, and Sanofi Pasteur MSD where she oversaw the epidemiological research programme for the quadrivalent human papillomavirus vaccine. She was part of the 7th EPIET cohort and completed her fellowship at the Robert Koch Institute (RKI) in Berlin, Germany.

Plenary C: Magic bullet to control antimicrobial resistance (AMR): behaviour change or new technologies?



Dr. Esmita Charani

Lead Pharmacist, Faculty of Medicine, Department of Infectious Disease, Imperial College London

Dr Charani's research interests are in understanding the role of social constructs in relation to health-seeking and health-providing behaviours in infection, antimicrobial resistance (AMR) and antimicrobial stewardship (AS).

Her research to date has enabled multinational collaborations and research, including both lowand middle-income and high-income countries. Her research opened the field of conducting social science research to tackle AMR and AS in national and international contexts influencing the approach to research in this field.

With a background in clinical pharmacy and through her research she has forged cross-disciplinary collaborations as well as championing and supporting greater pharmacist role in AS internationally (France, Norway and India, South Africa, Uganda). She has contributed to capacity building of researchers in India and South Africa, and is recipient of the Academy of Medical Sciences Hamied Foundation UK-India AMR Visiting Professor Award. She is also a Global Health Fellow with the Office of the Chief Pharmaceutical Officer.



Prof. Dr. Alex W. Friedrich

Head of department and Chair, Medical Microbiology and Infection Prevention, University Medical Center Groningen (UMCG)

Prof. dr. Alex W. Friedrich, MD PhD is head of the department and Chair of Medical Microbiology and Infection Prevention at the University Medical Center Groningen (UMCG) in the Netherlands. He is specialist in medical microbiology. He coordinates large international and cross border research networks for the prevention of infections due to antimicrobial resistant microorganisms (http://www.eurhealth-1health.eu; http://mrsa-net.org; http://eursafety.eu/; http://www.health-i-care.eu).

He is member of the Executive Committee of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) and Clinical Coordinator of the European Committee on Infection Control (EUCIC) of the ESCMID. He is member of the coordination team of the regional prevention network against antimicrobial resistance (www.remis-plus.net) and is chair of the non-profit EurSafety-Fund of the UMCG for fostering patient safety and infection prevention.

In 2019 he received the Robert Koch Award for Hospital Hygiene and Infection Prevention. His research activities comprise basic and clinical-microbiological research in the field of Bacteriology, Molecular Typing of multi-drug resistant microorganisms (e.g. MRSA, CRE) with the goal of prevention of Healthcare associated Infections (HCAI) due to Antimicrobial resistant microorganisms.



Plenary C:

Magic bullet to control antimicrobial resistance (AMR): behaviour change or new technologies?



Prof. Stephan Harbarth

Professor, Infection Control Program, Geneva Univ. Hospitals

Prof. Stephan Harbarth earned in 1993 his medical degree from Ludwig-Maximilians-University in Munich, Germany, and completed his residency in internal medicine and tropical medicine at Munich University Hospitals.

After serving as a clinical fellow in the Infectious Diseases Division in the Department of Internal Medicine at Geneva University Hospitals, Dr Harbarth completed his master's degree in epidemiology at Harvard University in Boston. He is board certified in infectious diseases and was appointed full professor at the University of Geneva in 2018.

Dr Harbarth's work has garnered several awards. His group is currently conducting several clinical and epidemiological studies to evaluate key questions related to the control of the acquisition, transmission and infection by multidrug-resistant microorganisms. He participates in several ongoing large-scale EU-funded studies (R-GNOSIS, AIDA, COMBACTE) and coodinates the DRIVE-AB project to address this public health threat.

Plenary D: Field-epidemiology in the coming decade: where we have come from and where we should be going



Dr. Chikwe Ihekweazu

Director General, Nigeria Centre for Disease Control (NCDC)

Dr. Chikwe Ihekweazu is the Director General of the Nigeria Centre for Disease Control (NCDC) and was until January 2018, the Acting Director of the Regional Centre for Disease Control for West Africa.

Dr Ihekweazu trained as an infectious disease epidemiologist and has over 20 years' experience working in senior public health and leadership positions in several National Public Health Institutes, including the South African National Institute for Communicable Diseases (NICD), the UK's Health Protection Agency, and Germany's Robert Koch Institute (RKI).

Dr Ihekweazu has led several short- term engagements for WHO, mainly in response to major infectious disease outbreaks around the world including the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19).



Dr. Adam Roth

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

Dr. Adam Roth is a medical doctor (M.D.) specialized in Clinical Bacteriology and Virology and an associate professor with a PhD in epidemiology.

He has several years of experience from running research and public health projects in low-, middle- and high-income countries with developing epidemiology training in the Pacific Region.

Prior to joining ECDC as Head of Fellowship Programme, Adam headed the Unit for Vaccination Programmes at the Public Health Agency in Sweden.

Plenary D:



Dr. Carl Reddy

Director, TEPHINET, Task Force for Global Health

Carl Reddy, MB. ChB, FCPHM, M.Sc. (Epi) is the director of the Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET) at the Task Force for Global Health. Dr. Reddy provides strategic, technical and operational direction to the TEPHINET network which comprises 73 member FETPs, regional networks and numerous partners and stakeholders across the globe.

Before joining TEPHINET, Dr. Reddy was the director of the South African Field Epidemiology Training Programme (SAFETP) in Johannesburg and during his tenure the programme transitioned from being dependent upon CDC funding to becoming owned by the National Institute of Communicable Diseases (NICD). During his time with SAFETP, Dr. Reddy served on various subcommittees and was on the board of the African Field Epidemiology Network (AFENET) based in Kampala, Uganda. He also attended program director meetings for TEPHINET, and in 2016, the organization elected him as Chairman of its Advisory Board.

Dr. Reddy completed his medical degree at the Nelson R Mandela School of Medicine in Durban, South Africa and has extensive clinical experience; as a medical officer in pediatrics, and primary health care including general practice locums in Saskatchewan, Canada. This was followed by stints in Accident and Emergency in South Africa and Southend Hospital in Essex, England. He then pursued the Diploma in Anaesthetics after which he recognized his calling and pursued a four-year residency in public health graduating with the Fellowship of the College of Public Health Medicine (FCPHM).

In 1998, Dr. Reddy won a scholarship from the Mexican government, which enabled him to study Spanish, do a year of public health-related research and complete his epidemiology training in that country. Armed with his MSc. Epidemiology, he returned to South Africa and joined its Medical Research Council, investigating ways to shorten treatment regimens for tuberculosis through clinical trials sponsored by the World Health Organization (WHO).

In 2008, he was seconded to the WHO's Tropical Diseases Research and Training Program in Geneva to oversee the safety of patients enrolled into WHO sponsored clinical trials in Africa. From there he joined the Global Fund and then UNAIDS, later returning to South Africa to direct efforts for the UNAIDS Technical Support Facility in Johannesburg.

22 PLENARY SESSION ABSTRACTS

23	PLENARY SESSION A	DAY 3, Thursday 26. November	10:15-11:45
25	PLENARY SESSION B	DAY 3, Thursday 26. Novemberr	16:00-17:30
27	PLENARY SESSION C	DAY 4, Friday 27 November	10:15-11:45
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PLENARY SESSION A DAY 3, Thursday 26. November 10:15-11:45

Chairs:

Mike Catchpole (ECDC) Magdalena Rosińska (National Institute of Public Health - National Institute of Hygiene, Poland)

Keynote session on COVID-19

Presented by

George Fu Gao, China CDC Andrea Ammon, ECDC Maria van Kerkhove, WHO, Switzerland

Abstract

Strategies and lessons learned from COVID-19 response in China.

Presented by Prof. George Fu Gao

The keynote speech shares the control strategies and lessons learned from COVID-19 response in China. Strategies were timely adjusted within the first 100 days since the outbreak. The diagnostic & treatment protocols and the prevention & control protocols were both developed and revised timely. COVID-19 epicurve shows the pandemic situation in China. For controlling outbreaks rapidly, 4 "Earlies" strategy was adopted: early detection, early reporting, early isolation, and early treatment and care. Rapid and large scale screening PCR tests were implemented. All cases were treated free of charge.

Affiliations:

Chinese Center for Disease Control and Prevention **Keywords:** COVID-19, China

Key developments, drivers, lessons and future trends of COVID-19 pandemic: the European perspective Presented by Dr. Andrea Ammon

Since the first cases of COVID-19 were detected in Europe in late January 2020, over 12 million cases and nearly 300,000 deaths

have been reported. Strict control measures put the first wave under control; once they were relaxed, resurgence of cases was observed since September. Partially, this could be attributed to increased testing, but the growing test positivity rate, hospitalisation and death rates signal true resurgence. Data show that younger age groups drive the spread. With control measures put in place, the case rate has started decreasing, however, more hospitalisation and deaths are to be expected among the vulnerable older age groups.

Many lessons have been learned, among those the importance of identifying and quickly responding to the many localised clusters that constitute the bigger epidemic 'waves'. It has been a challenge to set up population-based surveillance for case detection. Difficulties were observed in some areas of preparedness such as surge capacity, stockpiling of materials and local level preparedness. The importance of strengthening inter-sectorial and cross-border cooperation and improving community engagement are to be noted as well.

Efforts should be made to prevent and minimise future waves. ECDC forecast based on mathematical modelling demonstrates that relaxing the current control measures in December would result in resurgence of cases within a few weeks. A level of measures will need to be in place while vaccines are rolled out, initially to priority groups. Ensuring timely and transparent monitoring of vaccine safety and effectiveness will be crucial. Analysing and addressing gaps in preparedness should be started, as well as harnessing the potential of new developments such as contact tracing applications and rapid tests.

Affiliations:

European Centre for Disease Prevention and Control **Keywords:**

COVID-19 Pandemic; COVID-19 Virus Infection; SARS-CoV-2 Infection; pandemic preparedness

PLENARY SESSION B DAY 3, Thursday 26. November 16:00-17:30

Chairs: Vicky Lefevre (ECDC) Frode Forland (Norwegian Institute of Public Health)

Pandemic preparedness in times of COVID-19: how have pandemic preparedness plans contributed to responding to this global public health threat?

Presented by

Devi Sridhar, University of Edinburgh, United Kingdom Gabrielle Breugelmans, CEPI, Norway Anders Tegnell, Public Health Agency, Sweden Francesco Maraglino, Ministry of Health, Italy

Abstract

Global perspective on the race to develop a COVID-19 vaccine

Presented by Dr. Gabrielle Breugelmans

Over the past two decades, the scientific community and the vaccine industry have been asked to respond urgently to epidemics of SARS, H1N1 influenza, MERS, Ebola, and Zika. After the 2014-2016 Ebola outbreak in West-Africa, the world realized it needed to be better prepared for disease threats and there was global consensus that new and sustainable partnership models were needed.

CEPI, a public-private partnership established in 2017, focuses on R&D for vaccines against pathogens that have pandemic potential and preparing for "disease X". When the novel coronavirus was identified in January 2020, CEPI was able to quickly leverage on its initial investments in MERS vaccines and preparing for Disease X, to develop its COVID-19 portfolio. To date, CEPI has nine vaccines in its portfolio; eight in clinical trials, and three of these in late stage development. In the last week, Moderna and Oxford/Astrazeneca, which received initial funding from CEPI, have announced promising efficacy results.

In April 2020, the Access to COVID-19 Tools (ACT) Accelerator global collaboration was established to accelerate the development, production and deployment of vaccines, diagnostics and therapeutics. COVAX, the vaccine pillar under this global initiative, is coordinated by CEPI, GAVI and WHO. This platform is coordinating the research, development, manufacturing and fair

allocation of a diverse portfolio of COVID-19 vaccine candidates. CEPI's portfolio has been built on the principles of Speed, Scale, and Access and is aiming to make two billion doses available to countries in 2021. The COVID-19 pandemic has shown the need to revolutionize the full vaccine ecosystem and the need for a global financing system that supports end-to-end development, large-scale manufacturing and deployment, and ensures fair allocation.

Affiliation: Coalition for Epidemic Preparedness Innovation (CEPI) Marcus Thranes gate 2, 0473 Oslo, Norway Keywords:

CEPI, COVID-19 vaccine, ACT Accelerator, COVAX, R&D, equitable access

Pandemic preparedness in times of COVID-19: the experience from Sweden

Presented by Dr. Anders Tegnell

Sweden saw a surge of COVID-19 cases in late February and early March that was due to import cases from several countries and not only from countries with known community transmission at the time. There were over one million arrival and departures to and from Sweden during the annual winter holiday between 24 February and 15 March, which coincided with an extensive spread of the disease in many countries.

After the peak in late March and early April, there was a significant decline in seriously ill cases with the need for intensive care. The June peak in cases was due to increased testing rather than an increased spread.

A large proportion of deaths in the early part of the pandemic was amongst elderly people in long term care facilities. A visitor ban to care homes for older people was issued between March-October.

In October, Sweden started to see an increase of cases, and additional local measures have been implemented in close collaboration with regional authorities.

Context, strategies and measures

Key factors to be considered:

- 1. The response builds on the overarching goals set in the pandemic plan, with the aim to minimize mortality and morbidity in the entire population.
- 2. Shared responsibility with Sweden's 21 semi-autonomus regions, other government agencies etc. based on the Swedish government structure and health care system.
- 3. Legally binding regulations have been combined with nonbinding recommendations and advice, with strong focus on clear public communication.
- 4. Evidence based as much as possible.



5. Sustainable approach with a long-term perspective.

- 6. Strong reciprocal trust, based on a strong tradition of voluntary measures with an emphasis on individual responsibility not to spread disease. Similar to the childhood vaccination programme, where 97% of 2-year old children are vaccinated according to the recommendations of the Agency.
- 7. Supportive social security system. Action was taken by the government to enable people to follow the measures, for example the qualifying day for sick leave was abolished and a decision was made to remove the need for a medical certificate for up to 21 days of sick leave.
- 8. Taking into account potential impact on public health in general and growing health inequalities. That was part of the rationale behind keeping primary schools open.

Affiliations:

State Epidemiologist, Deputy Director General, Public Health Agency Sweden

Global health security and pandemic preparedness: the experience of Italy

Presented by Dr Francesco Maraglino

After the new coronavirus was discovered in China, Italy immediately implemented public health measures, including health surveillance, case definition, laboratory capacity, related organization measures and entry screenings. A high-level committee was appointed, chaired by the Minister of Health. Italy declared the national health emergency immediately after the PHEIC statement, and appointed the head of the Civil Protection to lead the response, supported by a Technical-Scientific Committee. This model allowed a whole-of-government approach with the most relevant measures issued by the Prime Minister. When the first local cases were detected, it was clear that the epidemiological features differed from China, with higher proportion of severe cases and mortality due to the different age stratification. In addition, residents in long-term care facilities were particularly affected. Response measures were implemented first in red-zones, then at national level until complete lock down, accompanied by financial intervention to sustain the country's economy. In late April, a de-escalation phase started monitored weekly. Due to increasing international travelling in summer, contact tracing was strengthened. This period was also used to surge hospital capacity (including ICU), primary health care, laboratory capacity, including validation of Antigenic tests, to improve logistic and procurement and to adopt a new case management model based on home-care, whenever possible. Several preparedness strategies were developed: management of SARS-CoV-2 cases and outbreak in schools and kindergartens; correct use of laboratory tests for SARS-CoV-2 in public health; and activities in the transition phase for the autumn-winter season, describing four scenarios

and eight pillars. During the second wave, challenges include the lower acceptance of public health measures and the high socioeconomic impact, increasing inequality and marginalization. For this, a "Ristori" decree has been released by the Governent for the relief of the economic loss of some categories.

Affiliations:

Ministry of Health, Directorate General of Prevention, Office for prevention of communicable diseases and international prophylaxis, Rome, Italy

Keywords:

COVID-19, Preparedness, Health emergency, Global health, Italy

PLENARY SESSION C DAY 4, Friday 27. November 10:15-11:45

Chairs:

Bojana Beović (University of Ljubljana Slovenia) Bruno Coignard (Santé publique France)

Magic bullet to control antimicrobial resistance (AMR): behaviour change or new technologies?

Presented by

Esmita Charani, Imperial College London, United Kingdom Alexander Friedrich, University of Groningen, The Netherlands Stephan Harbarth. Hôpitaux Universitaires de Genève, Switzerland

Abstract

How to support sustained behaviour change to optimise antimicrobial use in human Presented by Dr. Esmita Charani

Human and animal antimicrobial over and misuse remain key drivers of antimicrobial resistance (AMR). Antimicrobial stewardship (AMS) aims to address this, often through some form of technology, especially the process and outcome indicators. But the structural indicators and resources determine how technology is used and accessed and it is important to understand that technologies will remain ineffective if they do not recognise the end users. Currently in global funding for AMR most funding is in technology, but neglects evaluation, implementation, and adoption (e.g., cultural and contextual drivers of use) of such technologies. Historical precedent and scientific evidence highlight the social aspects of antibiotic use, setting it apart from other therapies. The political, cultural and economic drivers of antibiotic use are diverse, creating ethical dilemmas of what antibiotic therapies appropriate or inappropriate mean in different context. Resources and technology mean different things in different settings e.g., examples of drug charts (central to antibiotic review and surveillance) in different countries or medical laboratories to diagnostics. Understanding the context is key to developing fit and sustainable solutions including technological solutions. Optimising antimicrobial use is complex and needs to be considered within the contexts of healthcare as well as general prescribing and goes beyond simply providing single or even bundles of interventions such as evidence-based guidelines, better diagnostics, and new antimicrobial agents for the treatment of infection. These alone do not take into account structural and social determinants of health including policy and

strategy, complex socioeconomic factors, fragmented healthcare systems, human behaviours and a lack of access to expertise and resources in many countries that exacerbate suboptimal antimicrobial use. To sustainably optimise antimicrobial use we must address the socio-cultural and behavioural factors

Affiliations:

NIHR Health Protection Research Unit in Healthcare Associated Infections and Antimicrobial Resistance, Imperial College London, UK Visiting Researcher, Amrita Institute of Medical Sciences, Kerala,

India

Academy of Medical Sciences Hamied Foundation UK-India AMR Visiting Professor

Keywords:

Antimicrobial Stewardship; Behaviour Change; Culture and Team **Dynamics**



PLENARY SESSION D DAY 4, Friday 27. November 16:00-17:30

Chairs: Susan Hahné (RIVM) Amrish Baidjoe (ICRC)

Field-epidemiology in the coming decade: where we have come from and where we should be going

collaboration. Among many opportunities in extended collaborations, the ECDC running of MediPIET from 2021 will especially enrich the networking, exchange and impact of the Programme.

Affiliation:

European Centre for Disease Prevention and Control, Solna, Sweden

Presented by

Chikwe Ihekweazu, Nigeria CDC Carl Reddy, TEPHINET Adam Roth, ECDC

Abstract

Competencies and future of the ECDC Fellowship Programme

Presented by Dr. Adam Roth

The external evaluation in 2019 concluded that the ECDC Fellowship Programme is relevant and contributes to a network of effective public health professionals and increased capacity in Member States (MS). Several challenges were raised, notably: addressing inequalities in MS benefiting from the programme, clarifying its format, simplifying administrative processes, and systematically consolidating Training Site Forum (TSF) input into curricular updates. The Programme objectives have subsequently been updated to include the contribution to the reduction of disparity in capacity across Europe. In consultation with the TSF, National Focal Points for Training and Advisory Forum, the current two-path format of EPIET and EUPHEM will be maintained to meet needs of specialization while further enhancing interdisciplinarity. Simplified administrative processes addressing inequalities between MS are being explored. To meet upcoming challenges, processes for continuous quality improvement will be key, including the work of updating the curriculum. The competency update of the Programme will build on the ongoing revision of the competencies for applied epidemiology as well as the competency framework on public health microbiology with a one health approach. The learning by service and emphasis on intervention epidemiology will continue to define the Programme. Introducing continuous innovation and elements of flexibility in the curriculum, placements and exchange, will allow to better meet emerging needs and strengthen the work force capacity to face future challenges. Lessons learned from running the Programme during COVID should guide development. Harnessing opportunities from currently lowered thresholds to digital teaching and communication will facilitate new and more effective teaching and

29	FIRESIDE PANEL		
30	FIRESIDE PANEL 1A Food and waterborne dis	DAY 1, Tuesday 24. November 2020 seases outbreaks	11:00-11:40
33	FIRESIDE PANEL 1B Food and waterborne dis	DAY 1, Tuesday 24. November 2020 seases outbreaks (other)	16:00-16:40
36	FIRESIDE PANEL 2A HIV, sexually transmitted	DAY 2, Wednesday 25. November 2020 infections and blood infections	11:00-11:30
38	FIRESIDE PANEL 2B Vaccine-preventable dis	DAY 2, Wednesday 25. November 2020 eases	15:00-15:30
41	FIRESIDE PANEL 2C Influenza and other resp	DAY 2, Wednesday 25. November 2020 iratory viruses	16:30-17:00
43	FIRESIDE PANEL 3A COVID-19 Serology and p	DAY 3, Thursday 26. November 2020 prevalence	13:00-13:30
45	FIRESIDE PANEL 3B COVID-19 response	DAY 3, Thursday 26. November 2020	14:10-14:40
48	FIRESIDE PANEL 3C COVID-19 Surveillance	DAY 3, Thursday 26. November 2020	15:20-15:50
50	FIRESIDE PANEL 4A Antimicrobial resistance	DAY 4, Friday 27. November 2020	13:00-13:30
53	FIRESIDE PANEL 4B COVID-19 Field epidemic	DAY 4, Friday 27. November 2020 blogy	14:10-14:40
55	FIRESIDE PANEL 4C Global health and Emerg	DAY 4, Friday 27. November 2020 ging diseases	15:20-15:50

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Fireside Panel 1a (Live Q&A session) DAY 1, Tuesday 24. November 2020 11:00-11:40

Food and waterborne diseases outbreaks

Moderator

Ettore Severi (ECDC)

Abstracts

1.Outbreak of Yersinia enterocolitica in Norway, 2020

T. Lyngstad¹

E. Seppälä², H. Lund³, P. Katsiouleri⁴, A. Wester⁵, U. Naseer⁶, L. Brandal⁷, E. Macdonald⁸, G. Johannessen⁹, L.Jensvoll¹⁰, T. Berglund¹¹, H. Lange¹²

¹ Norwegian Institute of Public Health; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

² Norwegian Institute of Public Health; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

3,4,5,6,8,12 Norwegian Institute of Public Health

⁷ Norwegian Institute of Public Health; European Public Health Microbiology Training Programme (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

⁹ Norwegian Veterinary Institute

^{10,11} Norwegian Food Safety Authority

Background:

In June 2020, the Norwegian National Reference Laboratory (NRL) informed the food- and waterborne diseases team at the Norwegian Institute of Public Health (NIPH) of a possible outbreak of Yersinia enterocolitica O3. A multidisciplinary investigation team was established in order to find the source and prevent further transmission.

Methods:

In collaboration with the Norwegian Food Safety Authority (NFSA) and the municipality doctors, we interviewed 24 of 25 cases to assess food consumption one week before symptom onset. Cash receipts were obtained from 16 cases, and traceback investigations were carried out. Leftover food samples were tested by the Norwegian Veterinary Institute (NVI). Human isolates were sequenced by whole genome sequencing (WGS).

Results:

Twenty-five cases with nearly identical genotype were identified. Seventeen (68 %) of the cases were female and the median age was 28 years (range 2-58). The cases were geographically widespread in Norway, and had become ill during mid to late May 2020. Twenty-three cases (92 %) had eaten a pre-washed baby spinach or spinach product. Traceback investigations indicated imported spinach as a possible source. No other product could be linked to the outbreak. Two tested leftover samples (frozen spinach) were negative for Y. enterocolitica.

Conclusions:

We concluded that pre-washed baby spinach or spinach was probably the source of infection, although this conclusion was not supported by microbiological investigation of the only available leftover sample. These results were communicated to the public trough websites and by press releases, and the NFSA carried out inspections at the production facilities in Norway aiming to check routines and increase awareness on the possible risk for contamination of pre-washed spinach products.

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

Keywords: Yersinia enterocolitica, outbreak investigation, food- and waterborne diseases, pre-washed spinach, tracing

ABSTRACT ID: 109

PRESENTED BY: Trude M Lyngstad / trudemarie.lyngstad@fhi.no

2. A Campylobacter jejuni outbreak linked to contaminated pasteurized milk in Denmark, 2020: a matched case-control study

L. Alves de Sousa 1

L. Müller ², L. Espenhain ³, S. Skou Voss ⁴, G. Benedetti ⁵, S. Schjørring ⁶, A. Frøling Pedersen ⁷, S. Ethelberg ⁸

¹ European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; Infectious Disease Epidemiology and Prevention, Statens Serum Institut

 $^{\scriptscriptstyle 2,3,8}$ Infectious Disease Epidemiology and Prevention, Statens Serum Institut

⁴ European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and

Control (ECDC), Stockholm, Sweden; Infectious Disease Epidemiology and Prevention, Statens Serum Institut

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Background:

On 31 May 2020, an unusually high number (70) Campylobacter cases in the Danish island of Bornholm was reported. We initiated an outbreak investigation aiming to identify its source and set control measures.

Methods:

A confirmed case was defined as an individual with laboratory-confirmed Campylobacter spp. diagnosed from 28 May to 9 June, living in Bornholm and who had not traveled during the 7 days before symptom onset.

Initially, we assessed food consumption seven days before symptom onset with a trawling questionnaire, followed by an age-, sex- and residence-matched case-control study. We randomly selected controls from the Danish Civil Registration System. We analysed data with logistic regression. We performed trace-back guided environmental investigation. Human isolates were sequenced with whole genome sequencing (WGS).

Results:

We identified 161 confirmed cases with an age range of 0-97 years; 97 of which were male (60%). Of 64 isolates analysed with WGS, 55 were identically identified as type $ST_50#9$.

A matched case-control study included 26 confirmed cases and 52 controls. Cases were more likely to have consumed brand A milk (mOR: 21.4; 95%CI: 2.8 - Inf). Brand A milk also presented a positive dose- and frequency-response association.

We identified coliform bacteria contamination (200-2000 CFU/mL) in a pasteurized milk sample from brand A dairy producer. No Campylobacter was isolated from raw or pasteurized milk samples. Dairy plant inspection did not identify a cause of contamination in pasteurization.

Conclusions:

Epidemiological and microbiological findings suggest brand A pasteurized milk as a probable source for this Campylobacter outbreak in Bornholm. We recommended reviewing the equipment and process of pasteurization and safe milk handling at all steps in the inspected dairy production chain.

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

Keywords: Campylobacter jejuni, Pasteurized milk, Outbreaks ABSTRACT ID: 204

PRESENTED BY: Luís Alves de Sousa / laas@ssi.dk

3. Nuts about salmonella: consumption of brazil nuts and nut bars identified as risk factor for Salmonella Typhimurium t5.6145 in casecontrol study, United Kingdom, May - July 2020

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Background:

In April 2020, a cluster of Salmonella Typhimurium t5.6145 was identified in the UK through whole genome sequencing. Cases continued to rise to a total of 85 cases by 31/07/2020. A case-control study was conducted to identify potential vehicle(s) of the outbreak.

Methods:

Cases were defined as a laboratory confirmed case of Salmonella Typhimurium with a PHE SNP address designated as 1.222.503.919.5052.6145.% (t5.6145), a sample date after 01/04/2020, and resident of Great Britain (GB). Controls were identified (through a UK market research panel) as over 18 years, GB resident, no foreign travel, and no diarrhoea or vomiting in the 7-days prior to questionnaire completion.

Descriptive epidemiology for cases and controls, and univariate analysis were conducted to calculate odds ratios (ORs) and corresponding 95% confidence intervals (CIs). Risk factors significant in the univariate analysis (p<0.001) or with OR > 20 were considered in a stepwise multivariable modelling procedure with age and gender as potential confounders.

Results:

The study comprised 26 cases and 113 controls. Nuts and seeds were identified as potential risk factors for illness (OR 7.8, Cl 2.5 - 34.2). Brazil nuts (adjusted OR 6.7, Cl 1.1 - 48.7), and two nut bar brands produced by the same company, (nut bar A [aOR 23.3, Cl 2.4 - 386] and nut bar B [aOR 54.6, Cl 3.3 - 1810]), were independently associated with infection. The most commonly reported nut bars A and B contained brazil nuts.

Conclusions:

The most likely vehicle(s) of infection were brazil nuts, and two nuts bars that contained brazil nuts. As brazil nuts and nut bars are an uncommon vehicle of Salmonella Typhimurium, it will be important to consider these in future outbreak investigations.

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

Keywords: Salmonella, Gastroenteritis, Field Epidemiology , Outbreak, Nuts, Analytical Epidemiology

ABSTRACT ID: 50

PRESENTED BY: Ranya Mulchandani / ranya.mulchandani@phe.gov.uk

4. An outbreak of nalidixic acid and ciprofloxacin resistant Salmonella Enteritidis linked to eggs from Poland, Austria, 2019

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Background:

On 29 July 2019, the National Reference Center for Salmonella reported 151 human isolates of nalidixic acid and ciprofloxacin resistant (NAL-CIP) Salmonella Enteritidis MLVA type 3-10-5-4-1 from Austrian residents identified since 11 May 2019, compared to no human-isolates of this MLVA type during the previous seven months. We conducted an investigation to confirm the outbreak, identify the source and implement control measures.

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Methods:

We defined an outbreak case as an infection with NAL-CIP-resistant S. Enteritidis, MLVA type 3-10-5-4-1 or 3-9-5-4-1 in an Austrian resident with symptom onset in May-August 2019. We identified cases through national surveillance and by active case finding. District public health authorities collected data on symptoms, travel history and food exposure using a standardized questionnaire. WGS followed by cgMLST was carried out for selected human and environmental isolates, and trace-back analysis was carried out for suspected food vehicles.

Results:

400 cases were identified (median age: 22 years, range 0-89; 56% males, 32% hospitalized). Food consumption information was available for 88%. 48 cases ate at four of 12 Asian restaurants with outbreak strain positive environmental isolates, obtaining eggs from a single batch supplied by one egg producer in Poland. A single cluster type with an allelic difference \leq 7 was found for 141/142 human isolates, and all 11 single batch egg isolates from 11 Asian restaurants.

