ESCAIDE

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology

Online,
16-19 November 2021

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EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

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Foreword

A very warm welcome to the 2021 ESCAIDE conference! I hope you will find attending this second virtual edition of ESCAIDE a stimulating and rewarding experience and enjoy the wide variety of sessions and online interactive opportunities on offer.

In contrast to last year's race against time to convert the conference into a virtual format, this 2021 edition of ESCAIDE was planned as an online conference from the outset, taking full advantage of the online format and allowing for the inclusion of many more features into the online Swapcard platform. We are expecting a record number of attendees as a result, and I would like to take this opportunity to invite you all to make use of the many interactive features available during the event to meet with old friends and colleagues, as well as to expand your professional and personal networks by meeting someone new!

As in every year, the ESCAIDE 2021 conference programme is built around the presentation of excellent abstracts with high public health relevance. This is made possible through the hard work of the many authors, the large number of reviewers who guide abstract selection, and finally the session moderators who steer the conference sessions themselves.

I would like to thank all the authors who made the effort to submit an abstract to the conference. It is remarkable that in face of the continued and unremitting pressure on communicable disease professionals, you remain committed to writing scientific summaries of your work, so others have an opportunity to learn from your experiences.

My enormous appreciation also goes out to my Scientific committee colleagues and all of our speakers and presenters, for contributing to the creation of the incredibly exciting, and especially pertinent, plenary programme this year. The keynote session opening the conference will address the difficulties many of us face communicating scientific data and uncertainty during a pandemic to different audiences including policy-makers, colleagues, journalists and the general public (Plenary A). The contribution of modelling in real time for communicable diseases, recent innovations during the COVID-19 pandemic, and how the data generated can inform public policy and the general public will be discussed in Plenary B. Plenary C will adopt an exciting new format, where four speakers that have pioneered digital health solutions and covered new ground in public health services will be given the opportunity to present their innovations in a TED talk format. The final plenary session, Plenary D, will discuss underlying inequality and inequity issues in our national and global health systems that have been thrown into sharp relief by the COVID-19 pandemic. This session will also debate how to tackle these inequalities and good practices to adopt.

Finally, I wish you a successful and enjoyable ESCAIDE 2021, and hope that you leave the conference with useful insights, new contacts, and renewed enthusiasm for your role in the fight to address communicable disease.

Prof. Mike Catchpole

Chair, ESCAIDE Scientific Committee

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Scientific Committee

Mike Catchpole

Chief Scientist, Chair of ESCAIDE Scientific Committee

Susan Hahne

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), Netherlands

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

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.

Frode Forland

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

Bruno Coignard

Director, Infectious Diseases Division, Santé publique France

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.

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)

Mircea Ioan Popa

Microbiology Professor, Carol Davila University of Medicine and Pharmacy, Romania

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.

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

Magdalena Rosińska

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

Petronille Bogaert

Project Researcher and Head of Unit, EU Health Information Systems, Sciensano, Belgium

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

Petronille Bogaert is project researcher and head of unit EU health information systems at Sciensano. Her work primarily focusses on European projects facilitating research in the area of population health information. This includes the coordination of the Population Health Information Research Infrastructure for COVID-19 and the Joint Action on Health Information (InfAct). She is also leading several activities in the Joint Action Towards the European Health Data Space (TEHDAS) and HealthyCloud. She holds a double Master degree in European Public Health and a Masters in Biomedical Sciences. She is also president of the EUPHA section on Public Health Monitoring and Reporting.

Scientific Committee

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, as well as in developing epidemiology training in the Pacific Region.

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

Stine Nielsen

Vice-president, EPIET Alumni Network (EAN)

Stine is the vice-president of the EPIET Alumni Network (www.epietalumni.net) which brings together more than 600 European field epidemiologists and public health microbiologists. She has a MSc in public health sciences from Copenhagen University and has submitted her doctorate in epidemiology to the Charité university in Berlin. She has worked mainly on HIV and viral hepatitis focusing mostly on increasing access to health and harm reduction services for people who use drugs. She has worked at WHO/Europe (2004-2008) and the Robert Koch Institute (2008-2015). Since 2015, she has been a home-based consultant in Madrid. In February 2021, she joined the Epiconcept team (www.epiconcept.fr). Stine is active on Twitter as @StineNielsenEPI.

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Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2021.

Belgium

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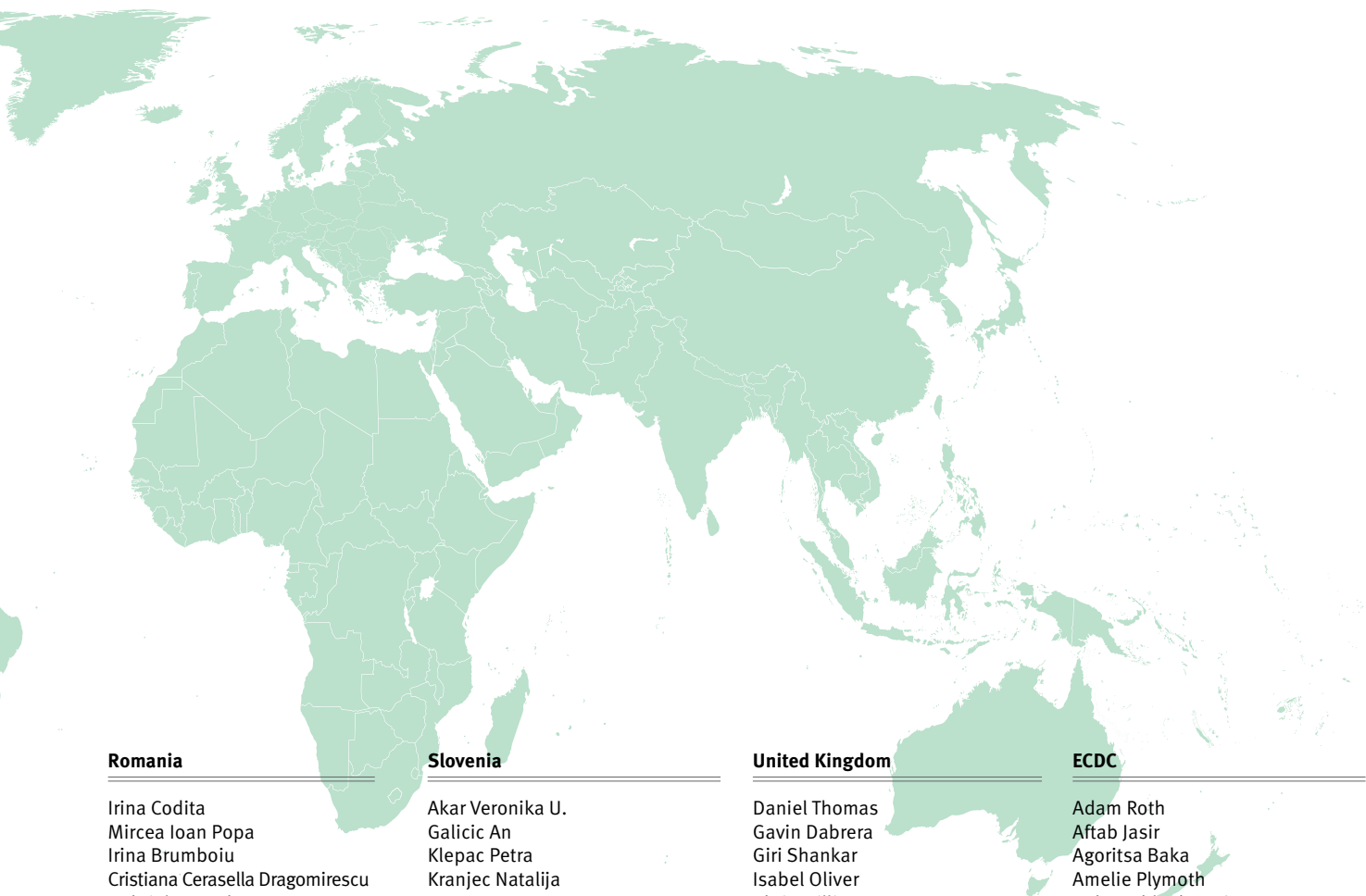## Norway

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Plenary Speakers

Plenary session A: Communicating science and scientific uncertainty during an evolving pandemic

Peter Piot

Belgium
Handa Professor of Global Health and Special Advisor on COVID-19 to the President of the European Commission

Peter Piot MD PhD is the Handa Professor of Global Health and former Director of the London School of Hygiene & Tropical Medicine (2010-2021). He is currently Special Advisor on COVID-19 to the President of the European Commission, and a visiting professor at the Rega Institute, KULeuven, Belgium, and the National University of Singapore.

He was the founding Executive Director of UNAIDS and Under Secretary-General of the United Nations (1995-2008).

A clinician and microbiologist by training, he co-discovered the Ebola virus in Zaire in 1976, and subsequently led pioneering research on HIV/AIDS, women's health and infectious diseases in Africa. He has held academic positions at the Institute of Tropical Medicine, Antwerp; the University of Nairobi; the University of Washington, Seattle; Imperial College London, and the College de France, Paris, and was a Senior Fellow at the Bill & Melinda Gates Foundation. He is a member of the US National Academy of Medicine, the National Academy of Medicine of France, the German National Academy of Sciences Leopoldina, and the Royal Academy of Medicine of his native Belgium, and is a fellow of the UK Academy of Medical Sciences and the Royal College of Physicians.

He is the Chair of the King Baudouin Foundation USA, New York, Vice-Chair of the Global Health Innovation Technology Fund, Tokyo, and member of the Board of the Novartis Foundation, Basel, and the Coalition for Epidemic Preparedness Innovation, and past President of the International AIDS Society.

In 1995 he was made a Baron by King Albert II of Belgium, and in 2016 was awarded an honorary knighthood KCMG in the UK, and in 2018 received the Grand Cordon of the Order of the Rising Sun in Japan. Professor Piot has received numerous awards for his research and service, including the Canada Gairdner Global Health Award (2015), the Robert Koch Gold Medal (2015), the Prince Mahidol Award for Public Health (2014), the Hideyo Noguchi Africa Prize for Medical Research (2013), and the Nelson Mandela Award for Health and Human Rights, (2001), and was named a 2014 TIME Person of the Year (The Ebola Fighters). He has published over 600 scientific articles and 16 books, including his memoir, No Time to Lose, translated into 5 languages.

Marta Hugas

Spain
Chief Scientist, European Food Safety Authority (EFSA)

Dr Marta Hugas is serving as Chief Scientist at the European Food Safety Authority. EFSA is a decentralized agency of the EU with a scope on risk assessment and risk communication on food and feed safety from the farm to fork. Marta holds a BSc in biological sciences, an MSc in genetics and microbial biotechnology and a PhD in food microbiology. Marta had a 20 year career on food safety applied research before joining EFSA in 2003. She has extensively published papers and book chapters. Since she joined EFSA in 2003, she's served in different position, mainly on risk assessment of biological hazards and contaminants as well as Head of the Risk assessment and Scientific Assistance Department. As Chief Scientist, she´s currently leading the reflections on EFSA's role regarding the sustainability of the food production systems from the safety assessment perspective as well as the possible uptake of scientific developments (microbiome, artificial intelligence, new genomic techniques etc) in EFSA's regulatory processes.

Recently she was appointed by the UN secretary general to the Scientific Group for the preparation of the 2021 UN summit on Food Systems as a co-coordinator of Action Track 2, Shifting to sustainable consumption habits.

Plenary Speakers

Plenary session A: Communicating science and scientific uncertainty during an evolving pandemic

Mirjam Jenny

Germany
Harding Center for Risk Literacy

I am a cognitive decision scientist, science communicator, and networker. My goal is to empower individuals and organizations to make evidence–informed, risk savvy, and sustainable decisions in our globalized and increasingly digitalized world. I aim to serve our democratic society by engaging with citizens, journalists, expert decision–makers, research organizations, funders, government organizations, private and public stakeholders, and policymakers. My areas of focus are health, crisis communication, transparent and accountable AI, and research and education. I currently run the science communication unit at the Robert Koch-Institute, Germany's National Public Health Institute, and support the WHO Hub for Pandemic and Epidemic Intelligence in Berlin. I am also still closely affiliated with the Harding Center for Risk Literacy at the University of Potsdam, which I directed until recently.

Vera Novais

Portugal
Science journalist, Observador

Vera Novais is a science journalist in Portugal. She's a staff writer for Observador and a freelancer for international news media. Vera writes about several topics in science but usually works on life sciences, health, astrophysics and scientific policy. Her favourite assignments are related to debunking misinformation about science, health and nutrition. Vera Novais is the President of the Portuguese science communication association SciComPt, is a member of the International Science Writers Association, and often collaborates with the World Federation of Science Journalists. Vera sees as her mission to help fellow science journalists and to contribute to the improvement of science journalism and science communication.

Plenary session B : Modelling epidemics in real time: coming of age?

Niel Hens

Belgium
Chair of evidence-based vaccinology, University of Antwerp

Niel Hens received a master degree in mathematics (1999) from KU Leuven and a master of science and PhD degree in biostatistics (2005) from Hasselt University. Since 2009 he is holder of the chair of evidence-based vaccinology at the University of Antwerp. He published work at the intersection between statistics and mathematical epidemiology focussing on semi-and non-parametric methods for handling missing data in his PhD work and after mainly focussing on bridging the gap between mathematical and statistical methods in infectious disease epidemiology. Next to biostatistics, Niel Hens teaches courses on computational biology and mathematical epidemiology to master of statistics and master of epidemiology students both in Antwerp and Hasselt. He is frequently consulted by federal and Flemish authorities especially for health-related topics.

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Plenary Speakers

Plenary session B : Modelling epidemics in real time: coming of age?

Vittoria Colizza

France
Head of Research, INSERM & Sorbonne Université

Vittoria Colizza is Head of Research at INSERM (French National Institute for Health and Medical Research) & Sorbonne Université, working in the Pierre Louis Institute of Epidemiology and Public Health where she leads the EPIcx lab (Epidemics in complex environments, www.epicx-lab.com). Through modeling, her research spans a wide array of issues on epidemic and pandemic risks, accounting for the role of social contact networks and mobility, and the interaction between population behavior and contagion dynamics. Integrating data from sensors and digital surveillance, her work provides actionable insights for the management of epidemic and pandemic crises. Since January 2020 she has been active in the response against COVID-19 pandemic, advising French governmental bodies and health agencies, and international authorities. For her work on the pandemic, in 2020 she received her knighthood of the Order of Merit of the Italian Republic by the Italian President, the highest-ranking honor of the Italian Republic.

Trained as a physicist (PhD in Statistical and Biological Physics in 2004 at the International School for Advanced Studies in Trieste, Italy), she worked at Indiana University (US, 2004-2007) in the School of Informatics as post-doc and visiting Assistant Professor, and joined ISI Foundation (Turin, Italy, 2007-2010) after being awarded an ERC Starting Grant in Life Sciences in 2007. In 2011 Colizza joined INSERM in Paris, and was promoted Head of research in 2017. Since 2020, she is Visiting Professor at the Tokyo Institute of Technology in Japan.

Jacco Wallinga

Netherlands
Head of Unit, Infectious Disease Modelling, National Institute for Public Health and the Environment (RIVM)

Prof. Dr. Doctor. J (Jacco) Wallinga heads the unit for Infectious Disease Modelling at the RIVM, and he holds the chair in Mathematical Modelling of Infectious Diseases at the department of Biomedical Data Sciences of the Leiden University Medical Center.

Jacco Wallinga graduated from Wageningen University in 1992, and obtained his doctoral degree at the same university in 1998. Since 1997, he analysed dynamics of infectious diseases at RIVMNational Institute for Public Health and the Environment. He became head of the RIVM department of Modelling of Infectious Diseases in 2005. He published over 150 articles in international peer-reviewed scientific journals and is a member of the editorial board of Epidemiology. He advises the Dutch government and international organizations on vaccination policies.

He is interested in understanding and predicting the impact of directed control measures on infection dynamics. In recent years, his research has been focused on three themes: real-time estimation of key epidemiological variables of infectious disease outbreaks, characterization of contact networks using information on social contact data, and using epidemic models to interpret molecular sequence data of pathogens.

Jacco Wallinga holds the chair in Mathematical Modelling of Infectious Diseases at the department of Biomedical Data Sciences of the Leiden University Medical Center (LUMC). As an extraordinary Professor, he works on the estimation and prediction of control measures on the dynamics of infectious diseases.

Plenary Speakers

Plenary session C : Digital health opportunities for Public Health: how far from reality?

Ran Balicer

Israel
Public health physician and researcher, Clalit Research Institute

Ran D. Balicer, a public health physician and researcher, serves as Founding Director of the Clalit Research Institute and Director of Health Policy Planning at Clalit - Israel's largest healthcare organization. In these roles, he is responsible for strategic planning and development of innovative organization-wide interventions for improving healthcare quality, reducing disparities, and introducing novel data and AI driven tools into practice to increase care effectiveness.

Prof. Balicer has been affiliated as faculty with the Ben-Gurion University since 2004, involved in research and teaching in the School of Public Health, and serves today as full professor and track director in the faculty' MPH program. He authored books, book chapters and over 150 peer-reviewed publications looking at various aspects of public health, quality improvement, and preventive medicine. In recent years, Prof. Balicer's research is focused on the study of extensive clinical databases in care provision and policymaking, as well as in applying and assessing innovative models of care aimed at increasing the effectiveness of non-communicable diseases care. In parallel, he is involved in the study of emerging infectious diseases prevention and control, through modeling and real-life big data.

Prof. Balicer serves as Chair of the Israeli Society for Quality in Healthcare, as an Advisor to Israeli Ministry of Health on infectious disease epidemiology, health policy and emergency preparedness. He also serves as a Board Member of the International Foundation for Integrated Care and of the European Federation of Medical Informatics.

Prof. Balicer serves in senior advisory groups to the World Health Organization (WHO) Regional Office for Europe - including the Region's Senators Group, and is involved in projects focusing on chronic diseases monitoring, prevention and control, and healthcare systems integration.

Gun Peggy Knudsen

Norway
Deputy Director General, Norwegian Institute of Public Health (NIPH)

Gun Peggy Knudsen is Deputy Director General of the Norwegian Institute of Public Health (NIPH), has been acting Executive Director for the Division of Infection Control for the past year and has previously served as Executive Director for the Division for Health Data and Digitalisation. Knudsen has a PhD in medical genetics and extensive experience in managing epidemiological and genetics research projects. She has in-depth knowledge of cohort data, biological material, previous and ongoing genetics projects based on materials at NIPH, and use of data from health registries in combination with other health data. She is also involved in national e-health work, representing NIPH on various committees and boards.

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Plenary Speakers

Plenary session C : Digital health opportunities for Public Health: how far from reality?

Dipak Kalra

Belgium
President, European Institute for Innovation through Health Data

Professor Dipak Kalra is President of the European Institute for Innovation through Health Data, which promotes the learning health ecosystem by developing solutions to scale up the trustworthy uses of health data. Dipak has led multiple European projects, and developed ISO standards, in EHR interoperability, data protection, business models and the reuse of EHRs for research. His current projects include the generation and acceptance of real world evidence in pregnancy, the governance of patient-centric clinical trials, policies and frameworks for the design and governance of mobile health programmes, scaling up the quality, interoperability and the reuse of health data for research including inputs to the European Health Data Space, the readiness of hospitals to generate evidence for value based care, and an initiative to explain the value of research using health data to the public.

Stefan Buttigieg

Malta
Specialist in Public Health Medicine, Digital Health and Social Media in Healthcare, University of Malta

Dr Buttigieg is a Specialist in Public Health Medicine with an avid interest in Clinical Informatics, Social Media and Digital Health. He currently lectures at the University of Malta Faculty of Health Sciences on the topics of Digital Health and Social Media in Healthcare. He is also an Author, Tutor and Digital Health Consultant focused on creating transformative and effective change. Within the World Federation of Public Health Association Governing Council, he represents the voices of Students and Young Professionals in Public Health and he is the Vice-President of the EUPHA Section on Digital Health.

Dr Buttigieg is consistently focused on expanding his knowledge within the field of Public Health, Social Media, Digital Health and Project Management with the main aim of empowering healthcare professionals to design, develop and distribute user-centric applications for healthcare.

Dr Buttigieg is on a mission to enable Digital Health for All and ensuring that no one is left behind.

Plenary Speakers

Plenary session D: The inequality pandemic

Ellen t'Hoen

Netherlands
Director, Medicines Law & Policy

Ellen 't Hoen is the director of Medicines Law & Policy, a group of legal and policy experts offering advice to international organizations and governments. From 1999 until 2009 she was the director of policy for Médecins sans Frontières. In 2009 she joined UNITAID in Geneva to set up the Medicines Patent Pool (MPP). She was the MPP's first executive director until 2012.

She has published widely and is the author of several books. In 2017 she received the Prix Prescrire for her book "Private Patents and Public Health: Changing intellectual property rules for public health."

In 2005, 2006, 2010, 2011 and in 2020 she was listed as one of the 50 most influential people in intellectual property by the journal Managing Intellectual Property. In 2020, she was appointed Officer of the Order of Oranje-Nassau, a royal award given in recognition of her work on access to medicines.

She has a master's degree in law from the University of Amsterdam and a PhD from the University of Groningen where she remains a Global Health Law Fellow at the law faculty.

Kevin Fenton

United Kingdom
Regional Director London, Department of Health and Social Care, Office of Health Improvement and Disparities

Professor Fenton has worked in a variety of public health roles across government and academia in the UK and internationally, most recently taking a leading role in London's response to the COVID-19 pandemic. Professor Fenton became the Regional Director for London in the Department of Health and Social Care's Office for Health Improvement and Disparities (OHID) in October 2021, having previously held the same position within Public Health England from April 2020 until its functions transferred to OHID. Within this role, he is also the statutory public health advisor to the Mayor of London and the Greater London Authority. He provides leadership across London for health, prevention of ill health, health protection and reduction of health inequalities.

In November 2020, Professor Fenton was named by Powerlist as the second most influential black person in Britain for his work leading the fight against coronavirus and his public health leadership on tackling inequalities. In Spring 2020, he oversaw the national PHE review of disparities in risks and outcomes of COVID-19, published as the ground-breaking 'Beyond the Data' report. The review led to recommendations which have shaped a more equitable COVID-19 pandemic response, both nationally and locally.

Professor Fenton previously held a joint position as Strategic Director of Place and Wellbeing and Director of Public Health at London Borough of Southwark. In this role he led the council's planning, regeneration, community engagement and public health portfolios driving inclusive regeneration, digital public health, asset-based community development and working in partnership with the NHS to promote health in all policies.

From 2012-2017, Kevin was PHE's National Director for Health and Wellbeing, leading national prevention programmes including screening for cancer, NHS Health Checks, obesity, mental health, e-cigarettes and tobacco harm reduction, HIV, sexual and reproductive health. He established and led PHE's Health Equity programme, focused on addressing the social determinants of health and promoting place-based approaches to health improvement.

Between 2005-2012, Professor Fenton was the Director of the National Centre for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention (NCHHSTP), within the Centres for Disease Control and Prevention (CDC) in America. He also served as chief of CDC's National Syphilis Elimination Effort, having worked in research, epidemiology, and the prevention of HIV and other STDs since 1995. Between 2000 and 2004, he was Director of the HIV and STI Department in the United Kingdom's Health Protection Agency and Senior Lecturer in HIV and STI epidemiology and control at University College London.

ESCAIDE

Plenary Speakers

Plenary session D: The inequality pandemic

Rossalina Latcheva

Austria
Programme Manager for Fair and Equal Societies, Research and Data Unit, European Union Agency for Fundamental Rights (FRA)

Rossalina Latcheva (PhD) is currently appointed as a senior Programme Manager for Fair and Equal Societies at the Research and Data Unit of the European Union Agency for Fundamental Rights (FRA) in Vienna. Her areas of expertise with respect to FRA's work include equality and non-discrimination, racism, xenophobia and related intolerance, migration and integration, gender-based violence, and mixed methods research. She is experienced in developing, collecting, and analysing primary and secondary data, as well as in applying diverse quantitative and qualitative research methodologies. Prior to joining FRA, she held a university post-doctoral position at the University of Zurich, Switzerland, and was appointed as a university lecturer at the University of Vienna, Austria. She holds a PhD in sociology from the Justus-Liebig University Giessen in Germany and has published a number of articles, book chapters and reports on migration, national and European identity, ethnic exclusion, violence against women and mixed methods research.

Information Stands

European Centre of Disease Prevention and Control

ECDC Public Health Training Section

The European Centre of Disease Prevention and Control (ECDC) is an EU agency aimed at strengthening Europe's defences against infectious diseases. The core functions cover a wide spectrum of activities: surveillance, epidemic intelligence, response, scientific advice, microbiology, preparedness, public health training, international relations, health communication, and the scientific journal Eurosurveillance.

ECDC disease programmes cover:
- Antimicrobial resistance and healthcare-associated infections
- Emerging and vector-borne diseases
- Food- and waterborne diseases and zoonoses
- HIV, sexually transmitted infections and viral hepatitis
- Influenza and other respiratory viruses
- Tuberculosis
- Vaccine-preventable diseases.

In 2021, ECDC continues to contribute to health security, giving particular attention to the following areas:
- Tackle antimicrobial resistance
- Improve vaccine coverage in the EU
- Support the European Commission and the Member States in addressing the Sustainable Development Goals in the area of HIV, TB and hepatitis
- Further support the European Commission and the Member States in strengthening the preparedness for cross-border health threats
- Focus on strategic partnerships to create synergy and avoid duplication of work
- Further enhance ECDC's operational performance and monitoring.
- The ECDC also monitors and provides information on COVID-19, and supports the response by Member States to the pandemic.

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

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.

www.ecdc.europa.eu/en/epiet-euphem

www.ecdc.europa.eu

Information Stands

ECDC Continuous Professional Development Programme

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).

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.

Eurosurveillance

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 post-print 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.

https://www.eurosurveillance.org/25years

Information Stands

EU Initiative on Health Security and MediPIET

The EU Initiative on Health Security aims to set up a regional workforce responsible for the prevention and control of challenges posed by communicable diseases and enhancing regional cooperation to tackle cross-border health security threats in EU candidate and potential candidates countries and European Neighbourhood Policy partner countries.

Project partners: Southern Neighbourhood (Algeria, Egypt, Israel, Jordan, Lebanon, Libya, Morocco, Palestine*, and Tunisia), Eastern Neighbourhood (Armenia, Azerbaijan, Belarus, Georgia, Moldova, and Ukraine) and EU Enlargement countries (Albania, Bosnia and Herzegovina, Kosovo**, Montenegro, North Macedonia, Serbia, and Turkey).

* This designation shall not be construed as recognition of a State of Palestine and is without prejudice to the individual positions of the Member States on this issue.
**This designation is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence

EPIET Alumni Network

The European Programme for Intervention Epidemiology Training (EPIET) Alumni Network (EAN) was founded in 2000 to help develop, maintain and fortify a network of European public health epidemiologists.

Members of the EAN are alumni of EPIET, the European Programme for Public Health Microbiology Training (EUPHEM) or alumni from Field Epimdemiology Training Programmes (FETP) of European Union (EU)/ European Economic Area (EEA) member states ot the United Kingdom. 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 seven elected members.

The objectives of the EAN are to:
- Provide EPIET, EUPHEM and FETP fellows with local support, including practical and technical assistance and including mentoring where appropriate.
- Facilitate the maintenance of the strong network within and between past EPIET, FETP and EUPHEM alumni and current fellows.
- Share and exchange professional experiences, information and skills among members.
- Constitute and enable access to a pool of expertise of trained European field epidemiologists and public health microbiologists, who can provide epidemiological, public health microbiological and public health expertise for members, their organisations, and other public and private organisations; the EAN participates in WHO's Global Outbreak Alert and Response Network (GOARN).
- Take part and assist in the promotion, development and delivery of training in field epidemiology, public health and public health microbiology.
- Contribute to both the logistical and scientific organisation of European field epidemiology and/or public health microbiology meetings, such as the annual European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE).

www.epietalumni.net

Information Stands

European Respiratory Society

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

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

Information Stands

European Society of Clinical Microbiology and Infectious Diseases

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 9,000 delegates virtually in 2021. ECCMID 2022 is planned as a hybrid congress (live + virtual) in Lisbon, Portugal.

www.escmid.org

TEPHINET

Founded in 1997, Training Programs in Epidemiology & Public Health Interventions Network (TEPHINET) is the global network of Field Epidemiology Training Programs (FETPs). With a secretariat based at The Task Force for Global Health in Atlanta, Georgia, USA, TEPHINET comprises more than 75 programs working across more than 100 countries to train «disease detectives» in disease surveillance and outbreak response. More than 19,000 FETP trainees have graduated from a TEPHINET member program.

Our vision is that all people are protected by a field epidemiology workforce capable of detecting and responding to health threats.

Our mission is to develop, connect, and mobilize a global field epidemiology workforce to strengthen public health systems and advance health security.

www.tephinet.org

Information Stands

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 21 years decades GOARN has conducted over 150 operations and deployed over 3500 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.

www.extranet.who.int/goarn

PANDEM-2

PREPARING FOR FUTURE PANDEMICS

PANDEM-2 is a H2020 EU-funded project that aims to develop new solutions for efficient, EU-wide pandemic management. The goal of PANDEM-2 is to prepare Europe for future pandemics through innovations in training and to build capacity between EU member states responding to pandemics on a cross-border basis.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No. 883285

https://pandem-2.eu/

Plenary Session Summaries

Plenary Session Summaries

Plenaries provide an opportunity to discuss public health challenges and scientific advances, bring together experts in cross-cutting fields to enable evidence from infectious disease research and epidemiology to be translated into improvements in public health.

The content of plenaries is proposed by the ESCAIDE Scientific Committee (10 cross-field members), who invite high level speakers to deliver inspiring presentations and address questions from the audience. There are four plenary sessions at ESCAIDE 2021, chaired by the ESCAIDE Scientific Committee. The format of each varies from panel discussions, interviews and debates.

PLENARY SESSION A
DAY 1, Tuesday 16 November
10:00-11:30

Chairs:
Mike Catchpole (ECDC)
Susan Hahné (RIVM, Netherlands)

Communicating science and scientific uncertainty during an evolving pandemic

Presented by

Peter Piot
European Commission
Marta Hugas
European Food Safety Authority (EFSA)
Mirjam Jenny
Harding Center for Risk Literacy, Germany
Vera Novais
Observador, Portugal

Summary

This session will provide ESCAIDE participants with insights into the challenges, but also the importance and the methods and approaches, to communicating scientific 'facts' and the scientific uncertainties in the face of a pandemic of an emerging infectious disease. The focus on this session is on the difficulties many scientists face communicating scientific data and uncertainty during a pandemic to different audiences including policy-makers, colleagues, journalists and the general public. The presentations will highlight the challenges of communicating in the context of sometimes conflicting societal, commercial and political needs and priorities, and reflect on the role of the internet and social media as channels for the dissemination of information and misinformation.

Abstract 1

Presented by Professor Peter Piot

COVID-19 is undeniably one of the most pressing global issues of our time. We were unprepared for a threat of this scale and immediately thrust into a state of mass uncertainty. When it came to communicating about the pandemic's evolving nature, oftentimes we faltered. Creating confusion and diminishing public trust.

Communicating science in a rapidly evolving, increasingly divided and highly politicized landscape is no easy task. Yet it is critical to do effectively if we are to build the political will and public trust needed to ensure a sustainable recovery.

In this conversation, Professor Peter Piot will reflect on some key learnings from the pandemic to date and offer insights for the road ahead.
How do we convey messages effectively when the truth changes? How do we counter narratives of skepticism and misinformation without minimizing valid questions, concerns or vaccine hesitancy? How do we maintain the integrity and independence of science in a context in which it is becoming increasingly politicized? Science is ever-changing and contested by its' very nature. How do we make space for scientific challenge and debate in a way that does not compound uncertainty in the midst of an emergency?

Addressing these questions will be crucial not only in the context of COVID-19 – the true impact of which remains to be felt – but also for the crises yet to come. We are entering an age of increasing public health threats. Good communication will be critical.

How the situation evolves in the months ahead depends not only on the virus but also on the policies we implement and the behaviours we engage in at an individual and societal level. Our words influence actions, and individual actions matter. For our messages to take true effect, we must ensure that we are speaking – and listening – to all voices.

Abstract 2

Presented by Marta Hugas and Anthony Smith

The EU food safety system and the European Food Safety Authority (EFSA) were conceived in the wake of the BSE food crisis of the late 1990s. Sporadic events over the past 20 years have tested and strengthened a robust crisis preparation and response system. EFSA has developed guidelines both for scientific risk assessment and for communication during food safety crisis situations. These focus on cooperation with national competent authorities to ensure there are procedures in place for long-term crisis preparedness and response situations. One of the lessons learnt during a 2011 multi-country e.Coli STEC outbreak was that contradictory messages from different authorities had played a role in confusing the public and jeopardizing their confidence in efforts to contain and trace the outbreak. Subsequently, EFSA re-invested in its Communication Expert Network (CEN) of Member State communicators and developed Crisis Communications Guidelines in 2016. These provide a four-step workflow for crisis communications: information gathering; preparation; communication; monitoring and review, that is repeated continuously throughout the stages of an incident: warning; risk assessment; response; management; resolution; and recovery. Dealing with uncertainty is a critical component in this framework, particularly in the early stages when 'facts are still uncertain'. Early-stage holding statements should address three basic questions even if all the answers are not known yet: what happened and how, what is being done about it. While doing so communication must make clear what is known, acknowledge what is uncertain, and indicate what is being done to address the knowledge gaps. EFSA's approach to uncertainty communication supports this framework by providing standardised numerical and verbal formats for expressing uncertainties, a requirement for positive framing about the extent of available knowledge, and the structured layering of information to support the goals of crisis communications.

Plenary Session Summaries

PLENARY SESSION B
DAY 2, Wednesday 17 November
10:00-11:30

Chairs:
Bruno Coignard (Santé publique France)
Magdalena Rosińska (NIPH-NIH, Poland)
Adam Roth (ECDC)

Modelling epidemics in real time: coming of age?

Presented by

Vittoria Colizza
INSERM and Sorbonne Université, France
Jacco Wallinga
RIVM and Leiden University Medical Centre, the Netherlands
Niel Hens
Hasselt University and University of Antwerp, Belgium

Summary

The COVID-19 pandemic has given new insights and built evidence through real-time modelling. In this session the panel will look at the contributions of real-time modelling to handling three different stages of the pandemic: early stages and the risk for importation and spread of the virus; forecasting cases and deaths and scenario building; and in evaluating the effectiveness of different interventions. They will give an insight into the major innovations in modelling during the pandemic and how these can be translated to other communicable diseases and how modelling can inform policy and communicate risk and uncertainty to press and policymakers. Finally, they will discuss how we can improve data-readiness to be better prepared in the future.

Abstract

Presented by Jacco Wallinga

Real-time modelling of the COVID-19 pandemic Both infectious disease experts and policy makers had to learn fast during the COVID-19 pandemic, in the sense that they frequently had to update any prior beliefs about infectious diseases and control measures in the face of new, unexpected observations. These observations could come from any of the data streams that have become available during the COVID-19 pandemic: daily case notifications, hospitalisations, deaths, vaccination coverage, vaccine efficacy, proportion infected by variant of the SARS-CoV-2 virus, contact patterns, mobility patterns. Real-time modelling can be used as a strategy to integrate the information from these data as observations come in, and it can be used to identify unexpected observations and learn from past observations by iteratively adapting the transmission model. We show how this strategy allows us to answer pragmatic questions such as: how transmissible is the circulating variant of the virus? how many notifications and hospitalisations do we expect today? how many IC admissions do we expect in the coming weeks? We highlight the importance of quantifying the uncertainty in forecasts and acknowledging the unknowns in the models.

PLENARY SESSION C
DAY 2, Wednesday 17 November
16:00-17:30

Chairs:
Vicky Lefevre (ECDC)
Petronille Bogaert (Sciensano, Belgium)

Digital health opportunities for Public Health: how far from reality?

Presented by

Ran Balicer
Clalit Research Institute, Israel
Gun Peggy Knudsen
Norwegian Institute of Public Health
Dipak Kalra
European Institute for Innovation through Health Data (i~HD)
Stefan Buttigieg
Digital Health Malta

Summary

This session will discuss insights on both the opportunities and the challenges of digital health for public health, and especially for infectious disease epidemiology, through presenting concrete examples. It will address how we can learn from digital technologies and digital health interventions used during the COVID-19 pandemic. It will cover the potential impacts of digital health on public health in the future, how to increase trust and how we move from talking about digital technologies in public health towards using digital health interventions as part public health systems.

ESCAIDE

Plenary Session Summaries

PLENARY SESSION D
DAY 3, Thursday 18 November
17:00-18:30

Chairs:
Stine Nielsen (EPIET Alumni Network)
Mircea Ioan Popa (Carol Davila University of Medicine and Pharmacy, Romania)
Frode Forland (Norwegian Institute of Public Health)

The inequality pandemic

Presented by

Ellen t'Hoen
Medicines Law & Policy, Netherlands
Kevin Fenton
UK Health Security Agency
Rossalina Latcheva
European Union Agency for Fundamental Rights (FRA)

Summary

There has been great inequity in how the coronavirus pandemic has impacted, and continues to impact, different groups – at both a global and country level – for cases, deaths, vaccine coverage and social and economic impact. How can this inequality be addressed? What can scientists, public health professionals, researchers, epidemiologists and medical practitioners do to contribute? This will address these questions, framed from the interlinking perspectives of access to healthcare, inequity in health provision for different communities and law and policy.

Fireside Session Abstracts

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

Fireside Session Abstracts

Fireside session 1 (Live Q&A panel)
Day 1, Tuesday 16 November 2021
13:30 – 15:00

Knowledge for policy and practice

Moderator

Ricardo Mexia (Instituto Nacional de Saúde Doutor Ricardo Jorge: INSA, Portugal)

Abstracts

a. Development of an Action Framework to mitigate vulnerabilities related to COVID-19 – the SONAR-Global VA-CE Study

T. Giles-Vernick [1]

A. Volkmann [2], J. Osborne [3], M. Geise [4], J. Paget [5], R. Kutalek [6], M. Dückers [7], D. Napier [8]

[1] Anthropology and Ecology of Disease Emergence Unit, Institut Pasteur, Paris

[2,8] Department of Anthropology, University College London

[3,4,5] Nivel

[6] Department of Social and Preventive Medicine, Medical University of Vienna

[7] Nivel; ARQ Psychotrauma Centre; Faculty of Social and Behavioural Sciences, University of Groningen,

Background:

We are developing an Action Framework to improve responses to infectious disease outbreaks with research methods and tools from the social sciences. The framework focusses on Community Engagement (CE) and is being drawn up in response to findings from the EU-funded SONAR-Global COVID-19 Vulnerability Assessment Study. The study is currently ongoing in five European countries and is assessing vulnerability and resilience in pandemic times through implementation of a large-scale Vulnerability Assessment (VA) protocol.

Methods:

Carried out in France, Germany, Italy, Malta, and Slovenia, each VA involves implementation of a demographic survey, interview protocol, and ethnographic observations in diverse participant pools (final N to exceed 100 per site and approximately 600 to 1000 overall). Data is coded and analyzed locally and, at various stages throughout the study, results are disseminated locally through various stakeholder engagement exercises, roundtables, and workshops. The proposed Action Framework builds on these engagement activities through established feedback and co-creation protocols.

Results:

To date, Partners in the study have identified and collaborated with multiple local stakeholders in each country (ranging from 2-23) to review and discuss implementation of the VA, first insights, and potential actions and interventions. Based on this, our research group (the SONAR-Global VA-CE Study) has drafted an Action Framework which lays out strategies for long-term Community Engagement around key issues identified in the VAs.

Conclusions:

The SONAR-Global VAs are providing valuable information to engage communities and local stakeholders around potential ways of mitigating the negative impacts of the COVID-19 pandemic and to strengthen community resilience. Our Action Framework is key to translating research findings into actions and has applications for other infectious disease outbreaks in Europe and elsewhere.

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

Keywords: stakeholder engagement, community participation, social sciences, COVID-19,vulnerable populations, Europe

ABSTRACT ID: 148

PRESENTED BY: Jacob Osborne / j.osborne@nivel.nl

b. COVID-19 vaccination prioritization: factors associated with mortality among COVID-19 cases in Sweden in 2020

M. Jansson Mörk [1]

H. Darabi [2], L. Martin [3]

[1] Public Health Agency of Sweden; European Programme for Intervention Epidemiology Training (EPIET)

[2,3] Public Health Agency of Sweden

Background:

Sweden's COVID-19 vaccination recommendations aim to protect individuals at increased risk of serious outcomes. Individuals living/working in long-term care or receiving/giving home care were given highest priority for vaccination. Based on the literature, individuals ≥70 years old were initially planned for the second highest priority group (Phase 2). However, to inform vaccination prioritization based on Swedish data, we investigated how age, sex, and comorbidities were related to mortality among COVID-19 cases.

Methods:

We conducted a retrospective cohort study of all laboratory-confirmed COVID-19 cases aged 50-69 years notified in Sweden (02/2020-12/2020). Comorbidity data for 2019 were assessed via the national patient register (ICD-10 codes) and via proxy definition using the drug prescription register (ATC codes). Multivariable Cox proportional hazards regression was used to model mortality ≤30 days from COVID-19 diagnosis. Independent variables included comorbidities, age, sex, pandemic period (February-May vs. June-December), and the interaction between age and sex.

Results:

We included 91,541 cases, 576 of whom died (0.63%). Most cases (53%) were female. Mortality increased with age and was higher for males. Compared to the reference group (females aged 50-54), the adjusted hazard ratio (aHR) was 28 (95% confidence interval [CI]=16-48) for males aged 65-69 and 13 (95% CI=7.2-23) for females aged 65-69. Compared to the absence of each comorbidity, liver disease (aHR=3.2, 95% CI=1.8-5.4), neuromuscular disease (aHR=2.2, 95% CI=1.4-3.4), and pulmonary disease (aHR=2.1, 95% CI=1.5-3.0) were most strongly associated with mortality.

Conclusions:

Older age and male sex were strongly positively associated with mortality, as previous studies have shown; these relationships were stronger than for any comorbidity. These results contributed to COVID-19 vaccine prioritization in Sweden, extending Phase 2 to include individuals ≥65 years of age.

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

Keywords: COVID-19, comorbidities, mortality, outcomes of disease

ABSTRACT ID: 122

PRESENTED BY: Marie Jansson Mörk /

Fireside Session Abstracts

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c. Impact of a pneumococcal polysaccharide vaccination program on invasive pneumococcal disease in elderly in the Netherlands

A. Niessen [1]

H. van Werkhoven [2], H. de Melker [3], N. van Sorge [4], R. van Gageldonk-Lafeber [5], M. Knol [6]

[1] RIVM

[2] UMC Utrecht

[3,5,6] RIVM

[4] Amsterdam UMC

Background:

In October 2020 a national program for pneumococcal vaccination in elderly was started in the Netherlands. All persons born between 1941 and 1947 were offered the 23-valent pneumococcal polysaccharide vaccine (PPV23). Vaccination coverage is estimated at 76% in the vaccine-eligible group. We evaluated the impact of this program on invasive pneumococcal disease (IPD) in the first respiratory season after implementation.

Methods :

IPD isolates from the majority of the Dutch hospital laboratories are routinely collected and serotyped. We calculated the odds ratio (OR) for having IPD due to a PPV23 vaccine type strain (VT-IPD) in elderly eligible for vaccination (73-79 years) compared to elderly ineligible for vaccination (60-72 years and 80 years and above) between 1 October 2020 and 30 April 2021. This was compared with an OR for the same months during the four previous respiratory seasons (2016/2017–2019/2020).

Results :

In the study period, 237 cases of IPD were reported among persons of 60 years and older, with 42 cases among the vaccine-eligible age-categories. The proportion of VT-IPD in those eligible for vaccination was 62% versus 74% in those not eligible with an OR of 0.56 (95% CI 0.28–1.15). The OR for having VT-IPD during the same period within the previous four seasons (n=3075) was 1.19 (95% CI 0.96-1.49). Corrected for the OR in the previous seasons, the impact of vaccination was 0.47 (95% CI 0.23–0.99).

Conclusions :

First results of the impact of PPV23 vaccination program show considerable impact among elderly eligible for vaccination. Overall IPD numbers this respiratory season are still small, presumably due to COVID-19-related social distancing, requiring a longer observation period. Vaccine effectiveness will be estimated when individual vaccination data become available.

d. Pertussis epidemiology and indirect impact of the childhood pertussis booster vaccinations, Norway, 1998-2019

E. Seppälä [1]

A. Kristoffersen [2], H. Bøås [3], D. Vestrheim [4], M. Greve-Isdahl [5], B. De Blasio [6], A. Steens [7]

[1] Norwegian Institute of Public Health; European Program for Intervention Epidemiology Training, European Centre for Disease Prevention and Control

[2,3,4,5,6,7] Norwegian Institute of Public Health

Background:

The acellular pertussis vaccine has been used in the Norwegian national immunisation programme since 1998. Following an increase in pertussis incidence in all age groups, booster doses were introduced for 7-8-year-olds in 2006, and for 15-16-year-olds in 2013/2014. We assessed the impact of the booster doses on pertussis incidence in different age groups.

Methods :

We included all pertussis cases notified to the Norwegian Surveillance System for Communicable Diseases in 1998-2019. We calculated annual incidence rates (IR, per 100,000 inhabitants) by age group. We estimated average annual changes in IRs (incidence rate ratios, IRR) for each age group for 2006-2012 and 2013-2019 using Poisson regression.

Results :

In 1998-2019, 74,675 cases of pertussis were notified. Coinciding with booster introduction, between 2006-2012 the IR decreased among 8-15-year-olds (from 433 to 199/100,000, IRR 0.89 [95% confidence interval 0.88-0.90]). A similar decrease was seen between 2013-2019 among 16-19-year-olds (from 171 to 77/100,000, IRR 0.84 [0.82-0.86]). There was no significant change in IRs among children <1 year of age between 2006-2012 (IRR 0.99 [0.95-1.04]) or 2013-2019 (IRR 0.96 [0.91-1.02]). The IR decreased in both periods among adults aged 20-39 and 40+ (IRR 0.94 [0.93-0.95] and 0.92 [0.91-0.92] in 2006-2012; IRR 0.97 [0.96-0.99] and 0.97 [0.96-0.99] in 2013-2019, respectively). Despite steady, high vaccination coverage, in 2013-2019, there was an increase in the IR among children aged 1-7 (63 to 86/100,000, IRR 1.05 [1.03-1.07]) and 8-15 (88 to 122/100,000, IRR 1.08 [1.06-1.10]) years.

Conclusions :

Pertussis booster doses have offered direct protection in the targeted age groups. We observed an indirect protection in adults, but not in infants. The recent increase in IRs among 1-15-year-olds warrants close monitoring and further evaluation of the vaccination schedule.

e. Improving understanding of HIV key populations through national surveillance in Ireland, 2019

M. Brady [1]

A. Shanley [2], E. Nugent [3], K. O'Donnell [4], C. Hurley [5], M. Fitzgerald [6], G. Fitzpatrick [7], E. Coughlan [8], C. Flynn [9], R. Carson [10], Y. Luky [11], C. Kennedy [12], J. McDonagh [13], D. Igoe [14]

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[4,14] Health Service Executive-Health Protection Surveillance Centre (HPSC), Ireland

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[6] Health Service Executive-Social Inclusion/Vulnerable Groups, Ireland

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[8] Safetynet Primary Care, Ireland

[9] Gender Orientation Sexual Health and HIV (GOSHH), Ireland

[10,11] AIDS Care Education and Training (ACET), Ireland

[12] Sexual Health Centre (SHC), Cork, Ireland

[13] Sexual Health West, Ireland

Background:

Since 2018, community-based organisations (CBOs) report anonymised voluntary community-based HIV testing (VCBT) data to the Health Protection Surveillance Centre (HPSC). VCBT services focus on key populations at higher risk of acquiring HIV, to support early diagnosis and treatment. We aimed to improve our understanding of HIV key populations in Ireland in order to provide public health guidance and recommendations for VCBT strategies.

Methods :

We carried out descriptive analysis of 2019 VCBT data, focusing on previously undiagnosed people for the first time. Variables analysed were: age, sex, country of birth, first time testing, and prior HIV diagnosis.

Results :

CBOs reported 5,607 HIV tests in 2019; 92 people (1.6%) had a reactive test result, similar to the proportion in 2018 (1.7%). The test reactive rate (seropositivity rate) among previously undiagnosed people was 0.5% (n=24), and was higher in females (0.9%) than in males (0.4%) (p <0.001). Of the 24 new diagnoses, 11 were female and were born in sub-Saharan African (SSA) countries of high HIV prevalence (median age 31 years; range 24-47); 3 were male and were born in high prevalence SSA countries (age range: 31-54); and 10 were men who have sex with men (MSM) born in a range of other countries (Ireland (n=3), Latin America (n=3), East Asia & Pacific (n=1), Western Europe (n=1), Central/Eastern Europe (n=1), and unknown (n=1)). Among newly diagnosed MSM, median age was 26 years (range: 19-34); 4 were first-time testers (range: 19-26) and 6 were repeat testers (range: 22-34).

Conclusions :

Considering the different demographic profile by sex among people with undiagnosed HIV in Ireland, a gender orientated approach to VCBT strategies could be beneficial. Continued monitoring and analysis can help inform future strategies.

Subject : Surveillance
Keywords: Surveillance, HIV Testing, Community,Key populations,Key marginalised populations,HIV
ABSTRACT ID: 90
PRESENTED BY: Melissa Brady / melissa.brady@hpsc.ie

Fireside session 2
Day 1, Tuesday 16 November 2021
13:30 – 15:00

COVID-19: Field Epidemiology

Moderator

Jan Walter (Robert Koch Institute, Germany)

Abstracts

a. Risk factors for SARS-CoV-2 antibody positivity in healthcare workers, a multicentre cross-sectional study of participants within SIREN, June – November 2020,

S. Foulkes [1]

V. Hall [2], A. Charlett [3], A. Atti [4], E. Wellington [5], P. Kirwan [6], R. Simmons [7], M. Kall [8], K. Munro [9], J. Khawam [10], A. Vusirikala [11], M. Shrotri [12], M. Chand [13], C. Brown [14], S. Hopkins [15]

[1,2,3,4,5,6,7,8,9,10,11,12,13,14,15] PHE

Background :
Healthcare workers have been disproportionately infected with SARS-CoV-2 and preventing future transmission requires characterisation of risk factors.

Methods :
This analysis is a cross-sectional study within SIREN, a large multi-centre cohort study among individuals working in hospitals in England. Upon enrolment participants undergo SARS-CoV-2 PCR and antibody testing and complete an online questionnaire, providing information on demographics, symptoms and occupational, household and community exposures. The primary outcome was being antibody positive at enrolment. Participants included if they had baseline testing within 30 days of enrolment and enrolled before December 2020 (to exclude antibody positivity following vaccination). Participants were described by their demographics and exposures and timing of primary infection, and factors associated with being antibody positive were investigated using a mixed effect multivariable in logistic regression analysis.

Results :
22,788 participants enrolled between June and November 2020 from 102 Trusts in England. There were 6,742 antibody positive participants (29.6%) and 16,046 (70.4%) antibody negative. The strongest risk factor for being antibody positive, was having contact with a confirmed COVID-19 case within the household (adjusted Odds Ratio 4.19 (95%CI 3.59-4.88). The strongest occupational risk was frequency of contact with COVID-19 patients, with those with daily contact having twice the odds of those with no contact (aOR 2.05 (95%CI 1.87-2.25)). Participants were also more likely to be antibody positive if they were from an ethnic minority, older or male.

Conclusions :

Whilst healthcare workers experienced specific exposures at work that increased their odds of infection, their greatest exposure was in the household and related to their ethnicity, age and gender. Protecting healthcare workers from SARSCoV-2 infection requires action to interrupt community transmission in addition to effective infection prevention and control strategies at work.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : COVID-19,healthcare workers,SARS-CoV-2
ABSTRACT ID: 207
PRESENTED BY: Sarah Foulkes / sarah.foulkes@phe.gov.uk

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b. Two choir outbreaks in March 2020 demonstrate the importance and determinants of aerosol-mediated long-range transmission of SARS-CoV-2, Berlin

F. Reichert [1]

O. Stier [2], A. Hartmann [3], C. Ruscher [4], A. Brinkmann [5], M. Grossegesse [6], M. Neumann [7], D. Werber [8], M. Hausner [9], M. Kunze [10], B. Weiß [11], J. Michel [12], A. Nitsche [13], M. Kriegel [14], V. Corman [15], T. Jones [16], C. Drosten [17], T. Brommann [18], U. Buchholz [19]

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[11] Local health authority "Charlottenburg-Wilmersdorf", Berlin, Germany

[12,13] Robert Koch Institute, Berlin, Germany

[14] Technical University of Berlin, Hermann Rietschel-Institute, Berlin, Germany

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[18] Berlin Cathedral Choir, Berlin, Germany

[19] Robert Koch Institute, Berlin, Germany

Background :

To date, few examples have convincingly demonstrated aerosol-mediated long-range (LR) transmission of SARS- CoV-2. In March 2020, two outbreaks occurred at different choir rehearsals in Berlin, Germany. We investigated these outbreaks to analyse the risk and determinants of indoor LR transmission (>1,5m).

Methods :

We performed two retrospective cohort studies and used clinical, diagnostic and contact data as well as whole genome sequencing to identify primary cases. Cases were confirmed by SARS-CoV-2 PCR or serology. We measured individual particle emission of choir members, calculated air particle concentrations and derived probabilities for LR transmission by Bayesian inference.

Results :

We included 65 (84%) and 42 (100%) participants of the two choir rehearsals. The primary case of choir 1 (mostly singing) infected the primary case of choir 2 (choir director, only occasional singing), both were pre-symptomatic at rehearsal. Attack rate in choir 1 (89%, 95%CI: 79-96%) was significantly higher than in choir 2 (24%, 12-39%). Median particle emission rate when singing was 7 times higher compared to talking. In choir 1, the median concentration of primary cases' emitted particles was 8 times higher, exposure at least 30 minutes longer and room volume smaller than in choir 2, resulting in markedly different estimated probabilities for LR transmission (median: 89% vs. 18%, 95%CI: 80-95% vs. 6-36%).

Conclusions :

Indoor activities may entail an LR transmission risk anywhere in the room.

Assuming comparable infectiousness of primary cases, we conclude that the duration of singing and particle emission, and smaller room volume led to higher concentrations of partially infectious aerosol, higher probability of LR transmission and a higher attack rate. These examples strongly support public health recommendations to avoid indoor contacts and singing.

c. Do antibody positive healthcare workers have lower SARS-CoV-2 infection rates than antibody negative healthcare workers in England: June 2020 to January 2021

S. Foulkes [1]

V. Hall [2], A. Charlett [3], A. Atti [4], E. Monk [5], E. Wellington [6], M. Cole [7], S. Rokadiya [8], B. Oguti [9], K. Munro [10], M. Zambon [11], M. Ramsay [12], T. Brooks [13], C. Brown [14], M. Chand [15], S. Hopkins [16]

[1] [2,3,4,5,6,7,8,9,10,11,12,13,14,15,16] PHE

Background :

There is an urgent need to better understand whether individuals who have recovered from Coronavirus Disease 2019 are protected from future SARS-CoV-2 infection.

Methods :

A large multi-centre prospective cohort recruiting hospital staff in the UK was established in Jun-2020. Participants attended regular SARS-CoV-2 PCR and antibody testing and completed fortnightly questionnaires on symptoms and exposures. At enrolment, participants are assigned to the antibody positive or negative cohort. The primary outcome was a reinfection in the positive cohort or primary infection in the negative cohort, determined by PCR tests. Potential reinfections were clinically reviewed and classified according to case definitions. Primary infections in the negative cohort were defined as a first PCR positive test and seroconversions were excluded when not associated PCR positive test. A proportional hazards frailty model using a Poisson distribution was used to estimate Incidence Rate Ratios (IRR), to compare infection rates in the two cohorts.

Results :

Between Jun-2020 and Jan-2021, 155 infections were detected in the positive cohort of 8,278 participants, collectively contributing 2,047,113 days of follow-up. This compares with 1,704 new PCR positive infections in the negative cohort of 17,383 participants, contributing 2,971,436 days of follow-up. The incidence density per 100,000 person days between June 2020 and January 2021 was 7.6 reinfections in the positive cohort, compared with 57.3 primary infections in the negative cohort. The adjusted IRR was 0.16 for all reinfections (95%CI 0.13-0.19) compared to PCR confirmed primary infections.

Conclusions :

A previous history of SARS-CoV-2 infection was associated with an 84% lower risk of infection, with median protective effect observed 7 months following primary infection. This study shows that previous infection with SARS-CoV-2 induces effective immunity to future infections in most individuals.

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PRESENTED BY: Sarah Foulkes / sarah.foulkes@phe.gov.uk

d. Factors associated with an outbreak of COVID-19 in oilfield workers, Kazakhstan, June-September 2020

D. Nabirova [1]

R. Taubayeva [2], A. Maratova [3], M. Kalkanbayeva [4], A. Yesmagambetova [5], S. Nassyrova [6]

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Background :

By June 2020 Kazakhstan suspended two-third of the oilfield workforce after 2,661 cases of COVID-19 were reported despite implemented preventive measures. We assessed individual and environmental factors associated with the COVID-19 transmission in the facility.

Methods :

Cases were employees of selected shift camps with the highest incidence who tested positive for SARS-CoV-2 during June-September 2020. We selected randomly controls from SARS-CoV-2 negative employees who concurrently lived at the same shift camps. Sociodemographic data, information on knowledge, attitude, practice towards COVID-19, working and living environment were collected. In addition to descriptive epidemiology, bivariate and multivariate logistic regression analyses were performed with R software. Factors significant in the bivariate analysis ($p < 0.05$) were considered in a multivariable analysis. Adjusted odds ratios (aOR), 95% confidence intervals (CI) were calculated by multivariate logistic regression.

Results :

The study had 296 cases and 536 controls with 627 (75%) men and 527 (63%) participants below 40 years of age. Of the seventeen studied individual factors, rare antiseptic use (adjusted odds ratios (aOR)=4.1, 95% confidence intervals (CI)=1.8-10.1), non-use at the workplace (OR=2.96, 95%CI=1.24-7.62), travel before shift work (aOR=2.8, 95%CI=1.0-7.9), and social interaction outside of work (aOR=1.8, 95%CI=1.2-2.9) were associated with increased COVID-19 transmission. Belief that asymptomatic COVID-19 is contagious (aOR=0.5, 96% CI=0.3-0.8), belief that facemasks protect in public places (aOR=0.4, 96% CI=0.2-0.8), and use of fabric facemasks (aOR=0.3, 96% CI=0.2-0.5) appeared to be protective against COVID-19. Of the nineteen environmental factors only air-conditioned premises (aOR=4.0, 95%CI:1.3-13.1) was associated with COVID-19 transmission.

Conclusions :

Individual factors were the main drivers of COVID-19 transmission; environmental factors contributed little to the transmission. Communication messages should enhance workers' individual responsibility and responsibility for the safety of others to reduce COVID-19 transmission.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : occupational setting, COVID-19, oil field, Kazakhstan, environmental factors, individual factors, outbreak

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e. [late breaker] Phylogeny-assisted estimation of secondary attack rate in a large regional COVID-19-Delta cluster in the South of Germany at the beginning of Delta-transmission, May/June 2021

Y. Zimnitskaya [1]

K. Licht [2], O. Tornseifer [3], C. Bauer [4], F. Burckhardt [5]

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[5] Department of Health Protection and Epidemiology, Baden-Wuerttemberg State Health Office, Stuttgart, Germany

Background :

After introduction of new variants-of-concern, critical parameters like secondary attack rates (SAR) need to be established quickly by analysing local outbreaks. In May/June 2021 a cluster of 94 SARS-CoV-2-positive cases with Delta variant occurred in Heidenheim, Germany at a time with Delta-prevalence still below 5%. PHE-reported SAR in household contacts for Delta variant at this time were about 15%. Using epidemiologic and phylogenetic data of this cluster, we calculated SAR for first (G1) and second (G2) generation cases.

Methods :

All close contacts according to national guidelines of a SARS-CoV-2-positive case were immediately tested by PCR after notification, at their symptom onset (if applicable) and at the end of quarantine. Samples were sent to our lab for sequencing. We calculated SAR with 95% confidence intervals (95%CI) for laboratory-confirmed Delta cases with transmission chains informed by a) epidemiology only and b) epidemiology and phylogeny. SAR was calculated for G1 and G2 generation cases.

Results :

The cluster consisted of 94 mostly household cases of which 51 were asymptomatic. 49 cases could be sequenced of which 47 shared 0-2 SNP differences. 55 of 94 cases had no contacts. Of 21 G1 cases with contacts, 146 contacts led to 58 infections (SAR 39.7%, 95%CI: 31.7-48.1). Of 12 G2 cases with contacts, 103 contacts led to 11 infections (SAR 10.7%, 95%CI: 5.5-8.3). Sequence-assisted confirmation of transmission chains could exclude transmission events and gave 23 G1 (13 G2) cases with 147 (102) contacts and 58 (10) PCR-confirmed infections (G1 SAR 39.5%, 95%CI: 31.5-47.8; G2 SAR 9.8%, 95%CI: 4.8-17.3).

Conclusions :

Rapid testing and quarantine of contacts stopped transmission chains by detecting asymptomatic cases and lowered SAR from 39.5% to 9.8% while sequencing information refined transmission data.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Secondary Attack Rate, Whole Genome Sequencing, Outbreaks,SARS-CoV-2 delta variant, Germany

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Fireside session 3
Day 1, Tuesday 16 November 2021
15:15 – 16:00

COVID-19: Surveillance

Moderator

Isabel Noguer (Instituto de Salud Carlos III, Spain)

Abstracts

a. The World Health Organization's global detection, assessment and monitoring of emerging SARS-CoV-2 variants of concern (VOCs)

R. Medialdea Carrera [1]

E. Kukielka [2], I. Nezu [3], Z. Kassamali [4], S. Mesfin [5], A. Awofisayo-Okuyelu [6], H. Laurenson-Schafer [7], L. Carter [8], L. Subissi [9], E. Hamblion [10], B. Archer [11]

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[8,9] Laboratory Networks, Infectious Hazards Management, WHO Emergencies Programme, World Health Organization

Background :

SARS-CoV-2 variants are emerging globally amidst high viral transmission rates, some potentially impacting transmission, disease severity, diagnostics, therapeutics and vaccines. WHO and partners developed a framework to routinely identify and assess potential public health implications of these variants to inform ongoing surveillance and mitigation measures.

Methods :

Through multidisciplinary collaboration, a risk assessment framework was applied to 1) identify signals of variants of potential interest or concern through event-based surveillance, Member States' (MS) notifications and expert information sharing; 2) undertake rapid epidemic intelligence to verify and gather suggestive or demonstrated impacts of these variants; and 3) assess risks posed to global public health based on criteria outlined in the WHO working definitions of variants of interest (VOIs) and variants of concern (VOCs), in collaboration with the WHO Viral Evolution Working Group (VEWG) and WHO teams worldwide.

Results :

The framework developed and facilitated the establishment of criteria and working definitions to categorise SARS-CoV-2 variant signals; the development of integrated systems and databases for daily global surveillance; and, the generation of surveillance guidance. Using this framework, as of 08 October 2021, WHO has designated 4 VOCs, 2 VOIs and 14 variants for further monitoring. Active communication to assist MS and the global scientific community in prioritizing surveillance, investigation and response activities is ongoing.

Conclusions :

As SARS-CoV-2 variants continue to emerge, early detection, rapid risk assessments and global surveillance are essential for timely responses and to inform mitigation measures against further spread of COVID-19. The WHO risk framework provides an objective evidence-based approach for characterising variants of global interest or concern, as well as a forum for multidisplinary collaboration to support the control of the COVID-19 pandemic.

b. Wastewater-based surveillance of SARS-CoV-2 to monitor the COVID-19 epidemic in Limassol, Cyprus

P. Karaolia [1]

A. Quattrocchi [2], I. Iakovides [3], P. Loutsiou [4], Y. Tsouloftas [5], D. Michaelides [6], O. Kalakouta [7], G. Nikolopoulos [8], D. Fatta-Kassinos [9]

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Background :

This study aimed to explore the potential link between community COVID-19 prevalence and wastewater concentrations of SARS-CoV-2-specific genes.

Methods :

Between 01/01-09/05/2021, composite 24-h samples collected from the Limassol wastewater treatment plant (WWTP) were analysed for the N2 and E SARS-CoV-2-specific genes, using reverse transcription-quantitative polymerase chain reaction. Viral concentrations were reported as $\log_{10}$ gene-copies/L (gc/L). Daily COVID-19 diagnosed cases in Limassol district were extracted from the national COVID-19 surveillance system and the 14-day cumulative number of COVID-19 cases was calculated as a proxy of active cases excreting the N2 and E genes. Notably, the weekly testing rate in Cyprus has been >5,000 tests per 100,000 population during the study period. Pearson correlation and time-series linear regression analyses were performed.

Results :

N2 and E wastewater concentrations very strongly correlated (r=0.95; p<0.001) and ranged between 1.5-6.1 gc/L. Furthermore, the 14-day cumulative number of cases strongly correlated with both N2 and E wastewater concentrations (r=0.83 and r=0.81, respectively; p<0.001). The pattern of decrease/increase of SARS-CoV-2 in wastewater was closely comparable to the change in active COVID-19 cases. The regression models explained 77% and 73% of the variability of the 14-day cumulative case number and its association with N2 and E wastewater concentrations was significant (p<0.001).

Conclusions :

In this study, monitoring the concentrations of SARS-CoV-2-specific genes in wastewater well depicted the trend of the COVID-19 epidemic. Wastewater-based surveillance may serve as a useful tool to support existing COVID-19 surveillance systems and as a valuable early-warning of the circulation and (re)emergence of SARS-CoV-2 infections. Additionally,

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it has the capacity to reflect the state of the pandemic, in settings with limited testing capacity. This research was funded by the Sewerage Board of Limassol-Amathus (SBLA).