Conclusions:

This outbreak was linked to consumption at Asian restaurants supplied with eggs by a single egg producer in Poland. Eggs from this farm were withdrawn from the Austrian market and cleaning and disinfection measures were implemented at the Polish farm. WGS analysis initiated at EU level identified human isolates belonging to the same cluster in six other Member States.

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

Keywords: Salmonella enteritidis, Disease Outbreaks, Nalidixic Acid, Ciprofloxacin, Eggs, Austria

ABSTRACT ID: 193

PRESENTED BY: Lukasz Henszel / henszel.lukasz@gmail.com

5. Investigation of an outbreak of ESBL- producing Salmonella Kentucky in humans linked to poultry in Malta, 2013-2020

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Background:

Salmonella enterica serotype Kentucky ST198 is frequently associated with human infections. The antimicrobial resistance of this serotype to multiple drugs is a growing concern worldwide. In 2016, an increase in the number of reported ESBL-producing Salmonella Kentucky (ESBL-SK) human infections prompted the launch of an investigation to determine the source of the outbreak.

Methods:

A retrospective epidemiological study was conducted including cases from January 2013 to February 2020. Laboratory diagnosis was conducted by PCR, susceptibility testing and Whole-Genome Sequencing (WGS) for both human and animal specimens. Data on ESBL-SK isolates in both human and animal samples was collected and epidemiological analyses were carried out.

Results:

As of February 2020, a total of 30 ESBL-SK infections in humans have been reported in Malta. Additionally, from 2016, a total of 16 animal isolates of ESBL-SK have been identified in poultry proceeding from four different farms and one slaughterhouse. No geographical cluster was identified. WGS confirmed a link between the poultry isolates and at least one of the human infections in 2019. WGS showed a link between the Maltese isolates and several isolates detected in the UK.

Conclusions:

The results of the combined phenotypic and genotypic analysis suggest a close relationship between the poultry and human strains and support the hypothesis that poultry production may play a role in the spread of ESBL-SK in the human community. Surveillance programs, rational use of antibiotics, collaboration with the animal health directorates and strict biosecurity measures must be implemented to identify the sources and to limit the spread of these bacteria in the poultry industries. We recommend rapid international collaboration for the management of ESBL-SK outbreaks and prevention of further spread.

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

Keywords: One Health, Salmonella, Antibiotic resistance, ESBL, Salmonella Kentucky

ABSTRACT ID: 201

PRESENTED BY: Raquel Medialdea Carrera / raquelmedialdeacarrera@gmail.com

Fireside Panel 1b (Live Q&A session) DAY 1, Tuesday 24. November 2020 16:00-16:40

Food and waterborne diseases outbreaks (other)

Moderator Therese Westrell (ECDC)

Abstracts

6. Epidemiological investigation of eight cases of lethal encephalitis caused by newly detected zoonotic Borna disease virus 1 in Germany, 2019-2020

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Background:

In 2018, Borna disease virus 1 (BoDV-1) was first confirmed as a zoonotic pathogen causing human encephalopathy in Germany with an extremely high fatality (19/20). Clinical spectrum, risk factors and transmission routes are unknown. In endemic areas, shrews (Crocidura leucodon) are shedding virus in saliva and excreta. We aimed to generate hypotheses about transmission routes and provide evidence for prevention.

Methods:

We defined cases as PCR-confirmed. BoDV-1 sequences were phylogenetically analysed with 120 animal sequences. We conducted interviews at patients homes (n=7) and by video call (n=1) using a standardized semiqualitative questionnaire covering potential exposures.

Results:

We interviewed family members of eight patients deceased in 1996-2019 (6 female, median age 28 years, range 11-78). Immunosuppression was known for none. All had developed fulminant encephalitis with confusion, deep coma and had died within a median of 4.5 weeks after symptom onset (range 3-43). All had spent their life in rural areas in Germany known to be endemic for animal BoDV-1. Six families kept domestic or farm animals. Family members did not know of any direct shrew contact, six families confirmed irregular peridomestic shrew presence. Four reported domestic cats bringing home shrews. BoDV-1 sequences from seven cases clustered with animal BoDV-1 sequences from the respective region.

Conclusions:

Rural residence is a common denominator of all cases. Shrew presence near cases' homes and phylogenetic analysis suggest peridomestic infection. In the absence of known direct shrew contact, environmental transmission cannot be excluded. We informed residents in endemic areas to minimize contact to shrews and their secretions. To enforce case finding we advised doctors to consider BoDV-1 as differential diagnosis in viral encephalitis and made direct pathogen detection mandatory to report.

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

Keywords: Borna Disease Virus, encephalitis, shrew, zoonosis, fatality **ABSTRACT ID:** 92

PRESENTED BY: Kirsten Pörtner / poertnerk@rki.de

7. Tracking the origin of Austrian human Brucellosis cases using whole genome sequencing, 2005-2019

J. Schaeffer¹

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Background:

Brucellosis is a zoonotic disease caused by Brucella spp. bacteria. Even though severity and incidence are low, brucellosis require heavy and long lasting treatment. Austria has official brucellosis-free (OBF) status in cattle, but a few human cases are still reported every year.

Methods:

Between 2005 and 2019, 19 B. melitensis strains were isolated in Austria, from patient (n=15) and cattle (n=4). The isolates were sequenced and analysed using core genome MLST (cgMLST). Patient and cattle isolates were compared with 63 reference strains from NCBI.

Results:

Among Austrian patient's isolates, 13/15 belonged to sequence type 8 (ST8). Two were isolated from the same patient, but two years apart. High similarity between the two strains suggests that the second brucellosis episode of this patient was a relapse. Nine ST8 isolates grouped together (<60 allelic differences). Among them, five patients were contaminated in Balkan countries, two in Turkey and one in Afghanistan. No epidemiological data was available for the last one, but the isolate was closest to a Turkish strain. The 2/15 remaining patient samples and 4 cattle isolates belonged to ST11, a European ST. The cattle isolates clustered together. They correspond to an Austrian outbreak from 2018: infected cattle contaminated a veterinarian and a farmer's child.

Conclusions:

For autochthonous outbreaks of brucellosis, WGS is key to identify the source of infection. For imported cases, especially those with missing epidemiological data, comparing strains with published sequences can suggest potential origins. Our genomic and epidemiologic data showed



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that a large proportion of Austrian cases were imported from the Balkans. Enhanced cooperation with these countries is planned to analyses this recurrent importation route and further reduce brucellosis incidence in Austria.

Subject: Microbiology

Keywords: brucellosis, Brucella melitensis, whole genome sequencing, imported cases

ABSTRACT ID: 27

PRESENTED BY: Justine Schaeffer /schaeffer.justine.91@gmail.com

8. Molecular typing as a tool to investigate the national increase of cryptosporidiosis cases in Sweden autumn/winter 2019

J. Beser¹

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¹⁰ Department of Safe Food, National Food Agency, Uppsala

Background:

In autumn 2019, an increase of cryptosporidiosis cases was noted in Sweden. Several regions were affected hence the Public Health Agency coordinated a multi-regional investigation.

Methods:

All clinical laboratories were asked to send positive Cryptosporidium samples to the Public Health Agency to identify species and subtypes, using sequence analysis of the 6okDa glycoprotein and rRNA small subunit genes. Regional departments of communicable disease control and prevention performed trawling interviews with cases by phone and/ or paper questionnaires. A case-case study compared cases of the most common subtypes in terms of food exposures using multivariable logistic regression analysis.

Results:

In total, 462 cases were reported between 1 October and 31 December. Most cases were detected in the regions of Stockholm (n=173), Västra Götaland (n=60) and Östergötland (n=59). To elucidate whether a national outbreak was ongoing, 300 samples were typed. Cryptosporidium parvum was found in 95% of the samples (n=285). The most common subtypes were IIdA22G1c (n=122; 41%) and IIdA24G1 (n=67; 22%).

The predominant subtype IIdA22G1c was identified in 10 regions,

confirming a national outbreak. Regional investigations revealed that many cases had been consuming an unpasteurized juice containing spinach. The epidemiological study confirmed this link, suggesting that IIdA22G1c cases were more likely to have consumed the juice compared to cases of IIdA24G1. Subtype IIdA24G1 was spread nationwide in 12 regions, but no source was identified.

Conclusions:

Molecular typing was crucial in the investigation, enabling the separation of two national outbreaks from smaller outbreaks and sporadic cases, and therefore enhancing the epidemiological investigations. The combined approach led to identifying unpasteurized juice as one outbreak source. Trace-back investigations revealed that no contaminated juice batches were left in stores and no withdrawal was needed.

Subject: Microbiology

Keywords: cryptosporidium, parasite, molecular epidemiology, outbreak, diarrhoea

ABSTRACT ID: 62

PRESENTED BY: Jessica Beser / jessica.beser@folkhalsomyndigheten.se

9. Risk assessment of foodborne Hepatitis E virus in Italy

Ornella Moro¹

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- ⁵ Region Sicily, Health Directorate

Background:

Hepatitis E virus (HEV) is an emerging pathogen transmitted to humans mainly by consumption of pork products. The heterogeneity of pork meat production in Italy required a specific study to quantify the importance of different foods in HEV transmission.

Methods:

A cross-sectional sampling study was performed in 2018-2019 to estimate the prevalence/concentration of HEV in different foods including vegetables, shellfish and pork products with/without liver (pork+/pork-). 730 samples were collected and examined by matrix-specific virus concentration methods followed by real-time RT-qPCR.

We developed a stochastic-parametric model to estimate the number of new infections per year, per food, based on consumption data by FAO/WHO GIFT. We estimated a dose-response model and a probability distribution for ingested HEV-RNA dose per year, per person, to obtain the overall number of new infections per year. A local sensitivity analysis quantified the dependencies between output and input parameters.

Results:

HEV point prevalence and concentration in pork+ products (N=92), pork- (N=104) and shellfish (N=204) samples was 12.0%, 2.9% and 0.5% with up to 3400gc/g, 960gc/g and 580gc/g, respectively. HEV was not detected in other food types. We estimated a total of 440,000 new infections per year caused by pork+ products consumption and 650,000 by pork-. The first estimation resulted highly dependent by input parameters (portion consumed, portion's weight, etc.). No infections resulted for other foods.

Conclusions:

Despite the larger fraction of cases are attributable to pork- products, the highly dependence of our estimation on the input parameters for pork+ make consumption of this foodstuff the top risky food for individual HEV infection. This study provides an estimate of expected HEV foodborne infections per year and highlight the data gap for a full quantitative risk assessment.

Subject: Modelling, bioinformatics and other biostatistical methods **Keywords:** Hepatitis E Virus, Epidemiology, Probability, Food Safety, Food Microbiology

ABSTRACT ID: 202

PRESENTED BY: Ornella Moro / ornella.moro@iss.it

10. A Campylobacter outbreak warning tool in Denmark: (less) time, (more) place and person

G. Benedetti¹

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Background:

Campylobacter is the most common cause of human bacterial enteritis in Denmark, while local point-source outbreaks are not easily identified due to low prevalence and lack of routine genotyping. Using recently available area-referenced data for all 98 Danish municipalities, we developed a warning tool that utilises pools of concomitant weekly observations to flag potential outbreaks at municipality level.

Methods:

Weekly Campylobacter incidences for 91 municipalities with population >20,000 were calculated using data from the Danish register of enteric infections (2008-2018). To account for less populated municipalities reporting higher incidences, municipalities were grouped by population size: 20-60,000 (Group1, n=67), 60-100,000 (Group2, n=17) and >100,000 (Group3, n=7) inhabitants. The warning tool identified outbreaks based on the skewness of the incidence distribution (exposure) per municipality group and week. The performance of the tool to flag weeks with the top 1% incidence and weeks with historically identified outbreaks (outcomes) was assessed as areas under receiver operating characteristic curves (AUC, 95% confidence interval) per group. Ninety-per-cent sensitivity thresholds of skewness were recorded. **Results:**

The top 1% incidences were flagged with an accuracy of 0.86 (0.82-0.91 95%Cl), 0.69 (0.59-0.79 95%Cl), 0.75 (0.65-0.85 95%Cl) in Group 1-3, respectively. With historical outbreaks, the tool had a lower performance: 0.82 (0.67-0.97 95%Cl), 0.69 (0.40-0.98 95%Cl), 0.46 (0.31-0.62

95%CI) in Group 1-3. Sensitivity thresholds of skewness decreased with municipality population size: 1.24, 0.38, 0.3 in Group 1-3.

Conclusions:

The tool showed good performance in flagging weeks with extreme Campylobacterincidences. However, the empirical definition of outcomes was a weakness of this analysis. We demonstrated the feasibility of a univariable approach that does not rely on historical data and we are currently applying the tool in a prospective manner.

Subject: Surveillance

Keywords: Campylobacter; Public Health Surveillance; Disease Outbreaks; Epidemiology

ABSTRACT ID: 185

PRESENTED BY: Guido Benedetti / gube@ssi.dk

Fireside Panel 2a (Live Q&A session) DAY 2, Wednesday 25. November 2020 11:00-11:30

HIV, sexually transmitted infections and blood infections

Moderator

Erika Duffell (ECDC)

Abstracts

11. CD4/CD8-ratio trajectories in ClinSurv, a large multicentre HIVcohort study from Germany 1999-2018

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Background:

Pathological CD4/CD8-ratios (≤1) are associated with elevated morbidity and mortality in HIV-patients. We investigated the trajectories of CD4/ CD8-ratios in the largest German multicentre long-term observational HIV-cohort study to provide evidence for treatment guidelines.

Methods:

We analysed ClinSurv-HIV cohort data from 1999-2018 including treatment-naïve patients with follow-up data for at least 3 years after starting continuous antiretroviral therapy (ART). Outcomes were the proportion reaching a normalised CD4/CD8-ratio (defined as >1 on two consecutive visits) within 3 years, and the time to normalisation. We compared proportions using x2-tests, medians using Wilcoxon rank-sum tests.

Results:

We included 4,154 patients, median (IQR) age at baseline was 40 years (33-48), and 53% were men who have sex with men. The median baseline-CD4-cell-count was 227 cells/µl (100-349). After 3 years of ART, 21% reached a normalised CD4/CD8-ratio within a median of 1.1 years (0.5-2). Normalisation differed by immune status: 1/1,850 of patients with baseline-CD4-counts ≤200 cells/µl had a normalised ratio at baseline. Within this group, 139/1,850 (8%) attained normalisation after a median

of 1.6 years (0.7-2.3). In contrast, 2/373 of patients with baseline-CD4counts > 500 cells/µl had a normalised ratio at baseline, and 192/373 (52%) (p<0.001) reached normalisation after a median of 0.7 years (0.2-1.6, p<0.001).

Restricting to patients continuously treated with an identical ARTclass-combination, 1,706/3,849 (44%) had baseline-CD4-counts <200. Those treated with regimens containing integrase inhibitors reached normalisation more often (15/141, 11%) than patients treated with nonnucleoside reverse transcriptase inhibitor or protease inhibitor regimens (87/1,565, 6%; p=0.015).

Conclusions:

Depending on baseline-CD4-cell-count, low CD4/CD8-ratios persist in the majority of patients after 3 years of ART. Particularly patients with poor immune status might benefit from integrase inhibitor containing regimens with respect to CD4/CD8-ratio normalisation.

Subject: Burden of disease

Keywords: HIV, CD4/CD8-ratio normalisation, trajectories

ABSTRACT ID: 93 PRESENTED BY: Kirsten Pörtner / poertnerk@rki.de

12. Low vaccination coverage for Human papillomavirus disease among men who have sex with men in France, 2019

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Background:

In France, human papillomavirus vaccination (HPV) has been recommended in 2016 for men who have sex with men (MSM) up to age 26 years. We aimed to estimate HPV vaccine coverage in MSM and identify uptake determinants.

Methods:

We collected data on socio-demographic characteristics, sexual behaviour, sexually transmitted diseases (STIs) screening and vaccination uptake using the "Enquête rapport au sexe", a voluntary cross-sectional online survey conducted in 2019. We calculated coverage of at least one dose of HPV vaccine and Prevalence Ratios of determinants with 95% confidence intervals using Poisson regression.

Results:

Of 9,469 respondents (age range 18-28 years), 15% (95%Cl 14-16) reported being vaccinated for HPV. HPV vaccination coverage was significantly higher among MSM younger than 24 years (PR:1.25; 95%Cl:1.13-1.39), with education level below university degree (PR:1.12; 95%Cl:1.08-1.32), living in rural areas (PR:1.21; 95%Cl:1.08-1.36), attending sex parties (PR:1.12; 95%Cl:1.03 - 1.33), using HIV related biomedical prevention methods (PR:1.31; 95%Cl:1.12-1.54), with a STI diagnosis (PR:1.22, 95%Cl:1.08-1.38), and being vaccinated for hepatitis A or B (PR:4.56; 95%Cl:3.63-5.81 and PR:3.35; 95%Cl:2.53-4.44, respectively).
Conclusions:

Our results indicated a low HPV vaccination coverage among MSM in France. Lower uptake was associated with older age, higher education level, and living in urban areas. Higher vaccine uptake was observed among MSM benefitting from other vaccinations and biomedical preventive methods against HIV, suggesting a synergistic effect of the implementation of the national preventive sexual health recommendations for MSM. Further efforts to improve HPV vaccination coverage targeting MSM are warranted.

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

Keywords: MSM, HPV, vaccination coverage

ABSTRACT ID: 33

PRESENTED BY: Giuseppina Ortu / giuseppina.ortu@santepubliquefrance.fr

13. An Evaluation of Gram-negative Bloodstream Infections Surveillance across Hospital Trusts in East of England, 2019

N. Chandra¹

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Background:

Gram-negative bloodstream infections (GNBSI) are subject to mandatory reporting via Public Health England's Health Care Associated Infections Data Capture System (DCS). The DCS includes non-mandatory information e.g. risk-factors, which Hospital Trusts anecdotally report limited-capacity and difficulties completing. We evaluated GNBSI surveillance in East of England for data-completeness, simplicity, acceptability and usefulness.

Methods:

We conducted face-to-face interviews with Infection Prevention and Control (IPC) staff from all 17 Trusts. Questionnaires captured ease, willingness and views on GNBSI surveillance. Average proportion of fieldcompleteness was calculated for E. coli by trust (April 2017-March 2019). **Results:**

16/17 (94%) reported that mandatory data (demographics/clinical/microbiology) were easy to collect. 64% (9/14) reported difficulty in collecting risk-factors. Average completeness of non-mandatory fields varied by Trust: 40% (range 0-89%) for 'source of infection', 21% (0-95%) for 'antibiotic history' and 45% (0-100%) for all 'risk-factors'.

All Trusts expressed willingness to report but were dissatisfied with the process. Common themes included excessive time-commitment and some irrelevant clinical questions.

13/17 (76%) reported receiving outputs, 6/14 (43%) considered them relevant to their role. 11/17 (65%) were unsure whether outputs informed public health action. Additional themes included: outputs untimely and difficult to interpret, and risk-factor data informative but not included.

Conclusions:

Engaging with GNBSI surveillance is reported here to be time-consuming and challenging. The relevance of providing data, particularly riskfactors, to inform public health action was not always apparent, further exacerbating low- completion. Surveillance outputs were regarded not sufficiently relevant, understandable or timely.

To improve data-quality and usefulness, we recommend PHE: reviews and rationalises DCS fields; engages with users on utility; provides training as appropriate; revises outputs; and considers alternative approaches to GNBSI surveillance such as sentinel reporting.

Subject: Surveillance

Keywords: Evaluation, Surveillance, Gram-negative bacteraemia, Healthcare associated infections, National Health Service, Infection Prevention and Control, Health Care Associated Infections Data Capture System

ABSTRACT ID: 32

PRESENTED BY: Nastassya Lakshmi Chandra / nastassya.chandra@phe.gov.uk

14. Evaluation of the National Surveillance System for Notifiable Sexually Transmitted Infections, Portugal, 2015-2018

H. Lucaccioni¹

R. Sá Machado 2

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Background:

In the early 2000's, Portugal formulated strategic orientations to tackle sexually transmitted infections (STIs), including the improvement of mandatory notification. We evaluated the national surveillance system (SINAVE) for Gonorrhoea, Chlamydia trachomatis infections and Lymphogranuloma venereum, and Syphilis, to assess whether it meets its main objective of monitoring the health status of the population. These are mandatory notifiable diseases and since 2015, the system is electronic-based.

Methods:

We extracted SINAVE data from 2015 to 2018. Positive predictive value was assessed as the proportion of validated cases. Data quality was assessed by completeness (proportion of "unknown"/blank fields), internal validity (proportion of inconsistent values), and record linkages between medical and laboratory notifications. Timeliness was calculated as median time length from symptoms onset/diagnosis/laboratory result/notification. Representativeness was assessed by comparing data (demographics, geographical distribution, transmission modes) to the literature in Europe and Portugal.



Results:

The performance of surveillance varied by attributes and diseases. Completeness was low (<90%), less than a quarter of notifications could be matched between medical and laboratory notifications, and 6.8% to 26.0% notifications had inconsistent values. Data quality attributes performed systematically higher for Chlamydia. Positive Predictive Value was high (70%-92%) for all four diseases. Timeliness varied from 5-17 days between the date of symptoms onset and diagnosis, though 13.7%-38.6% notifications were not notified within 24 hours from diagnosis. Surveillance data appeared consistent with the literature.

Conclusions:

The evaluation revealed unsatisfactory data quality, timeliness, and record linkage of medical and laboratory notifications. To improve the surveillance of STIs, we recommend limiting the notification forms to the most essential information, introducing validation rules in the information system, strengthening training, guidelines, and feedback for clinicians and laboratory professionals.

Subject: Surveillance

Keywords: Sexually Transmitted diseases, Portugal, Surveillance, Lymphogranuloma Venereum, Syphilis, Gonorrhea, Chlamydia

ABSTRACT ID: 16

PRESENTED BY: Héloïse Lucaccioni / heloiselucaccioni@dgs.min-saude.pt

Fireside Panel 2b (Live Q&A session) DAY 2, Wednesday 25. November 2020 15:00-15:30

Vaccine-preventable diseases

Moderator

Kari Johansen (ECDC)

Abstracts

15. Brand-specific influenza vaccine effectiveness against laboratoryconfirmed influenza in Europe – results from the DRIVE network 2019/20

A. Stuurman ¹

DRIVE consortium

¹P95 Epidemiology and Pharmacovigilance

Background:

DRIVE (Development of Robust and Innovative Vaccine Effectiveness) is a IMI funded public-private platform that aims to annually estimate brand-specific influenza vaccine effectiveness (IVE), for public health and regulatory purposes. IVE analyses and interpretation are conducted by public partners in the consortium.

Methods:

DRIVE (Development of Robust and Innovative Vaccine Effectiveness) is a IMI funded public-private platform that aims to annually estimate brand-specific influenza vaccine effectiveness (IVE), for public health and regulatory purposes. IVE analyses and interpretation are conducted by public partners in the consortium.

Results:

TND studies included 2235/2729 primary care-based cases/controls and 1296/2826 hospital-based cases/controls. IVE (95% CI) against influenza-like illness due to any influenza in children 6m-17y was 64% (44%-80%) for any vaccine, 81% (58%-92%) for Fluarix Tetra and 61% (38%-77%) for Vaxigrip Tetra. IVE (95% CI) against severe acute respiratory infection due to any influenza in adults ≥65y was 36% (7%-71%) for any vaccine and 52% (27%-68%) for Fluad. The population-based cohort covered 126,872/384,982 vaccinated/unvaccinated person-years. IVE (95% CI) of Fluenz Tetra was 64% (54%-73%) against influenza A and 80% (55%-91%) against influenza B in children aged 2-6y. IVE of Vaxigrip Tetra was 71% (54%-81%) against influenza A and 64% (12%-86%) against influenza B in children 6m-6y, and 27% (18%-35%) against influenza A and 64% (24%-83%) against influenza B in adults ≥65y.

Conclusions:

DRIVE is a growing platform. In 2019/20, the first precise brand-specific estimates were obtained from TND studies. In the next season, DRIVE will explore COVID-19 impact on IVE. Public health institutes with surveillance data and non- pediatric hospitals are encouraged to join DRIVE.

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

Keywords: HIV, CD4/CD8-ratio normalisation, trajectories

ABSTRACT ID: 84

PRESENTED BY: Anke Stuurman / anke.stuurman@p-95.com

Vaccine effectiveness against influenza A(H1N1)pdmo9, A(H3N2) and B: Results from the 2019/20 European I-MOVE primary care multicentre study

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Background:

In 2019/20 the I-MOVE network conducted a multicentre test-negative study using sentinel primary care networks in nine European countries to measure vaccine effectiveness (VE) against influenza A(H1N1)pdmo9, A(H3N2) and B.

Methods:

Primary care practitioners swabbed a systematic sample of patients presenting with influenza like illness (ILI), collecting also information on demographics, vaccination and clinical characteristics. Cases were RT-PCR positive for influenza A(H1N1)pdmo9, A(H3N2) or B 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 (o-14, 15–64, \geq 65 years).

Results:

We included 8457 ILI patients of whom 1499, 841 and 1214 were influenza A(H1N1)pdmo9, A(H3N2), and B positive, respectively. Where B/lineage was determined (938/1214 influenza B viruses), 923 (98%) were B/ Victoria.

Overall VE against influenza A(H1N1)pdmo9 was 45% (95%CI: 29–57), with 57% (95%CI: 17–78) and 50% (95%CI: 30–64) among those aged 0–14 and 15–64, respectively.

Overall VE against influenza A(H₃N₂) was 49% (95%CI: 30-62), with 60% (95%CI: 7-82) and 59% (95%CI: 37-74) among those aged 0-14 and 15-64, respectively.

Overall VE against influenza B was 57% (95%CI: 39–70), with 43% (95%CI: -3–69) and 63% (95%CI: 37–73 among those aged o–14 and 15–64, respectively.

Influenza positive cases among those aged ≥ 65 years were too few to measure adjusted VE.

Conclusions:

The 2019/20 VE against all circulating influenza (sub)types ranged between 43 and 63% overall and among those aged <65 years.

Our results suggest that influenza vaccination may have conferred protection in up to two-thirds of vaccinated individuals during the 2019/20 influenza season.

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, case control study, Europe

ABSTRACT ID: 84

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



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17. Healthcare provider knowledge of and barriers to pneumococcal vaccination in at risk adults: survey results in Ireland 2020

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Background:

Ireland has a high rate of invasive pneumococcal disease (IPD). National studies have identified that adults at risk of IPD have low uptake (16-36%) of pneumococcal vaccines. We aimed to determine healthcare provider (HCP) knowledge of, and beliefs regarding, pneumococcal vaccination in at-risk adults to identify potential barriers to vaccination.

Methods:

We distributed standardised questionnaires nationally to 24 oncology and haematology units. HCPs were questioned about their knowledge of, and their practice regarding, pneumococcal vaccination. A correct knowledge score was marked one out of a possible 10 correct answers. We conducted univariate and multivariate logistic regression using STATA to assess the association between recommending pneumococcal vaccine and knowledge and beliefs regarding pneumococcal vaccination.

Results:

The response rate was 77.8% (312/401); 21 units responded with at least one respondent. Among respondents, 147(47.1%) routinely recommend pneumococcal vaccine and 81(26%) routinely check their patients' vaccination status. Of those that don't routinely recommend vaccination, the most common barriers to recommending vaccination are uncertainty about which vaccines are needed [n=102 (61.8%)] and indications for pneumococcal vaccination[n=87 (52.7%)]. Having a knowledge score of 5 or greater[OR 2.1 (95%CI 1.32, 3.29], believing that pneumococcal vaccine is effective for preventing pneumonia[OR 3.5 (95%CI 1.66, 7.38)] and higher confidence in vaccine safety[OR 4.1 (95%CI 2.41, 6.95)] were predictive factors of recommending pneumococcal vaccine. Nearly all (98%) respondents said that further education is needed for HCPs regarding pneumococcal vaccination.

Conclusions:

This is the first Irish national study investigating factors associated with recommending pneumococcal vaccination among HCPs providing care to patients at increased risk of IPD. The study identifies the need for additional education to support HCPs to increase the likelihood that at-risk patients are appropriately vaccinated against pneumococcal infection.

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

Keywords: Vaccination, Pneumococcal infections, Health personnel, Surveys and questionnaires

ABSTRACT ID: 152

PRESENTED BY: Niamh Bambury / niamh.bambury1@hse.ie

18. Universal infant vaccination against hepatitis B: is the end of riskgroup HBV vaccination for MSM approaching?

M. Xiridou ¹

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Background:

Risk-group HBV vaccination for men who have sex with men (MSM) was introduced in the Netherlands in 2002, followed by universal infant HBV vaccination in 2011. The vaccination rate could be slightly increased, since MSM initiating pre- exposure prophylaxis (PrEP), for HIV prevention, have HBV tests and are offered HBV vaccination if tested negative. In this study, we investigated the impact of the transition from risk-group to universal HBV vaccination, accounting for the impact of PrEP.

Methods:

We developed a mathematical model for HBV transmission among MSM. Universal vaccination was modelled by assuming that, from 2033 onwards, 80-90% of MSM is vaccinated when they become sexually active. We investigated scenarios with and without termination of risk-group vaccination and assuming 0.5% extra vaccination rate and 0.5% extra testing rate due to PrEP consultations.

Results:

Universal vaccination in combination with risk-group vaccination resulted in a reduction of 24% in HBV infections among MSM in 2020-2070, compared to the situation with only risk-group vaccination. With universal vaccination, termination of risk-group vaccination in 2030 resulted in 32% more HBV infections over 2020-2070 (compared to continuation of risk- group vaccination until 2070) without PrEP and 27% more infections with PrEP. Termination of risk-group vaccination in 2040 resulted in 10% more HBV infections without PrEP and 8% more with PrEP.

Conclusions:

Universal HBV vaccination can lead to a major reduction in HBV incidence among MSM in the future. The reduction becomes smaller when ending risk-group HBV vaccination, but larger due to PrEP for HIV prevention. Efforts to keep high levels of HBV vaccination, testing, and treatment have to be continued in the coming 20-30 years to eliminate HBV as a health threat for MSM.

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

Keywords: HBV,Hepatitis B, Men who have sex with men, Risk-group HBV vac, Universal infant vaccination, Risk-group vaccination, Mathematical model

ABSTRACT ID: 51

PRESENTED BY: Maria Xiridou / maria.xiridou@rivm.nl

Fireside Panel 2c (Live Q&A session) DAY 2, Wednesday 25. November 2020 16:30-17:00

Influenza and other respiratory viruses

Moderator

Angeliki Melidou (ECDC)

Abstracts

19. Excess hospitalizations associated with RSV among children under 5 years old in France from 2010 to 2018

C.Demont 1

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Background:

Respiratory syncytial virus (RSV) is the most common cause of hospitalization among children with lower respiratory tract infection. As most children are not routinely tested to identify the etiology of their respiratory illness, estimating the burden of RSV is complex. The present study aimed at estimating the epidemiological excess burden due to RSV among <5 years in France from July 2010 through June 2018.

Methods:

Data on the hospitalization of infants due to respiratory diseases (Joo-J99 ICD10 codes) were taken from the French national hospital information database, PMSI. We applied an ecological approach based on Poisson cyclic regression to model weekly age- and respiratory hospitalization rates. We used surveillance data (Sentinelles Network) to account for the circulation of RSV and influenza during the study period to estimate excess hospitalization and related medical costs

Results:

The average seasonal number of respiratory hospitalizations associated with RSV was 48,681 (range: 42,509 - 56,732), representing 33% of all respiratory hospitalizations. Most hospitalizations concern infants with an average seasonal excess rate of 1,552 per 100,000 person-months for those 0-2 months, accounting for 63% of all respiratory hospitalizations. This rate decreased with age. Moreover, rate of excess hospitalizations increased during the study period, especially among children of 0-2 months, with a rate per 100,000 person-month of 1,283 in season 2010/2011 to 1,833 in season 2017/2018.

Conclusions:

In France, RSV is a significant cause of hospital admission in children < 5 years old and particularly for the o-2 months, representing most of respiratory hospitalizations in young infants. Public health interventions to prevent RSV among this age group could have important impact in healthcare utilization and should be considered in future analysis.

Subject: Burden of disease

Keywords: Respiratory Syncytial Virus, hospitalization, burden, children ABSTRACT ID: 179

PRESENTED BY: Clarisse Demont / clarisse.demont@sanofi.com

20. Burden of hospitalization due to respiratory syncytial virus (RSV)very severe associated lower respiratory tract infection (VS-ALRI) in the first year of life in a major urban city, Lyon, France

C. Horvat ¹

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Background:

Evaluation of burden and very severe ALRTI RSV-associated hospitalisation (VS-RsvH) in a major metropolitan area is of prime importance to guide future vaccine policies. We aimed to describe (VS-RsvH) incidence, factors associated with VS-RsvH and the prevalence of difficulty of breast-feeding or drinking in the VS-RsvH population.

Methods:

We conducted a retrospective study on a cohort of newborns (2014 to 2018) from a catchment area of approximately 1.3 million inhabitants using public hospital registry data from the Hospices Civils de Lyon. A case was defined as a laboratory confirmed RSV-infection with hospitalisation occurring in the first year of life and a severity grade as Very Severe LRTI according the WHO case definition. Population denominator was expressed as persons year-at-risk. Key variables (sex, month of birth, birth weight, gestational age, parity) were used for descriptive epidemiology and multivariate logistic regression.

Results:

Overall, 419 cases in 43,957 children were identified. Incidence was 9.5 cases per 1000 persons-year-at-risk the first year of life (95% Cl 8.0-10.0) and 25.5 cases per 1000 persons-year-at-risk the first three months of life (95% Cl 22.0–28.0). The factors independently associated with VS-RsvH were being born before the RSV season (OR = 8.00; 95% Cl: 5.71–11.20), being born premature (<=34 Week of A) (OR = 6.16; 95% Cl: 3.65–10.40). The proportion of nutritional support in this population was 67.5% (97.3% in the population aged below 3 months).

Conclusions:

Being born during the RSV season and prematurity are the two main risk factors that should be target as a priority by the national immunisation program. Breast-feeding or drinking difficulty account for a very high



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proportion of VS-RsvH. This issue should be addressed specifically in the future RSV surveillance programs.

Subject: Burden of disease

Keywords: Respiratory Syncytial Virus; RSV-associated hospitalisation, surveillance, epidemiology, hospitalization, very severe associated lower respiratory tract infection

ABSTRACT ID: 174

PRESENTED BY: Sebastien Casalegno/ jean-sebastien.casalegno@chu-lyon.fr

21. Novel methods in the surveillance of influenza-like illness (ILI): exploration of data from the symptom assessment app Ada

C. Cawley 1

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Background:

The freely available app 'Ada' allows users to enter symptoms they are experiencing, and applies a probabilistic reasoning algorithm to provide a list of possible causes for those symptoms. We compared data from Ada users in Germany with national influenza-like illness (ILI) surveillance data, in order to explore the potential role of novel digital tools in influenza surveillance.

Methods:

We extracted data for all assessments performed by Ada users in Germany in 2017-18, 2018-19 and 2019-20, and identified those which met the definition for ILI (report of fever with cough or sore throat). The proportion of assessments in which ILI was reported was calculated by calendar week, standardised for the German population, and compared with ILI rates reported by GrippeWeb (a web-portal for monitoring acute respiratory infections in Germany) using time series graphs, scatterplots, and Pearson's correlation coefficient.

Results:

In total 2.1 million assessments (for any symptoms) were performed by users in Germany between mid-2017 and mid-2020 (median number of assessments per week 13,410; interquartile range 10,489-16,623), among whom 2.2% reported ILI. As expected, estimated Ada ILI-rates were consistently higher than those reported by GrippeWeb. However, trends corresponded well, with both data sources identifying similar peak ILI weeks between early January and mid March each year. Correlations were significant for all three seasons: 2017-18 (r = 0.86, p<0.001), 2018-19 (r = 0.90, p<0.001) and 2019-20 (r = 0.64, p<0.001); the relatively weaker correlation observed in 2019-20 may be due to effects of the COVID-19 pandemic.

Conclusions:

Novel digital tools such as Ada could be an important source of ILI surveillance data, particularly in countries where robust surveillance systems don't exist and user numbers are high.

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

Keywords: influenza, ILI, surveillance, e-health

ABSTRACT ID: 59

PRESENTED BY: Caoimhe Cawley / caoimhe.cawley@ada.com

22. Supervised learning of syndromes from emergency department data to improve syndromic surveillance of influenza-like illness in Germany

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Background:

Emergency department (ED) data can serve as an important data source for syndromic surveillance systems (SyS), but missing data like diagnosis codes can make analyses relying on this information impossible. This study aims at enhancing an expert-defined syndrome to improve syndromic surveillance of influenza-like illness (ILI) with ED data from a SyS in Germany by using a supervised-learning approach.

Methods:

Routinely collected data from one ED were analysed, containing variables like chief complaints, vital parameters, diagnosis codes and demographic information. A binary naïve Bayes classifier and a logistic regression model were used to predict the ILI syndrome from all variables except the diagnosis code. The resulting ILI cases were evaluated on time series level with regard to seasonal patterns using internal reference cases (expert syndrome definition based on ICD-10 codes) and an external data source, a SyS of severe acute respiratory infections of 73 hospitals in Germany.

Results:

The predictions of the ILI syndrome had sufficient precision (F1-measure of 39.63%). The resulting ILI time series from both models showed high correlations with the time series of the internal reference cases (r = 0.861). Both models showed higher correlations with the external data source (r = 0.867 and r = 0.821) than the expert syndrome definition (r = 0.786). (p < 0.001 for all comparisons.)

Conclusions:

The expert syndrome definition based on ICD-10 diagnosis codes can be enhanced through supervised learning, enabling the syndromic surveillance of influenza-like illness, even if the diagnosis is missing. By changing the threshold of the syndrome classifiers, the sensitivity of these syndrome definitions can be adapted. This generic method can be applied to other syndromes and EDs, which will be evaluated in further research.

Subject: Surveillance

Keywords: Public Health Surveillance, Classification, Supervised Machine Learning, Syndrome

ABSTRACT ID: 173

PRESENTED BY: Birte Wagner / wagnerb@rki.de

Fireside Panel 3a (Live Q&A session) DAY 3, Thursday 26. November 2020 13:00-13:30

COVID-19 Serology and prevalence

Moderator

Eeva Broberg (ECDC)

Abstracts

23. The Study to Investigate COVID-19 Infection in People Living in Ireland (SCOPI): A national seroprevalence study, June-July 2020

P. Garvey ¹

A. Colgan ³, L. Thornton ⁴, J. Connell ⁵, T. Roux ⁶, M. Hunt ⁷, F. O'Callaghan ⁸, J. Bailie ⁹, P. Crowley ¹⁰, F.Culkin ¹¹, F. Kee ¹², M. Keogan ¹³, N. O'Connor ¹⁴, M. O'Sullivan ¹⁵, S. O'Sullivan ¹⁶, M. Tait ¹⁷, C. DeGascun ¹⁸, D. Igoe ¹⁹

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¹⁹ HSE Health Protection Surveillane Centre, Dublin, Ireland

Background:

Robust data on COVID-19 population prevalence supplements surveillance data in providing evidence for public health action. We conducted a COVID-19 population-based seroprevalence survey in June-July 2020 in Ireland.

Methods:

Using a cross-sectional prospective study design, we selected population samples aged 12-69 years in counties Dublin and Sligo using the Health Service Executive (HSE) Primary Care Reimbursement Service (PCRS) database as a sampling frame. Samples were selected with probability proportional to the general population age-sex distribution, and by simple random sampling within age-sex strata. Antibodies to SARS-CoV-2 were detected using the Abbott Architect SARS-CoV-2 IgG Assay (Architect) and confirmed using Fortress (Wantai). We estimated the population COVID-19 seroprevalence weighted for age, sex and geographical area.

Results:

Participation rates were 30% (913/3043) and 44% (820/1863) in Dublin and Sligo respectively. Thirty-three specimens had a positive result (1.9%). We estimated weighted seroprevalences of 3.12% (95% CI: 2.05-4.53%) and 0.58% (95% CI: 0.18-1.38%) for Dublin and Sligo, and 1.69% (95% CI: 1.13-2.41%) nationally. This equates to an estimated 59,482 (95% CI: 39,772-85,176) people aged 12-69 years nationally having had previous infection with SARS-CoV-2, 3.0 (95% Cl: 2.0-4.3) times higher than confirmed notifications. Ten participants (0.58%) reported a previous laboratory confirmed infection with COVID-19; eight (80%) of these were antibody positive. Seventy-six per cent of antibody positive participants had not reported laboratory confirmed infection.

Conclusions:

Our findings suggest that majority of people living in Ireland are unlikely to have been infected with COVID-19 and remain susceptible to infection. As it is unclear if antibodies to SARS-CoV-2 provide protective immunity to future COVID-19 infections, public health measures (including physical distancing, respiratory etiquette, etc) remain key until a vaccine and/or effective treatments become available.

Subject: Burden of disease

Keywords: cross-sectional studies, Seroepidemiologic studies, COVID-19, SARS-CoV-2

ABSTRACT ID: 184

PRESENTED BY: Patricia Garvey / patricia.garvey@hse.ie

24. SARS-CoV-2 prevalence and seroprevalence among healthcare workers in Belgian hospitals: preliminary results of a prospective cohort study

L. Mortgat 1

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Background:

In the current severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic, healthcare workers (HCW) play a crucial role in the chain of transmission. We aim to document prevalence of SARS-CoV-2 and seroprevalence of anti-SARS-CoV-2 IgG among HCW in Belgian hospitals, and to study potential risk factors for infection in order to guide infection prevention and control (IPC) measures in hospitals.

Methods:

We initiated a prospective cohort study late April 2020, including 7 followup points until the end of September 2020. 17 hospitals across Belgium



and 50 HCW per hospital were randomly selected. At each timepoint, RT-qPCR was performed to detect SARS-CoV-2 RNA on nasopharyngeal swabs, and a semi-quantitative IgG ELISA was used to detect anti-SARS-CoV-2 antibodies in sera. Two consecutive positive serologies defined seropositivity and the reverse defined seronegativity. Characteristics likely to be associated with seropositivity were collected using an online questionnaire.

Results:

849 participants completed the baseline questionnaire; 79.7% were women, median age was 40, and 59.6% were nurses. The weighted anti-SARS-CoV-2 IgG seroprevalence was 7.7% end of April and did not change significantly until end of August (7.8%). During follow-up, 2.2% (17/786) of the participants seroconverted and 2.5% (2/81) seroreverted. While 1.1% (8/699) of PCR tests were positive end of April, none were positive since end of May. Unprotected contact with a confirmed case was the only factor associated with seropositivity (PR 2.3, 95% CI, 1.6-3.2).

Conclusions:

Most Belgian hospital HCW did not show evidence of SARS-CoV-2 infection. Unprotected contact was the most important risk factor. This confirms the importance of widespread availability of protective equipment and use of adequate IPC measures in hospital settings.

Subject: Burden of disease

Keywords: SARS-CoV-2, Belgium, seroprevalence, healthcare workers, prospective cohort study

ABSTRACT ID: 240

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25. Seroepidemiologic study to detect antibody-mediated immunity against SARS-CoV-2 among residents and healthcare workers in the city of Plovdiv, Bulgaria, weeks 21-24, 2020

S. Stoitsova 1

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Background:

Anti-SARS-CoV-2 seroprevalence estimates complement routine surveillance data, and help assess relative population susceptibility. This study measured anti-SARS-CoV-2 seroprevalence among adult residents and high-risk healthcare workers (HCW) in Plovdiv city, Bulgaria. It started ten weeks after the first case was detected in Plovdiv, and took place during weeks 21-24 of 2020.

Methods:

We invited all adults residing in households, randomly selected through sampling with likelihood proportional to population density, and drew a random sample from a list of HCW in healthcare facilities attending to probable/confirmed COVID-19 patients. ELISA (detecting anti-SARS-CoV-2 IgA and IgG) was performed on participant serum samples. Crude rates (with 95% Wilson confidence intervals (CI)) and test performance-adjusted rates (with 95% Bayesian credible intervals (CrI)) were calculated.

Results:

Six out of 553 participating adult residents from 291 households and six out of 200 HCW were positive for anti-SARS- CoV-2 antibodies (IgA, IgG, or both), corresponding to crude seroprevalence rates of 1.08% (95% CI 0.5-2.35%) among adult residents and 3% (95% CI 1.38-6.39%) among HCW. Test performance-adjusted rates were: 0.17% (IgA) (95% Crl 0-0.37) and 0.04% (IgG) (95% Crl 0-0.12%) among adult residents; 1.36% (IgA) (95% Crl 0.23-2.40%) and 0.23% (IgG) (95% Crl 0-0.59%) among HCW. To help in other studies, we developed an online tool for Bayesian test performance adjustment (https://github.com/phyppl/prevestim/blob/master/basic.wppl).

Conclusions:

The results were comparable to those from studies carried out abroad, in areas with relatively lower cumulative incidence, and indicated high susceptibility to SARS-CoV-2. The evidence supported recommendations for continued adherence to personal protective measures, at a time when 14-day incidence of real-time RT-PCR confirmed cases was low and as a number of non-pharmaceutical interventions were removed to alleviate the burden of measures on society.

Subject: Surveillance

Keywords: COVID-19, seroepidemiologic studies, household survey, healthcare workers, COVID-19, immunoglobulin A, Immunoglobulin G, population, health personnel

ABSTRACT ID: 233

PRESENTED BY: Savina Stoitsova / stoitsova@ncipd.org

25. Seroprevalence for SARS-CoV-2 and associated factors in the Rinkeby- Kista district of Stockholm, Sweden, 22–24 June 2020

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Background:

Rinkeby-Kista district in Stockholm was identified as a COVID-19 hotspot with an incidence of 1410 cases/100,000 habitants as compared to 967/100,000 for whole Stockholm (August 30). In June, estimated from screening left-over blood samples, the seroprevalence in Stockholm was 11-12%. We aimed to estimate the seroprevalence in Rinkeby- Kista and identify risk factors of COVID-19 in order to determine the extent of the outbreak and gather information for additional preventive measures.

Methods:

We invited 2153 randomly selected individuals aged 16-70 in Rinkeby-Kista to have their blood samples analyzed for anti-SARS-CoV-2 antibodies (Abbott Architect SARS-CoV-2-IgG). We estimated seroprevalence as the proportion of individuals with detected antibodies with 95% exact confidence interval. The estimate was weighted for sampling-design and non-response, and corrected for test performance by Rogan-Blade formula. We investigated if socio-demographic indicators collected from population registers were associated to the presence of antibodies, using unweighted logistic regression.

Results:

In total 538 persons participated. We estimated seroprevalence in Rinkeby-Kista June 22-24 at 18.7% (95%Cl:14.8-23.3). Occupations in healthcare and other occupations entailing frequent contacts were associated with the presence of antibodies (OR=2.75, 95%Cl:1.28-5.92 and OR=2.63, 95%Cl:1.32-5.23) but no association was seen for occupations in schools (OR=0.82, 95%Cl:0.30-2.21), compared to other occupations. Living in a household with five or more persons was associated with presence of antibodies (OR=3.13, 95%Cl:1.38-7.06) compared to living alone. There were no statistical differences in seroprevalence by age groups, genders and if born in Sweden or not (p-values>0.5).

Conclusions:

The estimated seroprevalence in Rinkeby-Kista suggests that Rinkeby-Kista was more affected than Stockholm in general. Working in school was not identified as risk factor supporting previous findings. Preventive measures towards the risks with occupations entailing frequent contacts should be considered.

Subject: Surveillance

Keywords: seroprevalence, COVID-19,r andom sampling, population study

ABSTRACT ID: 178

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Fireside Panel 3b (Live Q&A session) DAY 3, Thursday 26. November 2020 14:10-14:40

COVID-19 response

Moderator

Tarik Derrough (ECDC)

Abstracts

27. Changes in behaviour of the UK population due to COVID-19, March to June 2020

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Background:

As part of the response to the COVID-19 outbreak in the United Kingdom (UK), FluSurvey, a surveillance system to monitor trends in influenza-like illness, was adapted to capture information on behaviour changes in the UK population during the outbreak. We described compliance of UK adults to the government's COVID-19 public health measures.

Methods:

Flusurvey participants received weekly COVID-19 questionnaires including questions on demographics, symptoms and behaviour changes. Incidence rates for hand washing, home working, social distancing and face mask use were calculated for three lockdown-related time-periods: early March (before), late March/April (during) and May/ June (easing). A compliance variable (hand washing, home working and social distancing) was also created.

Results:

There were 2,376 responses between 09-March and 07-June. Initially, 80.0% of participants stated that they had changed their behaviour due to COVID-19. This increased to 97.0% in the two weeks before lockdown and remained above 95.0% during the remaining study period.

Incidence rates for all behaviours were high and stable between the time-periods except for face mask use which increased from 10.6 per 1000 person-weeks before lockdown to 212.0 after. Incidence rates for compliance were 601.9, 816.0 and 840.2 per 1000 person-weeks during the three time-periods.

Conclusions:

Participants showed high and sustained compliance to the governments public health measures and changed their behaviour throughout the lockdown suggesting that the communication strategy was efficient and reached its target audience. Even without government recommendations, the use of face masks was widespread. The maintenance of a high compliance suggests the population is resilient to such changes in daily routine, resulting from the recommendations.

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

Keywords: COVID-19, Behaviour change

ABSTRACT ID: 25

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28. Changes in behaviour of the UK population due to COVID-19, March to June 2020

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Background:

In April 2020, "shielding" (separate living spaces with enhanced infection control support for groups at high risk of severe COVID-19 disease), was proposed for COVID-19 prevention in settings where lockdown is not feasible (i.e. displaced persons [IDP] camps). We conducted a qualitative study in two IDP sites supported by Médecins Sans Frontières in Benue state, Nigeria, to explore community perceptions of potential COVID-19 prevention measures.

Methods:

We conducted two rounds of participant led individual in-depth qualitative interviews in the study sites in April 2020. We first explored perspectives on health, COVID-19 disease, and prevention and control measures (including shielding) (n=12); then we explored acceptable measures without shielding (n=12). We recruited participants purposively, ensuring representative demographic and ethnic distribution. Data were coded in NVivo12 and analysed for key themes.

Results:

Participants have substantial knowledge of COVID-19 symptoms and prevention. Participants describe inter- generational reliance for decision-making, caring for the sick, and food provision. Shielding of high-risk persons in a specific area, especially elders, was only acceptable if they had access to medical care, COVID-testing, daily delivery of family food, mobile phones, and socially-distanced visitation. In the absence of shielding, self-enforced restrictions on social and commercial interactions within and outside the community were acceptable if food relief was provided. Other non-shielding interventions were proposed: organization of smaller markets, increased handwashing points, and provision of masks.

Conclusions:

In IDP camps in Benue, shielding of high-risk groups for COVID-19 requires substantial pre-conditions which are challenging to maintain in a camp setting. Measures favouring cohesion of communities and families were more likely to be accepted. COVID-19 prevention in IDP settings must be implemented in partnership with communities to ensure acceptance.

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

Keywords: Coronavirus, Conflict, Emergency, Humanitarian, Low- and middle-income countries, LMICs, COVID-19, Prevention, Shielding **ABSTRACT ID:** 76

PRESENTED BY: Emily Briskin / emily.briskin@gmail.com

29. Establishing a COVID-19 Pandemic Severity Assessment surveillance system in Ireland - preliminary findings

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Background:

Pandemic severity assessments (PSA) provide early warning signals and inform public health preparedness and response measures. We aimed to establish a COVID-19 PSA monitoring system (based on the WHO Pandemic Influenza Severity Assessment) and report on the findings from the first COVID-19 wave in Ireland.

Methods:

Transmissibility, severity and impact parameters were analysed by age-group and week: GP cough calls (%), sentinel GP influenza-like illness consultations/100,000, COVID-19 outbreaks and cases (all/ hospitalised/ICU/deaths-rates and case-fatality-rates-CFRs) and excess mortality (Z scores). Age-specific thresholds (baseline-extraordinary) were calculated on historic data using the Moving Epidemic Method for transmissibility/impact, means (+/-SDs) for severity and Z scores for excess deaths. As a COVID-19 proxy, historic influenza datasets were used. All parameters/thresholds were visualised with heat-maps.

Results:

During the first COVID-19 wave, transmissibility parameters initially exceeded baseline in early March 2020. COVID-19 incidence/100,000 exceeded extraordinary levels for five weeks (30/03-03/05/2020) and outbreaks exceeded baseline for 16 weeks. GP cough calls were sensitive and timely; exceeding extraordinary levels (age(15 years) for two weeks prior to school closures. COVID-19 hospitalisation/ICU rates (impact) varied by age-group; baseline/low levels for children and adults exceeding extraordinary levels. Excess all-cause mortality ≥ 65 years (March/April) was very high (Z>11). Hospitalised CFRs were high for 15-64-year olds (5.7%) and extraordinary for ≥ 65 years (33.9%). ICU CFRs were low in adults ($13.6\%, 15-64; 32.3\% \geq 65$), compared to historic data. There were no paediatric deaths.

Conclusions:

A PSA surveillance system using thresholds was successfully established, enabling assessment via heatmaps of the transmissibility, severity and

impact of COVID-19 in Ireland. GP cough calls were a timely and sensitive parameter. We recommend continued PSA monitoring in Ireland in order to inform public health measures as we transition through waves.

Subject: Surveillance

Keywords: COVID-19; Pandemic; Pandemic Severity Assessment; Surveillance;

ABSTRACT ID: 76

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ensure good quality education for children and to avoid long-term school closures, as future surges of COVID-19 are expected.

Subject: Toolkits

Keywords: COVID-19, school, infection prevention and control, adjustable control measures

ABSTRACT ID: 187

PRESENTED BY: Tone Johansen / tone.johansen@fhi.no

30. A traffic light model for infection prevention guidelines in Norwegian schools: experiences with adjusted levels of measures, COVID-19 pandemic, 2020.

T. Johansen 1

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Background:

Norway, as the majority of EU countries, closed schools in March 2020 in response to the COVID-19 pandemic. Beginning 27 April 2020, schools re-opened after infection prevention and control (IPC) guidelines were established. We developed a flexible traffic-light model (TLM) with three levels of measures adaptable to the local epidemiological situation. On the 02 June, the national level for the model was set at yellow (intermediate).

Methods:

The TLM has three levels of measures; green (normal situation), yellow (intermediate, normal class sizes) and red (strict, smaller groups). From o2 June to 10 September we monitored experiences with the TLM for all schools in Norway (students age 6-19.) Data were acquired from the Norwegian Surveillance System for Communicable Diseases (MSIS) and by reporting from county governors.

Results:

By 10 Sep, of a total of 11,746 COVID-19 cases, 399 (3.4%) were aged 6 - 13 and 644 (5.5%) 14 - 19 years. Four school outbreaks were reported, involving 48 students and 16 teachers, as well as isolated cases among teachers or students. In response to positive cases, most schools placed one or few classes in quarantine. 70 out of the total 3212 schools in Norway closed temporarily (average 2-5 days) to assess the situation, while four municipalities changed to red level.

Conclusions:

Our context adjustable COVID-19 control measures ensured a relatively normalized school situation for children in Norway. Few outbreaks were observed, and school closures were of short duration. Municipalities experiencing outbreaks could adjust from yellow to red level, instead of imposing long-term closure. We recommend flexible IPC guidelines to



Fireside Panel 3c (Live Q&A session) DAY 3, Thursday 26. November 2020 14:10-14:40

COVID-19 Surveillance

Moderator Cornelia Adlhoch (ECDC)

Abstracts

31. Comparison of secondary attack rates resulting from asymptomatic, presymptomatic and symptomatic cases in a COVID-19 outbreak in Freising district, Germany, February-March 2020

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Background:

In February/March 2020, a cluster of 59 SARS-CoV-2-positive, partially asymptomatic cases emerged around carnival events in Freising district, Germany. Because of its importance for public health management we used this cluster to analyse the transmission of SARS-CoV-2 by presymptomatic, symptomatic and asymptomatic cases to close contact persons.

Methods:

We surveyed cases regarding possible exposures, symptoms and information about household (HHC) and non- HHC/other contact persons (OC) in their infectious period (2 days prior to 10 days after symptom onset) with a standardized questionnaire. In detail, cases recalled HHC/ OC's test results and in which phase of infection the interaction occurred. We calculated secondary attack rates (SAR) for laboratory-confirmed SARS-CoV-2 infection and relative risks (RR) with 95% confidence intervals (95%CI). Additionally, we reconstructed the most probable transmission chain.

Results:

Fifty-three cases (90%) participated in the survey. Among the 46 symptomatic cases, fatigue (80%), headache (54%), cough (52%), ageusia (43%), and fever (43%) were the most frequently reported symptoms. In total, cases reported to have 96 HHC and 398 OC. None of

the 7 (13%) asymptomatic cases led to SARS-CoV-2-infection of their HHC or OC. SARHHC for symptomatic cases was 15%. We observed the highest SAR for OC who met their source cases in their presymptomatic phase (SAR=21%). The SAROC was 6.9% for meeting in symptomatic phase. The OCs of presymptomatic and symptomatic cases were 6.5-times (95%Cl: 1.1- ∞) and 1.8-times (95%Cl: 0.14- ∞) more likely to test positive for SARS-CoV-2 when compared with OCs of asymptomatic cases.

Conclusions:

While asymptomatic cases are unlikely to contribute to the spread of SARS-CoV-2, we observed the highest risk for transmission from presymptomatic cases. Therefore, our study stresses the need for immediate quarantine of close contact persons.

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

Keywords: SARS-CoV-2, relative risk, asymptomatic, presymptomatic, transmission

ABSTRACT ID: 176

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32. Role of returning travellers and control measures on the dynamics of COVID-19 in Bavaria

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Background:

The SARS-CoV-2 pandemic has affected health systems and economies worldwide. In Bavaria, implemented control measures included border controls, travel bans (notification week (NW) 11), contact restrictions (NW12), and 14-day-self- quarantining for risk-area-returnees (NW14), suspendable with a negative test from NW25. European travel restrictions were lifted in NW23. In NW32 (beginning school holidays) large-scale test-stations started operating (highways, train stations, airports). Here, we describe COVID-19 cases in Bavaria with regard to returning travellers and control measures.

Methods:

We describe the number of PCR-confirmed COVID-19 cases in Bavaria in NW9-36 (27.02.2020-06.09.2020) by NW and travel exposure abroad, notified until 09/09/2020.

Results:

Altogether 60,452 cases were reported. Weekly notifications rose rapidly, peaking in NW14 with 10,888 cases (spring peak). After decreasing until NW24 (n=268), notifications started increasing from NW26 (n=363), with a rapid rise from NW32 (n=700) to NW33 (n=1,265). Case numbers remained stable between NW34-NW36 (n=2,070-2,213) (summer peak). Travel exposure was 42% in NW10 (n=132) and 28% in NW11 (n=1,105), declined to \leq 3% between NW14-24 (n=623-10,888) and increased again to 5–11% in NW25-31 (n=268–679). Travel exposure rose to 27% in NW32, peaked at 58% in NW34 (n=2,070), and fell to 48% in NW35 and 34% in NW36.

Conclusions:

The peaks in spring and summer were both initially driven by returning travellers. So far, local transmission following infected risk-area-returnees occurred to a lower extent after the summer peak. Reasons may be heightened awareness, faster risk-area-declaration with resulting self-quarantining and testing policy for returnees. However, local transmissions still account for a substantial proportion of cases. As the holiday season ends, continuous efforts in contact tracing are necessary to avoid uncontrolled local spread, especially within high-risk populations.

Subject: Surveillance

Keywords: COVID-19, SARS-CoV-2, travel, containment strategy, control measures

ABSTRACT ID: 229

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33. The COVID-19 epidemic in Spain: Characterisation of cases and risk factors for severe outcomes

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Background:

COVID-19 epidemic spread rapidly in Spain which became one of the most affected countries in Europe. The aim of this work was to describe the epidemiological and clinical characteristics of reported cases in order to identify groups at higher risk of severe outcomes and tailor control measures.

Methods:

We used data from the National Epidemiological Surveillance Network to describe the PCR-confirmed cases from the beginning of the epidemic until 27 April 2020. We compared their characteristics among different severity levels (hospitalisation, admission to intensive care unit (ICU) and death) and identified risk factors for disease severity.