Subject : Surveillance

Keywords : Early-warning system,Wastewater,Cyprus,Surveillance

ABSTRACT ID: 200

PRESENTED BY: Annalisa Quattrocchi / quattrocchi.a@unic.ac.cy

c. Estimation of the serial interval of COVID-19 for two different time periods using contact data collected by the Irish Contact Management Programme

C. Carroll [1]

G. Cosgrove [2], S. Allwright [3], P. Kearney [4], C. McAloon [5], S. Doyle [6], G. Martin [7], J. Martin [8], C. Buckley [9]

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[9] COVID-19 Contact Management Programme, Health Service Executive; School of Public Health, University College Cork

Background :

The serial interval is an epidemiological parameter used in models predicting disease trends and healthcare demands. This study set out to estimate COVID-19 serial interval in the Republic of Ireland (RoI) across two time periods, to improve assessment of transmission dynamics and refine public health measures.

Methods :

Irish Contact Management Programme data were used to calculate the interval between symptom onset in primary and secondary cases (serial interval). Two periods were analysed, 1 September – 4 November 2020 and 1-28 February 2021. Sep-Nov saw a rapid growth in case numbers (mean 538.4 cases/day, range 84-1283) and an escalation from moderate to severe restrictions on 21 October. Severe restrictions remained in place in February following the third wave of COVID-19 in December/January and increasing prevalence of variant B.1.1.7 (mean 833.4 cases/day, range 556-1318).

Results :

2988 (Sep-Nov) and 2321 (February) eligible secondary cases were identified. The mean (median) serial interval decreased from 4.7 (4.0) days in Sep-Nov to 3.8 (3) days in February. The proportions symptomatic by time point were significantly higher in February than Sep-Nov: 56.4% vs 43.4%, 78.2% vs 67.4%, and 96.1% vs 93.8% by days 3, 5 and 10 respectively (all p<0.01). Earlier symptom onset in February was especially noticeable in secondary cases linked to younger index cases (e.g. 63.5% symptomatic at day 3 [index case 0-14 years] vs. 41.8% [index case 65+ years], p<0.01).

Conclusions :

These data show a reduction in the serial interval between late 2020 and early 2021. This may be attributable to the increasing predominance of the variant B.1.1.7 and/or different restrictions in place in February. These findings emphasize the importance of rapid identification of close contacts with an agile contact management programme.

Subject : Surveillance

Keywords : Communicable Disease Contact Tracing,COVID-19,Ireland / epidemiology,Infectious Disease Transmission,SARSCoV-2 B.1.1.7 variant,Time Factors

ABSTRACT ID: 227

PRESENTED BY: Ciara Carroll / ciara.carroll@ucdconnect.ie

d. Epidemiology of COVID-19 in children and adolescents in the EU/EEA

A. Baka [1]

N. Bundle [2], A. Danielsen [3], C. Deogan [4], A. Mougkou [5], A. Pharris [6], G. Spiteri [7], J. Suk [8], M. Tseroni [9], S. Sharma [10]

[1] ECDC

[2,3,4,5,6,7,8,9,10] ECDC

Background :

Children and adolescents represent 20.3% of the population in the European Union/European Economic Area (EU/EEA), but little is known about the epidemiology of COVID-19 in this group. Our aim is to provide an epidemiological overview of COVID-19 in children and adolescents.

Methods :

We obtained data from The European Surveillance System for individuals aged ≤19 years in 28 EU/EEA countries, from 31/01/2020 to 21/09/2021. We computed cumulative and age-sex specific COVID-19 incidence and mortality rates at EU/EEA-level. We calculated hospitalisation and intensive care unit (ICU) admission rates for 14 countries. Rates are reported per 100,000 population in the relevant sex-age stratum.

Results :

As of 21/9/2021, 5,693,583 cases and 170 deaths were reported, accounting for 16.8% and 0.01% of total COVID-19 cases and deaths, respectively. The incidence was highest among adolescents aged 15-19 years (126.34 [95% CI: 126,11-126,57]). Mortality was highest among adolescents (0.29 [0.19-0.39]), followed by children aged 0-4 years (0.23 [0.13-0.32]). In 14 EU/EEA countries reporting, 21,509 cases were hospitalised and 727 were admitted to an ICU, accounting for 0.37% and 0.01% of total COVID-19 related hospitalisations and ICU admissions, respectively Hospitalisation rates were highest among children aged 0-4 years (males: 78.7 [76-80]; females: 65.4 [63-67]), followed by adolescents (females: 61.7 [59-63]; males: 51.8 [50-53]). Males aged 15-19 and 0-4 years had the highest ICU admission rates: 2.5 [2.1-2.9] and 2.3 [1.9-2.7], respectively.

Conclusions :

COVID-19 incidence and mortality are lower in children/adolescents than in adults. In children/adolescents, COVID-19 is often mild and testing strategies vary. Therefore, COVID-19 is likely underreported in this group. Nevertheless, children/adolescents have emerged as a priority population for detection and control of COVID-19 as greater proportions of adults become fully vaccinated.

Subject : Burden of disease

Keywords : SARS-CoV-2, COVID-19, children, adolescents, paediatric, infants

ABSTRACT ID: 141

PRESENTED BY: Aikaterini Mougkou / aikaterini.mougkou@ecdc.europa.eu

Fireside Session Abstracts

e. [late breaker] COVID-19 outbreaks in long-term care facilities for older people, Ireland March 2020-August 2021; reduction in outbreak severity following vaccine rollout

P. Garvey [1]

A. Colgan [2], M. Madigan [3], C. Brehony [4], C. Dillon [5], U. Gurpinar [6], E. Robinson [7], J. O'Donnell [8], J. Cuddihy [9], L. O'Connor [10]

[1,2,3,4,5,6,8,9,10] Health Protection Surveillance Centre

Background :

The Irish COVID-19 vaccination programme prioritised vaccination of staff and residents in long-term care facilities (LTCFs) for older people in January 2021 because of the disproportionally high COVID-19 morbidity and mortality among elderly residents. We aimed to assess the impact on features of outbreaks in these settings following the implementation of the COVID-19 vaccination programme.

Methods :

We describe COVID-19 outbreaks notified in Ireland between March 1st 2020 and August 31st 2021, comparing the median outbreak size, number of deaths, case fatality and duration of outbreaks pre and post the vaccination program (31st January cut-off) using the Wilcoxon rank-sum test.

Results :

We included 582 outbreaks notified in LTCFs for older people, with 16,709 associated confirmed cases among staff and residents, and 2,047 deaths. Outbreaks ranged in size from 2 to149 cases, with time-interval between the first and last case of 0 to 204 days. Between 0 and 36 deaths among confirmed cases were reported per outbreak. This equated to case fatality rates of between 0% and 53.8% per outbreak (or 0% and 100% when analyses were confined to cases >65 years of age). Following the vaccination programme, there were statistically significant reductions in the median size of outbreaks from 22 to 9 cases (P=0.0001), the median duration of outbreaks from 25 to 13 days (P<0.0001), the median number of deaths from 2 to 0 per outbreak (P<0.0001), the median case fatality from 7.5% to 0% (P<0.0001) and the median case fatality in cases 65 years or older from 18% to 0% (P<0.0001).

Conclusions :

In conclusion, it appears that the January 2021 vaccination programme has been effective in reducing the severity of outbreaks in LTCFs for older people in Ireland.

Subject : Surveillance
Keywords : COVID-19; Long term care; disease outbreaks; vaccination
ABSTRACT ID: 302
PRESENTED BY: Patricia Garvey / patricia.garvey@hse.ie

Fireside session 4
Day 1, Tuesday 16. November 2021
15.15 – 16.00

Food and waterborne diseases and zoonoses: outbreaks

Moderator

Johanna Takkinen (ECDC)

Abstracts

a. Incubation period, spore shedding duration, and symptoms of Enterocytozoon bieneusi infection in a foodborne outbreak in Denmark, 2020

D. Michlmayr [1]

L. Alves de Sousa [2], L. Müller [3], P. Jokelainen [4], S. Ethelberg [5], L. Vestergaard [6], S. Schjørring [7], L. Dam Rasmussen [8] , C. Stensvold [9]

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[8] Department of Virus and Microbiological Special Diagnostics, Statens Serum Institut, Copenhagen, Denmark

Background :

Enterocytozoon bieneusi belongs to microsporidia, a group of spore-forming organisms rarely reported as causes of foodborne outbreaks. Nevertheless, E. bieneusi was identified as the causative agent in an outbreak of diarrheal disease affecting 77 employees who bought lunch from a workplace canteen in Denmark in November 2020.

Methods :

A web-based questionnaire was sent to the employees of the company; stool samples were tested by culture for bacterial pathogens and by PCR for viral and parasitic pathogens, including E. bieneusi. Employees positive for E. bieneusi were encouraged to continue submitting stool samples to determine the duration of spore shedding.

Results :

We conducted a retrospective cohort study including cases who worked at the affected company and reported at least one gastrointestinal symptom between November 4 to December 13, 2020. From the questionnaire, we identified 52 cases of which eight were laboratory-confirmed cases and all had E. bieneusi genotype C-positive. The risk estimates calculated for lunch events and specific food items, revealed that the egg/shrimp sandwich served in the canteen on November 4, 2020, was the likely source of infection (RR 3.6, 95% confidence interval 2.1 to 6.4). The incubation period was 5–12 days, and PCR positivity continued for up to 43 days after onset of symptoms. Diarrhea (90%), fatigue (83%), abdominal pain (79%), and nausea (71%) were the most commonly reported symptoms.

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Conclusions :

Enterocytozoon bieneusi should be part of the laboratory test panel for investigating potential causes of food-borne outbreaks. Spores may be shed in stool for weeks and therefore, testing for E. bieneusi can be useful even weeks after exposure.

b. Swimming associated paediatric hemolytic-uraemic syndrome outbreak due to Shiga toxin-producing Escherichia coli O26:H11

G. Terpant [1]

D. Sergentet [2], S. Lefèvre [3], P. Mariani [4], A. Cointe [5], C. Lamat [6], M. Fabre [7], E. Vaissière [8], T. Bénet [9], G. Jones [10], A. Nisavanh [11]

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[2] National Reference Laboratory for E. coli, VetAgro Sup, Marcy-l'Etoile

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[4,5] Associated Laboratory of the National Reference Center for E. coli, Department of Microbiology, Robert-Debré Hospital, AP-HP, Paris

[6] Regional Health Agency – Auvergne-Rhône-Alpes, Environmental Health Department, Lyon

[7] Regional Health Agency – Auvergne-Rhône-Alpes, Environmental Health Department, Annecy

[8,9] Santé publique France, Regional Division - Auvergne-Rhône-Alpes, Lyon

[10,11] Santé publique France, Infectious Diseases Division, Saint-Maurice

Background :

Shiga toxin-producing Escherichia coli (STEC) outbreaks in France are typically associated with consumption of raw milk cheeses or ground beef. From 27 July to 11 August 2020, Santé publique France was notified of five paediatric hemolytic-uraemic syndrome patients with reported exposure to swimming water at Lake Geneva. Epidemiological and microbiological investigations aimed to identify and confirm common at-risk exposures and guide control measures.

Methods :

Investigations used a trawling questionnaire and included active case searching. Stool samples and isolates were sent to the French National Reference Center for strain characterization and phylogenetic analysis to determine cluster affiliation (cgMSLT and SNP). Environmental investigations included water and sediment samples.

Results :

Cases, aged 15 months to 6 years, all visited the same beach at Lake Geneva between 11-26 July and reported symptom onset from 19-27 July. Isolates from all cases were STEC O26:H11 stx2 eae ehxA belonging to the same genomic cluster (cg MLST HC_65006). Parents reported ingestion of lake water or wet sand with no other common exposures identified. Environmental investigations collected 38 water and sediment samples during August and examined potential contamination sources (pastureland runoff, water-treatment plant malfunction…). Officials closed the swimming area during this period. Four E. coli O26 strains carrying the eae gene and one STEC non-O26 were isolated from the swimming water and sediment, none belonging to the outbreak genomic cluster. These results indicated persistent contamination of the swimming area with E. coli presenting potential health risks.

Conclusions :

This is the first recorded swimming-associated STEC outbreak in France. Health authorities and local officials continue environmental investigations in order to understand probable sources of contamination, and guide and strengthen control measures ahead of the upcoming summer season.

c. Tap water as a source of legionellosis outbreak spread to several residential buildings and one hospital

S. Mentula [1]

S. Kääriäinen [2], S. Jaakola [3], M. Niittynen [4], P. Airaksinen [5], H. Kirjavainen [6], I. Koivula [7], M. Lehtola [8], E. Mauranen [9], I. Mononen [10], R. Savolainen [11], O. Lyytikäinen [12]

[1] National Institute for Health and Welfare

[2] National Institute for Health and Welfare ; ECDC Fellowship Programme, Field Epidemiology path (EPIET)

[3,4,5] National Institute for Health and Welfare

[6] Environmental Health, City of Kuopio

[7] Kuopio University Hospital

[8] Kuopion Vesi

[9] Kuopio University Hospital

[10] Environmental Health, City of Kuopio

[11] Health Services, City of Kuopio

[12] National Institute for Health and Welfare

Background :

We report an unusual legionellosis outbreak with 12 cases extending over one year, all related to domestic and hospital water systems in the city of Kuopio (120 000 inhabitants) where usually only 1-2 cases are annually detected.

Methods :

Microbiology laboratories notify all Legionella sp. findings (urinary antigen test (UAG), PCR or culture) and physicians notify legionellosis cases to the National Infectious Disease Registry (NIDR). All cases are routinely interviewed to trace the source of infection and environmental water samples are obtained for each case from household, hospital and/or working place for PCR and culture. Human and environmental Legionella isolates were compared by whole-genomesequencing (WGS) as a part of outbreak investigation.

Results :

We identified 11 legionellosis cases notified to NIDR from late February to early May 2021 living in Kuopio; 10 diagnoses were based on UAG, 9 PCR and 4 culture. Median age was 69 years (range, 52-85), half of the cases were immunocompromised, one died. Six cases were living in the same residential area but all in different buildings and three cases were hospitalized patients. Household water samples from 5/6 cases and 17 water samples from the hospital were positive for L. pneumophila serogroup 1 with concentrations up to 649 000 cfu/l. All available human and water isolates were identical by WGS, including one isolate from a previous legionellosis case from January 2020.

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Conclusions :

Most of the cases were diagnosed by UAG which detects mainly L. pneumophila serogroup 1. By comparing the human and water isolates by WGS we were able to confirm the outbreak and its source. Positive water samples suggest inadequate maintenance measures taken at each building involved. Samples from regional water containers are under investigation.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Legionella, Legionella pneumophila, outbreaks, whole genome sequencing, drinking water, water-related Diseases
ABSTRACT ID: 210
PRESENTED BY: Silja Mentula / silja.mentula@thl.fi

d. Salmonella Typhimurium outbreak associated with frozen tomato cubes in Western Finland, January-February 2021

S. Kääriäinen [1]

D. Obach [2], D. Paspaliari [3], M. Tofferi [4], A. Nieminen [5], A. Pihlajasaari [6], H. Kuronen [7], A. Vainio [8], R. Rimhanen-Finne [9]

[1,2] National Institute for Health and Welfare; ECDC Fellowship Programme, Field Epidemiology path (EPIET)

[3] National Institute for Health and Welfare; ECDC Fellowship Programme, Public Health Microbiology path (EUPHEM)

[4] Central Ostrobothnia Environmental Health Care

[5] Central Osthrobothnia Federation on Municipalities for Social and Health Care Services

[6,7] Finnish Food Authority

[8,9] National Institute for Health and Welfare

Background :

Several individuals reported gastrointestinal symptoms following lunch-meals consumed January, 27-29 2021 in a restaurant in Western Finland. We investigated the outbreak to identify its extent and source to prevent further spread.

Methods :

We conducted a retrospective cohort study and asked the people exposed to participate via a media release on February 5. We defined a case as a person who, having had lunch at the restaurant during January 27-29, had stomach pain, vomiting or diarrhoea within seven days after the exposure and/or a laboratory confirmed Salmonella Typhimurium infection between 27 January and 26 February. We collected fecal and food samples for PCR and culture. We conducted whole-genome-sequencing (WGS) of positive samples and cluster analysis by cgMLST using Ridom SeqSphere+.

Results :

During January 27-29, 393 meals were sold. 101 persons, who ate 142 meals in total over the exposure period, participated in the study. Median age was 39 years (range, 16-77) and 39 (39%) were female. There were 49 cases (attack rate, 48.5%) including 23 laboratory confirmed cases. Two were hospitalized. Isolates from cases and frozen tomato cubes were closely related by cgMLST, based on analysis of 3235 loci. Tomato cubes were used uncooked in salads that were served in the lunch buffet and consumed by 76% of the cases. No statistical association was found between eating the salads and being a case (risk ratio, 1.8; 95% confidence interval: 0.8-3.8; p-value 0.08).

Conclusions :

The frozen tomato cubes were the suggested outbreak source based on cgMLST analysis, where all isolates clustered together. After a rapid recall of the product, no further cases were reported. Based on our results the manufacturer added a recommendation to cook the frozen product before consumption.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Salmonella Typhimurium, outbreak, frozen tomato cubes, whole genome sequencing
ABSTRACT ID: 116
PRESENTED BY: Sohvi Kääriäinen / sohvi.kaariainen@thl.fi

e. Sharp increase in Legionnaires' disease cases in EU/EEA in 2017 continues under 2018-2019

J. Samuelsson [1]

L. Payne Hallström [2], J. Gomes Dias [3]

[1,2,3] ECDC

Background :

Surveillance of Legionnaires' disease (LD) in the EU/EEA, carried out through the European Legionnaires' disease Surveillance Network (ELDSNet), showed a constant incidence in 2011-2016. In 2017, a 30% increase in the annual number of LD cases was observed. The aim of this study was to analyse if there was a significant increase in LD cases during 2017-2019, and if so to determine if there was an overall increase and/or the beginning of an increasing trend.

Methods :

We used two complimentary time-series analysis methods on LD data reported by 26 EU/EEA countries to TESSy, the European Surveillance System, for 2012-2019: 1) Harmonic regression models with Fourier terms and ARIMA errors using 2012-2016 data to predict 2017-2019 and estimate excess number of cases above 95% prediction interval; 2) Interrupted time series (ITS) to estimate a change in trend and level of LD cases from 2017.

Results :

The higher incidence of LD cases observed in 2017 continued into 2018 and 2019. The retrospective prediction showed a sustained excess of cases of 125 in 2017 (1.4%), 916 in 2018 (10.0%) and 481 in 2019 (5.0%), with excess distributed throughout the usual LD season. ITS also confirmed a significant increasing trend under 2017-2019 compared with 2012-2016.

Conclusions :

The unusual increase observed in 2017 was above what was expected based on a previous 5-year trend in and continued to be observed in 2018-2019. Different statistical methods confirmed the unusual increase in LD incidence, and an overall increasing trend since 2017. No specific outbreaks were reported within EU/EEA could explain the observations, demanding further exploration of the possible determinants driving this increase in the EU/EEA.

Subject : Surveillance
Keywords : Legionnaires' disease, time-series analysis, surveillance
ABSTRACT ID: 157
PRESENTED BY: Joana Gomes Dias / Joana.Gomes.Dias@ecdc.europa.eu

Fireside Session Abstracts

Fireside Session 5
Day 2, Wednesday 17 November 2021
13:30 – 14:15

COVID-19: Digital health

Moderator

Nienke Schutte (Siensano, Belgium)

Abstracts

a. Using genomic concordance to estimate COVID-19 transmission risk across different settings in England 2020/21

C. Cheng [1]

S. Packer [2], C. Turner [3], C. Anderson [4], G. Hughes [5], O. Edeghere [6], I. Oliver [7], E. Birney [8]

[1,2,3,4,5,6,7] Contact Tracing Cell, Public Health England
[8] European Bioinformatics Institute (EMBL-EBI)

Background :

Identifying areas that pose the greatest risk for community transmission of COVID-19 is essential to direct public health action and allow safe opening of society. Spread of B.1.1.7 lineage identifiable through S-gene target failure (SGTF) provided a unique opportunity to quantify the COVID-19 transmission risk associated with community settings in England 2020/21.

Methods :

All cases of COVID-19 in England were included through the NHS Test and Trace contact tracing system. Data between 11/2020 and 01/2021 (B.1.1.7 prevalence between 20-80%) was used. Community activities during a case's acquisition (7-3 days before symptom onset) period were used to defined case groups: >2 cases reporting the same activity, location and date. The genetic concordance (presence/absence of SGTF in grouped cases) was determined. Odds ratios for concordance and corresponding 95% confidence intervals were calculated by setting. Sensitivity analysis compared setting concordance in same day to 1-2-day case groups.

Results :

There were 41,325 clusters with SGTF data containing 115,410 community exposure events. Odds ratios ranged from 1.87 (95% CI:1.76 - 1.98) for shops to 29.9 (95% CI:23.1 - 38.7) nursery/preschool and 35.6 (95% CI:19.7 - 64.2) for visiting friends/relatives. We found an increasing trend in the odds of concordance with larger cluster sizes in educational settings. Sensitivity analysis showed a diminished effect when comparing clusters with exposure 1-2 days apart compared to same day.

Conclusions :

Transmission risk varies across community settings. This may be due to behavioural or environmental factors. Risk does not capture volume of users which also affects impact of settings on transmission. Data for some settings was limited due to non-pharmaceutical interventions in place. We recommend data are used to prioritise public health action when assessing and managing COVID-19 clusters.

Subject : Novel methods in epidemiology (e.g. digital disease detection, e-health)
Keywords : Contact tracing, Genomics,Transmission,COVID-19,Community
ABSTRACT ID: 238
PRESENTED BY: Athinna Nisavanh / athinna.nisavanh@santepubliquefrance.fr

b. Design and implementation of a tool for the identification of shared exposures from COVID-19 cases, a national system implemented in England 2020/21

A. Wensley [1]

S. Packer [2], K. Bamford [3], S. Spreadborough [4], O. Nsonwu [5], C. Chen [6], I. Florence [7], C. Anderson [8], G. Fraser [9], G. Hughes [10]

[1,2,3,4,5,6,7,8,9,10] Public Health England

Background :

During the COVID-19 pandemic a key requirement of control has been rapidly identifying, assessing and monitoring outbreaks, clusters and settings where transmission is occurring. The UK NHS Test and Trace system records locations an individual visited in 3 to 7 days before they became symptomatic. This allows the identification of clusters of COVID-19 and high-risk settings for public health action to supress community transmission.

Methods :

A common exposure algorithm was constructed to group cases based on place (same postal code and setting description) and time (attendance within a 7,2,1 day rolling window). Prioritisation metrics were calculated to assist stakeholder assessment and triage. Daily summaries were uploaded to a PowerBI dashboard for human review and action. To assist with the review process, a tool has been developed that links multiple sources of health protection information to common exposure data in a graphical html format generated in R.

Results :

The algorithm has identified 21400 potential common exposures attended by confirmed COVID-19 cases during their pre-symptomatic period in England between March and mid-May 2021. The tool to support prioritisation and investigation has an average of 28 unique users a day across 9 regions. It assists decision making by local stakeholders about what common exposures could merit closer review and possible public health action.

Conclusions :

The method used to identify possible exposures within NHS T&T data aims to be comprehensive and sensitive, favouring the inclusion of cases. This system of automated analysis and reporting utilising exposure information substantially reduces analytical burden and provides a mechanism for the identification of possible common exposures that may not be recognised through other mechanisms.

Subject : Novel methods in epidemiology (e.g. digital disease detection, e-health)
Keywords : COVID-19, Algorithms, Contact Tracing, Disease Outbreaks
ABSTRACT ID: 216
PRESENTED BY: Simon Packer / Simon.Packer@phe.gov.uk

c. Novel method for identification of COVID-19 outbreaks in residential property in England

D. Chudasama [1]

J. Lewis [2], F. Seeyah [3], B. Cook [4], J. Flannagan [5], G. Dabrera [6], T. Lamagni [7]

[1,2,3,4,5,6,7] Public Health England

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Background :

Establishing a means to geolocate cases to standardised residential address and property type is essential to the COVID-19 response function, particularly to identify outbreaks. We describe a novel process developed during the COVID-19 pandemic to provide this surveillance enrichment.

Methods :

All laboratory confirmed SARS-CoV-2 cases in England notified to PHE were address-matched daily against reference databases, namely Ordnance Survey (OS) CQC list of care homes and OS AddressBase Premium database. Unique Property Reference Number (UPRN) and Basic Land and Property Unit (BLPU) class, which identifies the nature of the property, were derived from this process. Enriched surveillance data were then used to identify outbreaks, defined as two or more cases at the same residence (determined by UPRN), within a 14-day period.

Results :

Of 3,874,406 laboratory confirmed COVID-19 cases, 3,678,065 (94.9%) were successfully address matched up to 09 Maty 2021. A wide array of different property types were identified, including prisons, HMOs and care homes, although the majority of positive cases resided in private dwellings (3,445,270 (88.9%)), followed by care homes, 146,902 (3.8%). A total of 744,730 residential outbreaks were identified over the study period, with the median size of an outbreak recorded as 3, and the largest outbreak with 908 positive cases at a university campus. Several large prison outbreaks were also noted, with the largest outbreak consisting of 582 inmates.

Conclusions :

Establishment of an address matching process provided vital epidemiological intelligence of use in characterising outbreaks in residential settings, facilitating monitoring and investigation of local transmission hotspots. As well as providing situational awareness, this process is providing a means to monitor the impact of targeted measures to control spread.

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

Keywords : COVID-19, Unique Property Reference Number, Basic Land Property Unit, Outbreak investigation

ABSTRACT ID: 187

PRESENTED BY: Dimple Chudasama / dimple.chudasama@phe.gov.uk

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d. Estimating asymptomatic and presymptomatic transmission of 2019 novel coronavirus (COVID-19) infection: a cohort study in Ho Chi Minh City, Vietnam

C. Valencia [1]

L. Quang [2], M. Handcock [3], D. Nguyen [4], Q. Ngoc [5], T. Nguyen [6], N. Le [7], T. Truong [8], H. Do [9], S. Otsu [10], L. Tuan [11], Q. Pham [12], T. Nguyen [13], P. Lan [14], L. Le [15]

[1] Global Alert and Response Network, World Health Organization, Geneva

[2,5,6,12,13,14] Department of Prevention and Control Diseases, Pasteur Institute, Ho Chi Minh City

[3] Department of Statistics, University of California, Los Angeles,

[4,7,8] Preventive Medicine Center, Ho Chi Minh Provincial Center for Disease Control, Ho Chi Minh City

[9] Disease Control and Health Emergency Program, World Health Organization Vietnam Country Office, Hanoi,

[10,11] Disease Control and Health Emergency Program, World Health Organization Vietnam Country Office, Hanoi

[15] Strategic Epidemiology and Modelling Group COVID-19, World Health Organization Regional Office for the Western Pacific, Manila

Background :

The rapid increase in the number of coronavirus disease 2019 (COVID-19) cases worldwide raised concerns of viral transmission from individuals displaying no or delayed clinical symptoms, even more so with the appearance of new variants and the introduction of vaccination campaings. We quantified the transmission potential of asymptomatic, presymptomatic and symptomatic cases using surveillance data from a bar gathering in Ho Chi Minh City, Vietnam.

Methods :

Between March 14 and April 25, 2020, we collected demographic, clinical and laboratory information of all COVID-19 confirmed cases and contacts from a bar gathering. We applied a Bayesian framework to estimate the proportions of asymptomatic, presymptomatic and symptomatic cases and transmissions with posterior modes and 90% credible intervals (CrI). Using Go.Data, we mapped chains of transmission and estimated the basic reproduction number (R0).

Results :

Of the 298 individuals attending the bar gathering on March 14, 2020, 13 tested positive for SARS-CoV-2. Another 6 tested positive from 4466 contacts further traced. The proportions asymptomatic, presymptomatic, and symptomatic were 0·43 (90% CrI 0·26–0·60), 0·35 (90% CrI 0·20–0·52) and 0·22 (90% CrI 0·09–0·37), respectively. The proportion of asymptomatic, presymptomatic and symptomatic transmissions were 0·45 (90% CrI 0.13–0·74), 0·24 (90% CrI 0.11–0.38), and 0·31 (90% CrI 0·15–0·49), respectively. The cluster-specific was 2·64 (90% CrI 1·41–3·68). The bar constituted 68%, workplace 21%, and household 11% of transmissions.

Conclusions :

We demonstrated using statistical models on surveillance data that high asymptomatic and presymptomatic transmission of COVID-19 occurred in a Vietnam cluster. Detecting, genotyping, and isolating presymptomatic and asymptomatic cases will be an important control measure as movement restrictions are lifted.

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

Keywords : Asymptomatic transmission, Quantifying transmission, Go.Data, Outbreak response, Cohort Study, COVID-19, Presymptomatic transmission, Bayesian analysis

ABSTRACT ID: 42

PRESENTED BY: Cristina Valencia / cvalencia@who.int

Fireside Session Abstracts

Fireside Session 6
Day 2, Wednesday 17 November 2021
13:30 – 14:15

Surveillance: implementation and evaluation

Moderator

Marlena Kaczmarek (ECDC)

Abstracts

a. Evaluating the propensity to test for SARS-CoV-2 infection and the risk of a positive result using national-level COVID-19 web-based syndromic surveillance

S. McDonald [1]

L. Soetens [2], M. Schipper [3], I. Friesema [4], C. van den Wijngaard [5], A. Teirlinck [6], N. Neppelenbroek [7], J. Wallinga [8], S. van den Hof [9], A. van Hoek [10]

[1,2,3,4,5,6,7,8,9,10] Netherlands National Institute for Public Health and the Environment

Background :

Voluntary testing for SARS-CoV-2 infection is an integral component of an effective response to the COVID-19 pandemic, but for many countries identifying and encouraging populations most at risk for infection to present for testing remains a challenge. Using internet-based participatory surveillance data from the Netherlands, we aimed to identify factors that are associated with a low propensity to be tested given symptom(s) and if tested, with a high risk of a positive test result.

Methods :

We analysed weekly survey data from the Infectieradar web-based syndromic surveillance system collected between 17 November 2020 and 18 April 2021 (50,946 surveys in which symptom(s) were reported; 12,026 unique participants). Multivariable regression analyses using generalised estimating equations for binomial outcomes yielded estimates of the associations between demographic, participant and household factors, as the odds of testing given COVID-19 compatible symptom(s) and if tested, the odds of a positive test result.

Results :

Males (adjusted odds ratio (OR) for testing=0.91; OR for positivity=1.50), age-groups <20 years (0.93; 1.35), 50-64 years (0.93; 1.20), 65+ years (0.78; 1.38), lower education level (0.77; 1.02), and diabetics (0.97; 1.08) were identified as potential target groups for encouraging testing among those with symptoms.

Conclusions :

This approach has suggested a set of risk factors or potential barriers to testing for SARS-Cov-2 infection, and therefore can assist in identifying subpopulations with a higher risk of a positive test outcome for which communication and/or accessibility can be improved. Enhancing the effectiveness of testing to reduce transmission in high risk groups is essential for the current response to the COVID-19 pandemic and for public health strategies in the longer term.

Subject : Surveillance

Keywords : COVID-19, Syndromic surveillance, Risk factors, Testing, Positivity

ABSTRACT ID: 37

PRESENTED BY: Scott McDonald / scott.mcdonald@rivm.nl

b. The benefits of large-scale community-based SARS-CoV-2 testing in low-income neighbourhoods in Rotterdam, the Netherlands

M. Vink [1]

Z. Igloi [2], F. Mevissen [3], J. van Beek [4], H. Voeten [5], R. Molenkamp [6], A. Vonk [7], M. de Graaf [8], T. Boelsums [9], E. Fanoy [10], M. Koopmans [11], N/A

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[3,5,7,9,10] Public Health Service Rotterdam-Rijnmond, Rotterdam

[4,6,11] Department of Viroscience, Erasmus MC, Rotterdam

[8] Department of Viroscience, Erasmus MC, Rotterdam; Waste water Surveillance group, KWR Water Institute, Nieuwegein

Background :

In November 2020 a high COVID-19 incidence was reported in Rotterdam, especially in low-income neighbourhoods. The proportion tested population in these areas was low. By introducing pop-up test facilities, we aimed to improve willingness and access to testing. In addition we evaluated the sensitivity of the rapid antigen test (RAT) in asymptomatic individuals to lower the threshold for testing.

Methods :

Between 24-11-2020 and 05-03-2021 12 free testing points were set up in public locations in three low-income neighbourhoods in Rotterdam, each with a daily capacity of about 200 persons. Background characteristics were collected at intake, after which nasopharyngeal swabs were taken and processed using both Polymerase Chain Reaction (PCR) and RAT. Upon leaving the test facility, visitors were asked to join a survey for evaluation purposes.

Results :

In total 19,795 visitors were tested, of whom 9,677 (49%) came without appointment. These walk-in visitors were generally older (median age: 50 versus 36 years) and lived more often in the proximity of the facilities (75% versus 29%) than visitors who came on appointment. For 67% of the visitors this was the first time they got tested. 1,211 persons (6%) tested SARS-CoV-2-positive, of whom 250 (21%) were asymptomatic. RAT could detect asymptomatic individuals with 84% (95%CI 73-92%) sensitivity compared to PCR. The test facilities were evaluated positively and visitors welcomed the easy access (low travel distance, no appointment needed) of the facilities.