Results:

The epidemic peaked on 20 March. Of the 218 652 COVID-19 cases, 45.4% were hospitalised, 4.6% were admitted to ICU and 11.9% died. Among those who died, 94.8% had at least one underlying disease. Healthcare workers represented 22.9% of the cases. Males were more likely to have more severe outcomes compared to females. Cardiovascular disease was a consistent risk factor across all severe outcomes. Patients with pneumonia had a higher odds of being hospitalised (OR=26.63; 95%Cl:25.03-28.33). The strongest predictor of death was age \geq 80 years (OR=28.4; 95%Cl:19.85-40.78). Among underlying diseases cases with chronic renal disease had the highest odds of death (OR=1.47; 95%Cl:1.29-1.68).

Conclusions:

The COVID-19 epidemic in Spain had a severe impact on the elderly. Patients with cardiovascular or renal preconditions were at higher risk for

severe outcomes. A high proportion of the cases were healthcare workers. Enhanced surveillance and control measures in these subgroups are crucial for preventing COVID-19 and mitigating transmission during this ongoing pandemic.

Subject: Surveillance

Keywords: COVID-19; Public Health Surveillance; Risk Factors; Pandemics; Spain;

ABSTRACT ID: 172

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34. COVID-19: Determinants of Hospitalization, ICU admission and Death among 20,293 reported cases in Portugal

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Background:

Determinants of hospitalization, intensive care unit (ICU) admission and death are still unclear for Covid-19. We used routine surveillance data from Portugal to identify risk factors for COVID-19 outcomes, in order to support risk stratification, clinical and public health interventions, and to plan health care resources.

Methods:

We conducted a retrospective cohort study including 20,293 laboratory confirmed cases of COVID-19 in Portugal extracted in April 28 2020, electronically through the National Epidemic Surveillance System of the Directorate-General of Health(DGS). We calculated absolute risks, relative risks (RR) and adjusted relative risks (aRR) to identify demographic and clinical factors associated with hospitalization, admission to ICU and death using Poisson regressions.

Results:

Increasing age after 60 years was the greatest determinant for all outcomes. Assuming 0-50 years as reference, being aged 80-89 years was the strongest determinant of hospital admission (aRR: 5.7, 95%Cl:5.1-6.4), 70-79 years for ICU(aRR:10.4 95%Cl:6.5-16.6) and >90 years for death(aRR: 226.8 95%Cl:82.7-622.1). Among comorbidities, Immunodeficiency, cardiac disease, kidney disease, and neurologic disease were independent risk factors for hospitalization (aRR: 1.83, 95%Cl:1.4-2.3; 1.79, 95%Cl:1.5-2.2; 1.56, 95%Cl:1.4-1.7; 1.82, 95%Cl:1.7-2.0), for ICU these were cardiac, Immunodeficiency, kidney and lung disease (aRR: 4.33, 95%Cl:2.5-7.4; 2.76, 95%Cl:2.5-7.4; 2.43, 95%Cl:1.6-



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3.7; 2.0, 95%Cl:1.4-2.9), and for death they were kidney, cardiac and chronic neurological disease (aRR: 2.9, 95%Cl:2.3-3.7; 2.6, 95%Cl:1.7-3.9; 2.0, 95%Cl:1.7-2.5) Male gender was a risk factor for all outcomes. There were small statistically significant differences for the 3 outcomes between regions.

Conclusions:

Older age was the strongest risk factor for severe Covid-19 outcomes, specially death. These findings have implications in terms of risk stratified public health measures that should prioritize protecting older people from infection.

Subject: Surveillance

Keywords: COVID-19, Risk Factors, Hospitalization, ICU, Death, Severe Outcomes, Surveillance

ABSTRACT ID: 219

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Fireside Panel 4a (Live Q&A session) DAY 4, Friday 27. November 2020 13:00-13:30

Antimicrobial resistance

Moderator

Pete Kinross (ECDC)

Abstracts

35. Comparison of phenotypic and genotypic antimicrobial susceptibility testing of VRE and ESBL isolates in Sweden, 2016-2018.

M. Riess 1

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Background:

PHAS conducts national microbial surveillance programmes including phenotypic antimicrobial resistance (AMR) surveillance of vancomycin resistant enterococci (VRE) and extended spectrum beta lactamase (ESBL) producing Enterobacteriaceae. We evaluated the performance of a genotypic AMR predictions pipeline versus phenotypic antimicrobial susceptibility testing (AST) data to improve testing algorithms.

Methods:

Phenotypic AST data (gradient and disc diffusion test) and genotypic predictions (using the ResFinder database on whole genome sequencing (WGS) data) were available. Samples included vancomycin resistant Enterococcus faecium (n=560) and ESBL producing Escherichia coli (n=357) and Klebsiella spp. (n=304; 259 K. pneumoniae). We calculated sensitivity, specificity, positive/negative predictive value and accuracy of the genotypic predictions versus phenotypic AST. Predicted genes were investigated for associated levels of resistance in terms of median minimum inhibitory concentrations or inhibitory zone values for some classes of antibiotics. Sequence types (based on WGS data) were investigated for frequencies of occurring resistance determinants.

Results:

Genotypic AMR predictions were fairly accurate for several drug species combinations: teicoplanin, vancomycin and linezolid resistance in E. faecium (97.5%, 98.0% and 99.5% respectively), gentamicin, amikacin and trimetoprim in E. coli (90.7%, 94.9 and 97.5%, respectively) and Klebsiella spp. (81.0%, 89.3 and 89.8%, respectively). Within classes of antibiotics, some genes conferred higher phenotypic resistance than others. Regarding standard-of-care antibiotics, we detected very few linezolid resistant VREs (6/560) and few amikacin resistant E.coli (40/357) and Klebsiella spp. (63/304).

Conclusions:

Genotypic AMR predictions can replace work intensive phenotypic AST for some drug species combinations but for Klebsiella spp. the bioinformatics analysis pipeline needs optimization. Including additional reference databases and refining relevant list of genes for specific antibiotics will increase the accuracy of genotypic predictions to

be able to substitute further phenotypic testing.

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

Keywords: VRE, ESBL, WGS, AST, genotypic, phenotypic, AMR

ABSTRACT ID: 21

PRESENTED BY: Maximilian Riess / Maximilian.riess@gmail.com

36. ESBL/pAmpC-producing Escherichia coli and Klebsiella pneumoniae carriage among veterinary healthcare workers in the Netherlands

A. Meijs 1

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Background:

Animals are a reservoir for ESBL/pAmpC-producing Escherichia coli/ Klebsiella pneumoniae (ESBL-E/K). We investigated the prevalence, molecular characteristics and duration of ESBL-E/K carriage among veterinary healthcare workers and determined the transmission frequency within households.

Methods:

Participants sent in a faecal sample and filled in an online questionnaire about their occupation, contact with animals, health, travel behaviour, and hygiene. Samples were cultured using selective enrichment/culture and resistance genes in positive samples were typed using PCR and sequencing. A subset of participants, including all ESBL-E/K positives, and their household members were asked to volunteer again 6 months later. Risk factors for ESBL-E/K carriage were analysed using multivariable logistic regression methods.

Results:

The prevalence of ESBL-E/K carriage was 9.8% (47/482; 95%Cl 7.4-12.7). The most frequently occurring ESBL genes were blaCTX-M-15 (n=26) and blaCTX-M-14 (n=7). The predominant E. coli sequence type was ST131 (n=9). Travel to Africa, Asia or Latin America in the past 6 months (OR 4.4), Crohn's disease (OR 7.6) and stomach/bowel complaints in the past 4 weeks (OR 2.1) were associated with ESBL-E/K carriage, whereas none of the occupation related factors were. Of the initially ESBL-E/K positive participants, 16/35 (45.7%) tested positive again 6 months later. In 14 (87.5%), the same ESBL gene and E. coli ST was found. Four of 32 household members carried ESBL-E/K, these were all partners of initially ESBL-E/K positive veterinary workers.

Conclusions:

This study showed that the prevalence of ESBL-E/K carriage in veterinary workers was higher compared to the general Dutch population. Increased risks due to occupational exposure to specific animals or high risk work activities could not be discerned. Transmission within households occurred, although the direction of transmission could not be determined.

Subject: Microbiology

Keywords: Enterobacteriaceae, Antibiotic Resistance, beta-Lactam Resistance , Veterinary Clinics, Veterinarians

ABSTRACT ID: 64

PRESENTED BY: Anouk Meijs / anouk.meijs@rivm.nl

37. Estimating the impact of stewardship programmes on antibiotic consumption in EU. Evidence from the Eurobarometer for the years 2009-2018.

N. Stamboglis 1

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² University of Birmingham

Background:

This study analyses the effectiveness of stewardship programmes in reducing antibiotics consumption across European countries. Existing knowledge shows that antibiotic over-consumption is a key factor in explaining antibiotic resistance. Understanding the effectiveness of stewardship programmes in reducing consumtpion, therefore, might prove useful in fighting resistance.

Methods:

Using data from the Eurobarometers 72.5 (Nov-Dec 2009), 79.4 (April 2013), 85.1 (April 2016), and 90.1 (September 2018), we estimate the impact of stewardship programmes on antibiotic consumption via difference-in-difference analysis, run on a representative sample of the European population. Difference-in-difference analysis allows us to estimate the impact such policy in reducing consumption by comparing countries where stewardship was introduced (treated group) with countries where such policy was not introduced (control group).

Results:

We identify a negative impact of stewardship programmes on antibiotic consumption. The effect is significant across years, as well as for individual years of policy implementation. We identify inter-temporal effects of the policy, with significant lead effects following its introduction. Our results on stewardship are confirmed, even when accounting for alternative national policies, such as National Action Plans. Stewardship programmes present an impact also on alternative dependent variables, such as receiving antibiotics from a doctor, patient's intention to consult a doctor for future use, as well as patients opinions on antibiotics. **Conclusions:**

The results presented in this paper expand the existing literature on policy interventions aimed at reducing antibiotic consumption by showing the effectiveness of stewardship programmes in reducing antibiotic use and in influencing patients' beeliefs on drug use. These results might be useful to policy makers who need empirical evidence on the effectiveness of stewardship programmes as a whole as well as on individual population segments.

Subject: Modelling, bioinformatics and other biostatistical methods Keywords: Antibiotic resistance, Difference-in-difference, Stewardship programmes

ABSTRACT ID: 243

PRESENTED BY: Niccolò Stamboglis / niccolo.stamboglis.1@city.ac.uk

38. CPE OXA-48 hospital ward outbreak in Ireland 2018-2019 -



investigation of transmission patterns using social network analysis and genomics

C. Brehony 1

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Background:

Carbapenemase-producing Enterobacterales (CPE) infection adversely impacts treatment, hospital stay, healthcare costs and mortality. In July 2018, a CPE hospital ward outbreak was declared. The aim of this study was to investigate transmission patterns on a ward using social network analysis and genomics.

Methods:

All patients admitted to ward A, July 2018 - December 2019, were included in a retrospective descriptive analysis. Cases were defined as patients with a negative admission screen, and subsequent positive CPE test. Genomic analysis was used to describe species, genotypes, CPE plasmids and genetic relatedness. Social networks of cases and patient contacts (>4 hours) were constructed.

Results:

Forty-five cases with 844 contacts were analysed. The median age of cases was 78 years (IQR 67-83), 58% (26/45) were male and 100% had co-morbidities. The median outbreak ward length-of-stay (LOS) was 17 days (IQR 10-34). OXA-48 CPE was confirmed in all cases and detected from 26 ward environmental samples. Two OXA-48 plasmid types among seven species were identified, with predominance of Enterobacter hormaechei (63%; 35/56 isolates) and ST78 (25%; 14/25) over time. Social networks identified temporal clusters by gender and species/ST/plasmid, coinciding with interventions. Network metrics indicated possible super-spreading events involving patients with behavioural disturbances.

Conclusions:

Social networks and genomics identified two OXA-48 plasmids, multiple species/genotypes and potential super- spreading in this CPE outbreak. Persistence of E.hormaechei ST₇8 and plasmid group-2, was possibly due to nosocomial adaptation. Interventions prevented intra-hospital spread and cases declined. An older patient cohort, extended hospital LOS, suboptimal ward infrastructure and multiple intra-ward transfers likely prolonged this outbreak. We recommend these novel methods for

complex nosocomial outbreaks, particularly for high-risk clones (ST78), systematic environmental sampling and tailored measures for patients with behavioural issues.

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

Keywords: Social network analysis; ,Genomics; ,CPE; ,Outbreak; ABSTRACT ID: 88

PRESENTED BY: Carina Brehony / carinabrehony@hotmail.com, Lisa Domegan/lisa.domegan@hse.ie

Fireside Panel 4b (Live Q&A session) DAY 4, Friday 27. November 2020 14:10-14:40

COVID-19 Field epidemiology

Moderator Anastasia Pharris (ECDC)

Abstracts

39. Risk factors for outbreaks of COVID-19 in adult care facilities following hospital discharge: a national cohort analysis

J. Adamson 1

C. Emmerson 2 , M. Gravenor 3 , D. Turner 4, J. Salmon 5, S. Cottrell 6, V. Middleton 7, B. Thomas 8, B. Mason 9, C. Williams $^{\rm 10}$

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Background:

Residents in long-term care facilities are vulnerable to COVID-19 outbreaks, causing high morbidity with over half of reported deaths in European facilities. Hospital discharges, staff and visitors were suggested as outbreak sources. We assessed the effect of hospital discharges on these outbreaks.

Methods:

We examined all hospital discharges (n=3,115), regardless of COVID-19 status, to Welsh care homes (n=1,068) and subsequent outbreaks between 22 February and 27 June 2020. A Cox proportional hazards regression model was used to assess the impact of time-dependent exposure to hospital discharge on the incidence of the first known outbreak, between 7-21 days after discharge, and adjusted for care home characteristics (size, type of provision and location).

Results:

A total of 544 homes received hospital discharges; 330 experienced outbreaks. In the univariable model, discharge was associated with an increased outbreak risk (hazard ratio 2.47, 95% Cl: 1.96, 3.11) but no association was found after adjusting for care home characteristics (1.15, 95% Cl 0.89, 1.47). Compared to homes of <10 residents, the hazard ratio (95% Cl) for homes of 50+ residents was 17.35 (9.65, 31.19). When stratified by home size, outbreak rates were similar for periods when homes were exposed to a hospital discharge, compared to unexposed periods.

Conclusions:

Care home size was the most significant predictor; after adjusting for home size, discharges from hospital were not associated with subsequent outbreaks. Our findings have influenced Welsh Government policy and the national incident response, improving infection control measures, staff testing, and advising avoidance of staff sharing. We recommend further investigation into outbreak sources, and support for care homes, as we approach the second winter of the COVID-19 epidemic.

Subject: Field epidemiology (e.g. outbreak investigations) **Keywords:** COVID-19, care facilities, hospital discharge, outbreak, time dependent Cox regression

ABSTRACT ID: 197

PRESENTED BY: James Adamson /james.adamson2@wales.nhs.uk

40. Risk factors associated with an outbreak of COVID-19 in a meatprocessing plant in Germany, April 2020

I. Finci 1

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Background:

A number of countries reported outbreaks of COVID-19 in meat-processing plants.

Following one such outbreak in Germany, we analysed factors that might contribute to the infection spread in affected meat-processing plant.

Methods:

As part of the outbreak investigation, all persons working in the facility were tested 4 times in 2 months, using nasopharyngeal specimen, ordered by the local health office. Sociodemographic data and information concerning working and living circumstances were collected. Univariate analysis was performed using binomial and multivariable analysis using logistic regression with R software. Risk ratios (RR) and adjusted odds ratios (aOR) for infection were calculated with 95% confidence intervals (95%Cl).

Results:

Among 1270 persons working at the meat-processing plant, 1253 were tested for SARS-CoV-2, 395 (32%) were positive. The highest attack rate was observed in beef-cutting workers (54%). Univariate analysis demonstrated that subcontracted workers had 2.7 times higher risk compared to workers directly employed by the enterprise. Sub-analysis of subcontracted workers revealed that living in congregate housing did not impose a higher risk of infection compared to not living with co-workers. Subcontracted workers living near the plant had the same risk of infection compared to workers living further and using shared transportation. Univariate analysis also identified certain ventilation sources to have higher risk. In multivariable analysis, working as subcontractor (aOR:2.2, 95%CI:1.3-3.8), work in meat-cutting (aOR:2.9, 95%CI:1.3-6.5) and work in veterinary inspection (aOR:7.3, 95%CI:1.0-51.7) were factors associated with infection.



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Conclusions:

Our results suggest working conditions as a factor involved in infection spread in this SARS-CoV-2 outbreak. Therefore, preventive measures targeting work place should be implemented to prevent infection spread. Face masks, distancing, staggering breaks, increased hygiene and entry-screening were implemented, possibly contributing to limiting the outbreak.

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

Keywords: COVID-19, SARS-CoV-2, Meat-processing plant

ABSTRACT ID: 200

PRESENTED BY: Iris Finci /iris.finci@gmail.com

41. Forgotten castles: What does serology tell us about the effect of the COVID-19 pandemic on care homes?

A. Jeffery-Smith 1

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Background:

Care homes have been significantly impacted by the COVD-19 pandemic with high morbidity and mortality reported in association with outbreaks in these settings. Understanding the degree of SARS-CoV-2 exposure in these settings, and the longevity of immunity associated with this is vital to prepare for the coming winter and ensure appropriate targeting of vaccine strategies.

Methods:

We investigated staff and residents of 13 care homes (506 staff and 447 residents) with different outbreak patterns across London, UK in a prospective cohort study. Six homes reported mature COVID-19 outbreaks and seven reported no cases or a single case. Five weeks after initial PCR for SARS-CoV-2 convalescent serum was obtained. Serological analysis involving live virus neutralisation and a range of different assays with recombinant and native virus proteins was undertaken.

Results:

In the six care homes reporting outbreaks PCR positivity was 30.5%. Convalescent seropositivity to SARS-CoV-2 was 71.7% (range 43.5% to 85.5%). In care homes reporting single or no cases PCR positivity was 4.0% and convalescent seropositivity 27.4%, ranging between 10.7% and 58.9%. Neutralising antibody responses were detected in 89.4% (118/132) of those with detectable antibody responses. Neutralising antibody titre was not associated with age (Chi square test, p=0.27).

Conclusions:

Contrasting the high SARS-CoV-2 seropositivity rates observed in care homes reporting outbreaks, seropositivity in care homes reporting single or no cases varied widely. Widespread silent transmission has occurred in some of these homes with PCR testing severely underestimating the extent of exposure. The use of serological analysis in conjunction with increasing understanding of the nature and longevity of immunity to SARS-CoV-2 will inform vaccine strategies and winter planning for high risk care home residents and the staff caring for them.

Subject: Field epidemiology (e.g. outbreak investigations)
Keywords: COVID-19, Outbreak, Care Home, Serology, Neutralising antibody

ABSTRACT ID: 220

PRESENTED BY: Anna Jeffery-Smith /anna.jefferysmith@phe.gov.uk

42. Control of a COVID-19 outbreak with high case fatality ratio in Tirschenreuth district, Germany, March-May 2020

M. Brandl¹

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Background:

In March 2020, Tirschenreuth district (TIR), Germany, reported a COVID-19 outbreak with exploding case load and high case fatality ratio (CFR). We investigated the outbreak to provide evidence for the control of similar outbreaks in the future.

Methods:

We analysed German national surveillance data with notification dates between 10March2020-11May2020. We interviewed early cases, defined as those with symptom onset until 12March2020, using a semistandardized questionnaire on exposures including contact to cases, private meetings, local festivities and travel. We calculated attack rates (AR) using the German population as denominator, and adjusted risk ratios (aRR) using robust Poisson regression.

Results:

In the analysed period, TIR reported 1,120 laboratory-confirmed cases (AR=1,500 cases per 100,000 population) and 138 deaths (CFR=12%). Of 110 early cases, 90 (82%) were interviewed: 30 (33%) had contact to confirmed cases, 15 (17%) visited a traditional local inn, 12 (13%) were skiing in Austria/Italy and 10 (11%) attended a one-day festival; 23 (26%) reported exclusively less common exposures and 15 (17%) no exposures at all. TIR's CFR exceeded Germany's CFR by factor two

(RR=2.5, 95%Cl=2.1-2.9). This difference was reduced by adjusting for sex, age, pre-existing conditions and living in nursing homes (aRR=1.3, 95%Cl=1.1-1.5). In hospitals, the CFR did not differ significantly between TIR and Germany (aRR=1.2, 95%Cl=0.97-1.4) but was higher in TIR for non-hospitalized cases (aRR=1.8, 95%Cl=1.4-2.3).

Conclusions:

The large number of cases with varying uncommon or no exposures suggests undetected community transmission. Spread among vulnerable groups (older people, those with preconditions or in care) partially explained the high CFR. Residual risk, especially outside hospitals, is likely overestimated due to undiscovered cases. Strengthening local health authorities is crucial to facilitate rigorous case finding and prevent undetected Sars-Cov-2 transmission.

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

Keywords: COVID-19, SARS-CoV-2, Public Health, Disease Outbreaks, Pandemics

ABSTRACT ID: 203

PRESENTED BY: Michael Brandl / brandlm@rki.de

Fireside Panel 4c (Live Q&A session) DAY 4, Friday 27. November 2020 15:20-15:50

Global health and Emerging diseases

Moderator

John Kinsman (ECDC)

Abstracts

43. Early detection of cholera epidemics to support control in fragile states: delays and potential impacts

R. Ratnayake 1

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² Epicentre

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Background:

Cholera epidemics continue to challenge disease control, particularly in fragile states. Rapid detection and response to cholera clusters may prevent epidemic propagation. We investigated delays in outbreak detection and response and their predictors, and estimated epidemic sizes and annual changes in response time.

Methods:

We systematically reviewed cholera outbreaks in fragile states (2008-2019), and epidemiological reports, to extract dates and potential predictors. We evaluated delays from the dates of symptom onset of the primary case, case presentation, outbreak detection, investigation, response, and confirmation. Branching process models were used to estimate epidemic size at each delay. Regression was used to investigate associations between predictors and delays to response.

Results:

Seventy-nine outbreaks from 34 countries were included. Median delays spanned 1-2 weeks: from symptom onset to case presentation (5 days, IQR 5–5), detection (5 days, IQR 5–6), investigation (7 days, IQR 5–13), response (10 days, IQR 7–18), and confirmation (11 days, IQR 7-16). Through model simulations, the median delay to response (10 days) generated a median epidemic size of 12 cases (upper range, 47), with 8% of outbreaks >20 cases (compared with 33% at 30-days delay). An annual decrease in delay to response of 5.3% (95% CI 0.6–9.7, p=0.03) was estimated. An immediate alert (versus weekly data analysis) predicted a reduction in delay to response of 40.2% (95% CI 7.2-61.5, p=0.02).



Conclusions:

The median delays from symptom onset to presentation and response were 5 and 10 days, respectively. Modelling suggests that in 8% of scenarios, such delays would result in large clusters that would be difficult to contain. Improving delays involves rethinking the local integration of rapid testing, alert systems, and early response.

Subject: International health and migration

Keywords: armed conflict, cholera, communicable disease control, epidemics, outbreaks, surveillance

ABSTRACT ID: 85

PRESENTED BY: Ruwan Ratnayake / ruwan.ratnayake@lshtm.ac.uk

distribution, discovery process and clinical manifestation all contributed to the probability of a virus disappearing. These results help make risk assessment for new viruses after their emergence.

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

Keywords: RNA Viruses; Risk Factors; Epidemiology; Machine Learning ABSTRACT ID: 108

PRESENTED BY: Feifei Zhang / feifei.zhang@ed.ac.uk

45. Strengthening country capacity for improving outbreak response to arboviral disease in West Africa

G. Ortu¹

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- ¹ Global health consultant
- ^{2,4} University of Edinburgh
- ³ University of Hong Kong

Background:

The emergence of Aedes-borne arboviral outbreaks in the West African region raised the question of the adequacy of health systems to respond to these outbreaks, and the need to assess the existing regional capacity. In 2018, WHO- TDR conducted a situation analysis of existing resources in 16 West African countries.

Methods:

47 questions on country epidemiological and entomological surveillance and vector control were sent to ministries of health. Countries' s responses coordinated by the department of public health and surveillance, were assessed by scoring each answer against indicators prepared for each question and by SWOT analysis

Results:

Results showed that capacity is mainly focusing on yellow fever surveillance and management. Countries have national strategies for disease surveillance and mandatory disease notification processes as well as epidemic preparedness task forces, but this capacity is not adequate for many other arboviruses, leading to weak implementation of activities for controlling arboviral outbreaks. For instance, routine virological surveillance for dengue and management of severe cases appeared limited. For entomological surveillance and control, capacity is more focused on Anopheles, vectors of malaria and not Aedes, reflecting the absence of a national strategic plan to control vectors of arboviral diseases

Conclusions:

This preliminary assessment identified some capacity and weaknesses of the region. Countries must be supported in defining annual operational plans for surveillance, prevention, management and control of arboviral diseases for strengthening their existing capacity and improving outbreaks prevention and response. Although the regional program of arboviral entomological surveillance has been set up, a regional consensus on the minimum technical requirements for adequate epidemiological surveillance and integrated vector management is

44. Geographical distribution of human infective RNA viruses and their disappearance

F. Zhang 1

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³ University of Hong Kong

Background:

Understanding the consequences of viruses after their emergence in humans is important for both preventing and controlling the associated outbreaks. However, the factors that determine why some viruses are able to establish sustained infections in humans across the globe, while others disappear from humans are not fully understood.

Methods:

We collated information for all 223 human RNA viruses on their geographical distributions and persistence in causing human infections from peer-reviewed literature. Next we explored what factors predicted sustained human infections using the Bernoulli Boosted Regression Tree models.

Results:

Seventy-eight (35%) human RNA virus species have wide geographic distributions (three or more continents). Viral features that predicted these wide distributions included transmissibility between humans, narrow host ranges (i.e. infecting humans only or humans and other primates only), a +ssRNA genome, and a reservoir host in non-human primates. Eighty-two (37%) viruses were found to have disappeared from humans for the past ten years or more. Viruses were more likely to disappear if they were incapable of transmission between humans, had a localised distribution, had a dsRNA genome, were discovered through active discovery programmes rather than passive investigation of the aetiology, were discovered from the old world (Africa, Asia, and Europe), were non-pathogenic, and/or were transmitted by vectors.

Conclusions:

Multiple characteristics determine the geographical distribution and disappearance of human RNA viruses; however, transmission ecology and structure were consistently the most important predictors. Host range was found to be an important predictor for geographical distribution, though less important for disappearance. Lastly, geographical

essential to fulfil the needs and determine where effort should be $\ensuremath{\mathsf{emphasized}}$

Subject: Surveillance

Keywords: Arboviral diseases; outbreak response; epidemiological surveillance; entomological surveillance; Western Africa ; capacity strengthening

ABSTRACT ID: 79

PRESENTED BY: Giuseppina Ortu / giuseppina_ortu@outlook.com

46. Seroprevalence of Measles Antibodies in Tunisia: First findings of 2019 National Survey

M. Osman¹

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Background:

In Tunisia, measles incidence declined significantly since introduction of vaccination in the national schedule in 1983 and plateaued around a total of 12 yearly cases, with a vaccine coverage greater than 90% since 2000. In January 2019, a nosocomial measles outbreak started in Kasserine and Sfax, and reached countrywide with a total of 3896 cases in September.

Our aim was to estimate the seroprevalence of measles-specific IgG antibodies in the Tunisian population by age and region.

Methods:

It was a seroprevalence study, on serum bank of 19663 samples collected in 2015 across Tunisia, with a representativeness of all age groups.

Considering an 85% vaccination coverage, we required a sub-sample of 3500 randomly selected specimens. ELISA technique was used by the microbiology and biochemistry laboratory of Aziza Othmana hospital and the microbiology laboratory of the Charles Nicolle hospital.

Results:

Out of 3454 samples tested, overall seroprevalence of anti-measles IgG was 94.9% (95%CI:94.3%-95.6%). In urban areas, seropositivity was 95.5% (95%CI: 94.7%-96.2%). By gender, anti-measles IgG was almost equal betwen the two sexes. Individuals born between 1982 and 1997 were more susceptible to measles; seroprevalence among those 20-30 years-old was 83.2% (95%CI: 79.7%-86.1%) and only 70.0% for those

1989-born. Governorates of Sidi Bouzid and Tataouine had the lowest proportions of measles seropositivity (<90%).

Conclusions:

The 2019 national serosurvey showed relatively high overall measles seropositivity in the Tunisian population. However, Tunisians born during 1982-1997 are unprotected against measles. Strengthening surveillance and raising healthcare workers and public awareness is essential. Also, vaccination of subjects aged 20 to 35, a childbearing age, is strongly recommended.

Subject: Surveillance

Keywords: Measles, Antibodies, Seroepidemiologic studies, Tunisia ABSTRACT ID: 118

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Disease Group: Food and waterborne diseases and zoonoses

Abstracts

1.1. Multi-country occurrence of non-cholera Vibrio infections in the Nordic countries and countries bordering the Baltic Sea in 2018

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Background:

Vibrio bacteria are ubiquitous in aquatic and marine habitats. Noncholera Vibrio species cause self-limiting vibriosis, but can rarely lead to severe clinical presentation. In the last years, countries in northern Europe have witnessed an increase in Vibrio infections during heatwaves, including 2018. We aimed to describe the epidemiology and map the genetic diversity of the isolates collected from seven countries (Norway, Sweden, Finland, Denmark, Poland, Estonia and Latvia) in 2018 in order to propose recommendations for control measures.

Methods:

We conducted a retrospective cross-sectional study using laboratorybased or passive surveillance data, analysing demographics, geographical distribution, seasonality and severity of vibriosis cases. Travel-related cases were excluded. Relatedness of isolates was investigated by phylogenetic single-nucleotide-polymorphism (SNP) analysis of whole genome sequencing data.

Results:

We identified 441 vibriosis cases with median age of 52 years (1-101) and male-to-female ratio of 1.6. Exposure was known for 112 cases of which 106 (95%) reported exposure to seawater. Infections by species showed a geographical disparity and were unevenly distributed across age groups. The odds of developing severe infection was associated with (i) age group

>65 years old (OR=14.2; 95%Cl:4.0-50.8), (ii) V. vulnificus (OR=23.7; 95%Cl:4.1-139.2) and V. parahaemolyticus (OR=3.2; 95%Cl:1.2-8.3) and (iii) summer season (OR=6.2; 95%Cl:2.8-13.7). Although phylogenetic analysis showed diversity between Vibrio isolates, two V. vulnificus clusters (<10 SNPs) were identified in Norway and Sweden.