Conclusions :

The intervention did increase test coverage in low-income neighborhoods, especially among older residents living in the vicinity of the test locations. RATs are useful diagnostics to detect asymptomatic individuals. We recommend the use of large-scale community-based SARS-CoV-2 testing in other high-risk situations and populations.

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

Keywords : COVID-19 testing, mass screening, ethnic groups

ABSTRACT ID: 240

PRESENTED BY: Martijn Vink / m.vink3@rotterdam.nl

c. Identification of subgroups in the Danish population for targeted human papillomavirus vaccination efforts,

S. Voss [1]

S. Nørgaard [2], P. Valentiner-Branth [3]

Fireside Session Abstracts

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Background :

In the Danish childhood vaccination program, the human papillomavirus (HPV) vaccination coverage is lower than for other vaccines. To tailor a targeted HPV vaccination effort, we aimed to identify girls in Denmark with lower first dose HVP vaccination coverage than girls in general.

Methods :

A population-based retrospective cohort study was performed of girls born in 2001-2004, residing in Denmark in September 2019 (N= 128,351). Data from the Danish Vaccination Register was linked to sociodemographic data from the Danish Civil Registration System and Statistics Denmark. Cox's proportional hazard regression models were used to compare vaccination uptake rates between subgroups of girls.

Results :

HPV vaccination coverage at 14 years of age varied widely by municipality (53.4-80.6%). Girls living with neither of their parents had a lower chance of being vaccinated compared to girls living with both their parents (aHR 0.51; 95% CI 0.48-0.54), likewise for girls attending special need education compared with public schools (aHR 0.62; 95% CI 0.53-0.74). The vaccination uptake among immigrants was lower compared to Danish born girls (aHR 0.88; 95% CI 0.83-0.92), especially among immigrant girls whose parents had not passed any Danish exams. Finally, girls who had received the TdaP-IPV booster had a 50% greater chance of being HPV vaccinated compared to girls who had not received it (aHR 1.50; 95% CI 1.47-1.53).

Conclusions :

To increase the HPV vaccination uptake, we recommend vaccination efforts targeting girls living without any of their parents, girls attending special need education, immigrants, and girls who have not been vaccinated with the TdaP-IPV booster. When targeting immigrants, the effort should focus on disseminating sufficient and understandable information about the Danish childhood vaccination program to the parents.

Subject : Surveillance

Keywords : Papillomavirus Vaccines, Vaccination Coverage, Immunization Programs, Social Determinants of Health

ABSTRACT ID: 32

PRESENTED BY: Sidsel Skou Voss / sisv@ssi.dk

d. Evaluation of WGS-based methods for molecular surveillance of Mycobacterium tuberculosis complex isolates in Ireland, 1999-2019

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Background :

MIRU-VNTR is a reference method globally for molecular typing of Mycobacterium tuberculosis complex (MTBC) isolates. However, as a PCR-based method that amplifies specific repetitive regions, it lacks discriminatory power to correctly infer phylogenetic relationships. The aim of this work was to evaluate two WGS-based methods, core-genome MLST and SNP analysis, and choose the optimum method for enhanced molecular characterisation and inference of phylogenetic relatedness of MTBC isolates.

Methods :

188 Irish MTBC clinical isolates, corresponding to 5% of the culture positive cases from 1999 to 2019 and previously characterised by MIRU-VNTR, were sequenced by Illumina's MiniSeq platform and analysed anonymously. cgMLST was performed using Ridom SeqSphere+ (version 7): 2,891 core-genome genes scheme with a threshold of ≤ 12 alleles to identify clusters. SNP analysis was performed by the MTBseq pipeline, with clusters defined with a maximum distance threshold of 5 SNPs. Methods were evaluated based on concordance of the results and discriminatory power compared to MIRU-VNTR, coupled with ease of use.

Results :

While MIRU-VNTR detected 13 clusters and 0 sporadic strains, cgMLST and SNP analysis produced a smaller number of clusters (9 & 11) and a greater number of sporadic strains (26 & 28). Three MIRU-VNTR clusters were disassembled. cgMLST and SNP analysis showed a higher discriminatory power and 96% concordance of results with each other, but only 86% and 63% concordance with MIRU-VNTR, respectively. cgMLST is preferable to SNP analysis, combining high discriminatory power with improved ease of use.

Conclusions :

cgMLST and SNP-analysis are both suitable for inference of genetic relatedness, however, based on our analysis, we recommend the implementation of cgMLST at the Irish Mycobacterial Reference Laboratory to enhance public health interventions for MTBC mitigation in Ireland.

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

Keywords : MIRU-VNTR, cgMLST, SNP analysis, molecular typing, Mycobacterium tuberculosis complex

ABSTRACT ID: 209

PRESENTED BY: Diana Espadinha / diana.costa@hse.ie

e. Development of an NGS-based typing method for surveillance of rotaviruses circulating in Sweden

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Background :

Vaccination against rotaviruses was included in the Swedish childhood vaccination programme in 2019. However, the gold standard molecular typing method, based on Sanger sequencing and targeting VP4 and VP7 genes, does not allow complete differentiation between wild-type and vaccine G1P[8] genotypes. Using the genetic diversity of the NSP2 segment between Rotarix and wild-type G1P[8] genotypes, we developed a novel typing method based on MinION sequencing, which identifies rotavirus genotypes and allows vaccine vs wild-type differentiation.

Fireside Session Abstracts

Methods :

We designed primers targeting NSP2, and redesigned primers targeting VP4 and VP7. 12 individual amplicons corresponding to NSP2, VP4 and VP7 gene fragments of Rotarix G1P[8] and three of the genotypes circulating in Sweden, G2P[4], G3P[8] and G4P[8], were generated. The amplicons were barcoded, pooled, and then sequenced on the MinION platform. Raw sequencing reads were base-called using guppy v4.5.4 (Oxford Nanopore Technologies), and adapters and barcodes were deplexed and trimmed using porechop (GitHub). Full-length amplicons were assembled using spoa and Pomoxis, and analysed in BLAST.

Results :

We tested genotyping accuracy of MinION sequencing vs gold standard method. Analysis of VP4 and VP7 sequences led to correct rotavirus gene and genotype identification by MinION in all samples. Pairwise alignment of the Rotarix G1P[8] NSP2 sample showed 99.9% identity to Rotarix G1P[8] and 90.1% to wild-type G1P[8], indicating differentiation capacity of the new method.

Conclusions :

This proof of concept study shows that the MinION sequencing can accurately identify rotavirus genotypes and has the potential to differentiate Rotarix from wild-type virus G1P[8] genotype. MinION genotyping will be further evaluated using other rotavirus genotypes. If successful, it will become the method of choice for the epidemiological surveillance of rotavirus in Sweden.

Subject : Novel methods in microbiology (e.g. new diagnostic tools)
Keywords : Rotavirus, molecular typing, NGS, vaccine strain differentiation
Keywords : Rotavirus, molecular typing, NGS, vaccine strain differentiation
ABSTRACT ID: 112
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Fireside session 7
Day 3, Thursday 18 November 2021
13:30 – 14:15

Burden of disease

Moderator

Piotr Kramaz (ECDC)

Abstracts

a. Incidence of first syphilis infection in the Lisbon Cohort of Men who have Sex with Men (MSM)

S. Ribeiro [1]

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Background :

The incidence of syphilis has been rising in the European Union since 2011. The rise has disproportionally affected men, particularly men who have sex with men (MSM). However, there is little information on the risk factors and predictors of seroconversion. This study's main objectives were to estimate syphilis antibodies seroconversion rate in the Lisbon MSM Cohort and to identify predictors of seroconversion.

Methods :

The Lisbon MSM prospective cohort participants were recruited at CheckpointLX, a community-based peer-led sexual health centre tailored for MSM. Participants were followed up according to their convenience, ideally in 6-month intervals. Demographic characteristics and risk factor data were collected using a Community Health Worker (CHW) administered survey. Syphilis rapid testing was offered to MSM with no prior history of syphilis or unaware of their status. The incidence rate was calculated for the period 2013-2017. Cox proportional hazards regression was used to test for association between participant characteristics and incident syphilis during follow-up.

Results :

A total of 110 syphilis cases were diagnosed in the cohort. The overall incidence rate of syphilis in the cohort was 35.10 per 1000 person-years (95% CI 29.0, 42.1). Low educational attainment was significantly associated with higher syphilis incidence. This association was attenuated after adjusting for drug and condom use.

Conclusions :

This study updates a previous estimate of syphilis infection in this cohort and provides the first analysis of its predictors in MSM participating in the Lisbon MSM Cohort. We found an incidence rate of syphilis comparable to other cohorts in similar settings. Our results suggest that a policy aimed at reducing risky behaviours in individuals with low educational attainment is warranted.

Subject : Burden of disease
Keywords : syphilis, incidence, MSM
ABSTRACT ID: 162

Fireside Session Abstracts

PRESENTED BY: Sofia Ribeiro / sofiafigribeiro@gmail.com

b. Prevalence estimates of genital Chlamydia trachomatis infection in Belgium – results from a cross-sectional study

N. Fischer [1]

I. Peeters [2], S. Klamer [3], M. Montourcy [4], V. Cuylaerts [5], I. De Baetselier [6], W. Vanden Berghe [7]

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Background :

Chlamydia trachomatis (CT) is the most diagnosed sexually transmitted infection (STI) in Belgium. National screening programs focus on young women, due to the medical implications of chronic asymptomatic infections for reproductive health. Thereby, the frequency of infections in men and older adults is underestimated. The objective of this study was to estimate the point-prevalence of CT in the broader population of Belgium, to inform evidence-based prevention campaigns and control strategies.

Methods :

In a cross-sectional survey 12.000 representative Belgians aged 16-59 years were randomly selected from the national register and invited by letter to collect a urine sample at home and complete a questionnaire on socio-demographics and sexual behavior. CT DNA in urine was detected by Xpert® CT/NG assay. Weighted estimated prevalence and 95% confidence interval (CI) was calculated per gender and age groups of 16-29, 30-44 and 45-59 years. Odds ratios (ORs) were calculated to identify potential risk factors for infection. Data analysis was performed using R.

Results :

A total of 6.5% (775/12.000) of individuals completed the questionnaire and submitted a urine sample. The populationwide weighted estimated prevalence was 1.53% (95%CI 0.78-3.0): 1.75% (95%CI 0.62-4) in men and 1.31% (95%CI 0.52-3.0) in women, and highest in age group 30-44 years. Sexual intercourse with a casual partner (OR = 6.3, 95% CI =1.7-24) and ›3 sexual partners in the last 12 months (OR = 4.5, 95% CI = 1.1-18) were associated with CT infection.

Conclusions :

Nationwide prevalence studies are relevant to assess the distribution of CT. Screening efforts should include men and individuals who report casual sex and frequent partner change. Moreover, the use of condoms and frequent STI testing should be emphasized in these screening campaigns.

c. Risk of hospitalisation and risk of death for healthcare workers with COVID-19 in nine EU/EEA countries, January 2020–January 2021

C. Carvalho [1]

L. Ferland [2], J. Gomes Dias [3], F. Lamb [4], C. Adlhoch [5], C. Suetens [6], J. Beauté [7], P. Kinross [8], D. Plachouras [9], T. HannilaHandelberg [10], M. Fabiani [11], F. Riccardo [12], J. Mossong [13], A. Vergison [14], R. van Gageldonk-Lafeber [15], A. Teirlinck [16], J. Melillo [17], T. Melillo [18], P. Mook [19], R. Pebody [20], A. Coutinho Rehse [21], D. Monnet [22]

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[11,12] Italian National Institute of Health

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[15,16] Dutch National Institute for Public Health and the Environment

[17,18] Ministry for Health Malta

[19,20,21] World Health Organization Regional Office for Europe

Background :

The impact of the COVID-19 pandemic on healthcare workers (HCWs), many of whom are professionally exposed to COVID-19 patients, has been unprecedented. We aimed to describe the effect of being HCW on the risk of disease and other outcomes, identifying independent risk factors for death.

Methods :

We used case-based data reported to The European Surveillance System between 31 January 2020 and 13 January 2021 to calculate COVID-19 attack rates (ARs) and attack rate ratios (ARRs) with 95% confidence intervals (CIs) for disease, hospitalisation, admission to ICU and death, in HCWs and non-HCWs. We used negative binomial regression, accounting for country heterogeneity and adjusting for age group, sex, comorbidities, and reporting period, to identify risk factors for death.

Results :

Nine EU/EEA countries (total population aged 20-69 years: 70.4 million; HCWs: 2.6 million) reported 2.9 million COVID-19 cases (overall AR: 4.1%; HCW AR: 10.1%; non-HCW AR: 3.9%). The ARRs for hospitalisation, ICU admission and death in HCW (compared to non-HCW) were 1.8 [95%CI 1.2-2.7], 1.9 [95%CI 1.1-3.2] and 0.9 [95%CI 0.4-2.0], respectively. Of 127,712 hospitalised cases, 6.4% were HCWs. Of these 1.8% died, compared to 8.2% in non-HCWs. Risk of death was lower in hospitalised HCWs than in non-HCWs, especially among cases not requiring ICU admission (adjusted IRR 0.3 [95%CI 0.2-0.6]), as well as in cases reported in June-September 2020 compared to the early phase of the pandemic (aIRR 0.5 [95%CI 0.4 to 0.7]).

Conclusions :

Amongst all cases, HCWs were at significantly increased risk of COVID-19 infection and hospitalisation, but not of death. In hospitalised cases, the adjusted risk of death was significantly lower for HCWs, possibly due to the healthy worker effect, better/earlier access to treatment, and differential under-ascertainment.

Fireside Session Abstracts

d. Sex differences in COVID-19 mortality in the Netherlands

A. Niessen [1]

A. Teirlinck [2], S. McDonald [3], W. van der Hoek [4], R. van Gageldonk-Lafeber [5], M. Knol [6], RIVM COVID-19 epidemiology and surveillance group

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Background :

Since the first reports of COVID-19 cases, sex-discrepancies have been reported in COVID-19 mortality. We provide a detailed description of these sex differences in relation to age and comorbidities among notified cases and in relation to age and sex specific mortality in the general Dutch population.

Methods :

Data on COVID-19 cases and mortality until May 31st 2020 was extracted from the Netherlands national surveillance database, with exclusion of healthcare workers. Associations between sex and case fatality were analyzed with multivariable logistic regression. Subsequently, male-female ratio of standardized mortality ratios and population mortality rates relative to all-cause and infectious diseases-specific mortality were computed stratified by age.

Results :

Male-female odds ratio for case fatality was 1.33 [95% CI 1.26-1.41] and was 1.27 [95% CI 1.16-1.40] among hospitalized cases only. This remained significant after adjustment for age and comorbidities. The standardized mortality ratio was higher for males, with a male-female ratio of 1.70 [95%CI 1.62-1.78]. The population mortality rate was 35.1 per 100.000, with a male-female rate ratio of 1.25 (95% CI 1.18-1.31), which was higher than for all-cause and infectious disease mortality. Male-female population mortality differences where largest among 55-59 and decreased by older age. However, the power in lower agegroups was low.

Conclusions :

Our study confirms male sex is a predisposing factor for severe outcomes of COVID-19, independent of age and comorbidities. The underlying mechanisms are likely to be COVID-19 specific. It is evident that sex should be considered as an important factor in further studies concerning COVID-19. More knowledge regarding the specific underlying mechanisms can help prioritize and personalize treatment and preventive measures for COVID-19.

e. Characterisation of scarlet fever's presentation and management in the modern era: a cross-sectional survey of cases in London, 2018-2019

T. Herdman [1]

R. Cordery [2], B. Karo [3], A. Purba [4], L. Begum [5], T. Lamagni [6], C. Kee [7], S. Balasegaram [8], S. Sriskandan [9]

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Background :

Timely identification of scarlet fever—fever, rash, and sore throat that can accompany Group A Streptococcal (GAS) infection—can help control outbreaks and reduce disease burden. In response to increasing incidence in London, we investigated factors associated with delayed diagnosis, and the consequences of delays for cases and households, with the aim of identifying obstacles to diagnosis and treatment.

Methods :

All cases among children (0-16 years) diagnosed with scarlet fever and notified to Health Protection Teams in London 2018-2019 were eligible: parents/guardians were asked to complete an online survey to collect information on demographics, symptoms, care-seeking, and clinical management. Factors associated with delayed diagnosis, defined as diagnosis after the first consultation, were identified through stepwise backwards multivariable analyses--applied to logistic regression (assessing characteristics associated with delay) and Cox's regression (assessing duration of illness as a consequence of delay).

Results :

Responses represented 412 cases. 70% first sought care from general practice (GP); 31% required multiple GP consultations. At the first consultation, for 28% of cases, scarlet fever diagnosis was not considered. In these cases, symptoms were frequently attributed to viral infection (60%, 64/106). Delay in diagnosis occurred more frequently among children over 5 years presenting with sore throat (OR: 2.8; 95%CI 1.3-5.8). Cases with delayed diagnosis took, on average, one day longer to return to normal activities, and required an additional day off school compared to those diagnosed at first consultation.

Conclusions :

Diagnosis of scarlet fever may not be initially considered among older children presenting with sore throat—perhaps due to a lower index of suspicion in this age group. During local and seasonal peaks, raising awareness of scarlet fever among carers and practitioners may aid identification and timely treatment.

Fireside Session Abstracts

Fireside session 8
Day 3, Thursday 18 November 2021
15:15 – 16:00

Secondary public health impacts

Moderator

Ajibola Omokanye (ECDC)

Abstracts

a. Measles vaccine mandates may have detrimental effects on uptake of other vaccines

J. Neufeind [1]

N. Schmid-Küpke [2], O. Wichmann [3]

[1,2,3] Robert Koch Institute

Background :

In Germany, a measles vaccine mandate came into effect in March 2020, requiring proof of measles immunization for children attending kindergarten or school and staff in care facilities. Mandates can be successful if implemented with care and in consideration of context. They may, however, evoke reactance and lead to a decreased uptake of other vaccines. The aim of this study was to investigate the association between reactance to the mandate and vaccine uptake of other vaccines.

Methods :

As part of a larger evaluation project on the mandate, we conducted a prospective longitudinal study among parents. Data was collected online at three time points in 2020. We assessed reactance to the mandate and the 5C psychological determinants of vaccination as primary determinants. Vaccination status and intent for different childhood vaccines were used as outcome variables. Associations between outcomes and determinants were analyzed using linear and logistic regression analysis.

Results :

In total, 7,307 individuals were initially recruited to participate in the study (58.5% female, mean age = 38.3 years). Of these, 11.2% showed some level of reactance to the mandate. Parents' level of reactance was associated with their children's vaccination status for pneumococcal and hexavalent vaccine. Furthermore, the higher parents' level of reactance, the lower the vaccination intent for the HPV, meningococcal C, or TdaP vaccine. All analyses indicate the same results pattern when controlled for the 5C psychological determinants.

Conclusions :

Parents' level of reactance to the measles mandate affects their children's vaccination status and vaccination intent for other vaccines. Measles mandates may lead parents with higher levels of reactance to omit other childhood vaccines. Therefore, it is important to monitor unintended consequences of measles mandates and to address them.

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

Keywords : Measles, vaccine mandates, vaccine hesitancy, Germany

ABSTRACT ID: 223

PRESENTED BY: Julia Neufeind / neufeindj@rki.de

b. The impact of the COVID-19 pandemic on gastrointestinal infection trends in England

N. Love [1]

A. Elliot [2], R. Chalmers [3], A. Douglas [4], S. Gharbia [5], J. McCormick [6], H. Hughes [7], R. Morbey [8], I. Oliver [9], R. Vivancos [10] , G. Smith [11]

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Background :

There is growing evidence that the COVID-19 pandemic has had indirect impacts on other health conditions. This work sought to establish the impact of the COVID-19 response on gastrointestinal (GI) infection trends in England.

Methods :

A retrospective ecological study was performed using routinely collected national and regional surveillance data from eight Public Health England coordinated laboratory, outbreak and syndromic surveillance systems using key dates of UK governmental policy change to assign phases for comparison between 2020/21 and 5-year averages.

Results :

Decreases in GI illness activity were observed across all surveillance indicators as COVID-19 cases began to peak. During the first six months of the COVD-19 response there was a 52% decrease in GI outbreaks reported (1,544 vs. 3,208 (95% CI: 2,938 – 3,478) and a 34% decrease in laboratory confirmed cases (27,859 vs. 42,495 (95% CI: 40,068 – 44,922). GI indicators began to rise during lockdown easing, although remaining lower than historic figures. Reductions in laboratory confirmed cases were observed across all age groups and both sexes, with geographical heterogeneity observed in diagnosis trends. Health seeking behaviour

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changed substantially, with attendances decreasing prior to lockdown across all indicators.

Conclusions :

There has been a marked change in trends of GI infections in the context of the COVID-19 pandemic. The drivers of this change are likely to be multifactorial; while changes in health seeking behaviour, pressure on diagnostic services and surveillance system ascertainment have undoubtably played a role there has likely been a true decrease in the incidence for some pathogens resulting from the control measures and restrictions implemented. This suggests that behaviour modifications such as hand hygiene were maintained, we could potentially see sustained reductions in illness.

Subject : Surveillance

Keywords : COVID-19, Gastrointestinal infections, Surveillance, syndromic surveillance

ABSTRACT ID: 121

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

c. The impact of the COVID-19 pandemic on STI surveillance data: incidence drop or artefact?

A. Sentís [1]

A. Prats-Uribe [2], E. López-Corbeto [3], M. Montoro-Fernandez [4], D. Nomah [5], P. Garcia de Olalla [6], L. Mercuriali [7], N. Borrell [8], V. Guadalupe-Fernández [9], J. Reyes-Urueña [10], J. Casabona [11], Catalan HIV and STI Surveillance Group

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Background :

Before the COVID-19 pandemic, STI were increasing in Europe, Spain and Catalonia were not an exception. Catalonia has been one of the regions with the highest COVID-19 numbers of confirmed cases in Spain. The objective of this study was to estimate the decline, due to the COVID-19 pandemic, in the number of STI cases in Catalonia during the lockdown and de-escalation phases according to expected values.

Methods :

An interrupted time-series analysis was performed using STI confirmed cases notified in Catalonia from August 1st, 2017, and August 1st, 2020 in Catalonia. Notifications were modeled as ARIMA processes to estimate the expected number of STI notifications since lockdown, from March 13th to August 1st, 2020, based on pre-lockdown data. We calculated the overall drop in the number of STI notifications, to estimate the magnitude of underdiagnoses and underreporting.

Results :

We found that since the start of the COVID-19 pandemic the number of STI notifications was 51% less than expected, reaching an average of 56% during lockdown (50% and 45% during de-escalation and new normality) with a maximum decrease of 72% for chlamydia. Our results showed that fewer STI were reported in women, people living in more deprived areas, people with no previous STI episodes during the last three years, and in the HIV negative.

Conclusions :

The STI notification sharp decline was maintained almost five months since lockdown to the new normality, this fact can hardly be explained without significant underdiagnosis and underreporting. There is an urgent need to strengthen STI/HIV diagnostic programs and services, as well as surveillance, as the pandemic could be concealing the real size of the already described re-emergence of STI in most of the European countries.

Subject : Surveillance

Keywords : Communicable Disease Control, Epidemiological Monitoring, Sexually Transmitted Diseases, Interrupted Time Series Analysis, COVID-19 Pandemic

ABSTRACT ID: 190

PRESENTED BY: Alexis Sentís / asentis@epiconcept.fr

d. Core competencies for applied infectious disease epidemiologists in Europe

A. Plymoth [1]

M. Ndirangu [2], C. Varela Santos [3], R. Filipe [4], J. Pommier [5]

[1] ECDC

[2,3,4,5] ECDC

Background :

The European Centre for Disease Prevention and Control (ECDC) supports the Member States and the European Commission to have a competent public health workforce. The aim of this Competency project was to review and update the core competencies in applied infectious disease epidemiology for mid-career applied epidemiologist, based on previous

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ECDC work in this area.

Methods :

The methodology used included a literature review related to epidemiological competencies to identify new areas. Qualitative data was then collected from 40 experts to inform the content and structure of the competency set. The results of the qualitative survey were discussed with a Technical Advisory Group, through an online two-day meeting, focusing on the content and presentation of the competency set. Further consultation with a larger pool of European experts in epidemiology is being conducted using a quantitative online survey to ensure the completeness and accuracy of the competency set.

Results :

The result of this process is a list of competencies that is subdivided into six areas (Essential methods for applied infectious diseases epidemiology; Public health in action; Public health communication; Infectious diseases; Contextspecific systems; Leadership and management) and 26 domains including the new ones e.g. One health and climate change, Vaccinology, Infodemiology and infodemic management.

Conclusions :

The potential uses for this competency set include training needs assessments in public health institutions, individual assessments, writing of vacancy notices, and professional development planning. Harmonising the competencies used in applied epidemiology will facilitate collaboration and enhance the use of a common language among professionals who tackle cross-border health threats in Europe.

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

Keywords : prevention, control, epidemiology, public health

ABSTRACT ID: 203

PRESENTED BY: Amelie Plymoth / amelie.plymoth@ecdc.europa.eu

Fireside session 9
Day 3, Thursday 18 November 2021
15:15 – 16:00

Late breakers (vaccines)

Moderator

Marion Muehlen (WHO)

Abstracts

a. Effectiveness of homologous and mixed vaccine series against Covid-19 in 16-69-year-olds in Finland: A register-based cohort study

E. Poukka [1]

U. Baum [2], T. Kilpi [3], D. Obach [4], A. Palmu [5], H. Nohynek [6], T. Leino [7]

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[4] EPIET fellow/ECDC; Finnish Institute for Health and Welfare

Background :

More research evidence on the effectiveness of homologous and mixed Covid-19 vaccine series is needed. Three Covid-19 vaccines, two mRNA vaccines and one adenovirus vector vaccine (AdV), have been used in Finland. The objective of this study was to estimate the effectiveness of homologous and mixed vaccine series during April-August as delta variant emerged to Finland.

Methods :

We conducted a register-based cohort study including all 16-69-year-olds in Finland. The exposure was Covid-19 vaccination (since 27 December 2020) and the outcomes were SARS-CoV-2 infection and Covid-19 hospitalization (between 26 April and 26 August 2021). Using Cox regression, vaccine effectiveness (VE) was estimated as 1 minus the hazard ratio comparing those who received their second vaccination ≥7 days ago to those unvaccinated. Due to the prioritization of chronically ill and safety concerns, the chronically ill received more often two doses of AdV or AdV and mRNA vaccine (mixed vaccine series) than homologous mRNA vaccine series. Threrefore, the analysis was adjusted for age and presence of underlying chronic conditions.

Results :

The cohort had 3670227 individuals of which 44% received two doses of mRNA vaccine, 4% two doses of AdV, 4% mixed series (AdV+mRNA) and 28% only one dose. A fifth remained unvaccinated. VE of the homologous series was 78%% (CI95% 77-79%, mRNA vaccine) and 76% (71-81%, AdV) against SARS-CoV-2 infection, respectively. The corresponding VE of the mixed series was 79% (76-82%). VE against Covid-19 hospitalization was 98% (96-99%, mRNA vaccine), 95% (88-98%, AdV) and 94% (87-97%, mixed series).

Conclusions :

Both homologous and mixed vaccine series protect well against SARS-CoV-2 infection and even better against the severe outcome of Covid-19 hospitalization. The study adds evidence about the effectiveness of the mixed series.

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

Keywords : Covid-19 vaccines, SARS-CoV-2, mixed vaccine series, hospitalization

ABSTRACT ID: 278

PRESENTED BY: Eero Poukka / eero.poukka@thl.fi

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b. 2021 COVID-19 vaccine effectiveness against hospitalisation due to laboratory-confirmed SARS-CoV-2 infection in older adults: pooled results from eight European countries

A. Rose [1]

Z. Lovric Makaric [2], C. Mazagatos [3], O. Launay [4], S. Denayer [5], L. Seyler [6], C. Burgui [7], J. Baruch [8], A. Marin [9], A. Machado [10], R. Vaikutyte [11], P. Husa [12], A. Vasili [13], S. Michelaki [14], L. Domegan [15], G. Fagherazzi [16], G. Petrovic [17], A. Larrauri [18], L. Luong [19], N. Bossuyt [20], T. Demuyser [21], I. Martinez-Baz [22], M. Borg [23], M. Lazar [24], V. Gomez [25], G. Gefenaite [26], L. Souckova [27], I. Hasibra [28], M. Amerali [29], N. Petty-Saphon [30], F. Berthet [31], E. Kissling [32], C. Carstairs [33] , S. Bacci [34], M. Valenciano [35], V. Sandonis [36], F. Pozo [37], I-MOVE-COVID-19 VE hospital working group, ECDC COVID-19 VE hospital working group

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Background :

European vaccine effectiveness (VE) studies initiated and funded by the European Centre for Disease Prevention and Control (ECDC) and the European Commission (I-MOVE-COVID-19) include 38 hospitals across 13 European countries. Using a test-negative case–control design, we aimed to measure VE against hospitalisation due to COVID-19 in vaccination target group(s) overall and by vaccine product.

Methods :

Between 28 December 2020 and 06 June 2021, we recruited patients hospitalised with severe acute respiratory illness (SARI; ECDC case definition). Cases were SARI patients, laboratory-confirmed SARS-CoV-2 positive by RT-PCR within 24 hrs of admission or within the previous 2 weeks. Controls were SARI patients who were RT-PCR negative for SARSCoV-2 at admission. We pooled available data received from 34 hospitals in eight countries, and estimated VE in those aged ≥65 years using logistic regression, adjusting for study site (as fixed effect), swab date, age and chronic condition.

Results :

We included 1,670 SARI patients (1,095 cases, 575 controls). Seventy-nine cases (7%) and 244 controls (42%) were vaccinated; 73% (235/323) with Pfizer–BioNTech vaccine. Adjusted VE (aVE) for one and two doses of Pfizer–BioNTech was 69% (95%CI: 44–82) and 93% (95%CI: 85–97), respectively (sample size was too small to estimate aVE by other vaccine products). For one dose of Pfizer–BioNTech, aVE was 73% (95%CI: 49–86) in those aged 65–79 years and 64% (30–82) in those ≥80 years. For two doses in these age-groups, aVE was 97% (95%CI: 86–99) and 85% (95%CI: 66–94), respectively.

Conclusions :

Our results suggest good protection against severe COVID-19 conferred by one and two doses of Pfizer–BioNTech vaccine in adults ≥65 years.

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

Keywords : SARS-CoV-2, COVID-19 vaccines, vaccine effectiveness, hospitalisation, multicentre study

ABSTRACT ID: 296

PRESENTED BY: Angela Rose / a.rose@epiconcept.fr

c. Effectiveness of Comirnaty COVID-19 vaccine against SARS-CoV-2 Delta variant among elderly residents from a long-term care facility, south of France, May 2021

M. Sanchez Ruiz [1]

G. Adonias [2], A. Robaglia-Schlupp [3], F. Rapilly [4], M. Chabert [5], L. Ramalli [6], O. Reilhes [7], C. Bruel [8], P. Malfait [9], P. Chaud [10]

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[2,3,7,8] Agence régionale de santé, Provence-Alpes-Côte d'Azur, France

[4,5,6,9,10] Santé publique France, Marseille, France

Background :

In December 2020, France started coronavirus disease (COVID-19) vaccination, prioritising vulnerable groups such as long-term care facility (LTCF) elderly residents. The following summer, respiratory syndrome coronavirus 2 (SARSCoV-2) Delta variant became dominant; however, vaccine effectiveness (VE) against it was not well understood yet. We assessed Comirnaty (BNT162b2 mRNA, BioNTech-Pfizer) VE against SARS-CoV-2 Delta variant among LTCF elderly residents during an outbreak in the south of France, May 2021.

Methods :

We conducted a retrospective cohort study among LTCF residents. We described, sex, age, dependency level, reversetranscription polymerase chain reaction and sequencing results, clinical evolution, vaccination status. We compared attack rates of SARS-CoV-2 infection, symptomatic, and severe COVID-19 (respiratory support, hospitalisation, and/or death reported) by vaccination status (two doses administered versus none) to evaluate VE (1 – Relative Risk [RR]) with 95% confidence intervals (CI).

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Results :

Among 68 LTCF residents, 73.5% (n=50/68) were female, the mean age was 89 (standard deviation [SD] 8.2) years, 73.1% (n=49/67) were severely dependent. A SARS-CoV-2 infection was identified in 38 residents (55.9%), 11 with symptomatic, and eight with severe COVID-19. All sequenced samples (n=19/38, 50.0%) had the same genomic sequence of Delta variant. All residents completed vaccination within three months prior to outbreak onset. Vaccination coverage was 83.8% (n=57/68). Comirnaty VE against SARS-CoV-2 Delta variant infection was 14.5% (95%CI: - 41.8-48.5). It was 89.0% (CI: 68.6-96.1%) against symptomatic, and 93.6% (95%CI: 72.2-98.5) against severe COVID-19.

Conclusions :

We found a high Comirnaty VE against symptomatic and severe COVID-19 caused by SARS-CoV-2 Delta variant among LTCF elderly residents, but not against Delta variant infection. This supports vaccination rollout and the implementation of control measures for close case contacts among vaccinated LTCF elderly residents.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : SARS-CoV-2,COVID-19,COVID-19 Vaccines, Long-Term Care, Aged, RNA Messenger
ABSTRACT ID: 286
PRESENTED BY: Miguel Angel Sanchez Ruiz / sanchez.r.miguel.angel@gmail.com

d. Vaccine acceptance for vaccination against covid-19 over time in Sweden 2021

S. Earnshaw Blomquist [1]

E. Appelqvist [2], S. Scholtens [3], L. Maripuu [4], M. Danielsson [5], L. Mannheimer [6], A. Tegnell [7]

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Background :

It is important to follow Covid-19 vaccine acceptance as a complement to coverage data in order to reach high vaccination coverage. This study aimed to provide insights into reasons for accepting or delaying vaccination as well as practical aspects and information needs among the adult population in Sweden.

Methods :

Between March – June 2021, three web-based surveys were conducted by the Public Health Agency of Sweden (PHAS). The questions were based on WHO's Behavioural Insights survey tool and adapted to the Swedish context. A set of respondents were given the opportunity to reply to additional open-ended questions. Data was weighted for representativeness of the Swedish population. Quantitative data was analysed descriptively. Qualitative data was analysed thematically.

Results :

The results showed sustained high levels of vaccine acceptance – (Yes definitely – 69-70%; Yes probably 18-22%; no or probably no 5-6% or don't know 4-7%). Vaccine acceptance was high both amongst men and women, and across age groups. 91% responded that it is important to get vaccinated to protect others, as well as 81% to protect your own health. The thematic analysis segmented by acceptance showed that those who would probably say yes to vaccination have questions focused on vaccine safety. Perceived practical barriers regardless of vaccine acceptance included the booking system, travel to the vaccination and time off work. The results were shared with partners, published on PHAS website and included in the national press conferences as a complement to vaccine coverage data.

Conclusions :

The results reveal a high vaccine acceptance at the time of the study. Examples of where the results have been implemented include guidance for youth vaccination and informing the targeting of unvaccinated individuals.

Subject : Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)
Keywords : COVID-19 pandemic, attitudes, behavioural insights, public health surveillance
ABSTRACT ID: 315
PRESENTED BY: Sarah Earnshaw Blomquist and Emma Appelqvist / sarah.earnshaw@folkhalsomyndigheten.se

e. [late breaker] COVID-19 Vaccine Breakthrough infections in fully vaccinated people: characteristics of cases notified in Castilla y Leon, Spain

I. Martinez-Pino [1,12]

S. Carbajal [2], C. Ruiz [3], J. Oyague [4], E. Arranz [5], J. Rodriguez [6], S. Fernandez [7], M. Herranz [8], M. Marcos [9], M. Chamorro [10], N. Rincon [11], M. Rodriguez [12]

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[3,4,5,6,7,8,9,10,11] General Directorate of Public Health, Castilla y Leon Spain

[12] General Directorate of Public Health, Castilla y Leon Spain

Background :

COVID-19 vaccines are a critical tool to control pandemic, however, vaccine breakthrough cases are expected. Castilla y Leon (CyL) started COVID-19 vaccination campaign on 27/12/2020 and as of August 27, 2021 1.759.701 people were fully vaccinated (73,4%). The Regional Ministry of Health of CyL is monitoring these cases to better understand infections among vaccinated people.

Methods :

Description of COVID-19 cases notified from 27/12/2020 to 27/08/2021 through the Regional Notifiable Diseases Surveillance System (RNDSS) was carried out. Patient demographics, time since vaccination, clinical presentation, vaccine type, and SARS-CoV-2 lineage were analyzed. For every COVID-19 case, vaccination history data was available from the Regional Vaccination Registry. For this study, a vaccine breakthrough infection was defined as the detection of SARS-CoV-2 RNA or antigen in a respiratory specimen collected from a person ≥7 days (Comirnaty) or 14 days (rest of vaccines) after they have completed all recommended doses of COVID-19 vaccine, regardless clinical presentation.

Results :

During the first eight months of vaccination campaign, 160.216 COVID-19 cases were notified to the RNDSS. 25.123 of them received 1 or 2 doses before disease onset, and 12.290 were classified as breakthrough infections (69,5% Comirnaty, 4,5% Moderna, 14.6% AstraZeneca, 11,3 Janssen). Median age was 58,3 years (IQR: 48,7-76,1) and 58,8% were female. 74,1% were symptomatic, 9% (1.103) were hospitalized and 211 (1.7%) died. Lineage was available in 19,5% of the breakthrough infections. 85,7% out of them were identified as variants of concern (59.8% Delta).

Conclusions :

Up to date, characteristics of breakthrough infections reflects those of vaccinated population in CyL. For an adequate interpretation of vaccine effectiveness specific studies are needed. We recommend to continue monitoring breakthrough infections to evaluate trends and changes in these cases.

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Fireside session 10
Day 4, Friday 19. November 2021
13:30 – 14:15

COVID-19: Vaccines

Moderator

Hanna Nohynek (THL, Finland)

Abstracts

a. Protection from severe outcomes after vaccination with one dose of mRNA vaccine BNT162b2: A COVID-19 outbreak investigation in a nursing home in Kiel, Germany, December 2020 to January 2021

M. Sandfort [1]

E. Meyer [2], H. Fickenscher [3], W. Hellenbrand [4], K. Michaelis [5]

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[3] Institute for Infection Medicine and State Office Schleswig-Holstein for the Registration of Notifiable Diseases, Kiel, Germany

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

Background :

On 28/12/2020, residents and staff in a nursing home in Kiel, Germany, received the first BNT162b2 dose. Residents of one ward were excluded due to the occurrence of COVID-19 cases in the preceding week. Five days after vaccination, cases were detected by routine testing on other wards. We investigated the protection by one BNT162b2 dose in this outbreak.

Methods :

We included all residents and staff present in the facility from 21/12/2020 to 26/01/2021 in a retrospective cohort study. Cases were all persons tested SARS-CoV-2 PCR-positive after routine antigen testing and at PCR-screenings. We considered cases vaccinated if a positive test or symptom onset occurred at least 8 days after vaccination. We analysed the association of vaccination with severe outcomes (hospitalisation or death) by Poisson regression, adjusting for age and whether cases occurred later than 4 days after the entire facility was quarantined on 04/01/2021.

Results :

Among 152 residents and 138 employees, 121 (80%) residents and 24 (17%) employees were vaccinated. We detected 108 cases (attack rate: 37%): 79/152 (52%) residents and 29/138 (21%) employees. Twenty-one residents were hospitalised and 13 died. Risk for severe outcomes increased with age by 8% [95%-confidence interval: 5%-12%] per year. The effectiveness of one dose against severe outcomes was 68% overall [30%-86%] and 75% [45%-89%] for residents. Risk for severe outcomes was similar when diagnosis occurred 5-14 days after vaccination (11/54 cases with severe outcomes, 20%) or later (2/10, 20%, Fisher's exact test: p=1.0).

Conclusions :

One BNT162b2 dose rapidly protected against severe outcomes during a COVID-19 outbreak in a nursing home. This suggests that providing BNT162b2 vaccination to unvaccinated non-cases early in institutional outbreaks can mitigate COVID-19 severity should further transmission occur.

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b. COVID-19 vaccine coverage in healthcare workers in England and effectiveness of BNT162b2 mRNA vaccine against infection, multicentre prospective cohort study (the SIREN study)

V. Hall [1]

S. Foulkes [2], A. Saei [3], N. Andrews [4], A. Charlett [5], E. Wellington [6], J. Stowe [7], N. Gillson [8], A. Atti [9], J. Islam [10], I. Karagiannis [11], K. Munro [12], J. Khawam [13], M. Chand [14], C. Brown [15], M. Ramsay [16], J. Lopez-Bernal [17], S. Hopkins [18], The SIREN Study Group

[1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18] Public Health England

Background :

There is an urgent need to better understand whether individuals who have recovered from Coronavirus Disease 2019 are protected from future SARS-CoV-2 infection.

Methods :

A large multi-centre prospective cohort recruiting hospital staff in the UK was established in Jun-2020. Participants attended regular SARS-CoV-2 PCR and antibody testing and completed fortnightly questionnaires on symptoms and exposures. At enrolment, participants are assigned to the antibody positive or negative cohort. The primary outcome was a reinfection in the positive cohort or primary infection in the negative cohort, determined by PCR tests. Potential reinfections were clinically reviewed and classified according to case definitions. Primary infections in the negative cohort were defined as a first PCR positive test and seroconversions were excluded when not associated PCR positive test. A proportional hazards frailty model using a Poisson distribution was used to estimate Incidence Rate Ratios (IRR), to compare infection rates in the two cohorts.

Results :

Between Jun-2020 and Jan-2021, 155 infections were detected in the positive cohort of 8,278 participants, collectively contributing 2,047,113 days of follow-up. This compares with 1,704 new PCR positive infections in the negative cohort of 17,383 participants, contributing 2,971,436 days of follow-up. The incidence density per 100,000 person days between June 2020 and January 2021 was 7.6 reinfections in the positive cohort, compared with 57.3 primary infections in the negative cohort. The adjusted IRR was 0.16 for all reinfections (95%CI 0.13-0.19) compared to PCR confirmed primary infections.

Conclusions :

A previous history of SARS-CoV-2 infection was associated with an 84% lower risk of infection, with median protective effect observed 7 months following primary infection. This study shows that previous infection with SARS-CoV-2 induces effective immunity to future infections in most individuals.

c. Previous SARS-CoV-2 infection as a priming dose for Pfizer vaccinations - Antibody response by sex, time since infection and symptoms in Italian health care workers

T. Homan [1]

F. Fortunato [2], G. Corso [3], R. Prato [4], D. Martinelli [5]

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[3] Department of Clinical and Experimental Medicines, University of Foggia, Italy

Background :

A key global strategy to mitigate public health and societal consequences caused by COVID-19 is to protect as many people quickly through vaccination. Postponing or cutting the second dose in previously exposed SARS-CoV-2 persons is recommended by Italy but not by WHO. We aimed to evaluate if previous exposure to SARS-CoV-2 can act as a priming dose as assessed by antibody response, considering sex, time since infection and symptoms.

Methods :

Blood samples were drawn before and after (21 days) infection, and after (≥21 days) the first dose of anti-COVID-19 vaccine Pfizer-BioNTech from PCR-confirmed naïve (n=132) and exposed (n=126) health-care workers (HCW), in Foggia since May-1 2020. We compared IgG-titres of exposed HCWs pre-dose with naïve HCWs post-dose. Among exposed HCWs, post-dose titres were compared between those infected less (n=16) and more (n=6) than 6 months ago and between those with and without symptoms.

Results :

A 36-fold difference between IgG-titres of exposed HCWs pre-dose and HCW unexposed post-dose (Medians: 25.35-0.7; p-value <0.001) was found. Between exposed HCWs with an infection more or less than 6 months ago postdose (Medians: 96-291 days) titres were similar (Medians: 2010-1250; p-value =0.154). Post-dose titres among exposed HCWs did not vary by sex but differed between symptomatic and asymptomatic (Medians =1900, 1170; p-value =0.048).

Conclusions :

SARS-CoV-2 infection yielded higher IgG-antibody titres than a first dose vaccine (Pfizer-BioNTech) in HCWs, regardless of sex. Immunogenicity after the first dose did not depend on the time since infection and was stronger in symptomatic individuals, although high titres remained among asymptomatics. Our data suggests that SARS-CoV-2 infection may serve as a priming dose regarding antibody response, irrespective of sex, time since infection and symptoms.

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d. COVID-19 vaccination in the Netherlands: Effectiveness and impact in elderly

B. de Gier [1]

M. Kooijman [2], S. Wijburg [3], N. Smorenburg [4], J. van de Kassteele [5], H. de Melker [6], S. Hahné [7], M. Knol [8], RIVM COVID-19 epidemiology and surveillance group

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

Background :

In January 2021, COVID-19 vaccination started in the Netherlands, first targeting nursing home residents, elderly and health care workers. Surveillance data were used to evaluate vaccine effectiveness (VE) and impact of the vaccination program among people of 75 years and older.

Methods :

Retrospective analyses were done for January 18th to May 17th, 2021, using data from vaccination and disease registers. VE at 21 days after the first and second dose of Comirnaty® (BioNTech/Pfizer) was estimated using the screening method by comparing the proportion of cases vaccinated with the vaccination coverage matched by calendar week. The impact of vaccination was quantified by comparing the incidence of infections, hospitalizations and deaths at ten weeks after start of vaccination with the incidence in the week preceding start of vaccination in the given target group, and standardizing the resulting incidence rate ratio (IRR) by dividing it by the IRR among the not-yet-eligible 65-74 year-olds.

Results :

The estimated VE against infection was 45% (95%CI: 42-49%) after one dose and 82% (79-84%) after two doses. The VE against hospitalization was 72% (64-78%) after one dose and 94% (90-97%) after two doses. VE decreased with increasing age. We estimated a relative decline in infections and deaths of 92% (92-93%) and 90% (87-93%) among nursing home residents. Among people living at home aged 80-84 and 85 and older, we estimated a relative decline of 64% (59-68%) and 73% (92-93%) respectively in infections; 65% (56-72%) and 77% (72-82%) in hospitalizations; and 50% (17-71%) and 63% (43-76%) in deaths.

Conclusions :

We found a high VE and large impact on COVID-19 burden in elderly in the first months after start of the vaccination program in the Netherlands.

e. COVID-19 vaccine in Finnish elderly and chronically ill: A register based cohort study

E. Poukka [1]

U. Baum [2], A. Palmu [3], T. Leino [4]

[1,2,3,4] Finnish Institute for Health and Welfare

Background :

Three COVID-19 vaccines have been used in Finland: two mRNA (Comirnaty and Moderna) and one adenovirus vector vaccine (Vaxzevria). The latter was primarily given to the chronically ill, who are highly susceptible to severe COVID-19 disease. The recommended interval between doses was set to 12 weeks to reach higher 1st dose vaccine coverage sooner in the population. We evaluated vaccine effectiveness (VE) against SARS-CoV-2 infection and COVID-19 hospitalisation among the elderly aged ≥70 years and the chronically ill aged 16-69 years.

Methods :

From 27.12.2021 through 14.05.2021 we conducted a population-based cohort study using medical and demographic register data. Exposure and outcome of interest were vaccination against Covid-19 and Covid-19 hospitalisation timely associated with a SARS-CoV-2 positive laboratory finding, respectively. VE was estimated as 1 minus the hazard ratio comparing vaccinated and unvaccinated adjusted for age, sex, vaccination priority group and hospital district.

Results :

The elderly cohort included 901 074 individuals of whom 83% had received the first dose of mRNA vaccine. The chronically ill cohort included 1 219 4978 individuals of whom 18% had received the first dose of Vaxzevria. In elderly, VE against COVID-19 hospitalisation was 66% (95%CI 38%-81%) 21-27 days after the first mRNA vaccination. VE increased to 76% (57%-86%) 42+ days after the first vaccination. There were no hospitalisations after two mRNA vaccinations. In chronically ill, VE was 84% (57%-94%) 21-27 days after the first Vaxzevria dose and 79% (59%-89%) after 42+ days.

Conclusions :

Both mRNA and adenovirus vector vaccines had high VE against SARS-CoV-2 infection and COVID-19 hospitalisation after the first dose. A single dose provides decent protection. Postponing the 2nd doses can be beneficial in managing the pandemic for providing higher vaccination coverage.

Fireside Session Abstracts

Fireside session 11
Day 4, Friday 19: November 2021
13:30 – 14:15

Late breakers

Moderator

Alma Tostmann (Radboudumc, the Netherlands)

Abstracts

a. Multi-country collaboration on the investigation of a Salmonella Braenderup outbreak in the EU/EEA and United Kingdom 2021

M. Aabye [1]

B. Rosner [2], S. Lefèvre [3], E. Litrup [4], L. Müller [5], S. Ethelberg [6], S. Balasegaram [7], A. Hoban [8], J. Takkinen [9], C. Jernberg [10], H. Moore [11]

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Background :

A genomic cluster of S. Braenderup ST22 was notified by Denmark via Epidemic Intelligence Information System (EPIS) of European Centre for Disease Prevention and Control (ECDC) on 3rd May 2021. By July, 348 S. Braenderup outbreak cases were reported from 12 countries in the EU/EEA and UK, including 68 hospitalisations. With countries support, ECDC established an international team to investigate the source and prevent the spread of the outbreak.

Methods :

A confirmed EU/EEA and United Kingdom (UK) outbreak case was defined based on whole genome sequencing (WGS). Under ECDC coordination, affected countries participated in teleconferences, shared questionnaires and provided case data to a common line list. Standard interviews (telephone or online) were performed focusing on fruit consumption in the week prior to symptom onset. Country-adjusted case-control studies were conducted in the United Kingdom (UK), Denmark (DK) and Germany (DE). Food safety authorities sampled fruits and carried out trace back analyses.

Results :

A strong association between being a case and consumption of melons was found in the UK and DE (OR =672, 95% CI: 39-58,975 (UK); OR =10.2, 95% CI: 3.9-26.4 (DE)), but not in DK (OR=1.46, 95% CI: 0.46-4.27). Of 124 cases, 86% reported consumption of other melons than watermelons. The outbreak strain was found in two samples of Galia melons imported from Honduras. The outbreak ceased as the imported fruits gradually disappeared from the market.

Conclusions :

The investigation identified imported melons (other than watermelons) as probable vehicles of infection. Case-control studies in several countries, sharing information and data, including WGS results from food samples, and cross-border trace back investigations were crucial to identify the source. Multi-sectorial collaboration should be further strengthened for investigation of multi-country foodborne outbreaks.

b. National Hepatitis A Outbreak in England and Wales Linked to Medjool Dates With Potential Ongoing International Risk

D. Leeman [1]

T. Garcia Vilaplana [2], K. Balogun [3], S. Ngui [4], C. Handford [5], T. Potter [6], M. D'Agostino [7], W. Khan [8], E. Phipps [9], R. Smith [10], S. Balasegaram [11], National Incident Management Team (FSA, PHE & PHW)

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[10] Communicable Disease Surveillance Centre, Public Health Wales, Cardiff, UK

[11] South East and London Field Service, National Infection Service, Public Health England, London, UK

Background :

An outbreak of genetically related hepatitis A virus (HAV) infections in England and Wales was identified in March 2021. A multidisciplinary team from Public Health England, Public Health Wales and Food Standards Agency (FSA) undertook epidemiological, microbiological and international supply chain investigations to identify the source and prevent further cases.

Methods :

As part of enhanced surveillance, a food history is taken from all HAV cases and infections are microbiologically confirmed including genotyping and sequencing. We undertook two case-case studies using HAV cases with unrelated sequences and cases from a Salmonella outbreak as case-controls. We collected date product information from cases including batch numbers. FSA undertook national and international supply chain investigations. Campden BRI laboratory tested food samples using RT-PCR.

Results :

Between January and June 2021, 37 HAV cases with one of three highly related genetic sequences and two un- sequenced cases with an epidemiological link to a sequenced case were identified. Thirty-five cases (90%) reported date consumption, analytical studies showed a strong association with dates; product A gave an adjusted odds ratio of 47.36 (95% CI: 1.79–1,256.07; p=0.021). Microbiological testing confirmed the presence of HAV on Medjool dates reclaimed from cases.

Fireside Session Abstracts

Food traceback identified a common grower based in Jordan. Multiple UK retailers recalled dates from this grower between April and May with outbreak surveillance continuing until August. An alert was issued to the International Food Safety Authorities Network by FSA.

Conclusions :

While our investigations identified a contaminated food item, no source of contamination was found. In July, Australian authorities reported three HAV cases with identical sequences to the UK outbreak strain who consumed dates from Jordan indicating potential ongoing contaminated food products in the international supply chain.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Hepatitis A, HAV, Outbreak, Medjool Dates, Supply Chain
ABSTRACT ID: 305
PRESENTED BY: David Leeman / david.leeman@phe.gov.uk

c. In(tra)-Action Review (IAR): COVID-19 Management at IHR-designated Airports in Germany from September 2020 until May 2021

M. Schöll [1]

M. Boldt [2], H. Czerwonka [3], L. Ehlkes [4], L. Frühsammer [5], S. Ippisch [6], U. Rexroth [7], J. Seidel [8], M. an der Heiden [9]

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Background :

Within the aviation sector, COVID-19 containment measures have strongly affected the responsibilities and procedures of public health authorities (PHA) in Germany. Following concepts from the World Health Organization (WHO) and the European Centre for Disease Prevention and Control (ECDC), an in(tra)-action review (IAR) was conducted to review recurring challenges and good practices and draw lessons from the COVID-19 response, in line with temporary recommendations by the Emergency Committee under the International Health Regulations (IHR, 2005).

Methods :

On 20 May 2021, 20 representatives from PHA at local, state and federal level, security agencies as well as from the aviation sector participated in a virtual IAR on COVID-19 management at German IHR-designated airports. In facilitated break-out groups, they identified challenges, gaps, and good practices using pre-designed templates and applying root cause analysis. Results were collated, triangulated and cross-checked with respondents.

Results :

Participants prioritized the following challenges: the limited adaptability of airport infrastructure in a health crisis, insufficient timely access to relevant traveler data for contact tracing purposes, the short

implementation deadlines of measures, high political pressure, and lack of or inconsistent standards. Good practices entailed the establishment of a digital registration system for travelers from risk areas, cross-sectoral collaboration, the set-up of testing centers at airports and the increase in funding for the German public health service.

Conclusions :

The IAR provided an opportunity for intra- and intersectoral exchange across the IHR-designated airports and different federal levels. Participants recommended using the digital registration of travelers for contact tracing, establishing regular intersectoral exchanges, and making communication more timely, more targeted, and more coordinated between different sectors and institutions. The experience with the IAR method is relevant for additional lessons learned processes.

Subject : Preparedness (e.g. preparedness planning, simulation exercises, after action reviews)
Keywords : Points of entry – Airport – COVID-19 – SARS-CoV-2 – In(tra)-Action Review - IAR
ABSTRACT ID: 301
PRESENTED BY: Meike Schöll / schoellm@rki.de

d. Increased Household Transmission of COVID-19 Cases Associated with SARS-CoV-2 Delta Variant (B.1.617.2): national case-control study

A. Vusirikala [1]

H. Allen [2], J. Flannagan [3], K. Twohig [4], A. Zaidi [5], D. Chudasama [6], T. Lamagni [7], C. Turner [8], C. Rawlinson [9], J. LopezBernal [10], R. Harris [11], A. Charlett [12], G. Dabrera [13], M. Kall [14], COG-UK Consortium

[1,2,3,4,5,6,] [7,8,9,10,11,12,13,14] Public Health England

Background :

The SARS-CoV-2 Delta variant (B.1.617.2), first detected in India, has rapidly become the dominant variant in England. Early reports suggest this variant has an increased growth rate suggesting increased transmissibility. This study indirectly assessed differences in transmissibility between the emergent Delta variant compared to the previously dominant Alpha variant (B.1.1.7).

Methods :

A matched case-control study was conducted to estimate the odds of household transmission ($\geq$ 2 cases within 14 days) for Delta variant index cases compared with Alpha variant index cases. Cases and controls were derived from national surveillance data (March to June 2021) and assigned on the outcome of interest, household clustering. One-to-two matching was undertaken on geographical location of residence, time period of testing and property type, and a multivariable conditional logistic regression model was used for analysis.

Results :

In total 5,976 genomically sequenced index cases in household clusters were matched to 11,952 sporadic index cases (single case within a household). 43.3% (n=2,586) of cases in household clusters were confirmed Delta variant compared to 40.4% (n= 4,824) of sporadic cases. The odds ratio of household transmission was 1.70 among Delta variant cases (95% CI 1.48-1.95, p <0.001) compared to Alpha cases after adjusting for age, sex, ethnicity, index of multiple deprivation (IMD), number of household contacts and vaccination status of index case.

Conclusions :

We found evidence of increased household transmission of SARS-CoV-2 Delta variant, potentially explaining its success at displacing Alpha variant as the dominant strain in England. With the Delta variant now having been detected in many countries worldwide, the understanding of the transmissibility of this variant is important for informing infection

Fireside Session Abstracts

prevention and control policies internationally.

e. An outbreak of multi-drug resistant Pseudomonas aeruginosa in a UK haematology unit: a matched case-control study demonstrating increased risk associated with quinolone use

W. Rice [1]

J. Martin [2], M. Hodgkin [3], A. Barrasa [4], M. Denton [5], G. Hughes [6]

[1,4,6] Public Health England

[2,3] Leeds Teaching Hospitals NHS Trust

[5] Public Health England; Leeds Teaching Hospitals NHS Trust

Background :

Between September 2016 and December 2020, 17 haematology patients were diagnosed with the same strain of multidrug resistant Pseudomonas aeruginosa at a teaching hospital in Northern England. The high associated case fatality rate (71%, n=12) prompted this investigation aiming to identify risk factors for acquisition of the outbreak strain.

Methods :

A retrospective matched case-control study with three matched controls per case. Cases were admitted patients colonized or infected with the outbreak strain; matching was based on admission date to one of the haematology wards. Adjusted odds ratios (aOR) with 95% confidence intervals (95% CI) using conditional logistic regression were calculated.

Results :

In total, 17 cases and 51 controls were included in the study. Analysis on patient movement found admission to the study hospital from another hospital (aOR = 21.5; 95% CI: 1.7-271.56), length of admission on one of the haematology wards (aOR = 1.03; 95% CI: 1.01-1.06), and number of attendances at the out-patient haematology unit (aOR = 1.57; 95% CI: 1.01-2.47) were associated with increasing risk of P. aeruginosa acquisition. Additionally, the use of ciprofloxacin (aOR = 102.13; 95%CI: 1.5-6682.9) and under the care of the transplant team (aOR = 14.27; 95CI%: 1.02-186.6) were identified as independent risk factors.

Conclusions :

Associations with patient movement highlight the vulnerability of these patients to acquisition of environmental organisms. In these settings, the use of quinolones to prevent neutropenic sepsis in patients receiving stem cell transplant must be balanced against the risk of acquisition of multi-drug resistant P. aeruginosa where it is present in the environment. In addition, where care across multiple organisations is required, we recommend a joint review of antibiotic use involving all hospitals in the care pathway.

Poster Tour Abstracts

The posters can be viewed in the virtual poster exhibition. Participants can then message the presenters on the platform about their poster.

The poster tours give participants at ESCAIDE 2021 an opportunity to view five posters and engage with the authors.

Each poster tour lasts 30 minutes and the presenters have 2 minutes each to introduce their work, followed by a Q&A, where the moderator will ask questions to the presenters and address the questions received in the chat and redirect them to the presenters.

The time available is too short for a full discussion on the research, therefore the main aim of the poster tour is to set up connections between the researchers and interested participants.

We hope that after the tour, participants will contact the authors to further discuss the research. Poster tours and oral abstract fireside sessions are organised by topic and dispersed throughout the conference programme.

The posters will be available on the platform throughout the conference. Each will be linked to the profile of the presenters, allowing participants to get in touch through messaging feature of the platform.

| **56** | **POSTER TOUR** |

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Poster Tour Abstracts

Poster tour 1
COVID-19: Field epidemiology

Abstracts

a. Coronavirus-19: Evaluation of symptomatology and cycle threshold values among residents and healthcare staff in long-term care facilities in the Netherlands, February 2020 - June 2020

M. Van Hensbergen [1]

C. den Heijer [2], S. Mujakovic [3], N. Dukers [4], C. Hoebe [5]

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Background:

COVID-19 has caused a high burden of disease within long-term care facilities (LTCFs). Important in this respect is the challenge to recognize COVID-19 in an early phase. However, transmission often took place before infection control measures could be taken. Almost all (suspect) COVID cases were tested by the Public Health Services (PHS). This made it possible to evaluate COVID-19 information on positively and negatively tested LTCF residents and staff in South Limburg during the first wave of the pandemic (February 2020-June 2020).

Methods :

Data was gathered via regular channels used to notify COVID-19 to our PHS. CT- values were available from MUMC+ medical microbiology laboratory after real time PCR from combined nasopharyngeal and oropharyngeal swabs. Univariate and multivariate logistic regression analyses were performed on symptoms predictive of COVID-19, corrected for age and sex.

Results :

1461 LTCF staff and 1702 residents were included, of which 512 (35,0%) and 695 (40,8%) tested positive for COVID-19, respectively. LTCF staff showed a higher mean CT value (28,4) compared to residents (26,5). Symptoms of disease which were predictive of COVID-19 were fever (OR 1,9, CI 1,5-2,4) cough (OR 1,4, CI 1,1-18), muscle ache (OR 2,7, CI 1,9-3,8) and loss of taste and smell (OR 4,1, CI 2,9-5,8) for staff, whereas for residents this was subfebrility (OR 5,96, CI 2,6-13,9), fatigue (OR 6,9, CI 2,7-17,2) and diarrhoea (OR 2,9, CI 1,2-6,9).

Conclusions :

In conclusion, symptoms predictive of COVID-19 differ between LTCF staff and residents. Only aspecific symptoms, such as fatigue and diarrhoea, were predictive for COVID in residents, which complicates early detection. Moreover, viral load was higher in residents compared to staff. These findings support a low-level testing policy within LTCFs, especially among residents.

b. Impact of cross-border-associated cases on the severe acute respiratory syndrome coronavirus-2 epidemic in Switzerland from June to September 2020

M. Reichmuth [1]

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Background:

In Switzerland, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic grew from a few dozen confirmed cases to several hundred cases per day during summer 2020. During this time, holiday travel without quarantine was largely allowed. The impact of potential cross-border-associated cases (imports) on the national epidemic dynamics remained unclear. Our objective was to assess the impact of imports on the SARS-CoV-2 epidemic in Switzerland during summer 2020.

Methods :

We analyzed individual data on confirmed SARS-CoV-2 cases reported by the Swiss Federal Office of Public Health (FOPH) from 1 June to 30 September 2020. We used a stochastic branching process model that accounts for superspreading of SARS-CoV-2 to simulate epidemic trajectories in absence and presence of cross-border-associated cases.

Results :

From June to September 2020, 23,199 SARS-CoV-2 cases were reported in Switzerland. For 12,259 (53%) of these cases, the most likely country of exposure was available and 3,304 (27%) declared that exposure was most likely abroad. In absence of imported cases, we estimated the effective reproduction number Re above the critical threshold of one (1.08, 95% confidence interval, CI: 1.04-1.11). In contrast, we estimated Re = 0.84 (95% CI: 0.81-0.87) if imported cases are taken into account.

Conclusions :

In Switzerland, imports had a considerable impact on the national dynamics and can explain the growth of the SARS- CoV-2 epidemic during summer 2020. Our results underline the importance of improved surveillance for international travelers in order to better control the spread of SARS-CoV-2.

Poster Tour Abstracts

c. Using real time PCR reflex assays to detect evidence for Variants of Concern (VOCs) in an outbreak of COVID-19 in a closed setting in Wales, UK

C. Sawyer 1

N. Pacchiarini [2], C. Moore [3], I. Murrell [4], A. Couzens [5], S. Corden [6], Y. Lee [7], C. Griffiths [8], S. Jones [9], C. Williams [10], C. Johnson [11]

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[7,8,9] Conway County Borough Council

[10] Centre Disease Surveillance and Control, Public Health Wales

[11] Betsi Cadwaladr University Health Board, Public Health Wales

Background:

COVID-19 Variants of Concern (VOCs) have implications relating to vaccine efficacy and increased transmissibility. VOC cases in the UK, aside from the UK Variant, are typically associated with travel. Following detection of a VOC, enhanced case management is undertaken. On 08 March 2021, an Incident Management Team (IMT) was initiated for an outbreak of COVID-19 in a boarding school in Llandudno, North Wales. One case was a student, recently returned from South America.

Methods :

Whole school testing was initiated on 06 March 2021 by the local authority. On 09 March 2021, whole genome sequencing and novel PCR reflex assay testing of cases was requested due to the potential for the returning student having a VOC – specifically E484K containing VOC-21JAN-02 (Brazil variant, P1).

Results :

There were 41 cases identified (27 pupils, 14 staff) across all 4 boarding "houses". By 10 March, PCR assays identified that samples did not contain the E484K mutation – a feature of the Brazilian variant and other VOCs. Overall, 26 samples were suitable for sequencing (of 36 available samples), all were found to be UK variant. Phylogenetic analysis revealed samples fell in a single genetically related cluster, comprising of 6 phylotypes; suggesting both multiple introductions of COVID-19 into the school, and transmission within the school.

Conclusions :

The use of novel PCR reflex assays provide timely information for further case management and outbreak response. Genomic sequencing provided detail on the lineage and provided evidence of multiple introductions of COVID-19 to the school, a closed setting, suggesting a need for improved general infection prevention and control measures – however, as the UK variant is the dominant circulating virus across Wales, enhanced case management was not required.

Subject: Field epidemiology (e.g. outbreak investigations)
Keywords: COVID-19, Genomics,outbreak investigation
ABSTRACT ID: 128
PRESENTED BY: Clare Sawyer / clare.sawyer2@wales.nhs.uk

d. SARS-CoV-2 risk factors among adults attending Municipal Health testing locations in the Netherlands, February to April 2021

A. Shah 1

M. Middeldorp [2], S. Abbas Zadeh [3], F. Dijkstra [4], S. Raven [5], E. Fanoy [6], S. van Dam [7], S. Hahné [8], M. Knol [9]

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[7] Department of Infectious Disease Control, Public Health Service Hart voor Brabant (GGD), 's-Hertogenbosch, The Netherlands

Background:

In the SARS-CoV-2 pandemic, several risk factors for transmission among the general population are still unclear. We aimed to investigate risk factors for testing SARS-CoV-2 positive among the Dutch population attending Municipal Health COVID-19 testing locations.