Conclusions:

Severe infections with V. vulnificus and V. parahaemolyticus represent a public health threat during summer seasons for the population at risk in the Nordic region and countries bordering the Baltic Sea. These countries may consider introducing or harmonising vibriosis surveillance based on their own public health priorities in order to advise the public and authorities on control measures.

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

Keywords: Vibriosis, Emerging pathogen, Waterborne infections, Baltic Sea, Heatwaves

ABSTRACT ID: 4

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1.2. Outbreak of Shigella sonnei linked to imported snap peas, Norway, November-December 2019

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Background:

In December 2019, the Norwegian Institute of Public Health was notified about several employees of Company A with gastrointestinal illness, all of whom had eaten at its canteen. We investigated to identify the outbreak source and implement control measures.

Methods:

We defined a case as a person with gastroenteritis symptoms for ≥ 3 days, with onset from 3–10 December. We invited employees who had eaten at the canteen from 2–4 December to a retrospective cohort study, via online questionnaire. All food items consumed by $\ge 50\%$ of cases with a p-value of <0.10 were included in logistic regression analysis. Local laboratories tested stool samples for enteric pathogens; the National Reference Laboratory performed core-genome Multi-Locus Sequence Typing (cgMLST) on Shigella spp/enteroinvasive Escherichia coli isolates.

Results:

Of 170 employees, 28 met the case definition; 22/28 (79%) were female, with a median age of 49 years (range 28-64). 126 employees who had eaten at the canteen responded to the questionnaire. Eating uncooked snap peas (aOR 5.2, 95%Cl 1.3–20.3) and salmon (aOR 3.9, 95%Cl



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1.1–14.5) were associated with illness. No snap peas were available for sampling.

Seven employees tested positive for S. sonnei; all isolates belonged to a new outbreak strain, which was observed in 7 additional cases in the community. Six community cases reported eating uncooked snap peas, which had a common distributor as those served at Company A.

Conclusions:

Imported snap peas were the likely source of this outbreak, and have been associated with previous shigella outbreaks. While package labels instruct consumers to cook snap peas before serving, the public and food services must be reminded about the risks associated with raw imported snap peas.

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

Keywords: Disease outbreaks, Foodborne Diseases / epidemiology, Foodborne Diseases / microbiology, Norway / epidemiology, Shigella sonnei / genetics

ABSTRACT ID: 5

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1.3. Examining socio-economic drivers of Verotoxigenic Escherichia coli (VTEC) enteritis and cryptosporidiosis infection in the Republic of Ireland (2008-2017) using a Random Forest classification algorith

E. Cleary 1

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Background:

Socioeconomic profile can be an important determinant of infectious disease transmission. However, components of deprivation indices and their association with infection transmission have rarely been examined. The current study explores the associations between 16 components of the Pobal HP deprivation index with Verotoxigenic Escherichia coli (VTEC) enteritis and cryptosporidiosis in the Republic of Ireland.

Methods:

HP deprivation index data (2011, 2016) were merged with VTEC and cryptosporidiosis notification data for years 2013 to 2017 and 2008 to 2017, respectively, at Central Statistics Office (CSO) Small Area (SA) level using a unique spatial identifier. Random forest (RF) models were trained using significant explanatory variables from stepwise logistic regression to examine associations between HP deprivation components and infection presence in 18,488 SAs. Models were discretised based on urban/rural classification and year during which deprivation data was collected.

Results:

RF models exhibited high classification accuracy for both infections

in urban and rural areas (correctly classified infection range = 97.3% - 98.4%). SA population size (coefficient (coeff) = 0.0001) and age dependency ratio (coeff = 0.0012) were strongly associated with VTEC infection in urban areas while proportion of renters (coeff = -0.0125) and third-level education (coeff = -0.0204) were associated with VTEC in rural areas. Conversely, proportion of semi-skilled workers (coeff = 0.0324) and unemployment rates (OR = 0.0141) were more acutely associated with cryptosporidiosis in urban areas, while rates of owner-occupied housing (coeff = 0.0052) and unemployment (coeff = -0.0118) were linked in rural areas.

Conclusions:

Deprivation components are significantly associated with VTEC and cryptosporidiosis infection, with the explanatory power of these components differing depending on settlement type, indicating significantly different transmission dynamics between built-up and predominantly rural areas.

Subject: Burden of disease

Keywords: Verotoxigenic Escherichia coli ,cryptosporidiosis,Pobal HP deprivation index,Random forest modelling

ABSTRACT ID: 14

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1.4. National outbreak of Salmonella Mikawasima in the United Kingdom, 2019/2020: A comparison of outbreak investigation techniques

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Background:

Over the past decade, multiple large outbreaks of Salmonella Mikawasima have been reported across Europe. In October 2019, routine Whole Genome Sequencing identified 22 S. Mikawasima cases in the UK within a 5-single nucleotide polymorphism (SNP) cluster. We aimed to identify the source of the outbreak using a variety of investigation techniques.

Methods:

Cases were individuals with laboratory-confirmed S. Mikawasima infection within 5-SNP residing in the UK. Cases were interviewed using questionnaires. We performed a case-case study using data from historical Salmonella outbreaks (past 5 years) to compare the exposure profile of the current Salmonella outbreak to historical Salmonella outbreaks. Following this, we undertook a case-control study using market research panel controls and reviewed supermarket loyalty cards to find common items.

Results:

152 cases were identified from Sep-2019 to Jan-2020; 62% were female; median age 54 years (IQR 33-70 years). Case- case study used 22 cases and 90 control cases (historical Salmonella cases) and indicated pork, mixed salad leaves and peppers as a possible cause. Case-control study used 16 cases and 124 controls (market research panel) and indicated

strawberries and cucumbers. 29 supermarket loyalty cards (from 17 cases) were obtained; most common food items purchased were salad leaves, tomatoes and chicken.

Conclusions:

The studies produced incongruent findings, therefore highlighting potential issues with relying on a single analytical study. Each study had limitations such as sample size and differing exposure periods. We conclude that the vehicle of infection is likely a commonly consumed food item and therefore difficult to identify using standard epidemiological/ analytical approaches. Our recommendations are to continue to monitor this Salmonella strain, to act quickly to any future outbreak and use a multi-angled approach in outbreak investigation.

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

Keywords: Salmonella Mikawasima, Outbreak

ABSTRACT ID: 24

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1.5. Did the implementation of the National Salmonella Control Programmes in poultry have an impact on human salmonellosis in Greece?

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Background:

Salmonella Enteritidis (SE) and Typhimurium (ST) are the most frequently reported serotypes in humans in Greece. Since 2008, National Salmonella Control Programmes (NSCPs) have been implemented targeting these serotypes in poultry.

We aimed to assess impact of NSCPs on trends and number of human SE and ST cases.

Methods:

Using monthly serotype data from the National Reference Laboratory for 2006-2017 as proxy for the number of salmonellosis cases we defined two intervention (SE, ST) and one control time-series (consisting of serotypes not associated with poultry or eggs). For SE, analysis was also performed for 2006-2015 due to a large SE multicounty outbreak in 2016. We performed interrupted time series analysis. We used a negative binominal regression model with trend and Fourier terms to adjust for secular and cyclical trends, one lag to account for autocorrelation, an indicator variable to define intervention, and an interaction term for assessing changes in trend after the intervention. We calculated incidence rate ratio (IRR) values and respective (confidence intervals) CIs as measures of association.

Results:

Before NSCPs, there was no significant trend for SE, ST, and controls. The same applied for SE and ST (p>0.05) after NSCPs' introduction, while the trend was increasing (IRR:1.0045, 95%Cl:1.0010-1.0080) for controls. For 2006-2015, SE presented a decreasing trend after the NSCPs' introduction (IRR: 0.99, %95Cl:0.98-0.99).

NSCPs had a statistically significant impact on total SE cases, reduced

on average by 49% (IRR:0.51, 95%CI:0.35-0.74) and 47% ((IRR:0.52, 95%CI:0.38-0.72) for 2006-2017 and 2006-2015 respectively, while no impact was shown on the total ST and control cases.

Conclusions:

Significant decrease on human SE cases justifies added value of NSCPs. For ST however, control measures should be extended to other susceptible species.

Subject: Burden of disease

Keywords: Salmonella Enteritidis, Salmonellosis, Health Impact Assessment, Time series analysis, Public Health

ABSTRACT ID: 39

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1.6. Outbreak of Salmonella Newport linked to imported crayfish, Sweden, 2019

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Background:

In October 2019, the Public Health Agency of Sweden identified a cluster of Salmonella Newport cases by whole genome sequencing (WGS). Cases' dispersion in place and time indicated a nation-wide ongoing outbreak. Swedish authorities started an investigation to identify the source and prevent further cases.

Methods:

We identified cases and their demographic information through the electronic notification system. Cases' food exposures were collected using a trawling questionnaire. We compared 20 outbreak cases to 139 domestic cases of salmonellosis with serovars other than S. Newport, with disease onset in corresponding season 2017-2019 and not belonging to another large outbreak. Food exposures were compared by adjusted odds ratios (aOR, adjusting for gender, age and county) with 95% confidence interval (Cl) using logistic regression. Implicated foods were sampled by a retail chain and at border control. Isolates from positive samples were compared by WGS.

Results:

Thirty-three cases from 12 counties were confirmed, 20 cases were women and median age was 55 years (range 1-82). Onset of disease ranged from 31 July to 2 November 2019. Outbreak cases were more likely to have consumed crayfish (aOR: 26, 95% CI 6.3-105) and the investigation identified one specific brand of imported frozen crayfish in dill brine. The retail chain recalled all remaining packages. S. Newport was detected in 6/84 samples from different batches from retail and in one sample from border control. Isolates from all food samples clustered with the outbreak strain by WGS.

Conclusions:



Our investigation confirmed crayfish as the vehicle in this outbreak. Crayfish in dill brine is a ready-to-eat food product requiring strict microbiological control. The epidemiological evidence led to immediate extensive product recall which prevented further exposure.

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

Keywords: Salmonella ,case-case study,outbreak,crayfish

ABSTRACT ID: 101

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1.7. The added value of epidemiology in the investigation of a waterborne outbreak of mixed origin, in Peloponnese, Greece, 2020

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Background:

On 15/06/2020, two E.coli O157 gastroenteritis cases were reported in residents of a Peloponnese village, with symptoms onset on 31/05/2020. Local pharmacists confirmed an increase in diarrhea cases seeking medication in late May and early June, however, symptoms were mild, incompatible with E.coli O157 infection and few cases visited the hospital. We undertook a case-control study to test the hypothesis that there was contamination of the water supply.

Methods:

Cases were defined as residents with diarrhea from 29/05/2020 - 06/06/2020 and controls as residents without symptoms. Both were randomly selected from customer lists from the two local pharmacies. Data was collected through telephone interviews. Logistic regression model was used for multivariable analysis adjusted for age and sex.

Results:

In total, 58 cases and 57 controls were selected. Median age of cases and controls was 46 (8-78) and 55 (3-96) years, respectively. 57% of cases and 56% of controls were female. Case distribution over time was compatible with a common source. In multivariable analysis, gastroenteritis was significantly associated with consumption of ice cubes (aOR=39, 95%Cl=10-151, p<0.001) and tap water (aOR=11, 95%Cl=3-38, p<0.001). Two stool samples were positive for E.coli O157 and one each for E. coli STEC, Salmonella spp. and E.coli EPEC. No pathogen was found in water samples, however chlorine concentration was lower than required by legislation.

Conclusions:

Although delayed notification prevented laboratory confirmation of water contamination, epidemiological investigation identified water as the probable source of the outbreak. We asked public health measures to be implemented by the municipality responsible for water safety.

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

Keywords: mixed outbreak, waterborne,gastroenteritis,Greece

ABSTRACT ID: 113

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1.8. Salmonellosis outbreak following wedding dinner, September 2019, Croatia; the role of outbreak investigation in considering legal action against caterer

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Background:

On September 18, 2019, the Andrija Stampar Teaching Institute of Public Health (ASTIPH) was informed of an outbreak of gastrointestinal illness among guests at a wedding on 14 September. We investigated to identify the vehicle and to prevent further cases. Although the outbreak investigation proceeded per usual practice, the communication of findings had unforeseen implications: the wedding couple subsequently requested the outbreak report, as they considered legal actions against the caterer.

Methods:

We conducted a retrospective cohort study among wedding guests, through an online questionnaire. Probable cases were defined as guests who developed diarrhoea from 15-18 September, and confirmed cases as guests with laboratory confirmation of Salmonella from a stool sample. We assessed associations between food exposures at the wedding and illness. Microbiological testing was performed in local laboratories and the National Reference Laboratory for Salmonella. A Sanitary Inspector provided environmental investigation of the catering premises.

Results:

Forty-three of 92 guests (47%) completed the online questionnaire; 14 guests met the case definition (attack rate 33%). Salmonella Typhimurium and Salmonella type B were identified for 9 confirmed cases. Two food items were significantly associated with being a case; eating roasted piglet had the highest risk ratio (RR=5.18, 95%Cl:1.32-20.3) and explained 86% of cases. Eight (19%) respondents reported the piglet was visibly undercooked. The pathogen was not confirmed in leftover food or from environmental testing.

Conclusions:

The epidemiological investigation suggested that undercooked piglet was the vehicle of infection, but no microbiological results were available to support this hypothesis. We provided a report to the couple with the most important findings but we suggest that the State Inspectorate develops protocols with objectives and guidelines for communicating investigation results in such scenarios.

Subject: Field epidemiology (e.g. outbreak investigations) **Keywords:** salmonella, wedding, Croatia, cohort study

ABSTRACT ID: 134

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Background:

The Rapid Assessment & Surveys methods (RAS) module for Cohort 2018 fellows took place in Zagreb, Croatia, 13-18 May 2019. On 14 May, some fellows reported gastro-intestinal complaints and could not attend the module. Based on symptoms, we hypothesized a food-borne infection as a potential cause of the outbreak, the topic was discussed via informal chats during coffee breaks among fellows. We described the extent of the outbreak and investigated to identify the potential source.

Methods:

We designed a cohort study, including the RAS module participants. Via online questionnaire, we started case finding and asked about social events and food exposures to assess associations between exposures and illness. We defined cases as fellows who attended the module and who had any of the following symptoms on 14-16 May: diarrhoea, vomiting, abdominal cramps.

Results:

Thirty-seven fellows attended the module; among them we identified eight cases (attack rate 22%). The only social event visited by all cases was the dinner on 13 May. Eating goulash during the implicated dinner was significantly associated with being a case (RR=5.63; 95%Cl:1.37-23.10) and explained 63% cases. Stool sample from one case was negative for norovirus, adenovirus, rotavirus, Salmonella spp., Shigella spp., Campylobacter spp. and Escherichia coli. Sanitary inspection in the restaurant on 17 May did not find leftover food for testing.

Conclusions:

Our investigation suggested that goulash was the vehicle of infection. No microbiological results were available to support this hypothesis. Information bias could be the limitation of the study due to fact that fellows exchanged their thoughts on the potential vehicle, even before the study was conducted. We recommended proper hand hygiene for fellows during lectures and social activities.

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

Keywords: gastroenteritis, outbreak investigation, Croatia, EPIET

ABSTRACT ID: 135

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1.10. Triangulating epidemiological analyses to identify likely vehicles of infection in an outbreak of Salmonella Enteritidis.

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Background:

Since 2012, whole genome sequencing in the UK has identified over 1000 cases of Salmonella Enteritidis in the 25-single nucleotide polymorphism (SNP) single-linkage cluster 1.1.2.12.% (t25:12). Epidemic Intelligence Information System communications had identified the strain across Europe, corroborating suspicions of non-UK poultry products as the vehicle(s) of infection. UK investigations were reinitiated in 2020 due to escalation of cases in two 5-SNP sub- clusters.

Methods:

We interviewed S.Enteritidis t25:12 cases with targeted questionnaires. We compared exposures of cases at 25-SNP and 5-SNP to those of market panel controls surveyed during two recent Salmonella outbreak investigations not linked to chicken (case-control), then to cases in those outbreaks (case-case), using logistic regression.

Results:

Of 225 cases reported January-August 2020, 62 non-travel-associated cases completed questionnaires, revealing high frequency of chicken consumption (97%).

In the case-control study (273 controls), multivariable analysis demonstrated that S.Enteritidis t25:12 cases who had eaten reformed chicken products and shopped at Supermarket-1 had an adjusted odds ratio (aOR) of 211.6 (95%CI 25.2-1775.2; Pc0.001), those who ate reformed chicken and shopped at Supermarket-2 had an aOR of 77.6 (8.6-700.2; Pc0.001), and those who ate reformed chicken and shopped at neither had an aOR of 4.0 (1.2-13.5; P=0.024), compared to those who had not eaten reformed chicken nor shopped at either.

Compared to 71 case-comparators cases were more likely to have eaten reformed chicken and shopped at either Supermarket-1 or Supermarket-2 (aOR 76.4; 95%CI 8.6-680.9; P<0.001), with similar results in 5-SNP subclusters.

Conclusions:

Although each comparator presents distinct limitations, the same associations emerge consistently. With multiple reformed chicken products from multiple retailers reported by cases, these findings help focus food chain investigations and microbiological sampling on key products and supermarkets.

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

Keywords: Salmonella Enteritidis,Outbreak,Poultry,Case-control,Casecase

ABSTRACT ID: 148

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1.11. Increasing trend in Capnocytophaga canimorsus notifications in Finland, 2000–2019

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Background:

Zoonotic bacterium Capnocytophaga canimorsus can cause meningitis, endocarditis, sepsis and death in humans. Many patients, but not all, have underlying condition such as alcoholism or splenectomy. Infections are often associated with dog or cat bites, scratches or wound licking.

Methods:

A case is defined as person with C. canimorsus isolated from blood or cerebrospinal fluid and notified to Finnish Infectious Disease Register (FIDR). We characterized cases reported to FIDR in 2000–2019 according to age, gender, sampling site, case fatality and hospital district. Incidence rate ratios (IRR) were calculated to compare incidences.

Results:

In 2000–2019, 343 (annual range 6–39) C. canimorsus findings were notified to FIDR (mean annual incidence 3.17 per million). In 2010–2019, the incidence increased nearly 3-fold compared to 2000–2009 (IRR 2.66, 95% CI 2.09-3.38). Of the cases, 55% (187/343) were male. Median age was 58 years (range 12–94 years). Incidence was 3-fold in 50–69-year olds compared to other age groups (IRR 3.32, 95% CI 2.69–4.11). C. canimorsus was mostly detected in blood (336/343; 98%). 17 cases (5%) died within 30 days of sampling. Mean annual incidences in hospital districts ranged from 0.22 to 7.03 per million. Incidence was 1.5-fold in Eastern districts compared to other districts (IRR 1.55, 95% CI 1.19-2.0)

Conclusions:

In Finland, C. canimorsus infection incidence increased during past 10 years and is higher, while mortality rate is lower, than in reports from other countries. Risk groups should be informed how to prevent animal exposures and how to act after exposure. More detailed information on sources, risk factors and geographicality are needed to better understand Capnocytophaga infection epidemiology in Finland in order to target control measures.

Subject: Surveillance

Keywords: Capnocytophaga, Incidence, Humans, Finland

ABSTRACT ID: 177

PRESENTED BY: Kristiina Suominen / kristiina.suominen@thl.fi

1.12. Increasing trend in Capnocytophaga canimorsus notifications in Finland, 2000–2019

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Background:

Hantavirus-infections and Leptospirosis are re-emerging zoonotic diseases. Occupational and non-occupational risk- factors were studied

among forestry workers (FW) in Lower Saxony (LS) to develop targeted preventive measures.

Methods:

Sera sampled in 2016 among FW in LS were screened for anti-Hantavirus IgG (H) and anti-Leptospira IgG (L) by ELISA. Data on risk factors was collected by standardized questionnaire. Odds ratios adjusted for age and sex (aOR) and 95%-confidence-intervals (CI) were obtained by logistic regression analysis.

Results:

Of 601 FW (89.4% male, median age 53 years) 8.8 % were H-positive, 4.9 % L-positive. Males were more affected than females (p=0.04). Only one H-positive FW (n=53) recalled clinical diagnosis whereas none of the L-positive FW (n=27) did.

The chance of H-seropositivity was increased by working outdoors (2.8; 95%-Cl 1.3–6.4), keeping reptiles (3.1; 95%-Cl 1.2–8.5), cleaning attics (2.4; 95%-Cl 1.1–5.4) and canoeing (2.4; 95%-Cl: 1.2–4.6) increased and decreased by taking walks (aOR: 0.3; 95%-Cl: 0.1–0.9) and having pet cats (0.5; 95%-Cl: 0.3–0.9). The chance of L-seropositivity was increased by swimming in freshwater (2.7; 95%-Cl 1.4–5.2) and decreased by higher educational degree (aOR 0.6; 95%-Cl 0.5–0.9) and gardening > 10 years (aOR 0.3; 95%-Cl 0.1–0.9). Employers and friends were the most frequent sources of information related to the pathogens, diseases and corresponding preventive measures.

Conclusions:

H- and L-seroprevalences are found to be within the range reported in other studies on FW in Europe. Underreporting of the diseases and identification of leisure- and occupation-derived risk factors indicate that raising awareness among practitioners, at-risk groups, and the public, and employing multimodal communication strategies is of utmost importance. Employers are key players in developing and communicating work-related preventive measures.

Subject: Burden of disease

Keywords: zoonosis, seroprevalence, forestry workers, risk factors, Germany, rodent borne

ABSTRACT ID: 180

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Disease Group: Healthcare-associated infections

Abstracts

2.1. Investigation into a persistent recurring cluster of meticillinresistant staphylococcus aureus colonisations on a special care baby unit in Northern England, August 2016 to November 2019

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Background:

Between August 2016 and November 2019, a cluster of meticillinresistant staphylococcus aureus (MRSA) colonisations were reported on a special care baby unit (SCBU) in Northern England. A case control study was performed to identify the source of the infection and prevent further cases.

Methods:

We defined cases as an infant admitted to the SCBU, colonised or infected with MRSA (spa type t₃₁₆). We performed a retrospective matched case control study with two controls per case selected from SCBU patients, matched by exposure period (week prior to positive result). Exposures were determined by medical record review. Cases were described and compared with controls using conditional logistic regression. Environmental investigations and staff screening were undertaken.

Results:

We identified 31 colonised cases in eight temporal clusters across the three-year period, with no infections reported. Thirteen of the 31 cases were within a 25 SNP cluster, consistent with exposure to a common source over a prolonged period. Most cases had a previous negative screen prior to testing positive (n=22; 71%). Environmental sampling and staff screening was performed on several occasions with no positive specimens obtained. In the analytical study, 31 cases were compared with 62 controls. One ward location and one healthcare worker were identified as significant exposures in the multivariable analysis.

Conclusions:

Due to the sporadic nature of the colonisations it was hypothesised that MRSA was being introduced to the ward intermittently, likely by a colonised healthcare worker, with possible transmission between infants also occurring within each temporal cluster. It is recommended that further environmental investigations be undertaken, and in the event of further cases staff screening should be performed.

Subject: Field epidemiology (e.g. outbreak investigations)Keywords: MRSA, Outbreak investigation, Case control study, Neonates, HCAI

ABSTRACT ID: 19

PRESENTED BY: Nicola Love / nicola.love@phe.gov.uk

2.2. Healthcare associated infection - the impact on length of stay

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- ⁵ Public Health Scotland

Background:

Increased length of stay for patients is an important measure of the burden of HAI. This study estimated the excess length of stay attributable to HAI. Considering the impact on LOS of different HAI types is important in guiding investment in HAI prevention.

Methods:

A one-year prospective incidence study of HAIs was performed in a teaching hospital and a general hospital in NHS Scotland in 2018/19. All adult inpatients with an overnight stay were included. HAI was diagnosed using European Centre for Disease Prevention and Control case definitions. A multistate model was used to account for the time varying nature of HAI and the competing risks of death and discharge.

Results:

The excess length of stay attributable to HAI was 7.8 days (95% CI 5.7-9.9). Median length of stay for HAI patients was 30 days and for non-HAI patients was 3 days. Using a simple comparison of duration of hospital stay for HAI cases and non-cases would overestimate the excess LOS by 3.5 times (27 days compared with 7.8 days). The greatest impact on LOS was found for pneumonia 16.3 days (95%CI 7.5-25.2), blood stream infections 11.4 days (95%CI 5.8-17.0) and surgical site infection (SSI) 9.8 days (95%CI 4.5-15.0).

Conclusions:

With an estimated total of 58,000 bed-days being occupied annually due to HAI, even a reduction of 10% in HAI incidence has the potential to free up 5,800 bed-days which could be used to treat an average of 1,706 elective patients in Scotland annually and help to reduce the number of patients awaiting planned treatment. This study should support decisions in infection prevention and control interventions locally, nationally and internationally.

Subject: Burden of disease

Keywords: Healthcare associated infection, Infection prevention and control, length of stay, multistate models

ABSTRACT ID: 222

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2.3. Clostridioides difficile surveillance in Belgian hospitals since 2008: main incidence trends

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Background:

Clostridioides difficile infection (CDI) is the most important cause of infectious diarrhoea acquired in healthcare institutions and results in a high clinical and economic burden. We aim to describe the incidence trends since 2008, the year the national surveillance was implemented, until 2018.

Methods:

Two data sources were used to compute CDI incidence in Belgian hospitals. First, we analysed data from the national surveillance. Participation is voluntary but was mandatory for all acute care hospitals until 2014. Hospitals are required to report all CDI episodes in hospitalised patients for at least one semester per year. Second, we used hospital stay data provided by the Federal Public Service. We analysed all stays classified as "Enterocolitis due to Clostridioiodes difficile" by the International classification of diseases (ICD9-10).These data are comprehensive and provide better estimates of CDI burden while allowing validation of surveillance data.

Results:

Participation in surveillance remained high (>85%) even when voluntary. The proportion of "hospital-associated" cases (HA-CDI, date of onset \geq 2days after admission) was 55.5% in 2018, compared to 64.8% in 2008. Incidence of HA-CDI per 10.000 hospitalisation-days decreased between 2008 (1.53) and 2010 (1.26), stayed stable until 2014, increased in 2015 (1.49) and remained stable since then. Incidence trend was similar when using hospital stay data. However, incidence computed via surveillance was systematically lower than when computed via hospital stays. Incidence remained highest in Wallonia and lowest in Flanders and there were large variations between provinces and hospitals.

Conclusions:

The lower incidence during 2010 - 2014 and the variations across the country and between hospitals suggest room for improvement. We also recommend in-depth investigation on the differences in incidence measured via these two data sources.

Subject: Surveillance

Keywords: Clostridioides difficile infection,Belgium,incidence,hospital ABSTRACT ID: 238 PRESENTED BY: Laure Mortgat / laure.mortgat@sciensano.be

Disease Group: HIV, sexually transmitted infections and viral hepatitis

Abstracts

3.1. An area-level metric to monitor and evaluate public health and policy responses to the Hepatitis C virus (HCV) epidemic: An ecologic analysis of variations in HCV community viral load in New York City

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Background:

"Community viral load" (CVL), an aggregate of individual viral loads in a population, can serve as a potent metrics for measuring and predicting transmission potential at the population-level, and for evaluating interventions. We adapted the CVL construct, developed for HIV epidemiology, to study hepatitis C virus (HCV) epidemiology.

Methods:

Data were from 8,353 patients receiving methadone during 2013-2016 at an opioid treatment program in New York City. HCV treatment rates were calculated. HCV incidence was calculated among those HCV antibody negative at baseline and retested at least once. Incidence rates and incidence rate ratios were examined. HCV CVL was calculated among those with documented, active infection. HCV CVLs were compared among geographic areas s using linear regression.

Results:

The overall HCV CVL was 4,351,079 copies/mL (SD=7,149,888) and varied significantly among geographic areas (p=0.02). HCV treatment rates increased significantly over the study period (12% vs. 45%, p <0.01). For each 1 log10 increase in HCV CVL, incident HCV was expected to be multiplied by 2.7; although this association was not statistically significant it was in the hypothesized direction suggesting that CVL may be a valuable metric for HCV epidemiology and suggesting the importance of further study of the association between HCV CVL and HCV incidence.

Conclusions:

There are significant area-level disparities in HCV CVL suggesting the need to geographically focus HCV control efforts. While HCV treatment rates increased during the study period, HCV CVL did not decrease suggesting the need for greater expansion of HCV treatment. As acute HCV and HCV incidence are difficult to measure directly, HCV CVL metrics hold promise as predictors of HCV incidence.

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

Keywords: novel metric; hepatitis C virus; policy and program evaluation; ecologic analysis

ABSTRACT ID: 42 PRESENTED BY: Ashly Jordan / ae.jordan@nyu.edu

3.2. Consultation rate and chlamydia positivity among ethnic minority clients at STI clinics in the Netherlands

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Background:

Although ethnic minority clients (EM) from STI endemic countries have increased risk of STI, little is known on the proportionality of their STI clinic consultation rates. The aim was to assess consultation and chlamydia positivity rates among different EM visiting STI clinics in the Netherlands.

Methods:

Consultation rates were calculated in EM groups dividing the number of STI consultations by the total number of inhabitants in the region belonging to an EM. Consultation rates and chlamydia positivity rates in EM were compared to native Dutch. Multivariable regression analysis was used to determine factors associated with chlamydia positivity.

Results:

23,841 clients visiting an STI clinic in the Eastern part of the Netherlands were included in the analysis, of which 7% were an EM. The consultation rate among native Dutch was 22.5 per 1000, compared to a mean rate of 8.5 per 1000 among EM. In all EM, consultation rates were lower than in Dutch, except for Antillean or Aruban EM and Latin American EM.

The chlamydia positivity rate among all clients was 15.5%, the highest rate was found among Antillean or Aruban ethnicity (27.1%). In multivariable analysis, factors associated with chlamydia positivity were: Eastern or Northern European EM, African EM, Antillean or Aruban EM, STI related symptoms, heterosexual preference, partner in a risk group, receiving a partner notification and having had 3 or more partners in the past 6 months.