Methods :

We conducted a test-negative study among adults attending Dutch COVID-19 testing locations from 8 February 2021. Participants were invited via appointment confirmation email. Eligibility included questionnaire completion prior to test result and not residing at a care facility. The association between demographic and chronic conditions with COVID-19 was assessed using univariable and multivariable logistic regression. Analysis was restricted to adults tested who experienced symptoms, had no close contact with a COVID-19 case, and were not previously tested SARS-CoV-2 positive since January 2020.

Results :

From 8 February-2 April 2021, 5912 adults met the inclusion criteria, of whom 245 tested positive (4%). 1902 (32%) were male, 5111 (86%) Dutch, and median age was 43 years (18-85). Of 280 (5%) persons vaccinated against COVID-19, 180 (3%) received two doses, 92 (2%) one dose, and information was missing for 8 (0.1%). Risk factors for acquiring COVID-19 included being aged 45-59 [OR:1.62, 1.11-2.39] and having a middle educational level (intermediate, lower vocational) [OR:1.43, 1.10-1.86]. Adjusting on age, gender, and educational level, adults living with adolescents (13-18 years) [adjusted OR:1.67, 1.04-2.72] had higher risk than persons living alone. Chronic conditions, contact professions, onsite occupations, and household size were not significantly associated with testing positive (p- values>0.5).

Conclusions :

Our study characterised symptomatic patients during the third wave in the Netherlands. Preliminary data indicated higher risk for acquiring COVID-19 for adults living with adolescents. We recommend monitoring transmission dynamics, adjusted by vaccination status when feasible, to inform public health strategies.

Subject: Field epidemiology (e.g. outbreak investigations)
Keywords: COVID-19, SARS-CoV-2, risk factors, test-negative study, Netherlands
ABSTRACT ID: 188
PRESENTED BY: Anita Shah / anita.shah@rivm.nl

Poster Tour Abstracts

e. Control of a nosocomial VOC B.1.1.7 outbreak with high secondary attack rates among household contacts in Berlin, Germany, January - February 2021

S. Burdi [1]

F. Reichert [2], S. Schink [3], P. Larscheid [4], J. Schumacher [5], C. Brandt [6], K. Jelavic [7], M. Ramthor [8], B. Schmitz [9], C. Drosten [10], J. Hofmann [11], J. Michel [12], T. Eckmanns [13], M. Abu Sin [14]

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Background:

VOC B.1.1.7 is assumed to have higher transmissibility than the wild-type SARS-CoV-2. We investigated a nosocomial outbreak with this variant to understand transmission dynamics and adapt recommendations for control measures to limit this and future B.1.1.7-outbreaks.

Methods :

Confirmed cases were defined as patients or health care workers (HCW) hospitalised or having worked at the hospital after 01.01.2021, or household contact (HHC) of cases, with N501Y and delH69/V70 mutations as detected by PCR. Information on symptoms and symptom onset were derived from surveillance data and clinical information. Based on collected information on contacts and exposures we constructed transmission chains.

Results :

The outbreak occurred at a tertiary hospital in Berlin, Germany, affecting mainly the cardiology ward. 18 cases among patients, 20 among HCW and 33 secondary cases outside the hospital (including four cases in a care facility) were identified (N=71). Transmissions occurred patient-to-patient (secondary attack rate (SAR)=35%;9/26), HCW-to-patient, patient-to-HCW and HCW-to-HCW. SAR among HHC was 75% (24/32). After the detection of the first three cases, control measures were implemented including a twice weekly screening of all inpatients (N=452) and HCW (N=1270). Close contacts were tested daily on days 10-16 after exposure. Nine cases were identified in the pre-symptomatic phase (16%;9/57 with available information on symptom onset; median=2 days before onset), six remained asymptomatic (8.7%;6/69 with available information on symptoms). The outbreak was declared over after 38 days.

Conclusions :

Despite high SAR of B.1.1.7, especially among HHC the outbreak could be controlled. Transmissions were observed to and from HCW during patient care, emphasizing the importance of strict adherence to infection prevention and control measures. In addition, immediate widespread PCR-testing of patients and HCW should be implemented to control outbreaks with B.1.1.7.

Poster Tour Abstracts

Poster tour 2
COVID-19: Implementation science

Abstracts

a. Low positive predictive value of SARS-CoV-2 rapid antigen tests in screenings of specific settings in Northern Region of Portugal

D. Queiroz Almeida [1]

R. Carvalho [2], A. Mendes [3], J. Vidal Castro [4], R. Areias [5], G. Cruz Alves [6], M. Neto [7]

[1] Public Health Departament, Northern Region Health Administration, Portugal; Matosinhos Public Health Unit

[2] Gerês/Cabreira Public Health Unit

[3,4,5,6,7] Public Health Department; Northern Regional Health Administration

Background :

It has been over a year since WHO declared the COVID-19 pandemic. Multiple strategies have been implemented to minimize the impact of the disease. In Portugal, one of the strategies consists of mass testing for SARS-CoV-2 in some specific contexts, because of the vulnerability of its population or the impact of an outbreak. These screenings were performed with rapid antigen test (RAT). However, there was no evaluation of the strategy. We aimed to assess the predictive value of RAT performed in screening tests.

Methods :

We conducted an observational study, using data from screenings in different settings (occupational, schools, nursing and care homes) for COVID-19 in the Northern Region of Portugal, from the National Surveillance System, between January 2021 and May 14Th 2021. For each positive result, a confirmatory test by PCR was searched for and calculated the positive predictive value.

Results :

A total of 29038 tests were performed, among three different settings (3867 in caring homes, 23367 in schools and 2049 in occupational settings). The positivity rate was 0,0930% (n=27). 70,8% (n=18) had a confirmatory test. Within these PCR test results, 6 were positive. This leaded to a positive predictive value of 33,3%. A post-hoc analysis revealed that 4 of these 6 people had mild symptoms when the first sample was collected (not eligible for screening).

Conclusions :

The positive predictive value of the RAT for SARS-CoV-2 in these settings was in line with the literature. Despite some COVID-19 cases were detected, it must be considered the economic, social and health costs of these interventions. Further studies are needed to better inform Public Health interventions and policies.

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

Keywords : COVID-19; Predictive Value of Tests; Mass screening; diagnostic test

ABSTRACT ID: 260

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b. I-MOVE-COVID-19 study of risk factors for in-hospital death in hospitalised COVID-19 patients in Europe, January 2020–January 2021

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Background :

Early in the COVID-19 pandemic, mortality from COVID-19 was known to increase with age (e.g. <2% in <50 year-olds, >20% in 70+ year-olds). Within this multicentre European study (11 sites in eight countries), we measured the risk of in- hospital death in COVID-19 patients, January 2020–January 2021.

Methods :

The cohort included patients aged 20+ hospitalised ≥24 hrs with laboratory-confirmed SARS-CoV-2. We collected information on age, sex, symptoms, chronic conditions (asthma, diabetes, cancer, heart, liver, and kidney disease, and immunodeficiency), and laboratory results. We computed odds ratios (OR), adjusting for admission date, age, sex, and

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co-morbidities. Sites with ≥15% missing values for any variables were excluded.

Results :

We included 11,307 patients from eight sites in the pooled analysis, of whom 2,110 (18.66%; 95%CI: 17.95–19.39) died in hospital. Odds of death was greater in males (OR=1.68, 95%CI:1.51–1.87), those with immunosuppression (OR: 1.49, 95%CI 1.01–2.19), heart disease (OR: 0.1.32, 95%CI: 1.18–1.48), kidney disease (OR: 1.31, 95%CI: 1.16–1.49), or diabetes (OR: 1.16, 95%CI:1.03-1.31). Compared with the 20–39-year-olds, odds of dying increased from 2.16 (95%CI: 1.17–3.99) in 50–59 year-olds to 32.47 (95%CI: 17.94–58.79) in 90+ year-olds. Compared with those admitted in Jul–Aug 2020, patients admitted in Jan–Feb or Mar–Apr 2020 had higher odds of death (OR: 2.22, 95%CI 1.38–3.58; 1.70, 95%CI 1.22–2.35; 1.48, respectively).

Conclusions :

The I-MOVE-COVID-19 study results suggest that the odds of in-hospital death from COVID-19 was higher among those who were older, male, who had heart or kidney disease, or who were admitted in January–April 2020. We will include further 2021 data to investigate additional potential risk/protective factors and outcomes, and to understand changes after vaccination rollout.

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

Keywords : COVID-19, SARS-CoV-2, risk factors, cohort, multicentre study

ABSTRACT ID: 169

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c. SARS CoV-2 PCR-testing in school-aged children in the first semester of school year 2020/2021 in Croatia. – An analysis based on the Croatian laboratory COVID-19 database

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Background :

In Croatia, an increase of COVID-19 case numbers has been observed since summer 2020. A fast surge of new cases was noted from week 42 and peaking in week 50. Primary and secondary schools remained open despite high community transmission. Testing was recommended primarily to symptomatic individuals. We aimed to investigate PCR-testing and PCR-test positivity rate (TPR) in school aged children and adults.

Methods :

Data from the Croatian laboratory COVID-19 database was used, including school-aged children defined as those aged 6 -18 years and adults aged above 18 years before April 1st, 2020. Those with missing of the following data were excluded from analysis: date of birth, date of testing and PCR-test results. We calculated PCR-testing rate (TR) and TPR for the study period (week 37-52 2020) for the two groups separately.

Results :

Of all PCR-test performed during the study period, 90,2% were in adults and 7,6% in school-aged children. Mean TR during the study period was 784/100,000 in school-aged children, 1.7 times lowercompared toadults (1,313/100,000).The TPR increased gradually in both groups (from 5% to maximum of 38%), being even higher in children between weeks 37 and

46 and roughly the same afterwards (>30%).

Conclusions :

Although the mean TR in children was lower than in adults, the TPR in both groups was roughly the same and even higher in school-aged children from the beginning of the study period until week 46. This could indicate more transmission in school-aged children than in adults. We recommend increasing testing in school-aged children regardless of their symptoms to better understand their role on community transmission and adjust non- pharmaceutical interventions accordingly

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

Keywords : COVID-19, PCR-testing, community transmission, children

ABSTRACT ID: 255

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d. SARS-CoV-2 incidence and its determinants in six ethnic groups of Amsterdam, the Netherlands: a population-based longitudinal study

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Background :

Previous studies have shown differences in SARS-CoV-2 diagnoses between ethnic groups, yet little is known on the temporal trends in new

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infections between ethnic groups.

Methods :

Participants aged 25-79 years enrolled in a population-based prospective cohort (HELIUS) conducted in Amsterdam, the Netherlands, were tested twice for SARS-CoV-2-specific antibodies and answered COVID-19-related questions during two nested sub-studies in June-October 2020 (after the first wave) and November 2020-April 2021 (during the second wave). We compared SARS-CoV-2 incidence since 1 January 2020 between ethnic groups using a two-state Markov model adjusted for age and sex and identified determinants of SARS-CoV-2 exposure within ethnic groups.

Results :

We included 2,497 participants in the first round, of whom 1,993 participated in the second round up to 9 March 2021. Median age was 54 years [interquartile range 45-62] and 55.4% were female. SARS-CoV-2 incidence was higher in participants of South-Asian Surinamese (adjusted hazard ratio [aHR]=1.62;95%CI=1.12-2.35), African Surinamese (aHR=1.96;95%CI=1.36-2.82), Ghanaian (aHR=5.96;95%CI=4.28-8.28), Turkish (aHR=2.57;95%CI=1.81-3.66) and Moroccan origin (aHR=3.15;95%CI=2.22-4.45) compared to participants of Dutch origin. These differences in incidence became wider during the second versus first wave for all groups except the Ghanaian group (all p for interaction<0.05). Presence of household members with suspected SARS-CoV-2 infection was a common determinant of SARS-CoV-2 exposure across groups. Other determinants were specific to individual groups.

Conclusions :

SARS-CoV-2 incidence was higher in the largest ethnic minority groups of Amsterdam compared to the Dutch origin group, especially during the second wave of SARS-CoV-2. Targeted prevention efforts following the first wave were not sufficient enough to prevent further infections/ widening of infection rates between groups. More effective interventions are urgently needed, with focus on reaching high vaccine coverages in these groups.

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

Keywords : SARS-CoV-2,COVID-19,HELIUS study, infection, incidence, seroprevalence, serology, antibody, ethnicity

ABSTRACT ID: 174

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e. Self-assessment of SARS-CoV-2 infection in six ethnic groups during the first wave of the COVID-19 epidemic in Amsterdam, the Netherland

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Background :

National test and trace strategies depend on individuals being able to assess whether they may have SARS-CoV-2 infection. Few studies have investigated ethnic disparities in self-assessed infection. We evaluated differences in self- assessment of past SARS-CoV-2 infection between six ethnic groups in Amsterdam, the Netherlands.

Methods :

Participants aged 25-79 years were randomly selected within ethnic groups from a population-based cohort study. We asked participants whether they thought to have been infected with SARS-CoV-2 infection and if so, what their symptoms were. Participants were tested for SARS-CoV-2 antibodies. We calculated the proportion of participants positive for SARS-CoV-2 antibodies who had self-assessed infection (i.e. sensitivity), which was compared across ethnic groups. In participants with self-assessed infection, we compared self-reported symptoms between antibody positive and negative individuals, overall and per ethnicity.

Results :

Between 24 June-9 October 2020, we included 2497 participants. The proportion with self-assessed infection was distributed as follows: Dutch, 14.7% (n=74/429); African Surinamese, 14.0% (n=57/407); South-East Asian Surinamese, 11.3% (n=51/453); Ghanaian, 5.4% (n=18/331); Turkish, 16.9% (n=69/338); and Moroccan, 20.1% (n=79/394). The sensitivity of self-assessed infection was high in Dutch (76.0%, n=19/25) and African Surinamese participants (81.8%, n=18/22), moderate in South-Asian Surinamese (59.1%, n=13/22), Moroccan (59.1%, n=19/32) and Turkish (63.3%, n=19/30) participants and low in Ghanaian participants (9.5%, n=9/95). Loss of smell and taste (all ethnicities), less appetite (Moroccan, African Surinamese), and muscle ache and shortness of breath (Moroccan) were more often reported by participants who thought they had been infected and were antibody positive compared to antibody negative.

Conclusions :

SARS-CoV-2 self-assessment differs across ethnic groups. Expanding testing opportunities and promoting vaccination for individuals, particularly in groups with poor sensitivity to assess infection, is crucial in reducing onwards transmission.

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

Keywords : SARS-CoV-2,COVID-19,infection,self-assessment,ethnicity,sensitivity

ABSTRACT ID: 170

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f. Inequalities in initiation of COVID19 vaccination by age and population group in Israel- December 2020-April 2021

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Background :

COVID19 vaccination coverage in Israel varies widely among different population groups. Comparing crude coverage between groups may be misleading because of the different age structure underlying each group. In order to describe inequalities in COVID19 vaccine initiation in Israel we described the interaction of age and population groups in terms of dose 1 vaccine coverage

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Methods :

We calculated cumulative age-specific vaccine coverage by population group (Ultra-Orthodox Jewish, Arab, General Jewish) using first COVID19 vaccine doses administered by age group and municipality (Ministry of Health Data) as numerator and census data as denominator (Central Bureau of statistics data). We calculated the relative differences in vaccine coverage between population groups within each age group, and between age groups within each population, using binomial regression

Results :

8,507,723 individuals in 268 cities were included. Compared with the general Jewish population, coverage was lowest in the Ultra-Orthodox population in all age groups (range -13.3% among 60+ to -47.2% among 15-19 years olds, p<0.001). In all groups, the proportion of vaccinated individuals in younger age groups relative to those aged 60+ decreased with decreasing age and were smaller in the Ultra-Orthodox groups compared with other groups. For example within the general Jewish population, people aged 20-29 were 16.6% less likely to be vaccinated than those aged 60+, increasing to 40.6% in the Ultra-Orthodox population.

Conclusions :

COVID19 vaccine coverage varies in different groups comprising Israeli society. In all age groups, the Ultra-Orthodox population had the lowest vaccine coverage. The younger the age group, the more Ultra-Orthodox Jews are diverging from their age peers in terms of initiating COVID19 vaccination. The vaccination programme requires tailored approaches to encourage vaccination among under-immunized groups in Israel.

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

Keywords : vaccine; COVID-19; Israel; inequalities

ABSTRACT ID: 139

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Poster tour 3
COVID-19: surveillance

Abstracts

a. Low occurrence of secondary COVID-19 cases following exposure to SARS-CoV-2 at primary schools and early childhood education and care facilities between August 2020 and March 2021 in Finland

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Background :

Closure of schools is a controversial public health measure to curb SARS-CoV-2 transmission. To assess the risks related to keeping schools open during the pandemic, we studied the incidence of secondary infections after exposure events at schools and childcare facilities in comparison to the overall incidence of COVID-19 in the respective agegroups. According to Finnish contact-tracing data, the average secondary attack rate after any kind of SARS-CoV-2 exposure has been 9-19%.

Methods :

We calculated and compared COVID-19 secondary attack rates among children and adults exposed to SARS-CoV-2 at early childhood education and care (ECEC) facilities (0-6y), primary (7-12y) or lower secondary schools (13-15y) in Finland during 08.2020-03.2021. Local contact-tracing teams reported the number of individuals quarantined after school exposures and laboratory-confirmed secondary cases following these exposures. Age-specific COVID-19 incidences were derived from the National Infectious Disease Register.

Results :

In total, 3014 exposure events were reported, concerning 70244 exposed individuals, 1.9% of whom tested positive for SARS-CoV-2 (1343 individuals: 268 adults; 1054 children; 21 unspecified). The secondary attack rates for children were: 2.5% when exposed at ECEC, 1.4% at primary schools and 1.7% at lower secondary schools. For adults, the respective rates were 5.0%, 1.7% and 1.3%. The risk was significantly (p-value<10-7) higher for adults compared to children for ECEC settings, but not for the higher levels. The secondary cases associated with school/childcare exposures accounted for only 6.9% of the total COVID-19 cases among 0-15 year-olds during the study period.

Conclusions :

The risk of transmission within childcare and school settings was low overall. Therefore, given the negative impact of school closures on child well-being, we recommend against implementing closures as a precautionary measure for COVID-19 mitigation purposes in Finland

Subject: Surveillance

Keywords: COVID-19, SARS-CoV-2, coronavirus, schools, child

ABSTRACT ID: 236

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ESCAIDE

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b. Excess mortality during the first year of the COVID-19 epidemic in Slovenia, week 10/2020–week 10/202

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Background :

During the current COVID-19 pandemic, data on excess mortality are of key concern. We introduced monitoring of excess all-cause mortality within the national COVID-19 surveillance system in Slovenia to inform prevention and control measures.

Methods :

We applied the EuroMOMO algorithm accounting for reporting delay, trend and seasonality, to the weekly number of deaths in the Central Registry of Patient Data reported from week 10/2020–10/2021. We defined excess mortality as z- score ›2 and compared all-cause mortality to COVID-19 reported incidence and mortality. Algorithm detects upward shifts of 1.5 standard deviations during three consecutive weeks.

Results :

During the first epidemic wave (week 10–20/2020), we observed no excess all-cause mortality but upward shifts among 75–84-year olds during week 15–17. During the second wave (week 36/2020–week 10/2021), we observed excess mortality during week 42/2020–week 5/2021 (z-scores: 3–14). Excess deaths peaked in week 49/2020 with 384 deaths (95% CI: 383.9–384.0) coinciding with a peak of 404 COVID-19 deaths in long-term care facilities (LTCF), following the peak incidence of 1,444 COVID-19 cases in LTCF from week 46–47/2020. All-cause mortality fell before vaccination rollout in week 52/2020. After week 6/2021, we observed no excess all-cause mortality but upward shifts among 75–84 and 45–64-year olds. Average death reporting delay was 5-10 days.

Conclusions :

Modelling weekly all-cause mortality represents a complementary tool for timely assessment of epidemic impact. Identified incidence and mortality patterns highlighted the importance of non-pharmaceutical interventions in LTCF, when no vaccination was available. The impact of indirect factors e.g. access to healthcare was not quantified in this analysis. Nevertheless, we concluded that control measures in high-risk settings should be prioritized for mortality reduction.

Subject: Surveillance
Keywords: excess mortality, COVID-19, incidence, Slovenia
ABSTRACT ID: 98
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c. Increased risk of hospitalisation for COVID-19 patients infected with SARS-CoV-2 variant of concern B.1.1.7 in Cyprus, weeks 45/2020 - 10/2021

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Background :

We analysed the characteristics of COVID-19 cases for which SARS-CoV-2 whole-genome sequencing (WGS) information was performed and compared disease severity between cases infected with SARS-CoV-2 variants of concern (VOC) B.1.1.7 and cases infected with non-VOC.

Methods :

WGS was performed on a subset of samples collected between weeks 45/2020-10/2021, through the European Centre for Disease Prevention and Control genomic SARS-CoV-2 monitoring surveillance program. WGS information was linked to the COVID-19 national surveillance data to extract case-based information. Logistic regression adjusting for age, sex, pre-existing conditions and symptoms was conducted to compare disease severity between cases infected with SARS-CoV-2 VOC B.1.1.7 and cases infected with non-VOC.

Results :

During the study period, 31,955 COVID-19 cases were diagnosed and for 297 (0.9%) WGS was available. SARS-CoV-2 VOC B.1.1.7 was identified in 76 (26%) samples. Although first detected in week 50/2020, it became predominant

(›50%) since week 4/2021. Cases with available WGS significantly differ from those not sequenced for age (mean: 49 vs 39 years), presence of symptoms (82% vs 68%) and pre-existing conditions (45% vs 26%), but not for sex. COVID-19 cases infected with VOC B.1.1.7 did not statistically differ from cases infected with non-VOC for sex and age, however, they had significantly higher likelihood of being admitted to the hospital (aOR: 4.9, 95% confidence interval: 2.4-10.1), but not to intensive care/high-dependency units, or of dying.

Conclusions :

This study suggests a higher risk of hospitalisation for COVID-19 cases infected with VOC B.1.1.7. However, sequencing was performed on a small proportion of cases, possibly biased towards hospitalised cases, which could lead to an overestimation of the risk. Continuous genomic surveillance for the detection and monitoring of VOC is essential to support public health interventions.

Subject : Surveillance
Keywords : WGS, Variant of Concern, B.1.1.7, hospitalisation
ABSTRACT ID: 212
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d. High local COVID-19 incidences barely affected the timeliness and completeness of COVID-19 reporting in Germany in 2020

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Background :

During the COVID-19 pandemic, public health actors relied on daily updated case numbers and information for decision- making. We evaluated timeliness and completeness of variables relevant for local-level public health action of COVID-19 notifications in Germany and associations with local COVID-19 incidences.

Methods :

Based on data from the German mandatory notification system from 27.01.-31.12.2020, we assessed associations with local 7-day-COVID-19 incidences in multilevel regression models, correcting for effects at local level and adjusting for pandemic phases (pre-pandemic: calendar week (CW) 5-9, first wave: CW10-20, summer: CW21-39 (reference), second wave: CW>39), federal states and weekdays. We assessed local reporting time (LRT; laboratory to local notification), data transmission time (DTT; local level to Robert Koch Institute) and completeness of information on symptoms, risk factors and exposure to a known case.

Results :

In 2020, 1,756,107 COVID-19 cases were reported in Germany. Median LRT (Q25-Q75:0-1) and DTT (Q25-Q75:0-1) were both 0 days. Completeness for symptoms, risk factors and exposure was 70%, 53% and 40%, respectively. Per 100 cases/100,000 inhabitants/7days, timeliness increased by 0.1 days (95%CI:0.1-0.2). Completeness decreased with higher 7-day-incidences (risk factor/symptoms/exposure: OR:0.999, p<0.001). They varied across state (p<0.001) and weekdays (p<0.001). For exposure (OR:0.804, p<0.001) and risk factors (OR:0.359, p<0.001), completeness was lowest in the first and for symptoms in the second wave (OR:0.696, p<0.001). Compared to summer, DTT was 1.325 days (p<0.001) higher pre-pandemic, while LRT was 0.145 days (p<0.001) higher during the first wave.

Conclusions :

Timeliness was excellent, completeness was mediocre. Both were barely affected by local incidences but showed regional and temporal variations, suggesting structural and procedural differences within the notification system. The ongoing enhancement of the notification system should address these differences, increase completeness and maintain timeliness.

e. Estimating COVID-19 reinfection in northern Portugal: a surveillance case definition is needed!,

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Background :

Since the emergence of SARS-CoV-2 in December 2019, over 164 million people have been infected and 3,4 million people died of COVID-19 worldwide. Nowadays, COVID-19 reinfections and their estimated impact are one of Public's Health major challenges, due to the absence of guidelines for intervention. In Portugal there is no reinfection case definition. This study aims to estimate COVID-19 reinfections in northern region of Portugal.

Methods :

In this observational study, we collected data on patients who had tested positive for COVID-19 from the Portuguese National Surveillance System (SINAVE) in the northern region of Portugal, from 1st March 2020 to 17th May 2021. We included all patients who had two positive tests (PCR/RAT), accordingly to reinfection definitions used in EU/EEE (45, 60 and 90 days) and estimated reinfection rates.

Results :

From the 338.532 confirmed COVID-19 cases, we obtained that 1.338 patients had two SARS-CoV-2 positive-tests 90 days apart. With lower test intervals, we obtained 2.258 patients with positive tests 60 days apart, and 3.191 patients with two positive tests 45 days apart. We estimated that, reinfection rate in northern Portugal is between 0,4% (tests 90 days apart) and 1,0% (45 days interval).

Conclusions :

The absence of a reinfection case definition may jeopardize the implementation of Public Health measures. Moreover, it can decrease population's risk perception. Therefore, it is urgent to implement a case definition, guiding public health policies against the COVID-19 pandemic.

Poster Tour Abstracts

Poster tour 4
Food and waterborne diseases: outbreaks

Abstracts

a. Outbreak of Salmonella Enteritidis linked to beef, Norway, January to May 2021

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Background :

On 25 February 2021 the National Reference Laboratory informed the Norwegian Institute of Public Health (NIPH) of a possible outbreak of Salmonella Enteritidis (S. Enteritidis). We initiated a multidisciplinary outbreak investigation to identify its source and prevent further transmission.

Methods :

Cases were defined as individuals with laboratory confirmed S. Enteritidis infection, sequence type ST11 (MLST), and cluster type CT5784 (cgMLST, 3002 targets), living in Norway and with onset of symptom after 25 January 2021. In collaboration with the Norwegian Food Safety Authority (NFSA) we interviewed the first eight cases with a standardized trawling questionnaire focused on Salmonella to assess food consumption one week before symptom onset. The remaining cases (n=11) were interviewed with a targeted questionnaire focusing on minced meat and beef products.

Results :

We identified 29 cases, 13 (38%) were hospitalized, and 62% were females median age 59 years, (range 2 - 91). They were geographically widespread in Norway. Fifteen of the 19 cases interviewed reported eating bovine minced meat, and eight had consumed some of it raw. The Norwegian Veterinary Institute had whole-genome sequenced S. Enteritidis isolated from bovine carcasses imported from Germany, and a match with the outbreak strain was detected.

Conclusions :

We identified beef imported from Germany as source of this outbreak. Meat products from the imported batch were recalled, and all available stock was impounded by the NFSA. Consumers were recommended via the media not to eat raw minced meat. The S. Enteritidis outbreak strain was also detected in patients from Denmark and France. Even though traceback investigations could not confirm the same source, it does highlight the importance of routine testing of meat imported to Norway.

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

Keywords : Salmonella Enteritidis, outbreak investigation, food- and waterborne diseases, bovine carcasses, Foodborne Diseases/prevention & control

b. An outbreak of norovirus gastroenteritis after a New Year's Eve dinner at a hotel in North Rhine Westphalia, Germany

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Background :

On 6 January 2020 local health authority of Siegen Wittgenstein reported a gastroenteritis outbreak among guests who attended a New Year celebration at hotel X. An outbreak investigation was conducted to identify potential vehicle(s) and mode of transmission.

Methods :

A retrospective cohort study aimed to test the hypothesis that food served during celebration was the vehicle of infection. Structured questionnaire was emailed to hotel guests and staff to collect data on illness onset and food exposures. Cases were defined as guests or staff that experienced acute onset of diarrhoea and/or vomiting within 48 hours of attending the celebration. Food specific attack rates and risk ratios with 95% confidence intervals (CI) were calculated. All food items identified as risk in univariate analysis and with >50% completeness were included in a multivariable logistic regression analysis with backwards elimination to identify the main vehicle.

Results :

Of 164 guests at the celebration, 66.5% responded to the questionnaire. A total of 84 cases were identified (attack rate: 77%), reporting vomiting (85.7%), nausea (85.7%) and diarrhoea (76.2%). Most cases (84.5%) developed gastroenteritis on 1 January 2020 and the median symptom duration was 3 days. A staff member with gastrointestinal illness <48 hours before the event was identified as a potential index case. Consumption of roast beef served during dinner was the strongest risk factor associated with being a case (odds ratio 3.2; 1.2-8.1 CI, p<0.05) and could explain 77.4% of cases.

Conclusions :

This point-source norovirus outbreak most likely started with a symptomatic staff member with further person-to-person and/or food-to-person spread among guests attending the dinner. Findings emphasize the importance of exclusion of symptomatic staff from the workplace, particularly in hospitality and food service industry.

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

Keywords : Norovirus, outbreak, acute gastrointestinal disease, retrospective cohort

Poster Tour Abstracts

c. Outbreak of Shiga-toxin producing Escherichia coli (STEC) O157 linked to imported food product, United Kingdom, August 2020

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C. Jenkins [2], S. Butt [3], R. Smith [4], T. Dallman [5], C. Brehmer [6], E. Marchant [7], S. Gharbia [8], J. Hawker [9]

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Background :

In August 2020, an outbreak of Shiga toxin-producing Escherichia coli (STEC) O157 occurred in the United Kingdom.

Whole genome sequencing revealed these cases formed a genetically distinct cluster.

Methods :

Hypotheses generated from exploratory case interviews were tested in two analytical studies, and these results informed microbiological and food chain investigations. A case-case study used non-outbreak "comparison" STEC cases; a case- control study used a market research panel to recruit controls. Enterobase, a publicly accessible database of genomes of several bacterial genera, was queried for isolates within 50-SNPs of the outbreak strain.

Results :

A total of 36 cases were identified; all cases reported symptom onset between 3rd and 16th August 2020. The majority of cases (83%) resided in the Midlands region of England or Wales. A high proportion of cases reported eating out, with one fast-food restaurant chain mentioned by 64% (n=23) of cases. Both case-case (adjusted odds ratio (aOR) 31.8, 95% confidence interval (CI) 1.6 – 624.9) and case-control (aOR 9.19, 95% CI 1.0 – 8.2) studies provided statistically significant results that consumption of a specific fast-food product was independently associated with infection. The only ingredient specific to the product was cucumbers which were imported from the Netherlands. The most closely related international match to the outbreak strain was a sequence from a Dutch cattle isolate (<75 SNPs) taken in 2007.

Conclusions :

Consumption of a specific fast-food product was a likely cause of this outbreak. Supply of cucumbers was immediately halted, and no further cases have been identified since 16th August 2020. The combination of multidisciplinary investigations was essential in halting this outbreak.

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

Keywords : gastrointestinal, outbreak, case-case, case-control, whole genome sequencing

ABSTRACT ID: 49

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

d. [late breaker] Foodborne outbreak in a Greek high school through catered lunches, May 2021

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Background :

In May 2021, 20 gastroenteritis cases were reported among 126 students (12-18 years) and 48 employees in a Greek school. Lunches were delivered by a catering company and consumed in classrooms. An investigation was initiated to identify the source and implement control and preventive measures.

Methods :

We conducted a retrospective cohort study. A case was defined as any student/employee presenting abdominal pain and/or diarrhea during 27-29 May 2021. We collected data through a structured paper questionnaire. We calculated food- specific attack rates (AR), risk ratios (RR), and 95% confidence intervals (95% CI). School and catering company premises were inspected by the public health directorate. Stool and food samples were collected and microbiologically analysed.

Results :

In this point source outbreak, 30 cases were identified among 129 respondents (AR:23%); 26 students and 4 teachers. Most cases reported symptom onset on 28 May (00:00-06:00). In multivariable analysis, consumption of spaghetti with minced meat on 27 May (OR 53.4, 95% CI:3.9–736.1, 97% of cases exposed) was associated with acute gastroenteritis. Two of the three stool samples from students were positive for Clostridium perfringens. Six food samples of the spaghetti dish offered on 27 May, tested positive for Clostridium perfringens and four were positive for Bacillus cereus. Inadequate recording of procedures and temperature measurements did not allow the identification of the critical points that led to the outbreak during the environmental investigation.

Conclusions :

This investigation highlights the risk of foodborne outbreaks in school settings. Epidemiological and laboratory investigation identified a catered lunch as the most probable source of this outbreak. The importance of having a sufficient recording system to guide public health action in case of outbreaks is emphasised.

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

Keywords : gastroenteritis, school, Clostridium perfringens, outbreak, Greece.

ABSTRACT ID: 328

PRESENTED BY: Sofia Papanikou / sopavage@yahoo.gr

Poster Tour Abstracts

Poster tour 5
Respiratory viruses: surveillance

Abstracts

a. Establishing a novel European hospital surveillance platform in response to a newly emerging infection: lessons from the I-MOVE-COVID-19 hospital network

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Background :

The first signal of a new infection is often severe cases presenting at hospital. Enhanced surveillance of these cases is critical to learning more about disease epidemiology and patient outcomes, but national-level surveillance can lack power to draw conclusions. In response to the emergence of SARS-CoV-2, the Influenza-Monitoring Vaccine Effectiveness (I-MOVE) network, founded in 2007, expanded to establish the I-MOVE-COVID-19 Consortium in February 2020. The Consortium's surveillance objectives included using pooled data to describe clinical and epidemiological characteristics of hospitalised COVID-19 patients across Europe, in order to contribute to the knowledge base, guide patient management, and inform public health response.

Methods :

Eleven study sites participated in the surveillance, including 23 hospitals across six EU Member States and Albania, and hospitals nationally in England and Scotland. A standardised protocol and dataset for collection was agreed by April 2020. In England and Scotland, data were generated by linkage of routine datasets; other sites used bespoke paper or electronic questionnaires. Data were submitted, pooled and analysed quarterly.

Results :

Data were received regarding 84,297 COVID-19 patients hospitalised between 1 February 2020 and 31 January 2021. Three surveillance bulletins were published between September 2020 and March 2021, providing key insights into severe COVID-19 at European level. However, the unexpected, overwhelming workload at participating sites, and difficulties securing data protection and ethics permissions, delayed data submissions and presented challenges for timely analysis.

Conclusions :

Building on an existing network facilitated a novel European multicentre hospital surveillance system to be implemented during a pandemic; however, timeliness was nonetheless problematic. In future, processes could be streamlined e.g. by developing pre-approved template protocols with information governance and ethical approvals in place during the inter- pandemic period.

Subject : Surveillance
Keywords : SARS-CoV2, COVID-19, hospital, pandemic
ABSTRACT ID: 218
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b. Seroprevalence of SARS-CoV-2 antibodies across the European region, January - December 2020

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Background :

To assess the infection-severity of a novel pathogen, it is critical to understand the true extent of infection and population exposure. ECDC and WHO Europe have supported standardized population-based SARS-CoV-2 sero-prevalence surveys across the European Region. Our study aimed to review SARS-CoV-2 sero-prevalence studies conducted in the region in 2020, in order to understand infection levels and inform vaccination strategies and other public health responses.

Methods :

We undertook a systematic review and searched MEDLINE, the WHO COVID-19 database, ELSEVIER and the pre- print servers medRxiv and bioRxiv using a predefined search strategy. We included general

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population and blood donor studies performed in 2020, at national and regional levels. Study risk of bias was assessed using a quality scoring system based on sample size, sampling and testing methodologies.

Results :

In total, 98 studies from 23 countries across the European region were included. National SARS-CoV-2 sero-prevalence estimates ranged from 0.3% to 6%, while sub-national estimates ranged from 0% to 52%, with the highest estimates in areas reporting widespread local transmission. A range of prevalence was also found among blood donor studies, ranging from 0 to 17%.

Conclusions :

The review found evidence of low national SARS-CoV-2 seroprevalence (<10%) across the region during the study period, except in sub-national populations that had experienced intense community transmission. Seroprevalence varied between and within countries, with variations likely to reflect the differences in population, stage of the epidemic, public health measures implemented and heterogeneity of epidemiological and laboratory methods A large proportion of the population across Europe remained susceptible to SARS-CoV-2 at the end of 2020, highlighting the critical importance of vaccinating priority groups while maintaining low levels of transmission to minimise morbidity and mortality.

Subject : Surveillance
Keywords : SARS-CoV-2, sero-epidemiology, surveillance, immunity, Europe
ABSTRACT ID: 217
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c. Adapting and optimizing event-based surveillance to meet the needs of the evolving COVID-19 pandemic

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Background :

WHO has applied timely and context-specific epidemic intelligence through event-based surveillance (EBS) to inform COVID-19 pandemic response activities. Consistent and systematic EBS has however been challenging due to the extreme volume of information and rapid evolution of risks and response needs.

Methods :

We conducted EBS through the Epidemic Intelligence from Open Sources (EIOS) initiative, together with official reports and targeted online searches. Analysts identified, assessed and documented signals of interest from around the world based on predefined criteria including changes in epidemiology, healthcare capacity, testing and impact on vulnerable populations.

Results :

The first COVID-19-related signal of a cluster of pneumonia cases was identified on 31 December 2019. Over time, the scope and processes for EBS changed. In early 2020, we used EBS to detect case and death counts, complementing official reporting through the International Health Regulations mechanism. In mid-2020, we used EBS more regularly to identify unusual trends not otherwise captured by global

indicator-based surveillance and gain insights into these events. In late 2020, WHO headquarters and the six Regional Offices established a collaboration through EIOS to maximize use of resources and to jointly address challenges related to EBS, which has facilitated information sharing and increased efficiency, particularly around detection and assessment of SARS-CoV-2 variants. As of 14 May 2021, over 2800 signals from 206 countries have been documented from over 34.4 million articles categorized as coronavirus-related by the EIOS system.

Conclusions :

EBS is providing critical epidemic intelligence during the COVID-19 pandemic and can be adapted to align with evolving needs. Sustained multi-level collaboration is needed to enable continuous adaptation to the changing surveillance landscape. Approaches established and lessons learned should be applied to non-COVID-19 surveillance.

Subject : Surveillance
Keywords : COVID-19, Pandemics, Information Dissemination, International Health Regulations, Public Health Surveillance
ABSTRACT ID: 118
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d. Enhanced surveillance of COVID-19 in secondary care in Europe: a tale of two waves

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Poster Tour Abstracts

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Background :

The I-MOVE-COVID-19 Consortium was established to conduct surveillance of hospitalised COVID-19 cases in nine European countries, aiming to describe the clinical and epidemiological characteristics of severe COVID-19 in order to inform public health response.

Methods :

Data are pooled from 11 participating sites; two (England and Scotland) submitting national data, with the remainder being from a selection of hospitals. Descriptive analysis is performed on the pooled dataset overall and comparing data on patients admitted from week 5 to 28 of 2020 ("first wave") vs those admitted later ("second wave").

Results :

Data on 84,297 hospitalised patients were submitted for 01 February 2020 - 31 January 2021. Fifty-six percent of cases (46,907/84,193) were male and median age was 69 years. Where information was available, 44% (25,344 /57,769) patients were recorded as having at least one chronic condition. Ninety-five percent (7,868/8,270 and 90% (5,606/6,231) were reported with respiratory and febrile presentations respectively. Twenty-four percent (18,795/78,955) were admitted to intensive care units (ICU) and 26% (19,805/76,764) died in hospital (all sites); 12% (3,305/28,262) and 20% (5,454/27,066) respectively for all sites except England (where ICU reporting is mandated, biasing the dataset towards more severe outcomes as this site represents >50% of all cases). As a percentage of all hospital admissions, both ICU admissions and deaths decreased significantly between the first and second waves in both sexes and across all age- groups, apart from the over 75s.

Conclusions :

Results from this multicentre European surveillance system suggest that about one in 10 hospitalised COVID-19 patients are admitted to ICU and one in five have fatal outcomes. Fatality and ICU admission were lower in the second wave compared with the first

Subject : Surveillance

Keywords : COVID-19, Hospital admissions, Epidemiologic Surveillance, Respiratory infections

ABSTRACT ID: 171

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e. A comparative analysis of the epidemiology of influenza and RSV in Russia: data from a large and diverse country in Europe

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Background :

Influenza and respiratory syncytial virus (RSV) are among the leading causes of lower respiratory infections worldwide. We conducted a comparative analysis of the age distribution and spatiotemporal epidemiology of influenza and RSV in Russia using surveillance data from 2013-14 to 2018-19 in six cities located in the west (Kaliningrad & St Petersburg), centre (Lipetsk), and east (Chita, Vladivostok & Khabarovsk).

Methods :

We calculated the positivity rate for influenza and RSV (by month, season, and overall) in each city, separately for patients seen at the primary and secondary care level. We compared the age distribution of patients infected with the different influenza virus (sub)types and RSV.

Results :

A total of 17,551 respiratory specimens were included: the overall positivity rate was 13.5% for influenza and 4.4% for RSV. The A(H1N1)pdm09, A(H3N2) and B virus (sub)types caused 31.3%, 44.0% and, respectively, 24.7% of all influenza cases. The median age was older among influenza (15 years) than among RSV patients (3 years); differences across influenza virus (sub)types were seen only at the primary care level, with influenza A(H3N2) patients being significantly older than A(H1N1)pdm09 or B influenza patients. The timing of influenza epidemics was similar across cities, with the peak typically occurring in February or March. In contrast, the typical peak timing of RSV epidemics varied largely across cities, and the virus was often detected also in spring and summer months.

Conclusions :

Influenza and RSV epidemiology differed in many regards in Russia, especially in the timing of epidemics and the age distribution of infected subjects. Health policies aimed at containing the burden of diseases of viral respiratory infections in Russia should take these findings into account.

Subject : Surveillance

Keywords : Influenza, respiratory syncytial virus, Russian Federation, surveillance, epidemiology, age distribution, seasonality

ABSTRACT ID: 109

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Poster Tour Abstracts

Poster tour 6
Emerging and vector-borne diseases

Abstracts

a. Evaluation of the use of different sample types for mosquito-borne flaviviruses surveillance in birds

N. Atama [1]

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Background :

Wild birds are reservoirs of several arboviruses such as WNV and USUV and are often monitored as indicators of disease introduction or spread. To optimize the bird surveillance for arboviruses in the Netherlands, we investigated the suitability of using different specimens from live and dead (brain, heart, spleen, lungs, oropharyngeal and cloaca swabs) birds for surveillance purposes. To explore the potential use of non-invasive sampling, we also included testing for viral RNA in feathers and faeces.

Methods :

Samples of 66 USUV and 9 WNV positive birds, collected in 2016-2020, were included. Real-time PCR was used for viral RNA detection, and the proportion of positive samples as well as viral loads were compared across specimens using Fisher's exact and Kruskal-Wallis tests.

Results :

No significant difference was observed across viral loads of USUV RNA in spleen, heart, lung, or brain specimens. High viral loads were detected in feathers which were not significantly different from the detections in organs from dead birds. Additionally, no significant decrease in viral load was seen in feathers after stored dry at room temperature for 44 days. In live birds, viral loads detected in blood collected on protein saver cards were not significantly different from detections in pooled oropharyngeal-cloaca swabs. Of WNV positive live birds, 1 each of 5 fecal samples and 2 available feathers were also positive.

Conclusions :

Feathers and swabs of dead birds can serve as alternative sample types for USUV detection in dead birds, which are easier to collect compared to organ samples. Moreover, feathers may also be a less invasive alternative for live bird screening. These findings likely also apply to WNV surveillance, and provide opportunities for citizen science for sample collection.

Subject : Surveillance
Keywords : Surveillance,Wild birds,Arboviruses,Usutu virus,West Nile virus,Flaviviruses
ABSTRACT ID: 263
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b. Epidemiological Characteristics of Lyme Borreliosis in Georgia, 2019

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Background :

Lyme Borreliosis is the most common tick-borne disease in Georgia. Disease exposure characteristics have never been described before. We aimed to estimate burden and describe disease by demographics and exposure characteristics in 2020 to prioritize public health actions.

Methods :

We extracted case-based data from enhanced passive surveillance using the national Electronic Integrated Disease Surveillance System and performed descriptive analysis to estimate incidence and characterize the cases by time, place, age, gender, and exposures.

Results :

During 2020, 515 suspected cases were reported. Among them, in accordance with national case definition, 233 (45.2%) were probable and 23 (4.5%) confirmed, while 259 (50 %) were suspected and not analyzed. The overall disease incidence was 6.8 /100,000 population. The disease was widespread in the country with the highest incidence in the Racha-Lechkhumi (27.5,/100,000) and lowest in Kvemo Kartli (2.1/100,000) regions. From June to August, 128 (50%) cases occurred. The median age was 35 years (IQR:22-55 years). Out of 256 interviewed, 76 (30%) and 28 (11%) reported a tick bite and improper tick removal, respectively. Forty-seven (18.4%) cases reported being close to green areas, while contact with animals was reported by 6 (2.3%) of cases.

Conclusions :

In 2020, over half of the reported cases were just suspected, highlighting the need for raising awareness among clinicians, so that diagnosis is based on the geographic-specific burden, especially in regions with higher incidence. This result may suggest high sensitivity of case definition, which should be evaluated. Lyme disease is widespread and follows the typical seasonal pattern with people of productive age being mostly affected. We recommend countrywide awareness campaigns as only 30% of cases recalled a tick bite, and more than 18% reported visiting green areas

Subject : Surveillance
Keywords : Lyme Disease, Tick Bites, Morbidity, Georgia
ABSTRACT ID: 13
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c. Genomic monitoring to investigate emergence and transmission dynamics of arboviruses in the Netherlands

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Background :

Arboviruses are a growing One Health concern in Europe, with climate change, travel and trade influencing arthropod vectors, hosts, and disease dynamics. Computational analyses of arboviral genomes can be powerful to unravel evolution and transmission dynamics of these pathogens. In the Netherlands, extensive surveillance for arboviruses in wildlife has led to detection of the circulation of two mosquito-borne flaviviruses: Usutu virus in 2016, and West Nile virus in 2020. We aimed to gain insight in the emergence and spread of these two arboviruses.

Methods :

We submitted samples collected from mosquitoes, live and dead wild birds across the Netherlands to full genome Nanopore-based sequencing. 190 Usutu virus sequences form the period 2016-2020 and 9 West Nile viruses from the early detection period in 2020 were generated. We integrated this new genomic data with sequences from public databases and performed phylogenetic analyses and molecular clock analyses.

Results :

We provide evidence for the co-circulation of genetically diverse Usutu virus strains and for continued enzootic presence of the Usutu virus lineage Africa 3. Molecular clock analysis evaluated the most recent common ancestor of viruses from this lineage to 9 to 4 years before first detection of Usutu virus in the Netherlands. In contrast, the initial phylogenetic analysis of West Nile virus isolates shows that the obtained sequences are from closely related viruses of lineage 2, suggesting first detection closer to time of emergence in the country

Conclusions :

Our results provide critical insights in the emergence and evolution of Usutu virus and West Nile virus in the Netherlands. We establish a framework for genomic monitoring of arboviruses transmission in real time that will contribute to early warning surveillance

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Subject : Surveillance

Keywords : Arboviruses, One Health, Genomics, Epidemiological Monitoring

ABSTRACT ID: 266

PRESENTED BY: Emmanuelle Münger / e.munger@erasmusmc.nl

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d. Sensibilisation of general practitioners towards imported arboviral infections in the light of established populations of Aedes albopictus in Baden-Wuerttemberg, Germany

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Background :

Since 2007 Aedes albopictus populations are spreading northward into Germany. Due to their vector competence and the adaption to colder climate Ae. albopictus bears a potential risk for transmission of arboviral infections via viremic travel returnees and thus poses a threat to Public Health in Germany. Early diagnosis of arboviral infections in regions where Ae. albopictus is established is important to reduce the risk of localized autochthonous outbreaks.

Methods :

To estimate the preparedness of GPs for emerging arbovirus infections a random sample of 278 GPs working in cities and counties in Baden-Wuerttemberg with proven occurrence of Ae. albopictus were interviewed by an anonymized quantitative-qualitative questionnaire. 112 participants (40%) were recruited. In the control group 129 GPs were recruited (129/278, 46%).

Results :

Of those GPs working in infested areas 35% knew, that Ae. albopictus had been found (47% did not; 18% unsure) compared to only 7,75% in the control group (74% did not know, 17% unsure). 15% of all participants and 44% of those aware of the presence of Ae. albopictus had previously received information. In the control group only 6% of all GPs had received information. 50% of all GPs have performed laboratory testing for Malaria (29% DNV; 6% CHIKV). 32% have made the first diagnosis of Malaria (13% DNV; 2% CHIKV) in both groups. 91% (88% in control) of all GPS asked wanted to receive more information on vector competent mosquitoes in Germany.

Conclusions :

GPs are of vital importance for monitoring the population for those newly emerging diseases it is of utmost importance to increase awareness on clinical syndromes of arbovirus diseases and strengthen the preparedness by providing them with the tools and knowledge to do so.

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

Keywords : Aedes albopictus, general practicioner, autochthonous infections, arboviral diseases, Public Health

ABSTRACT ID: 145

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e. Autochthonous transmission of dengue, chikungunya and Zika virus in mainland France, 2010-2020

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Background :

The spread of Aedes albopictus favoured the autochthonous transmission of dengue, chikungunya, and Zika virus in Southern Europe, mainland France reporting most of events. We described characteristics of dengue, chikungunya, Zika transmission events in mainland France from 2010 to 2020 and provided prevention and control recommendations.

Methods :

Data from surveillance and autochthonous transmission investigations were described (cross-sectional design). Events were counted per year, causative agent, region. We described the number of cases, circulation period, affected areas, land cover, vector density (larvae-positive containers/100 households, Breteau index), primary case origin, prevention challenges, control measures.

Results :

From 2010 to 2020, we identified 17 events of autochthonous transmission of dengue (six occurring in 2020), three of chikungunya, and one of Zika with 80 autochthonous cases. All events happened in three vector-colonized southern regions from July to October. In most events, cases were ≤300 meters apart (n=20), areas were peri-urban ("Discontinuous Urban Fabric", n=18). When measured (n=7), Breteau index varied from 38 to 267. Identified primary cases travelled from outside the European and Eastern Mediterranean regions (n=12). Prevention challenges included missing (n=5) or reported insufficient (n=2) vector control around primary cases, unidentified (n=9) or lately identified (after local transmission, n=4; 40 days after symptom onset, n=1) primary cases. Autochthonous case identification mainly included door-to-door active case-finding and awareness-raising (n=33), health professional notifications (n=26), active laboratory screening (n=13).

Conclusions :

Mainland France presents dengue, chikungunya, and Zika transmission events, yet limited cases and affected areas might depend on surveillance. Time-place characteristics, prevention challenges, case identification patterns recommend: rigorous surveillance from July to October; enhanced vector control upon case identification in vector- colonized areas; awareness-raising among professionals for early diagnosis and notification; door-to-door active case- finding, community awareness

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

Keywords : Dengue, Chikungunya virus, Zika Virus, Disease Outbreaks, Europe, France

ABSTRACT ID: 123

PRESENTED BY: Miguel Angel Sanchez Ruiz / sanchez.r.miguel.angel@gmail.com

Poster tour 7
Food and waterborne diseases: outbreaks

Abstracts

a. Using WGS for the detection of a persistent low-level outbreak of Salmonella serotype 4,5,12:i:- (monophasic variant of S.Typhimurium) in Ile de France region in 2020, France

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Background :

In June 2020, the National Reference Centre for Salmonella (NRC) reported to Santé publique France a new genomic cluster of Salmonella serotype 4,5,12:i:- identified by Whole Genome Sequencing (WGS) since January 2020. We investigated to assess the extent of the outbreak, the vehicle of transmission and implement control measures.

Methods :

We defined a case as a person with S.4,5,12:i:- isolated in stool since January 2020, belonging to genomic cluster HC5_143285 (cgMLST). Data on risk exposures was collected by telephone interviews. Implicated premises were inspected, and trace-back/trace-forward investigations were conducted. Food and environmental samples were cultured for Salmonella and WGS was performed on all isolates.

Results :

Forty-nine cases were identified with 46 (94%) living in Ile-de-France region. Among cases interviewed (n=24), symptom onset ranged from 15 January-18 October. Twenty-three (96%) reported having eaten chicken. No other common exposures were identified. Eight cases (33%) reported buying meat directly from slaughterhouse X. Trace-back investigations for the place of purchase for other cases was hampered by inadequate documentation of distribution channels. Inspections at slaughterhouse X identified several hygiene deficiencies in equipment maintenance and staff practices. On 27 July, the outbreak strain was isolated in chicken and environmental samples at slaughterhouse X.

Conclusions :

Our findings identified chicken meat from slaughterhouse X as the most likely vehicle of transmission. To prevent further cases, slaughterhouse X was closed from 29 July-25 September, and hygiene practices were corrected. No further cases were identified after 20 October 2020. This outbreak highlights the importance of equipment maintenance and adherence to hygiene procedures among staff in slaughterhouses. Without WGS, this persistent low-level outbreak could have gone undetected. We recommend strengthening surveillance by systematic sequencing of all Salmonella isolates.

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

Keywords : persistent low-level outbreak, Salmonella serotype 4,5,12:i:-, whole genome sequencing

ABSTRACT ID: 238

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Poster Tour Abstracts

b. Cross-border outbreak of Listeria monocytogenes in Austria, Denmark, Germany and Switzerland linked to smoked trout, 2020

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Background :

In October 2020, whole genome sequencing (WGS) of human isolates detected a new molecular cluster type (13516 and 14488) of L. monocytogenes. We investigated the outbreak, and through exchange of genome sequences via the Epidemic Intelligence Information System discovered a cross-border outbreak involving Austria, Denmark, Germany and Switzerland.

Methods :

We defined confirmed cases as individuals notified with laboratory confirmed listeriosis and identification of the cg MLST (13516 or 14488) with disease onset from September 2020. Cases were interviewed to assess food consumption minimum two weeks prior to symptom onset. Microbiological investigations were conducted in Austria and Germany.

Results :

By 03.05.2021, fifty cases have been identified, of which 19 (38%) were female. Median age was 79 years (range: 0-93). Three cases were reported as deceased. Two cases were pregnancy-associated, of which one was a newborn with sepsis and meningitis. Forty-five cases were reported in Germany, two in Austria, two in Denmark and one in Switzerland. Fifteen of 18 interviewed cases (83%) had eaten smoked trout. Microbiological

investigations identified L. monocytogenes matching the cluster in smoked trout from Brand A. Investigations at the processing facility of Brand A in Denmark identified L. monocytogenes, but not belonging to this cluster. The source of contamination was not found.

Conclusions :

The smoked trout from Brand A was the probable vehicle of the outbreak, and it was publicly recalled. The Danish Food Authorities increased control in the trout processing facility. Since December 2020, the number of cases decreased, with the last case reported in January 2021 in Germany. To stop cross-border outbreaks quickly, we recommend timely molecular surveillance and investigations of outbreak clusters in cooperation between stakeholders to identify and withdraw vehicles

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

Keywords : outbreak investigation, Listeria monocytogenes, smoked trout, Austria, Denmark, Germany, Switzerland, whole genome sequencing

ABSTRACT ID: 44

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c. First confirmed domestic transmission of Brucella canis between dogs in the UK: outbreak investigation and public health risk assessment

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Background :

Brucella canis (B. canis) causes a zoonotic infection of dogs. It is primarily transmitted to humans via exposure to reproductive fluids, particularly from parturition and abortions. Human infections are rarely reported world-wide but could pose a serious risk for vulnerable individuals. Historically, UK B. canis cases have only been reported in imported dogs. In June 2020, a canine infected with B. canis was reported to Public Health England and an Incident Management Team convened. We aim to describe the outbreak and implications for the public health risk assessment.

Methods :

Self-reported information from the index and linked households, microchip database searches and site visits were used to identify humans and dogs potentially exposed to B. canis and assess ongoing risks. Humans and dogs were tested for B. canis serologically and cultures were performed on tissue samples from two dogs. Dogs were categorised as positive, non-infected or suspected for B. canis according to the long-term management plan.

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Results :

Nine households were potentially exposed to B. canis. There were nine canine abortions or stillbirths in the households in the preceding 18 months. Serological tests were negative in all 14 humans tested; 75% (27/36) of dogs tested were seropositive and both cultures grew B. canis. All seropositive dogs originated from the index household. Puppies born to seropositive parents were sold to a further six households and are being followed up.

Conclusions :

This outbreak of B. canis identified the first documented transmission of B. canis between dogs in the UK. No humans tested positive despite prolonged and high-risk exposures. Increased awareness is needed among dog owners, veterinarians and health professionals about the risks and prevention of transmission of B. canis.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Brucella canis,Epidemiology,Outbreaks
ABSTRACT ID: 96
PRESENTED BY: Gemma Smith / gemma.smith@phe.gov.uk

d. Questionnaire-based epidemiological analysis of acute gastroenteritis outbreak among employees of two neighbouring institutions sharing canteen in Prague 2019

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Background :

On 17th December 2019 gastroenteritis outbreak occurred among employees of National Institute of Public Health (NIPH) and State Institute for Drug Control (SIDC). We investigated outbreak, identify pathogen, source or vehicle and implement control measures.

Methods :

In retrospective cohort study among 960 employees, we defined cases as employees with acute onset of diarrhoea or abdominal pain or vomiting or nausea within 17th-19th December 2019. Data collected via online questionnaire (demographics, clinical symptoms and eaten food items from the canteen menu) were analysed using descriptive, univariable and stratified analysis, using odds ratios (OR) as the response was low. All ten canteen employees were interviewed during the on-site inspection. Stool samples from two cases and two asymptomatic canteen staff were tested by electron microscopy.

Results :

276 (187 NIPH, 15 SIDC and 74 unknown) employees responded (29%). We identified 39 (14%) cases (22 NIPH, 3 SIDC and 14 unknown), 75% were female, median age 49 years. One case tested positive for norovirus. No canteen staff reported illness. No food item or environmental sample was tested. Sichuan pork served on 17th December was most likely vehicle of outbreak with OR 5.02, 95% confidence interval (CI) 1.98-12.64. Another potential vehicle was Chinese soup with OR 2.40, 95% CI 0.97-5.85. Eating both Sichuan pork and Chinese soup showed OR 31.5, 95% CI 5.0-320.7 compared to people who ate neither. Twenty-two (56%) cases can be explained by consumption of these items.

Conclusions :

Two food items served in canteen were associated with acute gastroenteritis. We recommend microbiological testing of cases and all kitchen staff. Analytical epidemiology is important to determine potential vehicle if food samples are unavailable or no pathogen is detected in environmental samples

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : disease outbreaks, gastroenteritis, cohort studies, norovirus, epidemiology, foodborne diseases
ABSTRACT ID: 110
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e. [late breaker] An outbreak of Salmonella Typhimurium following an Eid al-Adha celebration barbecue in Wales (UK), July 2021

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Background :

On 23 July 2021, Public Health Wales received a notification of two PCR (polymerase chain reaction) positive cases of salmonellosis. Both were from a group in the Cardiff Sudanese community who purchased whole jointed lamb to barbecue in a public park in Cardiff, Wales on 20 July to celebrate the Muslim festival Eid-al-Adha. Investigation was undertaken to identify the source of the outbreak and to implement control measures.

Methods :

A cohort study was conducted. A questionnaire was administered to barbecue attenders asking about food consumed, and other possible exposures, including travel history and contact with animals. Interviews were carried out either face to face, or by telephone. Analysis was undertaken using STATA 15. Human and left-over raw lamb samples were sent for genomic sequencing at the Gastro-bacterial reference unit (GBRU) in Public Health England.

Results :

Of 33 attending the barbecue, 17 fulfilled the case definition. Four cases were admitted to hospital overnight and one patient to intensive care. Seven cases were confirmed as Salmonella Typhimurium, all with a genetically identical sequence. Sequences obtained from 11 meat samples were identical, and matched sequencing from human samples. Epidemiological evidence indicates that lamb meat was the food vehicle, with a greater risk of illness in those eating "marrara" a traditional Sudanese appetiser of marinated raw sheep's liver (Risk ratio: 2.5, 95% CI: 1.5-4.3).

Conclusions :

Consumption of raw and undercooked meat and offal continues to be an ongoing public health risk. Improving awareness in minority communities who consume raw or undercooked meat or offal either regularly, or during specific religious or cultural events, may help reduce this risk. Future outbreak investigations involving minority communities should consider dishes beyond those on routine questionnaires.

Poster Tour Abstracts

Poster tour 8
COVID-19: Field epidemiology

Abstracts

a. Potential impact of SARS-CoV-2 B.1.1.7 variant in school settings-results from an outbreak investigation in Croatia, March 2021

B. Mahmutovic [1]

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Background :

On 2nd March 2021, a COVID-19 outbreak in a 4th grade class in a primary school in Zabok, Croatia, was reported. The rapidly evolving situation raised the suspicion of more infectious SARS-CoV-2 variant of concern. An outbreak investigation was urgently carried out.

Methods :

We conducted telephone interviews of all cases and their contacts, and recommended testing to all exposed, including asymptomatic contacts, to early detect and promptly isolate potential additional cases and to extend contact tracing if needed. A total of 8 samples were selected for whole genome sequencing (WGS).

Results :

There were 38 COVID-19 cases identified between 26th February and 11th March 2021, of whom 37 confirmed and one probable case according to ECDC criteria. One of the children from the class was identified as the possible index case based on the date of symptom onset, with 13 secondary cases (12 classmates and their teacher), and 24 tertiary cases (20 household members, 2 school children, and 2 school teachers). AR in the class was 58,3%. The age range of children (21 cases) and adults (17 cases) was 1 month to 14 years and 32 years to 66 years, respectively. The majority of cases (34) presented with mild symptoms, while 4 children were asymptomatic. Performed WGS confirmed SARS- CoV-2 B.1.1.7 lineage (UK variant) in 7 samples, and B.1.258 in one specimen.

Conclusions :

It was generally perceived that younger children are less susceptible to infection with the wild-type variant and less often lead to onward transmission. This outbreak demonstrates the potential significant impact of B.1.1.7 lineage in school settings and further spill over to community, and the importance of aproprirate and timely outbreak control measures as well as genomic surveillance.

Poster Tour Abstracts

b. Investigation of a COVID-19 outbreak among employees of a supermarket in Dublin, Ireland, January-February 2021

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Background :

Workers in essential retail jobs have a high risk of exposure to COVID-19. During the first twelve months of the pandemic in Ireland, 493 COVID-19 cases were linked to outbreaks in retail workplaces. We investigated a COVID-19 outbreak among employees of a supermarket in Dublin to recommend control measures and inform future outbreak investigations.

Methods :

A public health investigation was carried out at the supermarket. We analysed surveillance data and conducted a cohort study using an online anonymised questionnaire of all staff to explore potential risk factors. Descriptive analysis was conducted, relative risk and 95% confidence intervals were calculated.

Results :

Among 189 employees, 26 confirmed COVID-19 cases (14%) were identified between 4 January and 6 February, 2021, including nine cases identified through single day on-site testing of asymptomatic employees. Cases were aged 19 – 65 years and worked in different work locations within the supermarket. A total of 77 (44%) employees participated in the cohort study, including 10 cases. No single risk factor was identified. Eighty percent of responders used the staff canteen. Twenty percent used the hand sanitiser rather than recommended hand-washing before eating and/or smoking.

Conclusions :

This was the largest COVID-19 outbreak reported in a retail workplace in Ireland. Identifying workplace-related risk of infection during a time of high incidence in the community was difficult. Cases were identified from several work locations, within the supermarket. Therefore, transmission might have occurred in the common areas e.g. canteen. We recommend the reinforcement of control measures already in place prior to the outbreak and communication of key times to wash hands with water and soap. Those measures and testing of asymptomatic staff successfully controlled the outbreak within one month.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : COVID-19, Outbreak Investigation, Retail outlet, Cohort study
ABSTRACT ID: 50
PRESENTED BY: Annamária Ferenczi / annamaria.ferenczi@gmail.com

c. First long-term care facility coronavirus outbreak in the Netherlands following cross-border introduction from Germany, March 2020

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Background :

The Dutch province of Limburg borders the German district of Heinsberg, which had a large cluster of COVID-19 cases before any cases were reported in the Netherlands. However, Heinsberg was not included as an area reporting local or community transmission per the national case definition at the time. In early March, two residents from a long-term care facility (LTCF) in Sittard, a Dutch town located in close vicinity to the district of Heinsberg, tested positive for COVID-19 during hospitalization. In this study we determined whether cross-border introduction of COVID-19 took place by analysing the LTCF outbreak in Sittard epidemiologically and microbiologically.

Methods :

Surveys and semi-structured oral interviews were conducted with all LTCF residents during regular points of care on new or unusual signs and symptoms of disease. Throat and nasopharyngeal swabs were taken from residents suspect of COVID-19 for the detection of SARS-CoV-2 by Real-time Polymerase Chain Reaction. Additionally, whole genome sequencing was performed using a SARS-CoV-2 specific amplicon-based Nanopore sequencing approach. Moreover, twelve random residents were sampled for possible asymptomatic infections.

Results :

Out of the 46 tested residents, nineteen (41%) tested positive for COVID-19, including three asymptomatic residents. Eleven samples were sequenced, along with three random samples from COVID-19 patients hospitalized in the regional hospital at the time of the LTCF outbreak. All samples were linked to COVID-19 cases from the cross-border region of Heinsberg, Germany.