Conclusions:

Most EM visit the STI clinic less often than native Dutch on a population level, while being more often chlamydia positive. STI clinics should increase outreach activities for EM clients as they are insufficiently reached by current care while contributing substantially to chlamydia rates.

Subject: Surveillance

Keywords: sexual health,STI,sexually transmitted infections, chlamydia, ethnic minorities, ethnic groups, consultation rate

ABSTRACT ID: 102

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3.3. High infection rate of Chlamydia trachomatis and Neisseria gonorrhoeae in people visiting the Sexual Transmitted Disease advice centers of Baden-Württemberg, Germany 2018-2019

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Background:

In Germany the costs for screening of Chlamydia trachomatis (CT) of asymptomatic people are only covered for sexually active women less than 25 years. In order to find out how many people are infected asymptomatically and should be screened regularly to interrupt the transmission we investigated CT and Neisseria gonorrhoeae (NG) infection in people visiting the Sexual Transmitted Disease (STD) advice centers of Baden-Württemberg (BW).

Methods:

We collected information including sexual and risk history from 26,197 people who consulted 35 STD advice centers from 1st-January-2018 to 31st-December-2019. Depending on the risk behavior and independently from any existing symptoms we investigated urine, cervical, urethral, vaginal, anal and/or pharyngeal swabs by Polymerase Chain Reaction (PCR), made a descriptive analysis and calculated Risk Ratios (RR) for CT/ NG infection with 95%-confident intervals (Cl).

Results:

15,870 (62%) specimens were from men, 9,620 (38%) from women. The positivity rate for CT/NG was 5.4%/1.7%. The rate for CT/NG infection was 7.2%/5.0% in men who have sex with men (MSM), 4.1%/2.4% in sex workers and 4.7%/0.4% in heterosexual people. MSM had 1.48 higher risk for CT infection (Cl 95%: 1.17 - 1.89) and 8.40 higher risk for NG infection (Cl 95%: 4.34 - 16.3). We detected the highest inhibition rate in rectal material (5.3%).

Conclusions:

For CT and NG we recommend a regular screening of sex workers and MSM with often changing sexual contacts. Heterosexual people with often changing sexual contacts should be investigated regular for CT infection. STD advice centers should give detailed advice on how to handle self-made rectal swabs to get useful material for analysis with PCR.

Subject: Surveillance

Keywords: Chlamydia trachomatis, Neisseria gonorrhoeae, screening, infected asymptomatically

ABSTRACT ID: 130

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3.4. Hepatitis C National Epidemiological Surveillance System Evaluation, Portugal – 2017/2018

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Background:

Hepatitis C National Epidemiological Surveillance System sets as objectives the monitoring of ongoing virus transmission, measuring incidence and early detection to implement prevention and control measures and provide linkage to care. We aimed to evaluate performance of the surveillance system through a set of attributes, in order to identify gaps in need of improvement.

Methods:

We extracted national surveillance data on all notified Hepatitis C cases from 2017 to 2018. Completeness was measured on proportion of compulsory fields filled. Positive predictive value was evaluated on the proportion of confirmed cases validated for surveillance purposes. We discussed representativeness comparing key characteristics of cases with reference literature. Timeliness was appraised by the proportion of notified cases in the first 24 hours after diagnosis.

Results:

There were 804 reported Hepatitis C cases. Data completeness on compulsory fields was 76.4%. Positive predictive value was 51.0% (410/804). Main cause for non-confirmed cases was year of diagnosis before 2017. Majority of cases were male (75.8%), within the age group of 45-54 years old. Regional incidence was highly asymmetrical, ranging from o to 10.7 cases per 100 000 inhabitants. More than half of cases (50.7%) had chronic disease. Disease transmission through non-occupational lesion (needles, tattoo, piercing, bites and injuries) represented the majority of cases (26.8%). Co-infection with HIV was 5.6%. Timeliness was 24.2%.

Conclusions:

Hepatitis C epidemiological surveillance system, whereas comprehensive, provides a sub-optimal picture of disease strategic indicators. We recommend improving data quality on completeness by making notification shorter on key variables and all fields compulsory. We endorse routine training of notifiers on disease reporting features. Timeliness can be enhanced by an automatic linkage between laboratorial and medical softwares.

Subject: Surveillance

Keywords: surveillance, hepatitis c,evaluation **ABSTRACT ID:** 182

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

Abstracts

4.1. Determinants of continuation influenza vaccination in the next season among Polish patients attending a primary care clinic (PCC)

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Background:

The influenza vaccination coverage among Polish population is disturbingly low. The study objective was to evaluate the uptake and influencing factors among PCCs patients followed in the next season after receiving a refunded immunisation.

Methods:

Between October-December 2018 consecutive patients ≥55 years of age, who attended a PCC in Gryfino, Poland, received the refunded quadrivalent influenza vaccine recommended by the WHO for the 2018/2019 season and were followed in the next (2019/2020) season regarding a flu shot. A questionnaire, distributed by a research team, was used to assess determinants influencing continuation of influenza vaccination. The Fisher exact test was used to detect significant differences.

Results:

Among 108 participants vaccinated in the 2018/2019 season (54.6% males, age 55-85 years, median 67 years), 63.9% declared they would vaccinate themselves for influenza in the next season (regardless of whether the vaccine would be refunded). However, only 25.9% took a flu shot in the 2019/2020 season; all declared a self-paid immunization. The percentage of vaccinated individuals was significantly higher among those married (p=0.002), employed (p=0.03), vaccinated in the 2017/2018 season (p=0.002) or anytime (p=0.06). There were no statistically significant differences between vaccinated/unvaccinated patients regarding age (p=0.18), gender (p=1.00), health status (p=0.82), recommendation of the vaccination by a GP/nurse (p=0.66), declaration of future vaccination (p=0.07), influenza knowledge (p=0.82).

Conclusions:

The increase in influenza vaccination uptake among Polish patients is urgently needed, particularly during the SARS- Cov-2 pandemic. Vaccination refunding in one season does not affect much the selfpaid immunization in the next season. Therefore, free-of-charge vaccinations should be universally provided to increase the uptake. Future interventions maximizing the uptake should be tailored, focusing especially on unmarried, non-working, never vaccinated patients. **Subject:** Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: vaccination, influenza vaccine, coverage, determinants, Primary Care Clinic, patients

ABSTRACT ID: 106

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4.2. Vaccine effectiveness against influenza A(H1N1)pdmo9 in older adults: Results from the I-MOVE hospital network, 2019–20 season

A. Rose 1

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Background:

Influenza A(H1N1)pdmo9, A(H3N2) and B viruses co-circulated in Europe in the 2019–20 season. The I-MOVE hospital network conducted a multicentre test-negative study in 16 hospitals in eight European countries to measure influenza vaccine effectiveness (IVE) against these subtypes among adults aged \geq 65 years.

Methods:

Hospital teams swabbed patients 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 any influenza (sub)-type; controls negative for any influenza virus. We calculated IVE adjusted for study site, date of onset; chronic conditions, sex, and age, stratified by age-group and statin use.

Results:

We included 294 A(H1N1)pdm09 cases and 1180 controls (numbers for influenza A(H3N2) and B were too small). Of 1468 (>99%) patients with this information, 493 (33%) were on statins.

Adjusted IVE against A(H1N1)pdmo9 was 49% (95%CI: 31–62) overall, 62% (95%CI: 41–75) in 65–79-year-olds, 30% (95%CI: -9–55) in those ≥80 years, 60% (95% CI: 35–76) in statin users and 41% (95%CI: 13–59) in non-users.

Conclusions:

Results suggest moderate IVE against influenza A(H1N1)pdmo9 among hospitalised patients aged ≥65 years, with higher A(H1N1)pdmo9 IVE point estimates among younger patients and among statin users, although 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 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, A(H1N1)pdm09, age-group, Europe, hospital, statins

ABSTRACT ID: 122

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4.3. Evaluation of the influenza sentinel surveillance system in primary health care in Latvia

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Background:

Regular and comprehensive evaluation of influenza surveillance systems is necessary to monitor the data quality. Information about the performance of established influenza surveillance systems at national level, including Latvia, is limited.

Methods:

We applied the ECDC's guidelines on Data Quality Monitoring and Surveillance System Evaluation to assess the performance of the influenza sentinel surveillance system in Latvia between the 2014/15 and 2018/19 seasons. The performance of the surveillance system was evaluated using seven surveillance attributes such as completeness, timeliness, stability, representativeness, simplicity and utility. For each attribute specific quantitative or qualitative indicators were described and used.

Results:

During the investigated influenza seasons data completeness for received reports was >90% by cities, seasons and weeks. All aggregated reports were timely submitted to the local and national levels, and to TESSy. The system was able to detect the beginning and end of each influenza season and correctly identify epidemic weeks as the data has a strong correlation with other system's data, e.g. number of positive specimens. The system was representative by the cities and covered 5.2% to 5.7% of all population. However, the number of tested sentinel specimens was

not representative by cities and throughout a season. The number of sentinel general practitioners (GP's) were stable by seasons and weeks. However, only one-third of GPs had participated in influenza surveillance more than one season. The system's simplicity and utility were rated as good by 66% of participated sentinel GP's.

Conclusions:

The influenza sentinel surveillance system's performance provides reliable information to characterize the seasonal influenza activity and trends in Latvia. A comprehensive evaluation of the influenza surveillance system should be performed regularly to identify major weaknesses and ensure system's stated objectives.

Subject: Surveillance

Keywords: influenza, sentinel surveillance system, surveillance evaluation

ABSTRACT ID: 228

PRESENTED BY: Oksana Martinuka / oksanamartinyk@gmail.com

Disease Group: Vaccine preventable diseases

Abstracts

5.1. Determinants of HPV-vaccination uptake over time in the Netherlands

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Background:

HPV-vaccination uptake in the Netherlands during the catch-up campaign in 2009 (birth cohorts 1993-1996) was 52%. The uptake among girls 12/13 years of age increased to 61% (birth cohorts 2000-2001) in the regular immunisation programme, but declined thereafter to 45.5% (birth cohorts 2003-2004). This study aimed to gain insight into the relationship between social, economic, cultural and political factors and the HPV-vaccination uptake and whether the influence of these factors changed over time.

Methods:

A database study was conducted to study determinants of HPVvaccination uptake on different aggregation levels: individual, postal code and municipality. The study population consisted of Dutch girls invited for HPV-vaccination in the years 2012, 2014 and 2017 (birth cohorts 1999, 2001 and 2004). Using multilevel multivariate logistic regression analysis the influence of determinants on HPV-vaccination uptake was analysed.

Results:

Results showed that having not received a MMR-vaccination, one or two parents born in Morocco or Turkey, a lower socioeconomic status, higher urbanisation level, higher road distance to the vaccination location and higher municipal voting proportions for Christian political parties or populist parties with liberal-conservative views were associated with a lower HPV-vaccination uptake. In several variables we found some small changes between the vaccination years, however, we did not find clear factors which could possibly explain the decrease in the HPV-vaccination uptake.

Conclusions:

This study gives insight into the relationship between social, economic, cultural and political factors and the HPV- vaccination uptake for public health relevance. Tailored information and/or consultation should be prepared for identified target groups that are associated with a lower

HPV-vaccination uptake. This might help to increase the HPV-vaccination uptake in the Netherlands in the future.

Subject: Surveillance

Keywords: Immunization, Human papillomavirus, Ethnic groups, Urbanization, Social class, Politics

ABSTRACT ID: 53

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5.2. Impact of pneumococcal conjugate vaccines on invasive pneumococcal disease in European children under five years of age: SpIDnet multicentre study

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Background:

During 2012-2019, ECDC funded the Streptococcus pneumoniae Invasive Disease network (SpIDnet) to strengthen the invasive pneumococcal disease (IPD) surveillance in European children. Using surveillance data from 11 sites in 10 countries, we measured the impact of pneumococcal conjugate vaccines on IPD in children <5 years old according to the vaccine(s) used in their childhood vaccination programmes: in 2018, seven sites used PCV13 (PCV13 sites), two used PCV10 and two used both vaccines (PCV10+/-PCV13 sites).

Methods:

We compared site-specific IPD incidence in 2018 with the mean incidence in the years when no conjugate vaccine was used (pre-vaccination period). We calculated the impact as (1-pooled IRR)*100 and 95% confidence interval (CI) using random-effects meta-analysis in the seven PCV13 sites and the four PCV10+/-PCV13 sites.

Results:

Compared to pre-vaccination period, IPD incidence caused by all, PCV7 and PCV10007 serotypes in the PCV13 sites decreased by 60% (95%Cl: 46%-70%), 97% (95%-98%) and 93% (76%-98%) respectively, while nonPCV13 incidence increased by 241% (136%-394%). In the PCV10+/-PCV13 sites, IPD incidence caused by all, PCV7 and PCV100007 serotypes decreased by 63% (54%-70%), 98% (94%-99%) and 83% (46%-95%) respectively, while nonPCV13 incidence increased by 109% (-7% to 368%). PCV13non10 incidence decreased by 60% (38%-74%) in PCV13 sites and increased by 10% (-66% to 27%) in PCV10+/-PCV13 sites.

Conclusions:

Both PCV10 and PCV13 childhood vaccination strategies led to similar decreases in the incidence of IPD caused by all, PCV7 and PCV10n0n7 serotypes compared with the pre-vaccination period. PCV13n0n10 incidence decreased only in PCV13 sites. Non-PCV13 IPD incidence increased in both groups of sites. IPD surveillance is crucial to measure the impact of new vaccines covering more serotypes that are likely to be introduced in the near future.

Subject: Surveillance

Keywords: Streptococcus pneumoniae, Pneumococcal Infections, Pneumococcal Vaccines, Vaccine effectiveness, Population Surveillance **ABSTRACT ID:** 68

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5.3. A qualitative analysis of caregivers' opinions about childhood vaccination and vaccination services from a Missed Opportunities for Vaccination assessment in Zimbabwe

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Background:

Globally more than one in ten children miss out on vaccinations, leaving them vulnerable to vaccine preventable diseases. In 2017, the Zimbabwe Expanded Programme on Immunization and immunization partners conducted a missed opportunities for vaccination (MOV) assessment to explore why children experience MOV, and thus inform improvements to increase immunization coverage and equity.

Methods:

Using the World Health Organization MOV strategy, we conducted focus group discussions (FGDs) with between eight to 11 caregivers of children <24 months of age at selected health facilities in 11 provinces. Caregivers were asked about satisfaction with healthcare and vaccination services, vaccination attitudes and compliance, reasons for MOV, retention of home-based records (HBRs) in their communities, and suggestions for improvement. We used a grounded theory approach to analysing the qualitative data.

Results:

Eleven caregivers FGDs were conducted. In general, caregivers had positive attitudes toward healthcare and vaccination services in Zimbabwe. However, three main themes emerged as reasons for MOV: 1) lack of caregiver knowledge about vaccination; 2) access issues, mainly in the form of long distances to vaccination sites; and 3) logistics, including issues with supply and management of vaccines and HBRs. Caregiver suggestions for improvement included a need for practical improvements to HBRs, improved management of vaccination services, as well as improved and frequent health education for caregivers.

Conclusions:

Strategies to improve access to vaccination, logistics and health education are key to reducing MOV in Zimbabwe. Therefore, strategies to address MOV should be included in long-term immunization plans and community driven, in order to ensure that gains in immunization coverage and equity are sustainable.

Subject: International health and migration

Keywords: vaccination services, missed opportunities for vaccination, childhood vaccination, qualitative methods

ABSTRACT ID: 80

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5.4. Safety profile of GSK's quadrivalent seasonal influenza vaccine in Germany, Belgium, and Spain: Enhanced passive safety assessment study in the 2019-2020 influenza season

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Background:

Seasonal influenza annually infects millions in Europe, with a higher hospitalisation risk among older adults and young children. Annual influenza vaccination is the most effective measure to reduce the risk of influenza complications. In compliance with European Medicines Agency guidance, we assessed the frequency of adverse events (AEs) after vaccination with GSK's inactivated quadrivalent seasonal influenza vaccine (IIV4).

Methods:

A passive enhanced safety surveillance (ESS) study was conducted in the 2019-2020 season in eight centres in Belgium, Germany, and Spain. Subjects ≥9 years received one GSK's IIV4 dose, while unprimed children (6 months - <9 years) received two. Subjects received diary cards to report any AEs experienced within seven days post-vaccination that were entered into an electronic database.

Results:

1,082 subjects (52% female) received GSK's IIV4, including 115 children <9 years (2 doses). The diary card return rates were 97% (Dose 1, n=1,049) and 100% (Dose 2, n=115). All subjects in Belgium and Germany were adults ≥18 years; 71% of participants in Spain were children (6 months-17 years). 39% (post-Dose 1) and 8% (post-Dose 2) reported at least one AE. Local AEs after Doses 1 and 2 include: injection-site pain (25% and 1%), swelling (6% and 2%), and erythema (5% and 1%) respectively. The most frequent general AEs were fatigue (8%), headache (7%), rhinorrhoea (5%), myalgia (5%), and pyrexia (3%) after Dose 1, and rhinorrhoea (3%), pyrexia (3%), and irritability (2%) after Dose 2. No GSK's IIV4-related serious AEs were reported during the study.

Conclusions:

The AEs in the 2019-2020 influenza season were comparable to those in the 2018-2019 GSK ESS study. The study supports GSK's IIV4 safety profile.

Subject: Surveillance

Keywords: Human Influenza; Influenza vaccines; At risk groups; Injection site reaction; Gneral adverse reaction; Europe.

ABSTRACT ID: 90

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5.5. Rubella IgG antibody levels detected in antenatal screening: a retrospective rubella seroprevalence study, Ireland 2015-2019

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Background:

Rubella vaccination has been included in Ireland's vaccination schedule since 1971 leading to the elimination of endemic rubella and the absence of immunity from natural infection. We analysed antenatal rubella IgG test results (n=134,977) to identify the proportion and trends of rubella susceptibility in pregnant women tested between 2015 and 2019 at the National Virus Reference Laboratory.

Methods:

Rubella-specific IgG-antibody levels were classified as immune, nonimmune or detected at low level according to rubella-specific IgG concentrations of ≥ 10 IU/ml, ≤ 1 U/ml and 5-9.99 IU/ml, respectively.

Cohorts of women were defined based on their birth year reflecting changes in the Irish vaccination schedule:

- Cohort 1 (1966-1979): was eligible for monovalent Rubella vaccination at age 12-14 years.
- Cohort 2 (1980-1994): was eligible for two doses of MMR vaccination, at age 15 months and 10-14 years.
- Cohort 3 (1995-2003): was eligible for two doses of MMR vaccination, at age 15 months and 4-5 years.

Adjusted odds ratios (aOR) were calculated using logistic regression.

Results:

The overall proportions of immune, non-immune and detected at low level, rubella-specific IgG results were 89.8%; 5.9% and 4.4%, respectively. Rubella immunity gradually decreased with increasing maternal birth year. Only 73.7% of the youngest cohort were rubella immune.

The odds of being rubella non-immune were 2.2 (95% Confidence Interval (CI):2.09-2.40) and 7.11 (95% CI:6.55-7.72) times higher in cohorts 2 and 3 respectively, compared to cohort 1.

Conclusions:

This study identifies an increase over time in the proportion of pregnant women who are rubella susceptible in Ireland. This highlights the need to enhance rubella awareness and additional measures are required to ensure women are fully vaccinated before pregnancy. More in depth analysis should identify at risk groups.



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

Keywords: Rubella, Antenatal screening, MMR vaccination, Congenital rubella syndrome

ABSTRACT ID: 98

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5.6. Seroprevalence of meningococcal serogroup C bactericidal antibodies in the Portuguese population, more than a decade after vaccine introduction

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Background:

The incidence of invasive meningococcal disease due to serogroup C (MenC) decreased in Portugal since the introduction of the conjugate vaccine (MCC) in 2001 (included in the National Immunisation Plan in 2006). Up to date, studies on the prevalence of serum bactericidal antibodies (SBA) against MenC had not been performed in the Portuguese population.

Methods:

We evaluated SBA levels against MenC in the population aged 2-65 years who participated in the 2015/2016 National Serological Survey, in order to identify the protected fraction of the population. SBA titres \geq 8 were considered protective.

Results:

31.1% of the 1500 individuals studied were protected against MenC. The geometric mean titre was 6.5. The proportion of seroprotected was particularly small in children 2-4 years (<16%) who underwent single dose vaccination at 12 months of age (vaccination strategy since 2012), and young adolescents 10-14 years (<24%) who were vaccinated with 3 doses at 3, 5 and 15 months of age (2006-2012 strategy) or with a single dose in a catch-up campaign (2006/2007) at 1-4 years of age. The proportion of seroprotected was higher (44.7% to 53.5%) in adolescent and young adults (15-24 years), resulting from vaccination during the catch-up campaign at 5-15 years of age. The highest protection rates were observed when the vaccine was administered during adolescence.

Conclusions:

The small fraction of population seroprotected, combined with the waning effect of the antibody response over time, known from the literature, may indicate that the Portuguese population will become progressively more exposed to the risk of infection. Taking in consideration our results, we recommend a variation of the vaccination strategy introducing a booster dose of the MCC vaccine during adolescence.

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

Keywords: Neisseria meningitidis serogroup C, Meningococcal disease, Seroprevalence, Serum bactericidal antibodies, MenC conjugate vaccine, National Serological Survey, Portugal

ABSTRACT ID: 104

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5.7. Meningococcal-C-Cluster in Bavaria, Germany, in 2019 – possibilities and needs for control and prevention measures

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Background:

Between March-August 2019, a cluster of invasive meningococcal disease (IMD), caused by serogroup C with identical isolates based on genome sequencing, occurred in Southern Bavaria, Germany. Vaccination is recommended for children ≥1 year since 2006, close contacts of cases and people at increased IMD-risk. Here, we describe the cluster and applied control measures.

Methods:

We analysed the outbreak regarding time, place and demography. We estimated incidences considering different geographical dimensions and age groups in order to identify populations at highest risk and target groups for prevention (extended vaccination recommendation).

Results:

Within 6 months, five individuals from two adjacent counties developed IMD; three 18–21-year-olds, one 13-year-old child, and a 56-year-old contact person. All were unvaccinated. Extensive investigations failed to identify an epidemiological link between four cases, pointing toward community circulation of the pathogen. Based on the three young adult cases, we determined an incidence of 39.5/100,000 inhabitants for 15–24 year-olds in the affected area (approximately 7,600 persons). In a vaccination campaign from mid-September to the end of October 2019, addressing this group, 1,257 people got vaccinated. Additionally, children and adolescents were requested to catch up meningococcal vaccination. One year after the last case, no further cases were assigned to the cluster.

Conclusions:

All cases might have been prevented by following existing vaccination recommendations. Health workers, especially general practitioners

and paediatricians need to promote vaccination of children and catchup vaccinations in older children, while public health officials should promote vaccination of close contacts. In case of unusual occurrence of IMD, extended vaccination recommendations for defined risk groups may help increase vaccination coverage and prevent further IMD cases.

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

Keywords: Cluster, outbreak, invasive meningococcal disease, vaccination recommendation, prevention and control measures
ABSTRACT ID: 126

Ab31144110.120

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5.8. Quantifying measles transmission in healthcare settings in England: Analysis of measles surveillance data 2017-2019

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Background:

In August 2019, the UK's measles elimination status was revoked due to a resurgence of cases in 2017-18. Measles is readily transmitted in healthcare facilities without proper triage and isolation, particularly when healthcare contacts are unvaccinated infants and patients with underlying medical conditions. We quantified the extent and characteristics of healthcare-acquired (HCA) measles in England to inform control measures.

Methods:

We analysed routine surveillance questionnaires for all laboratoryconfirmed and probable (clinically compatible/epidemiologicallylinked) measles cases reported in England in 2017-2019. Cases were linked to national case management data (HPZone) and case notes manually trawled to derive most likely transmission route. We present the proportion of HCA cases and their demographics, MMR history, and healthcare worker (HCW) status.

Results:

There were 2,550 measles cases in England in 2017-2019. Of those with a known transmission route, 9.9% were likely HCA (190/1916). Among them, 92.1% were exposed in hospital settings (164/178), 44.7% were HCWs (85/190), and 66.3% unvaccinated (120/181). More than half (55.8%, n=120) of unvaccinated cases were aged >5 years and eligible for vaccination. Of these, 30 were HCWs, who themselves made up 36% of all 82 HCW cases with vaccine history. These unvaccinated HCW cases were older than non-HCW unvaccinated adult cases (median age 40.0 vs 30.6, p=0.004).

Conclusions:

Measles transmission in healthcare settings accounts for around 10% of reported measles cases. HCWs are an important subgroup, particularly those in older birth cohorts missed by routine measles vaccination. We recommend campaigns to increase MMR uptake among HCWs alongside the systematic collection and reporting of HCW MMR vaccination status to interrupt transmission in this setting.

Subject: Surveillance

Keywords: Measles, MMR, Nosocomial, Healthcare acquired, Occupational health, Health records

ABSTRACT ID: 151

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5.9. The assessment of smartphones application reminders on vaccination series completion for a follow-up visit – A non-randomized trial at the Zaatari refugees camp, Jordan

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Background:

We evaluated the effectiveness of a smartphone application in improving children vaccination uptake at the Syrian refugees camp in Zaatari in north of Jordan. The app delivers three automated reminders prior to the vaccine appointment and two messages post the appointment; in case of a missed appointment.

Methods:

A non-randomized trial, during March-December 2019 at three vaccination clinics. The study included refugees living at the camp, own an Android smartphone and have one newborn that require between one and four first vaccination doses. We compared both study groups for returning back to one follow-up visit, using Kaplan-Meier survival analysis. Finally we identified factors associated with coming back within one week to the appointment using logistic regression analysis.

Results:

We recruited 935 babies (n=471; 50.4% in the intervention group, both study groups were similar at baseline). The majority of mothers were literate (94.2%) and median age 24. The majority of the babies had a vaccination card (n=878, 94%). One quarter (26%) of the intervention group came back within one week (versus 22% for the control group); When it comes to lost-follow-up, 22% and 28% did not have a history of returning back (intervention and comparison groups respectively, p=0.06) (Risk reduction: 9%). The Kaplan-Meier Survival Analysis showed a statistically significant progressive reduction in the duration of coming back late for the follow-up vaccine visit. The adjusted logistic regression analysis showed that fathers deciding on vaccination remained statistically significant (adjOR 1.8; 95%Cl 1.2; 2.5).

Conclusions:

Educating fathers about the importance of vaccination is important. The app can be used as a reminder for parents to come back on time for their children's vaccine follow-up visits.



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

Keywords: Vaccine preventable diseases, refugees, mHealth, e-health, Jordan, Syria

ABSTRACT ID: 164

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5.10. Assessment of Missed Opportunities for Vaccination among children below 24 months in Zimbabwe, 2017

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Background:

A missed opportunity for vaccination (MOV) occurs when vaccine-eligible persons do not receive vaccine(s) they were due during a health facility encounter. Zimbabwe conducted a MOV assessment to estimate the magnitude and explore possible reasons for MOV, in order to improve vaccination coverage and equity.

Methods:

Using the World Health Organization MOV strategy, the assessment was conducted in 22 districts during 15-23 November 2017. Data were collected by conducting health facility exit interviews with caregivers accompanying children below 24 months. A knowledge, attitude, practice (KAP) survey was self-administrated to healthcare workers (HCWs). We estimated the magnitude of MOV using only documented vaccination dates from records, and analysed possible reasons for MOV.

Results:

Of the 493 children with vaccination documentation, 60% (295/493) were vaccine-eligible on the day of the assessment. Of these children, 25% (73/295) had a MOV. Among 64 children attending for a non-vaccination visit, 66% (n=42) had a MOV, whilst 92% (34/37) of children aged 12-23 months had a MOV. With multi-dose vaccine series, the prevalence of MOV increased with subsequent doses and timeliness of vaccination decreased. Among 312 HCWs interviewed, 36%; (113/312) reported their vaccine knowledge was insufficient. Only 35% (109/308) of HCWs identified the correct contraindications against vaccination. Most HCWs were concerned about adverse effects following immunization (71%; 220/312) and believed that parents' negative beliefs (63%; 195/311) and distance from vaccination sites (65%; 203/311) were the main determinants for incomplete childhood vaccination.

Conclusions:

The MOV assessment in Zimbabwe highlighted areas for improvement that could increase vaccination coverage and equity. Interventions to reduce MOV should include providing training to HCWs and improving vaccination documentation checks, irrespective of the reason for visit or age of the child. Subject: International health and migration

Keywords: Vaccination; Health equity; Caregivers; Child; Health Personnel; Zimbabwe

ABSTRACT ID: 170

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5.11. Outbreaks of mumps genotype G viruses: clusters associated with multiple exposures in the Netherlands, October 2019 to March 2020

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Background:

From October 2019–March 2020, several clusters of mumps cases were identified in the Netherlands. Our objective was to describe clusterassociated mumps virus transmission using epidemiological and molecular information in order to help future mumps prevention efforts.

Methods:

An epidemiological cluster includes ≥2 mumps cases with an epidemiological link to a laboratory-confirmed mumps case. A molecular cluster includes ≥2 mumps cases with identical mumps virus sequences. Cases with a symptom onset date between 1 October 2019–31 March 2020 reported through the National Notifiable Diseases Surveillance System were included. We described epidemiological and clinical characteristics of mumps virus genomes (2270 nucleotides). Correlations between epidemiological and molecular information were investigated.

Results:

In total, 102 mumps cases were notified (90% laboratory-confirmed, 10% epidemiologically linked). Fourteen epidemiological clusters were identified containing 2–12 cases. Sequence data was obtained from 50 mumps genotype G viruses. Twelve molecular clusters were identified containing 2–13 cases, dispersed geographically and timewise. Twenty-one (30%) of 71 cluster-associated cases were identified using epidemiological information, 25 (35%) using molecular surveillance, and 25 (35%) using both. Combined information redefined 7 epidemiological clusters into 2 distinct molecular clusters. The first lasting for 14 weeks, the other for 6. Additionally, 1 molecular cluster was detected, linked by geography and time but without an epidemiological link.

Conclusions:

Both epidemiological and molecular information indicated ongoing mumps virus transmission for extended time periods. Sequence analysis provided valuable insights into epidemiological clustering. Our

findings illustrate the importance of combined information in cluster identification. If combined epidemiological and molecular information is available real- time, this would improve outbreak detection and generate further insight into mumps transmission.

Subject: Surveillance

Keywords: MMR; mumps; surveillance; genotype G viruses; the Netherlands

ABSTRACT ID: 171

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5.12. Molecular and epidemiological characterisation of toxigenic and non- toxigenic Corynebacterium diphtheriae and Corynebacterium ulcerans isolates identified in Spain from 2014 to 2019

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Background:

This study examines the microbiological and epidemiological characteristics of toxigenic and non-toxigenic Corynebacterium isolates submitted to the national reference laboratory in Spain, between 2014 and 2019 in order to describe the current situation and evaluate the need for improved diphtheria surveillance.

Methods:

We performed a descriptive analysis extracting the epidemiological information from the Spanish Surveillance System. The isolates were characterized using phenotypic and molecular methods including whole genome sequencing and ad hoc core genome MLST.

Results:

Thirty-nine isolates were analysed. Thirty-five were identified as C. diphtheriae (six toxigenic) and four as C. ulcerans (three toxigenic). One C. diphtheriae isolate was identified as non-toxigenic tox genebearing. Ages of patients ranged from one to 89 years. MLST identified 28 sequence types (STs) of which seven were described for the first time in Spain. WGS analysis showed that 10 isolates, including three toxigenic isolates, harboured a variety of antibiotic resistance genes in addition to the high prevalence of penicillin resistance phenotypically demonstrated. Phylogenetic analysis revealed one cluster of isolates from family members. Epidemiological data on non-toxigenic isolates was scarce and risk information was only available for toxigenic isolates (9/39); three patients reported recent travels to endemic countries

and three had contact with cats/dogs. One unvaccinated child with respiratory diphtheria had a fatal outcome.

Conclusions:

WGS analysis showed a high genetic variability between the strains. The study identifies the need for an improved surveillance system and reporting mechanism with more comprehensive and timely data including cases of non- toxigenic diphtheria in the disease surveillance as they could gain or recover toxin production capacities.

Subject: Surveillance

Keywords: Diphtheria, Corynebacterium, Diphtheria Toxin, Corynebacterium Infections, Microbiology, Epidemiology, Spain

ABSTRACT ID: 205

PRESENTED BY: Andreas Hoefer / ahoefer@isciii.es



Disease Group: COVID-19

Abstracts

6.1. 'In-action' evaluation of the Italian COVID-19 surveillance system

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Background:

In-action evaluation is a method for continuous quality improvement of surveillance systems. We used this method to improve the national COVID-19 surveillance system in Italy during the epidemic. The surveillance system, coordinated by Istituto Superiore di Sanità, collects data on laboratory confirmed SARS-CoV-2 infections through a web-based platform. We measured completeness, timeliness, and concordance of the surveillance system before and after introduction of our intervention.

Methods:

Data reported by 21 Regions/Autonomous Provinces were subject to an in-action evaluation and results were sent back weekly to regional focal points. When minimum quality requirements were not met, systematic telephone exchanges with Regional focal points solved technical issues and misunderstandings. Completeness was assessed for 5 key variables: date of onset, date of diagnosis, outcomes, case-allocation and clinical status. Timeliness was calculated as time between date of diagnosis and notification. We assessed concordance by comparing individual notifications with aggregated number of cases communicated daily to Civil Protection/Ministry of Health (gold standard). Here we report results of the first 2 months of activity (21 May-21 July) after introducing in-action evaluation.

Results:

Completeness of onset date, diagnosis date, outcomes, allocation, and clinical status were: 82.4%, 98.9%, 89.9%, 73.3% and 72.5% for cases in the first 3 months of Covid-19 surveillance in Italy. After introducing in-action evaluation, this improved to 93.2%, 99.9%, 97.3%, 77.2% and 96.8% in the subsequent 2 months. The median delay between diagnosis and notification improved from 5 to 4 days. The concordance level improved from 90.43% to 99.98%.

Conclusions:

In-action evaluation provides continuous feedback on data quality to regional focal points, allowing for rapid follow-up and problem solving.

This approach was successful in improving the quality of COVID-19 surveillance in Italy.

Subject: Surveillance

Keywords: Covid-19, Surveillance, In-action evaluation

ABSTRACT ID: 40

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6.2 Hospitalised COVID-19 patients in Malta; a single-centre restrospective study of the first wave

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Background:

This is a retrospective, single-centre study on all adult COVID-19 patients hospitalised in Mater Dei Hospital (MDH), Malta's only acute general teaching hospital, during the first wave of the pandemic, from 7th March to 24th April. It is a descriptive study in which comparisons have also been made between patients having mild disease and those with moderate-severe illness.

Methods:

Data was collected on demographics, comorbidities, laboratory and clinical parameters, treatment, admission to intensive care unit (ICU) and 30-day mortality.

Results:

Out of 447 cases of COVID-19, 89 adults were hospitalised at MDH. The average age was 50.3 years (S.D. 20.2 years) and sixty patients (67.4%) were males. The commonest presenting symptoms were cough (48.3%) and fever (39.3%), with 18.0% being asymptomatic and diagnosed incidentally during screening for elective procedures. Nineteen patients (21.3%) had moderate-severe disease (SpO2 <93% and/or bilateral pneumonia on imaging). Of these, 7 patients (7.9%) required admission to the ICU. Patients with moderate-severe disease had lower lymphocyte and eosinophil counts, and higher C-reactive protein levels on admission when compared to those with milder disease. All patients with moderate-severe disease were treated with hydroxychloroquine/azithromycin combination, in line with evidence available at the time. Patients with moderate-severe disease had significantly longer hospital stays than those with mild disease (p<0.001). Two of the latter died secondary to unrelated medical conditons.

Conclusions:

Patients with COVID-19 admitted to MDH generally had a good outcome, especially those with moderate-severe disease who all survived to 30-day follow up. A low threshold for admission to hospital and early stratification of disease severity with prompt referral to ICU are likely to have played an important role in attaining these positive outcomes.

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

Keywords: COVID-19, SARS-CoV-2, Malta, hospitalised, 30-day mortality **ABSTRACT ID:** 44

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6.3. Incidence and mortality for COVID-19 outbreaks in English care homes, April- May 2020

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Background:

As an identified risk group we aimed to assess incidence and outcomes of COVID-19 in English care home residents and staff.

Methods:

We collected individual (co-morbidities, exposure to visitors/hospitals) and care home (control measures, capacity) data from 95 care homes with suspected COVID-19 outbreaks (2+ cases with continuous cough/ temperature) between 6-9 April 2020. Initial data collection occurred 5 to 38 days (median 13 days) from first case onset. Case outcomes (recovery/ death) were ascertained one month after recruitment

Results:

A median of 19% (IQR 11%-30%) of residents and 7.8% (0%-21%) of staff per care home had suspected or confirmed COVID-19. The symptomatic incidence rate among residents was 1.0 cases (range 0.2-6.1 cases) per 100 person-days. One-fifth of resident cases were hospitalised before symptom onset (19%, 54/291). The resident case fatality risk (CFR) was 46% (176/386, 95% CI 41%-51%); higher among residents with dementia (52% vs 36%, p=0.0029) and cancer (63% vs 43%, p=0.012). Median time from symptom onset to death among fatal resident cases was 8 days (IQR 5-13 days). Recovery, defined as symptomatic improvement, was longer for residents in nursing than residential homes (18 vs 8 days p<0.001, Wilcoxon rank test), and with respiratory disease (21 vs 8.5 days, p<0.016). 97% of homes reported enhanced cleaning, 94% case isolation, 85% facility closure and 82% shared space restrictions. 20% (51/259) of residents received visitors in the 14 days before onset.

Conclusions:

In the early phase of the pandemic, residents of English care homes with COVID-19 outbreaks experienced high morbidity and mortality. Specific comorbidities were associated with higher fatality and longer recovery. Targeted surveillance, regular universal testing and prioritising potential vaccination will support an effective response to future outbreaks.

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

Keywords: COVID-19, Care homes, Pandemic, severe acute respiratory syndrome coronavirus 2, comorbidity, Frail elderly

ABSTRACT ID: 54

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6.4. Safety and Efficacy of Antiviral Drugs for the Treatment of Patients with SARS-CoV-2 Infection: A Systematic Review and Meta-analyses

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Background:

The objective of this systematic literature review (SLR) and metaanalyses is to assess the safety and efficacy of the antiviral drugs that have been proposed to treat COVID-19. The multiple uncertainties about the COVID-19 and a large amount of ongoing research make it necessary to provide the scientific community with high-quality, timely, and living systematic reviews of the relevant evidence.

Methods:

The literature search was conducted in PubMed, EMBASE, Medrxiv, Cochrane Central Register of Controlled Trials (CENTRAL), and LitCOVID databases from inception to 27-Aug-2020 to find articles providing information on the efficacy and safety of antiviral drugs in patients with COVID-19. Risk Ratios (RRs) with corresponding 95% confidence intervals (CIs) were pooled using random-effects models.

Results:

A total of 10 studies were identified which fulfill the inclusion criteria. Patients taking antivirals had 26% less risk of having a severe adverse event (SAE) compared to controls (RR, 0.74, Cl:0.62 to 0.89, P=0.002). Clinical improvement at day 14 was observed among the cases treated with antivirals compared to the control group (RR 1.24, Cl: 1.00 to 1.53 p=0.05).

Conclusions:

There is evidence that Remdesivir and LPV/r reduces the hospital length of stay and that patients to which antivirals were administered had less SAE and improvement when compared to patients not prescribed with antivirals. Due to a lack of power and the quality of the studies, it was not possible to determine which antivirals have a greater risk-benefit balance, and therefore the optimal approach to antiviral treatment is still uncertain.

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

Keywords: Antiviral agents; COVID-19; SARS-CoV-2; meta-analysis; systematic literature review.

ABSTRACT ID: 110

PRESENTED BY: Zuleika Aponte Torres / zullybort@gmail.com

6.5. Epidemiological characteristics of the COVID-19 outbreak in a secondary hospital in Spain

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Background:

On December 31, 2019, the authorities of the People's Republic of China alerted of the appearance of a new type of virus of the Coronaviridae family, called SARS-CoV-2. As of June 30, Spain is among the most affected countries with 248.970 confirmed cases and 28.346 deaths. Our aim is to describe the cases of COVID-19 during the first four months of the epidemic at Infanta Sofía University Hospital, San Sebastián de los Reyes (Madrid), a public secondary hospital.

Methods:

Retrospective descriptive study of cases that met COVID-19 clinical diagnosis criteria or had a positive PCR test during the period from February 27 to June 29, 2020. A description of demographic variables, hospital and ICU stay, nursing home residents, country of birth, mortality and distribution of the epidemiological curve was performed.

Results:

1828 confirmed cases were attended at our centre, of whom 64,4% were hospitalised. 5,6% were admitted to ICU. 51,6% of all confirmed cases were male. The median age was 64,4 years. 15,1% were nursing home residents. 18,3% of all confirmed cases were of Latin American origin of which 7,2% were admitted to the ICU. Overall case fatality was 14,7%. Significant differences were observed among PCR positive testing cases and clinically diagnosed cases where PCR positive had different basal characteristics and needed more ICU admission (6,7% vs 3,4%). We observed a biphasic epidemiological curve.

Conclusions:

60 to 79 year old males were admitted and deceased more often than women. 64,4% of all our confirmed cases were hospitalised and 5,6% were admitted to the ICU. Mortality reached 14,7%. People of Latin American origin and PCR positive cases were admitted more often to the ICU.

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

Keywords: Pandemics, coronavirus infections, SARS-CoV-2, Epidemiology, infection control

ABSTRACT ID: 120

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6.6. Low secondary attack rate of COVID-19 in the Republic of Cyprus from a nationwide contact-tracing strategy during March-May 2020

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Background:

Contact tracing is an essential public health tool in the effort to break community transmission. We investigated the secondary attack rate (SAR) and transmission networks among COVID-19 cases in Cyprus.

Methods:

We used case-based surveillance data of COVID-19 confirmed cases, between March 9-May 3, 2020.

Primary cases were individuals who tested positive for SARS-CoV-2 and had the earliest onset date in Cyprus or individuals with travel history in the previous 14 days, without close contact with a confirmed case. Secondary cases were individuals with confirmed close contact with a known primary case.

We calculated SAR and 95%CI of COVID-19 by dividing the number of confirmed secondary cases by the total number of close contacts of the primary cases.

We used Cytoscape v3.8.0 to perform network analysis.

Results:

During the study period, 870 cases were confirmed; origin of infection was known for 769 (88.4%) cases, of which 108 (14%) were imported, 87 (11.3%) primary and 574 (74.6%) secondary. Overall 119 primary/ imported cases reported 616 close contacts (mean number close contacts: 5.2±6.1). The SAR was 12% (95%CI: 9.6-14.8%). Notably, two cases infected 7 and 11 individuals, respectively.

Network analysis revealed that 531 cases (61%) were detected in 40 independent networks with > 4 individuals, 24 triads and 53 dyads, while 339 (38.9%) cases could not be linked with any other confirmed case. The largest network consisted of 50 individuals from a community cluster, two independent families and an intrahospital transmission cluster.

Conclusions:

In Cyprus, SAR estimate is similar to what reported elsewhere among household contacts. Network analysis suggests absence of widespread community transmission, achieved through timely application of strict preventive measures, allowing the control of the COVID-19 epidemic.

Subject: Surveillance

Keywords: Secondary attack rate, Network analysis, Contact-tracing ABSTRACT ID: 124

ADJIKACI ID: 124

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6.7. Epidemiological characteristics of COVID-19 cases in non-Italian nationals diagnosed in Italy: results from the national integrated surveillance system

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Background:

International literature suggests that disadvantaged groups could be at higher risk of morbidity and mortality from SARS- CoV-2 infection due to poorer living/working conditions and barriers to healthcare access. Yet, to date, there is no concrete evidence of this disproportionate impact on non-national individuals, including international migrants, short- term travellers, and refugees.

Methods:

We analysed data from the Italian integrated surveillance system of all COVID-19 confirmed cases diagnosed from the 20th of February to the 19th of July 2020. We used multilevel negative-binomial regression models to compare attack rates, case-fatality rates and rates of admission to hospital and intensive care unit (ICU) between the Italian and non-Italian nationals. The analysis was adjusted for differences in sociodemographic characteristics and differences in the week and region of diagnosis.

Results:

We analysed 213,180 COVID-19 cases, including 15,974 (7.5%) non-Italian nationals. We found that, compared to Italian cases, non-Italian cases were diagnosed at a later date and were more likely to be hospitalised [(adjusted relative risk (ARR)=1.39, 95% confidence interval (CI): 1.33-1.44)] and admitted to ICU (ARR=1.19, 95% CI: 1.07-1.32), with differences being more pronounced in those coming from countries with lower HDI. We also observed an increased risk of death in non-Italian cases from low-HDI countries (ARR=1.32, 95% CI: 1.01-1.75).

Conclusions:

A delayed diagnosis in non-Italian cases could explain their worse outcomes compared to Italian cases. Ensuring early access to diagnosis

and treatment to non-Italians could facilitate the control of SARS-CoV-2 transmission and improve health outcomes in all people living in Italy, regardless of nationality.

Subject: Surveillance

Keywords: COVID-19; migration, health inequalities, immigrants, case fatality

ABSTRACT ID: 125

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6.8. Risk of symptomatic COVID-19 due to aircraft transmission: a retrospective cohort study of contact-traced flights during England's containment phase

P. Blomquist 1

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Background:

As air travel resumed post-lockdown during the COVID-19 pandemic, knowledge gaps remained regarding SARS-CoV-2 transmission on flights. We conducted a retrospective cohort study using contact tracing data to estimate risk of acquiring symptomatic SARS-CoV-2 on aircraft, to inform contact tracing and infection control efforts.

Methods:

We identified co-passengers of infectious passengers on 18 Englandbound flights from European cities up to 12/03/2020, using manifests received for contact tracing. Infectious passengers were laboratoryconfirmed cases with symptom onset from 7 days before to 2 days after the flight. Possible aircraft-acquired cases were laboratory-confirmed with onset 3-14 days post-flight with no known non-flight exposure to infectious passengers. Manifest data was merged with the national case management dataset (identifying cases, onset dates, contact tracing status) and the national COVID-19 linelist. Contact tracing notes were manually reviewed to identify non-flight exposures. We calculated attack rates (ARs) among all co-passengers and within subgroups, including by distance from the infectious case and number of infectious cases onboard.

Results:

There were 55 infectious passengers and 2,313 co-passengers, of which 2,221 co-passengers had only known flight exposure. Five possible aircraft-acquired cases were identified, representing ARs of 0.2% (95%CI 0.1-0.5) among all flight-only contacts and 3.8% (95%CI 1.3-10.6) among flight-only contacts sat within a two-seat radius and contact- traced. The AR among 92 co-travellers with known non-flight exposure to infectious cases was 13.0% (95%CI 7.6-21.4%). There were insufficient numbers to assess differences between subgroups.



Conclusions:

We conclude that risk of symptomatic COVID-19 due to transmission on short to medium-haul flights is likely low, and recommend prioritising contact-tracing of close contacts and co-travellers where resources are limited. Further research on risk on aircraft is encouraged, particularly with larger sample sizes.

Subject: International health and migration

Keywords: COVID-19, Aircraft, Transmission, Epidemiology

ABSTRACT ID: 149

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6.9. The risk of SARS-CoV-2 transmission by infected general practitioners (GPs): a cohort of contacts from a GP practice in Nuremberg, Germany, February – March 2020

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Background:

Early March 2020, two GPs were infected with SARS-CoV-2 in Nuremberg, Germany. Before symptoms onset, both GPs had been attending to patients; GP1 also while being symptomatic, but only until laboratory confirmation of SARS- CoV-2 infection.

Methods:

We conducted a retrospective cohort study of all GP-patient-contacts to analyse the type of contact and incidence rate ratio (IRR) of SARS-CoV-2 infection within 14 days after exposure. Case definitions were based on clinical criteria (onset of ≥ 2 COVID-19-symptoms = possible; when including pneumonia, anosmia, ageusia or dysgeusia = probable) and laboratory confirmation (SARS-CoV-2 PCR-positive = confirmed).

Results:

We interviewed 83/131 (63%) contact-persons; 56 (68%) were female, median age was 45 years [IQR 7-87] and 54 (65%) reported underlying condition(s). Due to multiple GP visits by the same contact-person, 89 contact-events were included. Median contact-event duration was 10 minutes [IQR 10-20]. GPs wore face masks during 31/89 contact- events (35%); more often during contact-events with a physical examination (25/56) compared to without examination (6/32; p-value=0.046).

We identified 22 (27%) cases: 17 (21%) possible, 3 (4%) probable and 2 (2%) confirmed. All cases had contact with a GP when they did not wear a mask or when contact was >10 minutes (p-value=0.018). Overall, contact time >10 minutes (IRR=1.5, 95%Cl=0.5-6.6) or contact during the pre-symptomatic period (IRR=1.3, 95%Cl=0.5-4.5) showed a trend towards increased risk. The trend for wearing a face mask was towards a protective effect (IRR= 0.85, 95%Cl=0.3-2.05).

Conclusions:

SARS-Cov-2 transmission was observed in a GP-patient-setting. The risk of transmission was reduced when GPs wore face masks and when contacts were short. Our findings support the use of face mask for GPs, and reduction of contact time, to minimize risk of SARS-CoV-2 transmission.

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

Keywords: SARS-CoV-2,transmission,health-care setting,GP,face mask ABSTRACT ID: 163

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6.10. Gender-specific differences in perception of quarantine of SARS-CoV-2 exposed repatriates from Wuhan, China, to Germany, February 2020

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Background:

After declaration of a PHEIC 01/2020, 124 Germans and their families were repatriated from Wuhan, China, and quarantined in army barracks in Rhineland-Palatinate. This study aims at improving state-run quarantines by analysing the sex-specific perception of communication, wellbeing, and social responsibility of adult repatriates.

Methods:

On day 11 of the quarantine, we distributed a self-administered Likertscale questionnaire and analysed associations between questions by gender using Spearman Rank correlation and tested differences between sex-specific correlation coefficients.

Results:

Of 78 adults, 66 (85%) responded; 62/66 (94%) felt safe: 27/30 (90%) female and 35/36 (97%) male. "Feeling safe" was associated with being less "afraid of infection during quarantine" among women (rho=0.6, p=0.0005), but not in men (rho=0.06, p=0.7), difference between women and men (p=0.015).

22/66 (33%) felt bored, 9/30 (30%) female and 13/36 (36%) male. Among women, "feeling bored" correlated with "fear of social isolation", "job insecurity", "financial distress", "fear of stigmatisation", and "wish for psychosocial care" (rho ranging from 0.39 to 0.66, all p<0.03). Among men, however, "feeling bored" correlated negatively with "fear of social isolation" (rho= -0.32, p=0.06). All above mentioned correlation coefficients were different between men and women (all p<0.04).

"Financial distress" correlated with "wish for psychosocial care" in women (rho=0.65, p=0.0001) only (men: rho=0.06, p=0.7; difference between women and men p=0.006).

"Fear of stigmatisation" correlated with "fear of social isolation" for both sexes (rho=0.68, p<0.0001), confirming internal validity.

Conclusions:

Repatriates of both sexes perceived the state-run quarantine as safe. Quarantine-related fears and concerns were strongly associated with gender and being bored. Gender-tailored communication and activities should be considered for increasing wellbeing in state-run quarantine.

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

Keywords: Quarantine, perception, repatriation, SARS-COV-2, evacuation, pandemic, gender, sex

ABSTRACT ID: 166

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6.11. SARS-CoV-2 wastewater surveillance as part of a national COVID-19 control strategy in Ireland

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Background:

By 07/09/2020 Ireland (population 4.9 million) reported 30,080 total confirmed cases of COVID-19 infection. National testing protocol comprises testing of symptomatic individuals, close contacts of confirmed cases, and mass targeted testing of at-risk groups e.g.,

meat-processing plants. However, many other asymptomatic cases are not detected, limiting surveillance strategies that inform Public Health policy. SARS-CoV-2 wastewater surveillance has recently emerged as a novel tool for detecting early GI viral shedding from symptomatic and asymptomatic cases, notably up to 4-10 days in advance of case detection by standard testing protocols. Following the easing of national restrictions COVID-19 activity surged from August 2020. We describe the first Irish experience of using SARS-CoV-2 wastewater surveillance to detect increased COVID-19 activity.

Methods:

From June 2020 24-hour influent samples from 3 wastewater treatment plants in the East of the country were collected; collective capacity approx. 2.1 million population equivalent. Following ultrafiltration, RNA extraction and a validated SARS-CoV-2 RT-qPCR assay targeting nucleocapsid gene (regions N1, N3) and envelope protein (E) markers were performed once weekly. Positive results were confirmed by sequence analysis. National COVID-19 datasets from Health Protection Surveillance Centre (HPSC) were reviewed.

Results:

On 17thAugust 2020 all 3 markers tested positive in all 3 wastewater plants for the first time. This corresponded with a subsequent surge in detection/notification of confirmed cases of COVID-19 infection in the areas covered by the wastewater treatment facilities.

Conclusions:

This proof of concept study highlights the utility of SARS-CoV-2 wastewater surveillance as an early warning tool for increased COVID-19 activity. An optimal strategy for sampling, reporting and rapid use of these surveillance data to inform specific Public Health actions for COVID-19 control is critical and remains to be determined.

Subject: Surveillance

Keywords: SARS-CoV-2, Wastewater surveillance, Infection Prevention and Control, COVID-19, Pandemic, Public Health

ABSTRACT ID: 186

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6.12. SARS-CoV-2 seroprevalence among inmates of a penitentiary complex during a COVID-19 outbreak – Federal District, Brazil: a cross-sectional study

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Background:

A COVID-19 outbreak started in a Penitentiary Complex in the Federal District, Brazil, on April 1, 2020. By the end of June, over 1 000 cases had been confirmed among the more than 13 000 inmates. An outbreak investigation was conducted, which raised the hypothesis that the



proportion of infected inmates was higher than the captured cases by local health teams. The objective of this study was to estimate the SARS-CoV-2 antibody prevalence among inmates.

Methods:

A cross sectional study was performed in two stages, with the use of IgM/ IgG rapid tests between June and July 2020. A stratified sampling was conducted among the four prison units within the penitentiary complex, and 485 inmates were randomly selected to be interviewed and tested. Those with negative results were tested again 21 days later. Complex sampling and analysis were considered for data processing, and both prevalence and incidence were adjusted considering the overall test sensibility (90.6%) and specificity (99.2%).

Results:

A total of 460 inmates were enrolled in the study, and by the end of the first phase the seroprevalence was 57.0% (95%Cl: 51.9-62.0). Among the positive cases, 75.3% were symptomatic, and the most reported symptoms were fever, changes in taste and smell, and headache, which were present in 63.9% of all symptomatic patients. In the second stage, there was an incidence of 10.5%, and the overall seroprevalence was 62.3% (95%Cl: 57.2-67.3).

Conclusions:

The study demonstrates that in overcrowded populations, the SARS-CoV-2 can be capable of rapidly infecting great part of the population. Recommendations include maintaining biosecurity protocols, including the use of personal protective equipment, constant sanitation of public spaces, and case isolation.

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

Keywords: COVID-19, severe acute respiratory syndrome coronavirus 2, outbreak, prisons, seroepidemiologic studies, Brazil

ABSTRACT ID: 188

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6.13. COVID-19 outbreak among employees of a meat-processing facility in the Netherlands

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Background:

SARS-CoV-2 emerged in December 2019 and reached pandemic levels by March 2020. Due to wide-spread virus circulation clusters were seen in workplace environments. Hereby, we describe a part of the COVID-19 outbreak investigation in a meat-processing facility in the Netherlands in June 2020.

Methods:

We performed a cross-sectional study aiming to assess the situation after control measures' implementation. A random sample among the approximately 600 employees working in cooled areas were interviewed (questionnaires in 5 languages) and sampled (oro-nasopharyngeal swabs) on a single day at two timepoints. Any participant with \geq 1 swab testing positive for SARS-CoV-2 RNA was defined as laboratory-confirmed case. Environmental samples were also collected inside the facility on the same day.

Results:

A total of 76 employees (97% questionnaires response rate, none using Dutch) participated in the study. Twenty-seven cases were laboratory-confirmed (35.5%), all provided questionnaires. Only four employees (two cases) reported mild symptoms. SARS-CoV-2 RNA was detected in both samples in 6 cases (22%), whereas 21 cases (78%) had one sample testing positive, mostly at the beginning of the shift. The mean Ct values for all samples were >30 (range 29.69-negative), none could be sequenced. A total of 6.7% (7/105) of the environmental samples were positive (Ct>38).

Conclusions:

Approximately one third of the surveyed meat-processing facility employees tested positive for SARS-CoV-2 RNA and were predominantly asymptomatic. The high Ct values and lack of symptoms led to two possible scenarios: recovering from mild infection, or truly asymptomatic. The environmental sampling showed a low positivity rate and could not be linked by sequencing to the diagnosed cases. Widespread transmission of SARS-CoV-2 within this production location did not seem likely after the implementation of the control measures.

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

Keywords: COVID-19, SARS-CoV-2, Coronavirus Infections, Disease Outbreaks

ABSTRACT ID: 192

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6.14. Management of a COVID-19 outbreak in a Hotel in Tenerife, Spain

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Background:

In February 24th a hotel in Tenerife was placed under quarantine after a guest travelling from an at risk region of Italy presented to a hospital with symptoms of an acute respiratory infection and tested positive for SAR-CoV-2. We describe a timeline with the main events, including the measures taken and the extent of the outbreak in the Hotel, for the consideration of public health officials that may encounter similar situations.

Methods:

Daily clinical and laboratory information collected by the Canary Islands Public Health Authorities was used to describe the evolution of the events related to the COVID-19 outbreak reported in the hotel during the period of February 24th – March 5th 2020.

Results:

After confirmation of the index case, Public Health Authorities immediately quarantined the hotel and implemented measures to prevent and control further transmission. A group of nine individuals that were considered close contacts with the index case and were tested by RT-PCR. Five of them ultimately tested positive and were transferred to local hospitals for treatment and isolation. Any other guests or hotel workers that developed symptoms were immediately tested. Among them, only one tested positive for SARS-CoV-2 and was isolated. After 14 days, the quarantine ended and the guests were allowed to return to their countries.

Conclusions:

The measures applied have thus far proven effective in mitigating a situation that may have resulted in the formation of a cluster with potential for subsequent international transmission considering the international nature of the guests. Measures implemented need to be assessed on a case by case basis and recommendations should be adapted depending on the risk of exposure and relevant social- culturalor sanitary -aspects.

Subject: Field epidemiology (e.g. outbreak investigations) Keywords: COVID-19, Outbreak, Hotel, Quarantine, Rapid Response,

Outbreak Control

ABSTRACT ID: 207

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6.15. The evolution of the COVID-19 epidemic in Spain based on indicators of healthcare system capacity, February-August 2020

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Background:

During the first wave of the COVID-19 epidemic in Spain, diagnosis, hospitalisation and admission to intensive care unit (ICU) was prioritised to severe cases. The aim of this work was to describe two indicators that can be applied to monitor disease burden and capacity of the healthcare system.

Methods:

We used data on COVID-19 confirmed cases notified to the National Epidemiological Surveillance Network with reported or calculated onset of symptoms from week 5 to 35. We calculated the weekly ratio of deaths over admissions to ICU stratified by age. We also computed the weekly proportion of hospitalised cases relative to the total cases. Results were compared between two periods, weeks 5-19 and 20-35, based on the beginning of phase 1 of the lockdown de- escalation.

Results:

Median of the weekly ratio of deaths over ICU admissions for $(65 \text{ years} \text{ during the first and the second periods was 0.54 (IQR: 0.33-0.74, Max: 1.0) and 0.25 (IQR: 0.18-0.33, Max: 0.4), respectively. In cases <math>\geq 65 \text{ years}$, the median ratio was 5.6 (IQR: 2.8-14.0, Max: 21) and 3.0 (IQR: 1.9-4.2, Max: 11), respectively. Median proportion of hospitalised cases over the first period was 37% (IQR: 19-56, Max: 59) and decreased to 5.4% (IQR: 4.9-10, Max: 13) over the second.

Conclusions:

Ratio of deaths over ICU cases was higher during the first period compared to the second one, which may reflect the overburden of the healthcare system. The ratio was higher for the older group in both periods. The lower proportion of hospitalisation in the second period may be related to the improved capacity of case detection. These indicators, in conjunction with others, may help to rapidly guide response and allocation of resources.

Subject: Surveillance

Keywords: COVID-19; Mortality; Intensive Care Units; Hospitalization; Pandemics; Spain;

ABSTRACT ID: 208

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6.16. The impact of the COVID-19 pandemic and associated public health measures on other notifiable infectious diseases under surveillance in Germany

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Background:

The COVID-19 pandemic and associated public health measures affect healthcare seeking behaviour, access to healthcare, test strategies, disease notification and workload at public health authorities, but may also lead to a true change in transmission. We aimed to assess the impact on notifiable infectious diseases under surveillance in Germany, to understand the epidemiology of all infectious diseases during the pandemic.

Methods:

We selected all nationally notifiable diseases with case numbers >100/ year. We used a Poisson regression analysis on a weekly aggregated time series to compute the change in case numbers during week 2020-10 to 2020-32 (pandemic), in comparison to the previous four years (week 2016-01 to 2020-09). The model incorporated trend and seasonal components, and the pandemic as a binary variable.

Results:

Between week 2020-10 and 2020-32, 216,825 COVID-19 cases, and 139,571 (-35%) other infectious diseases, were notified. Notifications decreased across all ages: 0-4yrs -57%; 5-14yrs -45%; 15-34yrs -26%; 35-59yrs -24%; 60-79yrs -34%; 80+yrs -44%.

The largest mean decreases were seen for childhood-related illnesses -58% (from -86% for measles to -33% for mumps), hospital-associated infections -47% (from 63% for Acinetobacter to -28% for MRSA), gastro-intestinal infections -46% (from -83% for Rotavirus to -7% for Yersiniose), and respiratory diseases -28% (from -54% for seasonal influenza to -12% for tuberculosis). Conversely, tick-borne encephalitis (+58%) increased strongly. (All categories p- value < 0.005.)

Conclusions:

The COVID-19 pandemic led to a drastic decrease of notifications for most infectious diseases in Germany, especially among younger and older age groups. The largest decrease has been seen among childhoodrelated illnesses. Clear understanding of changes in trends is essential for long-term public health protection of all infectious diseases. Further investigations are necessary to understand these multi-causal effects.

Subject: Surveillance

Keywords: Public Health Surveillance, COVID-19, Pandemics

ABSTRACT ID: 209

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6.17. COVID-19 seroprevalence among workers of the Catalan Institute of Oncology (ICO) in Catalonia, Spain.

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Background:

Cancer patients are at higher risk for severe COVID-19 infection. Hence, COVID-19 surveillance of workers from oncological centers is crucial to assess infection burden and transmission This study aims to estimate the SARS-CoV-2 seroprevalence among the Catalan Institute of Oncology (ICO) workers, a comprehensive cancer center (four hospitals in Catalonia, Spain), and to assess associated factors

Methods:

In a cross-sectional study (21st May-26th June 2020) all ICO workers (N=1,949) were invited to complete an online self- administered epidemiological survey (demographics, lifestyles, professional information, clinic, and exposure and protection measures) and to provide a blood sample to test IgM and IgG against SARS-CoV-2. Odds ratios (OR) for seropositivity adjusted by age, sex, and ICO center as well as and 95% confidence intervals (95%CI) were estimated.

Results:

A total of 1,235 employees filled the survey and performed serology (participation rate: 63%). The median age was 44 years (IQR:16), 76% were female, 52% were medical care staff (physicians, nurses or nursing assistants), and 79% worked on-site during the pandemic period. Overall, SARS-CoV-2 seroprevalence was 8.9% (95%Cl:7.44-10.63), with no differences by age and sex. Seropositive participants were twice more likely to be medical care workers (OR:2.09, 95%Cl:1.40-3.27) and to be in contact with COVID-19 patients (OR:1.60; 95%Cl:0.97-2.66). Seropositivity was lower on those who referred not to be exposed by interacting with colleagues (OR:0.28, 95%Cl:0.13-0.63). Seropositivity was associated cohabiting with a COVID-19 patient (OR:5.09, 95%Cl:3.15-8.24).

Conclusions:

SARS-CoV-2 seroprevalence among ICO workers was lower than in other Catalan hospitals. Whereas the main risk factor was cohabiting with infected people, contact with COVID-19 patients and other colleagues stood out as risk factors of nosocomial infection. Strengthening preventive measures and health education among health-care workers is fundamental.

Subject: Burden of disease

Keywords: SARS-CoV-2,COVID-19,Health Personnel,seroprevalence,Risk Factors,Oncology

ABSTRACT ID: 211

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6.18. Ethnic variation in outcome of people hospitalised with Covid-19 in Wales (UK): A rapid analysis of surveillance data using Onomap, a name-based ethnicity classification tool

O. Orife 1

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Background:

There is emerging evidence that Black, Asian and other minority ethnic (BAME) individuals living in Europe are at increased risk of SARS-CoV-2 infection (COVID-19) and experience worse clinical outcomes. We used Onomap, a name-based ethnicity classifier, to investigate ethnic health inequalities in Covid-19 in Wales (UK).

Methods:

We analysed routine surveillance data on 4,046 individuals hospitalised in Wales with Covid-19 between 1st March and 31st May. Ethnicity was assigned to individuals using Onomap and classified according to 2001 UK Census classifications. A 'BAME' field was created, containing all ethnicities except 'White' or 'unclassified'. We conducted multivariable logistic regression to identify risk of severe outcomes (intensive care (ICU) admission and mortality) in BAME individuals hospitalised with confirmed Covid-19.

Results:

After controlling for age, sex and social deprivation, we found that hospitalised BAME individuals were younger (median age: 53 years compared to 76 years for White individuals; (p<0.01; Mann Whitney 2 sample test) and more likely to be admitted to ICU. Bangladeshi (adjusted odds ratio: 9.80, 95%CI 1.21-79.40) and 'White – Other' (aOR: 1.99, 95%CI: 1.15- 3.44) ethnic groups were most likely to be admitted to ICU. In Wales, older age (aOR for over 70 years: 10.29, 95%CI: 6.78– 15.64) and male gender (aOR: 1.38, 95%CI: 1.19–1.59), but not ethnicity, were associated with death in hospitalised patients.

Conclusions:

Based on the available data, hospitalised ethnic minority individuals were more likely to be admitted to ICU with COVID-19 but less likely to die. These results improve our understanding of the pandemic and have contributed to Welsh Government initiatives to mitigate the risk of infection in those most vulnerable to severe infection.

Subject: Surveillance

Keywords: Covid-19, ethnicity, outcomes, epidemiology

ABSTRACT ID: 217

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6.19. Incubation time estimation and epidemiology of the COVID-19 outbreak in the first two weeks of the epidemic in Baden-Württemberg, South- Germany, February and March, 2020

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Background:

Baden-Württemberg (BW) has been the German state with the second highest COVID-19 incidence in Germany. In this study, we describe the start of the epidemic in BW, and estimate the incubation time for COVID-19 using data of travellers and other cases with known exposure intervals.

Methods:

We analysed data of all SARS-CoV-2 positive cases notified to the state health office between 25 February and 9 March 2020. Data was collected from electronic notification software and supplementary information on exposures was provided by local health authorities. Incubation time was estimated assuming equal probability of infection during each day of travel abroad to risk regions or during close contact with a confirmed case before onset of symptoms.

Results:

Out of 217 cases, 123 (56.7%) were male and median age was 46 years (range: 1-90). Most cases (148; 68.2%) had travel exposure, 55 had contact with a confirmed case (25.3%); for 14 (6.4%) the exposure was unknown. Altogether, 40 (18.4%) cases were asymptomatic, 158 (72.8%) had mild disease, 11 (5.1%) had severe disease and for 8 cases (3.7%), symptom information was not available. Four (1.8%) cases died. We estimated the incubation time based on 100 cases with known exposure period and disease onset. It lasted less than 5 days in 49.3% of cases, less than 7 days for 73.4% and less than 11 days for 97%.

Conclusions:

Our estimate of the incubation time distribution confirms the findings of previous studies. Based on our study and estimation of other researchers, the duration of quarantine of 10 days might be a reasonable decision.



Subject: Surveillance

Keywords: Incubation time, SARS-CoV-2, Quarantine duration ABSTRACT ID: 221

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6.20. COVID-19: Cross-border contact tracing in Germany, February-April 2020

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Background:

The Robert Koch Institute (RKI) manages the exchange of data for crossborder contact tracing related to COVID-19 between public health authorities (PHA) in Germany and abroad. We aimed to describe the extent of RKI cross-border contact tracing activities and challenges experienced.

Methods:

For data exchange the RKI used different communication channels including the single-window system "Early Warning Response System" (EWRS) for communication within Europe and e-mail within Germany and for International Health Regulation (IHR) National Focal Points (NFP) outside EU/EEA. For the latter, personal data was shared encrypted in a separate message. We analysed RKI activities from o3/02/2020 to o5/04/2020 by the number of PHA contacted, communication channel, number of contact persons and exposure context.

Results:

The RKI processed 467 activities initiating contact to PHA 1,099 times (median 1, confidence interval [1;16]). EWRS was used for 345 (31%) contacts. Of 327 (70%) events with known exposure context, 64 (14%) exposures occurred on aircrafts, 24 (5%) on cruise ships and 210 (45%) related to non-transport contexts. Cruise ship and aircraft exposures yielded higher median numbers of authorities contacted (10 [2;16], 4[2;11] vs 1[1;6]) and contact persons (60 [9;269], 2[1;3] vs 1[1;2]) than non-transport related exposures.

Conclusions:

While transport related events didn't reflect the majority of the contact tracing activities, they contributed substantially to the workload. Therefore, the role of transport in transmission of COVID-19 should be further evaluated in order to determine an efficient use of resources. Due to the single-window function, EWRS was perceived as a fast and secure communication option but was not available for the large proportion of communication. Communication structures on national and international level should be synchronized using EWRS as best practice example.

Subject: Surveillance

Keywords: cross-border contact tracing, surveillance, pandemic prepardness, International Health Regulations, Germany , COVID-19

ABSTRACT ID: 234

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6.21. Portuguese National Serological Survey to Coronavirus Disease 19

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Background:

Seroepidemiological studies allow estimating more precise cumulative incidence when compared with results obtained from the SARS-CoV-2 RNA detection test. In this context, the first Portuguese COVID-19 National Serological Survey (ISN-COVID-19) had as primary objectives to: characterize the extent of SARS-CoV-2 infection; determine seroprevalence in specific age groups and Health Regions; and determine the proportion of asymptomatic SARS-CoV-2 infections within Portuguese population.

Methods:

ISN-COVID-19 was an observational, cross-sectional study. A nonprobabilistic sample of 2,301 people residing in Portugal, aged over 1 year old, was analyzed. Sociodemographic, epidemiological and clinical data were collected using a questionnaire and a blood sample was collected from each participant, at 114 collection points, between May 21-July 8, 2020. SARS-Cov-2 specific IgG and IgM were measured in serum by ELISA.

Results:

National seroprevalence was 2.9% (2.0-4.2%), being higher than the accumulated incidence of the infection reported by the National Surveillance System (0.44%). The estimated seroprevalence was higher in males than in females (4.1% vs 1.8%). It ranged from 2.2% in the 10-19 age group to 3.2% in the 40-59 age group. At the regional level, seroprevalence varied between 1.2% in Alentejo and 3.5% in Lisbon and Tagus Valley. Age and regional differences were not statistical significant. About 44% of individuals with SARS-CoV-2 antibodies did not report previous COVID-19 symptoms.

Conclusions:

The estimated seroprevalence is compatible with a limited extent of infection in the Portuguese population, between March and June 2020. Differences observed between seroprevalence and cumulative incidence

¹ INSA

of the infection are consistent with the evidence of lesser capacity to capture mild or asymptomatic cases by surveillance systems. These results advise universal maintenance of protection measures.

Subject: Surveillance

Keywords: Severe Acute Respiratory Syndrome Coronavirus 2, COVID-19, Seroepidemiological Studies; Cross-sectional studies, Immunoglobulin M, Immunoglobulin G.

ABSTRACT ID: 236

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Disease Group: Antimicrobial resistance

Abstracts

7.1. No association between use of alcohol-based hand rub and antimicrobial resistance in Finland, 2014-2018

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Background:

Antimicrobial resistance (AMR) varies across Finland's five regions, but the variation is not explained by regional differences in consumption of antimicrobials. As infection control practices are critical in controlling the spread of antimicrobial resistant pathogens, we assessed the association between AMR and the consumption of alcohol-based hand rub (ABHR) in acute care hospitals, in order to improve infection control guidelines.

Methods:

We used antimicrobial susceptibility data from FinRes surveillance from 2014-2018. FinRes data included: methicillin for Staphylococcus aureus, vancomycin for Enterococcus faecium and faecalis, carbapenems for Enterobacteriaceae (Escherichia coli, Klebsiella pneumoniae, Klebsiella oxytoca, and Enterobacter cloacae), Acinetobacter baumannii and Pseudomonas aeruginosa. We used data from national surveys on infection prevention and control indicators from the same period, to estimate ABHR consumption in litres per 1000 patient-days in 58 hospitals. AMR index was calculated as the proportion of resistant isolates of all isolates tested. We imputed missing data for ABHR consumption for the year 2016, and used a fixed negative binomial regression model to assess the association between AMR index and ABHR consumption over time with year, ABHR and region as explanatory variables.

Results:

ABHR consumption (regional range 19-85 litre/1000 patient-days) increased in all five regions during 2014-2018 (p<0.05) but the AMR index did not (regional range 1.2-2.9%). We found no association between ABHR use and AMR index, r [Cl95%] = 0.35[-3.04-4.08](p=0.83).

Conclusions:

Our ecological analysis found no correlation between ABHR consumption in acute care hospitals and regional AMR measures. As AMR isolates are likely to have originated in different care settings and community, further research on factors such as hand hygiene compliance and other infection control practices in long-term care facilities, is needed.

Subject: Surveillance

Keywords: Antimicrobial resistance, Hand hygiene, Alcohol-based hand rubs, Finland

ABSTRACT ID: 35 PRESENTED BY: Veronica Cristea /cristeaveronica91@gmail.com

7.2. Increasingly limited options for the treatment of enteric fever in travellers returning to England, 2014-2017: a cross-sectional analytical study

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Background:

Effective treatment of travel-related enteric fever (Salmonella enterica serovar Typhi or Paratyphi) depends upon understanding the geographical distribution of antimicrobial resistance. The aim of this work was to characterise the changing patterns of resistance to inform empirical treatment recommendations.

Methods:

All S.Typhi or S.Paratyphi isolates from patients resident in England 2014-2017 underwent antimicrobial susceptibility testing; results were compared to a London survey 2005-2012 by chi-squared test. Demographic and travel-related risk factors for resistance identified through national surveillance questionnaires were used to construct a multivariable logistic regression model for each organism to predict adjusted odds ratios (aOR) for multi-drug resistance (MDR).

Results:

We characterised 584 S.Typhi and 499 S.Paratyphi isolates. 87% of S.Typhi and 97% of S.Paratyphi isolates were resistant to ciprofloxacin; 21% of S.Typhi were resistant to ciprofloxacin, amoxicillin, co-trimoxazole, and chloramphenicol (MDR4). One isolate of S.Paratyphi A was resistant to third-generation cephalosporins; none were resistant to azithromycin.

Comparison with the 2005-2012 survey indicated increased S.Typhi resistance to ciprofloxacin among travellers to Pakistan (79% to 98%; P<0.001) and Africa (12% to 63%; P<0.001).

S.Typhi ciprofloxacin resistance was associated with travel to Pakistan (aOR 27.6, 95%Cl: 9.2-83.0), India (aOR 5.3, 95%Cl: 2.8-9.9), and Bangladesh (aOR 3.2, 95%Cl: 1.3-8.3) compared to other destinations.

MDR4 in S.Typhi was associated with travel to Pakistan (aOR 3.1, 95%Cl: 1.8-5.4) and less likely with travel to India (aOR 0.15, 95%Cl: 0.07-0.33) compared to other destinations, after adjustment for sex.

Conclusions:

Third-generation cephalosporins and azithromycin remain appropriate choices for empirical treatment in returning travellers. Prescribing guidelines should reflect high rates of S.Typhi ciprofloxacin resistance globally—especially in South Asia, and increasingly in Africa—and MDR in Pakistan. Forthcoming national treatment guidelines will reflect these recommendations.

Subject: Microbiology

Keywords: Enteric Fever, Antimicrobial Resistance, Travel, Salmonella Typhi, Salmonella Paratyphi

ABSTRACT ID: 146

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7.3. Bugs that can resist antibiotics but not men: Sex-specific differences in population-based incidence rates for colonisations and infections with antimicrobial-resistant bacteria in Germany, 2011-2019

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Background:

Data from surveillance networks show that men have a higher incidence of infections with anti-microbial resistant (AMR) pathogens than women. We systematically analysed infections plus colonisations with all AMR pathogens that are notifiable in Germany after laboratory confirmation. We aimed to assess the magnitude of sex-specific differences in order to guide prevention and treatment measures.

Methods:

We calculated incidence rates (IR) per 100,000 person-years for notified colonisations and infections with Carbapenem- non-susceptible Acinetobacter spp. (ABC) and Enterobacterales (EBC), and invasive infections with Methicillin-resistant Staphylococcus aureus (MRSA), using the entire German population as denominator. We limited the study periods to years in which they were notifiable (ABC/EBC: 2017-2019, MRSA: 2011-2019) and used Poisson regression to adjust for sex, age, federal state and year of notification.

Results:

In the study periods, 2,278 colonisations/infections with ABC (median age 66 years, interquartile range [IQR] 53-76), 11,937 with EBC (median age 68 years, IQR 55-78), and 30,778 with MRSA (median age 74 years, IQR 64-81) were notified, resulting in IR of 0.90 for ABC, 4.7 for EBC and 4.1 for MRSA per 100,000 person-years. The adjusted IR ratio of men compared to women was 2.2 (95% confidence interval [CI]=2.0-2.4) for ABC, 1.9 (95%CI=1.8-2.0) for EBC, and 2.3 (95%CI=2.2-2.3) for MRSA. Multivariable models with interaction terms revealed stronger associations in older age groups and regional differences. Stratified by colonization/infection for ABC and EBC, the effect size did not differ.

Conclusions:

Men in Germany have a notably higher risk for both colonisation and infection with AMR pathogens than women. Regionally specific hospital guidelines for antibiotic screening and associated hygiene measures, as well as directed antibiotic therapies, should take both age and sex of patients into account.

Subject: Surveillance

Keywords: Microbial Drug Resistance, Sex Distribution, Methicillin-resistant Staphylococcus aureus, Carbapenem-resistant Enterobacterales, Carbapenem-resistant Acinetobacter

ABSTRACT ID: 199

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7.4. Multi-drug resistance in food-producing animals from Portugal: Escherichia coli and food-borne pathogens

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Background:

Food production animals are seen as a major source of widespread antimicrobial resistance transmission to humans, including multiresistance. Hence, we assessed multi-resistance (MDR) prevalence and MDR profiles in Escherichia coli and food-borne pathogens isolated from foodproducing animals in Portugal.

Methods:

Data from the Portuguese AMR surveillance program on broilers (2014, 2015, 2016, 2018) and pigs (2015 and 2017) was used. MDR was defined as isolates resistant to three or more antimicrobial classes. MDR prevalence was calculated for each bacteria (E. coli, Campylobacter and Salmonella) and stratified by animal population species and year. MDR-profiles were obtained by aggregating antimicrobial classes with resistant results from antimicrobial susceptibility testing and compared among isolates.

Results:

We included 584 E. coli, 362 Campylobacter and 386 Salmonella isolates from broilers and 406 E. coli isolates from pigs. In food-borne pathogens, theoverallMDRfrequencybetween 2014-2018 waslowerfor Campylobacter (14%) and Salmonella (18%) isolates than for E. coli. In broilers E. coli isolates, MDR increased from 2014 (76%) to 2018 (86%) and decreased in pigs from 2015 (92%) to 2017 (82%). In broilers, the most common E. coli MDR-profile across all surveillance years was to (fluoro)quinolonesamphenicols-penicillin's-sulphonamides-tetracyclines-trimethoprim. Nevertheless, in 2018 the MDR-profile included 4thgeneration cephalosporins instead of amphenicols. The most prevalent MDR-profile in Campylobacter was (fluoro)quinolones-macrolides-tetracyclines while in Salmonella the MDR-profile was (fluoro)quinolones-penicillin'ssulphonamides-trimethoprim. In pigs, the most observed MDR was penicillin's-amphenicols-sulphonamides-tetracyclines-trimethoprim. **Conclusions:**

Extremely high MDR was observed in E. coli from broilers with presence of 4th generation cephalosporin resistance in the most prevalent MDR-



profile. Lower levels of multi-resistant food-borne pathogens are a positive result, although fluoroquinolones and macrolides are present in the main MDRprofiles. These findings provide valuable information towards AMR stewardship.

Subject: Surveillance

Keywords: Multi-Drug Resistance, Animals, Escherichia coli, Population Surveillance

ABSTRACT ID: 223

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Disease Group: Global health and Emerging diseases

Abstracts

8.1. Insecticide thermal fogging in hyrax dens is effective in the control of leismaniasis vectors in rural Palestine, 2019

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Background:

Zoonotic cutaneous leishmaniasis (ZCL) is endemic in Tubas, Palestine and transmitted by the sandfly Phlebotomus sergenti that inhabits dens of hyraxes, the reservoir animal. Since 1996, control measures include pyrethroid spraying of affected domestic areas, however cases still occur. We evaluated the effectiveness of thermal fogging using Permethrin insecticide inside hyrax dens on decreasing sandfly density and leishmania infection and consequently the ZCL incidence.

Methods:

From July to October 2019, we conducted a 12-week prospective study using a controlled interrupted time series design in two control and one intervention sites each containing three hyrax dens. At week 6, we applied thermal fogging to the intervention site. We measured weekly (pre- and post-intervention) and 36 hours post-intervention the sandfly species' abundance using CDC light traps inside dens and identified sandfly species. We used PCR and next-generation sequencing (NGS) to identify Leishmania spp. infection in engorged or blood-fed Phlebotomus female sandflies. We calculated the abundance reduction in sandflies and in Leishmania spp. infection using Mulla's formula.

Results:

Among 11427 sandflies collected, 7339 (64%) were female and 1786 (16%) of Phlebotomus genus; the remaining were Sergentomyia spp. Phlebotomus comprised ten species of which P. sergenti was the dominant (N=773, 43%). We report P. arabicus (N=6) for the first time in Palestine. Sandfly abundance reduction at 36 hours and five weeks post- intervention was 97% and 38% respectively. Overall Leishmania spp. infection was 6.5% with PCR (15/231) and 9.5% (22/231) with NGS. Abundance reduction of sandfly infection by NGS five weeks post-intervention was 82% with zero infections during the first two weeks.

Conclusions:

Fogging inside hyrax dens could be an effective complementary method for "source reduction of ZCL vector" especially when applied bimonthly.

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

evaluation of programmes)

Keywords: Cutaneous Leishmaniasis, Hyrax, Interrupted Time Series, Permethrin, Prevention and Control, Sandfly

ABSTRACT ID: 37

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8.2. West Nile virus transmission in Europe is shaped by spring temperature

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Background:

West Nile Virus (WNV) is now endemic in many European countries, causing hundreds of human cases every year, with a high spatial and temporal heterogeneity. Several previous studies suggested that spring temperature might play a key role at shaping WNV transmission. In particular, in a recent analysis, by calibrating an epidemiological model using data gathered over several years in northern Italy, we found a strong positive association between April-May temperature and WNV estimated prevalence both in mosquito and avian hosts during summer, which resulted in a higher risk for human spillover. Here we investigate whether such relationship holds at a broad spatial and temporal scale.

Methods:

We collated publicly available data on the number of human infections recorded in Europe between 2011 and 2019. We then applied generalized linear models to quantify the relationship between human cases and spring temperature, considering both average conditions (over years 2003-2010) and deviations from the average for subsequent years (2011-2019).

Results:

We found that larger WNV outbreaks are associated both with warmer average spring conditions and positive deviations. We also found a positive association with WNV detection during the previous year, which can be interpreted as an indication of the reliability of the surveillance system but also of WNV overwintering capacity.

Conclusions:

Weather anomalies at the beginning of the mosquito breeding season might act as an early warning signal for public health authorities, enabling them to design in advance efficient surveillance and prevention strategies.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Arboviruses, Epidemiology, Culex, Public Health

ABSTRACT ID: 43

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8.3. Retrospective study of risk factors of keratitis by Fusarium and Acanthamoeba in the Netherlands (FUSACA study)

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Background:

Since 2015, laboratories notifications of severe keratitis caused by Fusarium or Acanthamoeba increased in the Netherlands. This rare but serious infection is most common among individuals who wear contact lenses (CL). It is however not clear which factors put CL users at a higher risk for infections. We investigated here risk factors for Fusarium and Acanthamoeba keratitis among contact-lens users.

Methods:

Since Fusarium and Acanthamoeba keratitis are not under systematic surveillance, we designed a retrospective case- control study approaching Acanthamoeba and Fusarium cases diagnosed between 2009-2020 by 16 cornea reference centers across the Netherlands. Controls were recruited in spring 2020 online via social media. Both cases and controls completed a questionnaire containing data on demographics, comorbidities, CL habits and hygiene practices. Risk factors were assessed using logistic regression.

Results:

In total, 227 cases (184 Acanthamoeba, 42 Fusarium and 1 unknown) and 1020 controls using CL were included in the analysis. The risk of acquiring keratitis was higher for persons having a history of prior eye trauma (OR 4.4, 95%Cl: 1.9-9.8). Traveling abroad (OR 4.3, 95%Cl: 1.9-9.4), CL contact with water (OR 3.3, 95%Cl: 1.2-8.8) and swimming with CL (OR 2.7, 95%Cl: 1.3-5.5) also put CL users more at risk of acquiring keratitis. Washing hands with antibacterial soap before manipulating contact-lenses as well as being advised by a contact lens specialist were protective factors (OR 0.2, 95Cl%: 0.03-0.7; OR 0.4, 95Cl%: 0.2-0.9, respectively).

Conclusions:

With the exception of prior eye trauma, all identified risk factors are related to non-compliant practices when handling CL. Hence, we recommend reinforced communication on appropriate CL habits and hygiene practices among CL users since those could prevent infections.

Subject: Burden of disease

Keywords: Keratitis, Risk factors, Case-control, Acanthamoeba **ABSTRACT ID:** 97

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8.4. Knowledge, attitude and practice towards West Nile virus infection among final year medical students in Belgrade, Serbia, 2019

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Background:

In 2018, Serbia ranked 2nd in Europe in the number of the reported human West Nile virus (WNV) infection cases. This implicates that Serbian health sciences' students as future health workers should be familiar with WNV infection. Therefore, we aimed to assess the medical students' knowledge, attitude, and practice (KAP) towards WNV infection in order to guide education recommendations.

Methods:

We conducted a cross-sectional study among all final year students at School of Medicine, University of Belgrade between 16th and 20th December 2019. Information on KAP, sociodemographic and academic performance data earned within courses were collected by self-administered pretested questionnaire. We used univariate and multivariable binomial regression analysis to investigate factors associated with KAP after dichotomizing the scores using 70% cut off- points.

Results:

Among a total of 489 students, 488 (99.7%) [median age (interquartile range), 24 (1), years] answered the questionnaire. Among respondents 58% (281/488) were categorized as have been knowledgeable about WNV infection, 68% (332/488) had adequate attitudes towards the disease and only 8% (38/479) practiced effective personal protective behaviors against mosquito bites. A students' grade point average (GPA) earned in courses, over time, at School of Medicine was independent predictor of better knowledge [prevalence ratio=1.19 (95% Confidence Interval: 1.08-1.32)] on WNV infection. Female sex of participants [PR=1.18 (95%CI: 1.03-1.36)] and GPA [PR=1.14 (95%CI: 1.04-1.24)] independently predicted adequate attitude towards WNV infection.

Conclusions:

Moderate knowledge, adequate attitude, and poor practice towards WNV infection among final year medical students at School of Medicine, University of Belgrade, indicate a need for educational interventions such as extending the curriculum with the content on WNV infection to create higher awareness regarding this disease and its prevention.

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

Keywords: Health knowledge, attitudes, practice,West Nile virus,medical students, Serbia

ABSTRACT ID: 143

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8.5. Five Year Review of Malaria Case Management-Yobe state, Northeast Nigeria, 2013-2017: An Analysis of Routine Surveillance Data

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Background:

Malaria remains an important communicable disease in Sub-Saharan Africa. Nigeria accounts for 25% and 19% of the global malaria cases and death respectively. Nigeria's malaria policy stipulates testing for all fever cases and administration of artemisinin-based combination therapy (ACTs) to confirmed cases. We described malaria diagnosis and treatment practice in Yobe state, Nigeria.

Methods:

We obtained the 2013 – 2017 Yobe state malaria surveillance data from the District Health Information System (DHIS). We conducted a crosssectional analysis of reported fever cases for all the state population, malaria tests done and treatment given to confirmed malaria cases during the period. Data were summarized in frequencies and proportions.

Results:

Overall, 1, 263,290 fever cases were reported, with an increase from 112,059 in 2013 to 358,521 in 2017 capturing only public health facilities. A total of 946,244 (75%) were tested using malaria microscopy or rapid diagnostic test (mRDT) kit, 671,917 (71%) were positive. A total of 217,275 cases were tested with microscopy, 173,153 (80%) were positive. Of 728,969 tested with mRDT, 498,764(68%) were positive. There was an increase confirmed malaria cases over the years, 62,398 in 2013 against 198,717 in 2017. Overall, 553,846 (83%) of the 665,306 uncomplicated confirmed malaria received the recommended ACT, however, there was an improvement in the proportion of cases receiving the drugs from 74% in 2013 to 91% in 2017.

Conclusions:

There was an increase in the reported malaria cases in Yobe state during the review period. The use of ACT improved by 17%, but the state did not meet the country's case management target of 100%. We recommended the intensification of malaria control activities, and inclusion of private health providers data into the surveillance system.

Subject: Burden of disease Keywords: malaria,Case Management,ACT,Nigeria ABSTRACT ID: 160

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