Conclusions :

Sequencing combined with epidemiological data was able to virtually prove cross-border transmission at the start of the Dutch COVID-19 epidemic. Our results highlight the need for cross-border collaboration and adjustment of national policy to emerging region-specific needs along borders in order to establish coordinated implementation of infection control measures.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : SARS-CoV-2, COVID-19,Long-Term Care, Infection Control, Whole Genome Sequencing, Disease Outbreaks
ABSTRACT ID: 111
PRESENTED BY: Mitch Van Hensbergen / mitch.vanhensbergen@ggdzl.nl

ESCAIDE

Poster Tour Abstracts

d. Are saunas safe in the COVID-19 pandemic? Results from an outbreak at a Danish boarding school, 2020

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Background :

A large COVID-19 outbreak occurred at a Danish boarding school (højskole) in late 2020. The primary case was known, and had recently spent the weekend outside the school. Settings of potential widespread transmission included a sauna visit shortly before the primary case's symptom onset, and a school-wide party after the primary case had started isolation. We investigated students' behaviour during the outbreak, to identify high-risk settings and inform control measures.

Methods :

All 138 students were tested for COVID-19 by PCR. We conducted a retrospective cohort study, using an online questionnaire to ask students about sauna use, party attendance, and adherence to school COVID-19 rules such as avoiding close contact with students outside designated "family groups". The analysis used logistic regression, adjusting for sex.

Results :

77 students tested positive (attack rate 56%) and 78 answered the questionnaire (41 cases, 37 non-cases, ages 18-26). Attending the sauna was the only behaviour associated with infection (odds ratio 6.1, 95% confidence interval 1.8-23.3), but only 46% of cases attended. All other risk behaviours were near universal and showed no association with infection: more than 90% reported contact outside "family groups", spending time in prohibited common areas, and attendance at the party.

Conclusions :

There was likely widespread transmission at the sauna, suggesting saunas are not safe to open when COVID-19 incidence is high. However, the sauna could account for fewer than half of the cases, and there were many other opportunities for infection to spread due to low adherence to COVID-19 rules. If social distancing measures are unenforceable, the only realistic measure to prevent large outbreaks in similar closed setting s may be strict quarantines of people entering from outside.

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

Keywords : covid-19, disease outbreaks, retrospective studies, disease transmission infectious, epidemiology

ABSTRACT ID: 120

PRESENTED BY: Oliver McManus / olmc@ssi.dk

Poster tour 9
COVID-19: Burden of disease

Abstracts

a. Seroprevalence study of SARS-CoV-2 infection in Romania, 2020, Teodora Vremera

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Background :

Detection of anti-SARS-CoV-2 antibodies helps evaluate the extent of COVID-19 in a population. The aim of the study was to estimate the burden of SARS-CoV-2 infection in order to substantiate preventive measures, such as vaccination strategy.

Methods :

The study was conducted between June - November 2020 and involved the collection of residual sera from a representative sample of the Romanian population, in each county of the 8 regions (South, South-East, South-West, West, North-West, North-East, Center and Bucharest-Ilfov). Samples were tested at the National Institute for Public Health Laboratory for detection of IgG antibodies, using chemiluminescent technology.

Resu1lts :

A total of 19597 samples were tested from persons aged between 0 - 97 years (median 48 years). Of the total, 1213 (6.19%, 95%CI:5.45-8.14) showed anti-SARS-CoV-2 IgG antibodies, with no significant differences between females and males (p=0.95). Seropositivity rate by age group was: 6.1% in 0-19 years, 5.5% in 20-39 years, 8.4% in 40-59 years, and 4.6% in those > 60 years. The seropositivity rate by regions was 3% in North-West, 3.6% in Bucharest-Ilfov, 4.1% in Center, 6.8% in West, 6.9% in South-East, 7.6% in South-West and 8% in the North-East and South.

Conclusions :

The prevalence of the immune response varied across the eight regions of Romania, being higher in the North-East and South and lower in the North-West and Center (p<0.00001). Seroprevalence also showed differences between age groups, with higher prevalence in middle age population than in elderly (>60 years) (p<0.00001), which suggests that vaccination policies could take into account targeting certain age groups. We recommend that seroprevalence studies are repeated after the introduction of anti-SARS-CoV-2 vaccination in order to assess the percentage of immune population.

Subject : Burden of disease

Keywords : SARS-CoV-2, antibodies, infection, prevalence , vaccination

ABSTRACT ID: 102

PRESENTED BY: Teodora Vremera / teodora.vremera@insp.gov.ro

Poster Tour Abstracts

b. Long-term effects of COVID-19 in Malta, Charmaine Zahra

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Background :

COVID-19 long-term effects are still unknown. The aim of this study was to describe long-term symptoms in SARS- CoV-2 PCR-positive persons in Malta during 2020.

Methods :

We conducted a cross-sectional survey asserting symptoms persistence after COVID-19 isolation discharge. Patients with a registered email and onset date in 2020 were sent a questionnaire 3 months after their positive test result. Data were analysed descriptively to estimate symptom prevalence. Multivariable logistic regressions were used to determine risk factors for long-term effects. Age, sex, and hospitalization during COVID-19 were used as covariates and symptoms (>1 month from isolation discharge) were used as outcomes.

Results :

For data before 8th July 2020, 516 patients (out of 674) met our inclusion criteria, and 219 responded (42.6%). Median age was 35 years (range, 3-99), and 56.6% were women. 73.0% presented symptoms initially and 16.4% were hospitalized. After discharge from isolation, 44% presented symptoms, and a month after, 14.1%, 12.7%, 7.3%, 11.9%, and 14.2% presented fatigue, shortness of breath (SOB), cough, anxiety, and depression, respectively. Males were associated with having lower odds of fatigue (OR = 0.40, P = 0.03) and SOB (OR = 0.36, P = 0.03) than females, but no association was found with hospitalisation or age. Hospitalised patients were associated with higher odds of anxiety (OR = 2.81, P = 0.03) than non-hospitalised patients, but no association with sex or age were found.

Conclusions :

This is the first study to highlight COVID-19 long-term effects in Malta. Data from after 8th July are being quality-checked, and will be included in the final report. This information can help us in taking evidence-based decisions for COVID-19 case management, to offer support to long COVID-19 consequences.

Subject : Burden of disease

Keywords : Long-term effects, COVID-19 Pandemic , Cross-Sectional Survey, Risk factors

ABSTRACT ID: 156

PRESENTED BY: Charmaine Zahra / charmaine.e.zahra@gov.mt

c. Seroreversion and antibody waning to SARS-CoV-2 in an ongoing, population-based longitudinal study in Germany 2020/2021

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Background :

Understanding the duration of natural and vaccine-acquired immunity is essential to stop the spread of COVID-19. Most current investigations are based on data from symptomatic or notified infections of SARS-CoV-2. We aimed to investigate antibody waning in a population-based sample of seropositive individuals as well as to determine titre status in vaccinated persons.

Methods :

We conducted a population-based longitudinal seroprevalence study of SARS-CoV-2 antibodies (MuSPAD) sampling 5,318 adults two times in a three months interval in in the German cities of Aachen, Osnabrück, Magdeburg, and Chemnitz. IgG antibodies were measured with Spike S1-specific IgG ELISA. We investigated seroreversion in seropositive individuals at baseline compared to follow up (excluding those who received a vaccination) and compared titres of vaccinated and non-vaccinated individuals at follow up.

Results :

Of the 161 individuals that were seropositive at baseline (median age 54, 60% female) and had not received a vaccination yet, 125 were seropositive and 36 seronegative (IgG seroreversion 22%, 95% CI: 16–30%) at follow up. Median antibody titre ratios in those seropositive decreased from 2.7 (95% CI: 2.38-3.20) to 1.8 (95% CI: 1.49-2.24) within the observation period. Of 1,282 persons fully vaccinated at follow up, 1,268 (98%, 95% CI: 97-99) were seropositive, with a median antibody titre ratio of 7.57 (95% CI: 7.41-7.71).

Conclusions :

We show high seroreversion in a small longitudinal population-based sample in a three month interval in line with previously published data from non-population based studies. Almost all fully vaccinated individuals were seropositive and had high antibody titre.

Subject : Burden of disease

Keywords : COVID-19 testing, Antibodies, Vaccination, Seroepidemiologic studies

ABSTRACT ID: 239

PRESENTED BY: Julia Ortmann / juliaortmann@protonmail.com

Poster Tour Abstracts

d. The impact of lockdown on COVID-19 burden in specific age groups, 2020-2021, Slovenia

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Background :

Until May 2021 Slovenia had two lockdowns to control COVID-19 spread. Lockdowns included several non-pharmaceutical interventions (NPIs). The second lockdown differed in terms of less focus on closure of workplaces. In order to assess the differences in lockdown impact on specific age groups we evaluated disease burden before and after intervention.

Methods :

We defined COVID-19 burden in different population age groups as an index calculated as the fraction of new cases in a given age group relative to its size. A value of 1 represents an occurrence of disease proportionate to population size. We performed the calculations for a 7-day time period, 7 days before lockdown implementation and 7 days after.

Results :

First lockdown (16.3.2020-19.4.2020): before implementation the highest burden of infections was in the 20–49 age group (index 2.6). After lockdown burden decreased (index 0.9) with a shift of the highest burden in the 60+ age group, mainly due to outbreaks in long term care facilities (LTCF) (index 3.3). Second lockdown (1.4.2021-11.4.2021): before implementation highest burden was in the 10-59 age group (index 1.5). After lockdown, burden reduction in this age group was observed (index 1.2), while distribution among age groups remained unchanged.

Conclusions :

First lockdown showed the effect on the working population but did not shield the older age groups. Second lockdown did not shift the burden of infections away from the working population with the highest burden of infection. Our results support the need to tailor NPIs to address the main drivers of the epidemic. High risk environments (LTCF) and safe work environments should be addressed specifically avoiding unnecessary lockdown restrictions

e. Attribution of nosocomial seeding to COVID-19 outbreaks in long-term care facilities (LTCFs): population-based surveillance in England, 2020-21

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Background :

Residents of long-term care facilities (LTCFs) have been disproportionately affected by the COVID-19 pandemic worldwide. While there is considerable movement of residents between hospitals and LTCFs, there are few assessments of the extent to which COVID-19 cases contributing to outbreaks in LTCFs are hospital-associated.

Methods :

We matched residential addresses from COVID-19 laboratory notifications in England between March 2020 and January 2021 to reference databases to identify LTCF residence and enable outbreak identification. Hospital-associated COVID-19 was identified through linkage to NHS secondary care records and defined based on length of hospital admission and timing of specimen collection. Nosocomial seeding of outbreaks was defined based on the index case's hospital-associated status plus their specimen and discharge dates in relation to possible secondary cases' specimen date.

Results :

We identified 138,022 COVID-19 cases among LTCF residents, of which 17,973 (13%) had a recent hospital admission. Of those, 11,904 (66%) met one of the hospital-acquired definitions and of these, 7,330 (62%) were discharged to a LTCF. A total of 1,131 outbreaks ensued (8% of all LTCF outbreaks), consisting of 12,955 resident cases (9% of all LTCF cases) and 3,780 deaths (11% of all LTCF deaths). For most of these outbreaks the potential seeds were community-onset hospital-associated cases (86.1%; n=974) and for those who were hospital-onset hospital-associated the median time between diagnosis and discharge was 3 days (interquartile range (IQR) 0-7).

Conclusions :

Nosocomial seeding potentially contributed to 1 in 13 COVID-19 outbreaks in LTCFs in England, accounting for around 1 in 10 LTCF cases and deaths of residents. Further cases and deaths in LTCFs therefore may be reduced with more policy and resource directed to reduce this route of COVID-19 introduction.

Poster Tour Abstracts

Poster tour 10
Implementation science

Abstracts

a. Barriers and facilitators to infection prevention and control (IPC) in Dutch psychiatric institutions: a theory-informed qualitative study

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Background :

Care institutions are a high-risk setting for emergence and spread of infections, which stresses the importance of infection prevention and control (IPC). Accurate implementation is crucial for optimal IPC practice. Despite wide IPC promotion and research thereof in the hospital and nursing home setting, similar efforts are lacking in disability care settings. Therefore, our study assessed perceived facilitators and barriers to IPC among professionals from residential care facilities (RCFs) for people with intellectual and developmental disabilities (IDD), as well as to identify professional- reported recommendations for IPC improvement.

Methods :

This qualitative study involved semi-structured interviews (before covid-19) with twelve professionals from five Dutch RCFs for people with IDD. Thematic analysis was conducted (by two researchers independently) to identify barriers and facilitators, which were structured across an integrated theoretical framework for implementing change.

Results :

Findings revealed barriers and facilitators at the guideline, client, professional, professional interaction, professional- client interaction, client interaction, organisational, community and societal level. The main barriers included a lack of tailored and practical guidelines, client's defiant behaviour, lack of professionals' awareness, lack of structural organisational attention, and high work pressure and staff shortages. The main facilitators included professionals' positive attitude, organisational awareness and sense of urgency, structural and universal education, and professionals responsible for or taking the lead regarding IPC. The main recommendations were (structural) IPC education of professionals, introduction of tailored and practical IPC guidelines, and client participation.

Conclusions :

To promote IPC, interventions should be implemented on multiple levels (e.g., the professional and organisational level) and target multiple factors (e.g., professional's attitude and support by board of directors). There is a need for a tailored and comprehensive approach to successfully implement and sustain IPC in disability care.

b. Analyses of blood donor samples from eight provinces in Lao PDR suggest considerable variation concerning HBV exposure and carriage

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Background :

The epidemiology of hepatitis B in the Lao PDR is not well understood, even though hepatitis B is endemic. In previous studies, more than 40% of the adult Lao population, born before introduction of the vaccine, were likely to have been exposed to the virus. Here, we investigate hepatitis B markers in Lao blood donors to determine regional, occupational, age and sex-related differences.

Methods :

5017 voluntary blood donors from 8 different provinces were tested for hepatitis B markers. Predictors for the prevalence of hepatitis B surface antigen (HBsAg), considered as a marker of chronic infection, and antibodies against the core antigen (anti-HBc), a marker for hepatitis B exposure, were assessed by bivariate and multivariable analyses.

Results :

In total, 41% of the participants were positive for anti-HBc; the HBsAg prevalence was estimated at 6.9% among all participants and 3.9% among repeat donors. Among first-time donors, HBsAg was highest in males (11.5% versus 4.7% in females; p<0.001), soldiers (15.5%) and participants from Northern provinces (13.1%). Anti-HBc was highest in first- time donors who were from the North (62.5%), at least 36 years old (54.5%) and males (48.2% versus 35.8% in females; p<0.001).

Conclusions :

Our study confirmed an overall high HBsAg and anti-HBc prevalence in Lao PDR, albeit with considerable and previously undescribed regional variations. Follow-up studies to investigate the regional differences are warranted and should capture potential risk factors. The identification of a sizeable number of HBsAg positives among repeat donors warrants a thorough investigation of current blood screening, record keeping and counseling practices. The findings are important for blood donor management in the country and will hopefully also raise awareness for the identified issues in similar resource-limited settings.

ESCAIDE

Poster Tour Abstracts

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c. Molecular epidemiology of Bordetella pertussis in Norway 1996-2019: Allelic variants of vaccine related antigens

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Background :

Pertussis is a public health concern globally, despite high vaccine coverage. Pathogen adaptation to acellular vaccines (ACVs) is suggested to contribute to the recent resurgence. We aimed at describing the population structure of Bordetella pertussis in Norway, 1996-2019, and determine if there was an evolutionary shift in the wake of ACV introduction in 1998.

Methods :

We included 180 B. pertussis isolates referred to the national reference laboratory 1996-2019. The isolates underwent whole genome sequencing. We determined the distribution and frequency of allele variants and temporal changes of genes encoding vaccine antigens.

Results :

Two out of six different allelic profiles were dominating; 47% (n=85) with profile A (introduced 1994) and 42% (n=75) with profile B (introduced 1970), both carrying pertussis toxin (ptxA1, ptxP3), pertactin (prn2), fimbriae (fim2-1 and fim3-2 (A) or fim3-1 (B), respectively). Sixteen percent (n=29) showed deletions in prn. Isolates with ptxP1 and prn1 disappeared around 2007. The prn2 allele likely emerged prior to 1972, and ptxP3 before the early 1980s. Recently circulating clones of B. pertussis have the ptxP3 and prn2 alleles fixed, with increasing incidence of prn deletions. The isolates were evenly distributed across a global phylogeny.

Conclusions :

The Norwegian B. pertussis population harbor allelic profiles of ACV antigens with mismatch to components of the ACV. Mutations in ACV antigens occurred as early as 1950, prior to the ACV era, however ACV might have contributed to evolvement of a more uniform B. pertussis population. This could have implications for vaccine efficiency and therefore prevention and control of pertussis. We recommend continued collection of B. pertussis for surveillance purposes, and to further explore the role of genetic adaptation.

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

Keywords : Bordetella pertussis, whooping cough, whole genome sequencing, evolution, genomic variation, vaccine related antigens

ABSTRACT ID: 97

PRESENTED BY: Lin Thorstensen Brandal /

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d. Easy access to vaccination important for adherence during the 2016-2019 HPV catch-up vaccination of young women in Norway

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Background :

Human papillomavirus (HPV)?infections are the most common sexually transmitted viral infections among young women. In 2018 Norway reported 11 cases per 100,000 women-years. A random sample of 10,000 women born between 1991-1996 who were offered catch-up HPV vaccination were invited to participate in the cross-sectional online survey between 23 September and 6 October 2019. In this catch-up programme, 59% of eligible women accepted HPV vaccination.

Methods :

We defined vaccination adherence as receiving all three doses. Non-adherence was defined as starting but not completing the vaccine schedule. Determinants of HPV vaccination adherence were investigated using descriptive, univariable and multivariable logistic regression analyses providing adjusted odds ratios (aOR).

Results :

Data from 4,967 respondents (49.7%) were included. Overall, 91% (95%CI=89.3-91.9) of those initiating vaccination, adhered to the complete schedule. The following factors were significantly associated with HPV vaccination adherence compared to non-adherence: born outside Norway (aOR=0.43; 95%CI=0.47-0.97), having children (aOR=0.51; 95%CI=0.35-0.73), vaccination being readily available (aOR=2.28; 95%CI=1.50-3.37), difficulty of finding a vaccination site (aOR=1.94; 95%CI=1.69-2.23) and preference for receiving information from health authorities (aOR=1.37; 95%CI=1.04-1.81). SMS and social media were negatively associated for Norwegians (aOR=0.68, 95%CI=0.46-1.01) while an opposite trend was found for those of not-Norwegian origin (aOR=1.48, 95%CI=0.69-3.14; not significant). Study participants who did not adhere to the full vaccination schedule reported that they had forgotten (40.4%; 95%CI=33.5-47.8) or had no time (32.9%; 95%CI=26.2-40.4).

Conclusions :

Despite NIPH's targeted communication campaign including frequent reminders through SMS and social media, main barriers for HPV vaccination adherence were difficulty to find a vaccination site, forgetting to take the vaccine or not having time to complete the schedule. Intervention programs to strengthen a targeted HPV vaccine reminders system for vaccination are needed.

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

Keywords : Papillomavirus Infections, Papillomavirus Vaccinations, Cross-Sectional Studies, Vaccination, Communication

ABSTRACT ID: 164

PRESENTED BY: Elburg Van Boetzelaer / elburg.vanboetzelaer@fhi.no

Poster Tour Abstracts

e. [late breaker] Vaccine hesitancy and public participation in Ukraine: An exploratory qualitative study on attitudes and barriers to measles vaccination

J. Osborne [1]

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Background :

Despite the proven effectiveness of many vaccines, some parents in Ukraine still have doubts about vaccinating their children, a persistent problem for measles outbreaks and the COVID-19 response in the country. This study, part of the European Union-funded Sonar-Global, aims to present the case of vaccine hesitancy in Ukraine, focusing on vulnerability and participatory solutions for parents of children under 6.

Methods :

This study uses in-depth interviews with 15 parents of children under 6 years of age and 15 experts (e.g., healthcare practitioners, community representatives) to produce an analysis of the current barriers for vaccination and the implications for policy and public participation. Typical state-recognized vulnerable groups were included, with a particular focus on access to information and services. Stakeholders were conducted to establish how a connection can be made to the already-institutionalized public consultation process in the country.

Results :

The results of the interviews showed that differently situated groups had varying access to reliable information and healthcare. Some groups were found to face structural barriers to vaccine access, such as Roma people living in remote areas and low-income families. Other groups received information about vaccines from others in their communities, such as family members or religious organizations. A stakeholder consultative process resulted in recommendations, including enabling easier access to vaccinations for Roma communities and incorporating study results into trainings and information campaigns.

Conclusions :

This study highlights the importance of qualitative methods in vaccine-related research within communities. Certain public and community-based institutions may be well-suited to improve communication about vaccines. These insights resulted in policy recommendations for sustained public engagement surrounding measles vaccination in Ukraine, with clear implications for COVID-19 vaccination and future emerging diseases.

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

Keywords : Measles vaccine, Anti-vaccination movement, Community participation, social sciences, Ukraine

ABSTRACT ID: 311

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Poster tour 11
Food and waterborne diseases and zoo-noses

Abstracts

a. Trends in Shiga Toxin Producing Escherichia coli other than serotype O157:H7 (non-O157 STEC) in Wales before and after introduction of multiplex PCR testing (2015-2019)

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Background :

Following severe outbreaks of O157:H7 STEC–HUS (Haemolytic Uraemic Syndrome) in the 1980s, laboratory protocols in the UK focused on detecting this serotype. Consequently, until recently, STEC O157:H7 was the most detected serotype in all 4 UK nations. In August 2018, Wales implemented multiplex PCR assays on all faecal samples in order to detect stx genes – enabling identification of all STEC serotypes. We describe the effect of this change in Wales on overall non-O157 case numbers, and those with virulence factors of public health concern.

Methods :

All stx positive faecal specimens identified in Wales sent for culture confirmation and typing at the PHE Gastrointestinal Bacteria Reference Unit between 2015 and 2019 were included. Descriptive analysis of identified non-O157 STEC, and their virulence profiles, before (2015-2017) and after (2018-2019) the introduction of the multiplex PCR assay was completed.

Results :

160 non-O157 and 153 O157:H7 culture positive STEC cases were sequenced. Between 2015 and 2017 2 non-O157 STECs were identified, compared to 44 in August - December 2018 and 114 in 2019. The most commonly identified non- O157 serotype was O26:H11 (n=38) followed by O146:H21 (n=19). 19 of 20 non-O157 isolates with stx2a + eae genes (12.5%) (the virulence profile associated with STEC-HUS), were identified in 2018/2019.

Conclusions :

Implementation of the stx PCR assay has significantly increased the number of non-O157 STECs identified in Wales by 175% – from 2 cases in three years, to 114 cases in 2018. Implementation has enabled not only rapid diagnosis of clinically severe STEC-HUS non-O157 cases, but early detection of outbreaks and insights into sources and transmission of, this potentially severe zoonotic, foodborne pathogen - enabling rapid response for appropriate public health action.

Subject : Surveillance

Keywords : STEC, STEC-HUS, Non-O157, Surveillance

ABSTRACT ID: 228

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Poster Tour Abstracts

b. Salmonellosis has markedly declined in Finland: 25-year experience of infectious disease surveillance

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Background :

In 2020, salmonellosis was the fourth most common gastroenteritis in Finland after campylobacteriosis, norovirus infection and cryptosporidiosis. Clinical laboratories are obliged to notify salmonellosis findings to Finnish Infectious Disease Register (FIDR). We describe demographics of salmonellosis cases in Finland in 1995–2020.

Methods :

A case is defined as a person with laboratory confirmed salmonellosis notified to FIDR in 1995–2020. We characterized cases according to age, gender and travel history. We compared cases' travel history with Finns' travel records in 2012–2020 (data from Statistics Finland).

Results :

In 1995–2020, 59 616 salmonellosis cases were notified to FIDR, of which 73% were travel-related, 18% domestic, and for 10% the traveling data was missing. Of all cases, 54% were women. The incidence of domestic cases decreased 5-fold (annual incidences 4-22/ 100 000) and travel-related 4-fold (annual incidences 11-48/ 100 000) from 1995 to 2019; in 2020, incidences were 3.1/100 000 for travel-related and 3.8/100 000 for domestic cases. The incidence was highest in 0–4 year-old domestic, and 25–29 year-old travel-related cases (16 and 54/ 100 000). According to Statistics Finland, 25–64 year-olds travel more than other age groups. In 2020, traveling decreased in all age groups. Compared to number of travels, most infections were contracted in Asia and Oceania region and in Africa.

Conclusions :

Both domestic and travel-related salmonellosis have markedly declined over the past 25 years in Finland. Salmonellosis in Finland is mostly travel-related. Decrease in salmonellosis suggests better food safety and improved hygienic practices both in Finland and elsewhere. In 2020, travelling decreased due to COVID-19 restrictions.

Subject : Surveillance

Keywords : Gastroenteritis, Salmonella Infections, Humans, Finland

ABSTRACT ID: 40

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

c. Seroprevalence and risk factors for hantavirus disease and leptospirosis in a hantavirus high-risk region in Lower Saxony, Germany 2019

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Background :

Hantavirus disease and leptospirosis are rodent-borne zoonoses, commonly causing unspecific symptoms, with potential severe course. With no human vaccine available in Europe, protective behaviour is essential. We examined risk factors and disease knowledge in residents of a hantavirus high-risk region.

Methods :

Patient sera from two general practitioners were tested for IgG antibodies against common hantavirus and Leptospira strains via ELISA. Questionnaires inquired potential exposures, and associations with serostatus were assessed by calculating adjusted odds ratios (aORs) via multivariable logistic regression analysis.

Results :

Of 451 participants aged 18-85 (median: 59) 232 (51.4%) were female. Seroprevalences were 11.1% (8.5-14.4) and 2.5% (1.4-4.5) for hantavirus and Leptospira respectively. 38% of anti-hantavirus IgG positive but none of the anti-Leptospira IgG positive participants had been clinically diagnosed. Frequent exposure to dead rodents (aOR: 3.1; 95%CI: 1.2-8.2) or wood handling (2.8; 1.4-5.8) corresponded with higher, living close to water (0.3; 0.2-0.7) with lower odds of positive anti-hantavirus IgG. Spending 2h/ week minimum in the forest (9.1; 1.9-44.0) was positively, frequent cleaning of storage rooms (0.3; 0.1-0.95) negatively associated with anti-Leptospira IgG. More participants were aware of hantaviruses than Leptospira (92% vs. 14%) but only 22% knew about the disease-specific press releases of their local health authority.

Conclusions :

We derive recommendations for the public and health authorities: to prevent hantavirus infections keep home and work environments free of rodents and wear protective equipment like gloves and FFP3-masks when handling wood. To prevent Leptospira infections clean storage rooms regularly and avoid contact to material potentially contaminated with rodent urine when in the forest. Local health authorities need to communicate information more efficiently. Increasing awareness of leptospirosis might increase diagnosis and improve secondary prevention.

Subject : Burden of disease

Keywords : Seroprevalence, Zoonoses, Hantavirus, Leptospira, Risk factor

ABSTRACT ID: 117

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d. [late breaker] Scratching the surface: a Salmonella Infantis outbreak linked to contaminated pork rind snack in the UK, 2021; a case-control study

M. Bardsley [1]

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Poster Tour Abstracts

Background :

Whole genome sequencing identified a cluster of genetically similar Salmonella Infantis cases in the UK, reaching 129 cases by 30 July 2021. A case-control study was conducted to identify potential vehicle(s) of infection.

Methods :

Cases were adult UK residents with laboratory confirmed Salmonella Infantis within a 5-single nucleotide polymorphism (SNP) single linkage cluster. Controls, identified via a market research panel, were adult UK residents with no foreign travel or diarrhoea/vomiting in the previous 7 days. Controls were frequency matched by age and sex to cases. Questionnaires collected data on food exposures and special diets.

Descriptive epidemiology and univariable analyses were conducted, including calculating odds ratios (OR) and corresponding 95% confidence intervals (95%CI). Risk factors with a p-value <0.2 were considered in a stepwise modelling process using multivariable logistic regression. Environmental investigations were undertaken.

Results :

The study contained 19 cases and 87 controls. Pork scratchings were identified as potential risk factor for illness, with an attack rate of 79% (OR: 78, 95%CI: 15- 454). Pork scratchings (adjusted OR: 152, 95%CI: 17- 1358) and following an 'other' diet (aOR: 39, 95%CI: 1.8-83) were independently associated with infection. Among cases who named a brand of scratchings (8/15), all reported consuming Brand A. Microbiological investigations identified isolates within the same cluster at production premises and in final product for Brand A.

Conclusions :

Epidemiological and microbiological findings strongly associate Brand A pork scratchings with Salmonella infection. The manufacturer, who distributes to UK, EU and third country customers, voluntarily suspended production and withdrew/recalled products. To date, over 300 cases in the UK have been linked to this outbreak with likely exposure dates pre-dating public health actions.

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

Keywords : Salmonella, Gastroenteritis, Field Epidemiology, Outbreak, Pork scratchings, Analytical Epidemiology

ABSTRACT ID: 324

PRESENTED BY: Megan Bardsley / megan.bardsley@phe.gov.uk

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e. [late breaker] Water, Sanitation and Hygiene coverage in Bentiu Internally Displaced Population Camp, South Sudan, August 2021

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Background :

Approximately 100,000 people live in Bentiu Internally Displaced Population (IDP) camp, South Sudan, residing in five sectors. Following a recent Hepatitis E outbreak and fund cuts for water, sanitation and hygiene (WASH) services in the camp, an assessment of the current WASH situation was conducted to identify gaps in service provision.

Methods :

A cross sectional lot quality assurance sampling (LQAS) survey was conducted. Nineteen households were sampled from each sector using geographic positioning system random sampling. Data were collected using KoBoCollect mobile application. Weighted averages and confidence intervals were calculated.

Results :

Weighted average of 95% (95% CI 90.5%-99.5%) households use potable water for drinking, however only 46% (95% CI 36%-57%) get minimum 15 liters of water/person/day. Households storing water for longer than one day was 36.6% (95% CI 26.4%-48.6%), and 37% (95% CI 27%-46%) have containers in adequate condition.

In 97.4% (95% CI 94.5%-100%) households, menstruating women and girls use acceptable dignity kits. Hygiene promotion coverage in the previous week was 49% (95% CI 39.6%-58.5%). 26.6% (95% CI 17.4%-35.3%) of households had a piece of soap.

22.8% (95% CI 15.6%-30.1%) of pit latrines were found in an acceptable condition. Similarly, 13.2% (95 % CI 6.6%-19.9%) of households had functioning hand washing points near the latrines.

Over the previous two weeks, 57.9% (95% CI 49.6-69.7%) households reported no diarrhea and 71.3% (95% CI 62.1%-80.6%) no eye infections among children under five.

Conclusions :

The WASH condition in the camp is precarious and requires urgent intervention to prevent and control WASH-related outbreaks.

Subject : Array

Keywords : Water, sanitation and hygiene, South Sudan

ABSTRACT ID: 321

PRESENTED BY: Berhe Tesfay / berhe.etsay@gmail.com

Poster Tour Abstracts

Poster tour 12
COVID-19: Knowledge for policy and practice

Abstracts

a. Evaluation of an Antigen Rapid Diagnostic Test for SARS-CoV-2 at a south Italian field site: despite limitations, could it serve as a useful screening tool?

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Background :

To control the pandemic and quickly identify COVID-19 cases, a key strategy is mass testing for SARS-CoV-2. Real- time, quantitative PCR (RT-qPCR) is the gold standard, however lab capacity and costs are limiting factors. We evaluated the low-cost, Boditech Rapid Antigen Test (RAT) for point-of-care diagnosis of COVID-19.

Methods :

We enrolled health-care workers (HCW), medical students and symptomatic patients at the Foggia university hospital. Participant's nasopharyngeal swabs were analysed by RT-qPCR and RAT. Samples were processed using a fluorescence immunoassay test-kit. We stratified the analysis for sensitivity and specificity by age, gender, symptoms, and days since symptoms onset. We also reported the diagnostic accuracy, the positive and negative predictive value (PPV, NPV).

Results :

We collected samples of 261 participants, including 36 RT-qPCR positive. 47 persons reported symptoms, the median age was 42 years. The overall sensitivity and specificity were 94% (CI95: 81-98) and 83% (CI95: 78-88), respectively. The diagnostic accuracy was 85% with a Kappa coefficient of 55% (CI95: 44-67). The PPV was 48%, and the NPV 98%. Among symptomatic persons the specificity was 42% (CI95: 21-67). All RT-qPCR positive subjects reporting symptoms ≥7 days before the test (n=4) resulted in a negative RAT.

Conclusions :

This evaluation study found that the Boditech-RAT does not meet the minimum performance requirement for RAT set by WHO (≥80% sensitivity and ≥97% specificity). The specificity was considerably lower (83%), whereas the sensitivity (94%) was in line with some of the best RATs tested. We conclude that the Boditech-RAT is suitable for screening purposes, but should not be used for symptomatic patients arriving late for diagnosis to avoid false positivity.

b. Integrating mapping, whole genome sequencing and staff interviewing to determine the source of infection and inform control measures in a prison COVID-19 outbreak

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Background :

Prison residents are vulnerable to COVID-19 outbreaks. In December 2020, there were 75 cases per 1,000 prison population compared to 46 cases per 1,000 general population (England and Wales). In October 2020, an outbreak was declared in the Wales's second-largest prison (population = 1,693 men). We aimed to control the outbreak to ensure operational continuity and resident welfare.

Methods :

We examined COVID-19 cases in staff and residents between 14th October 2020 and 21st April 2021. We integrated staff interviews, epidemiological descriptive analysis, maps of case location and density, network information and whole genome sequencing (WGS). WGS determined relatedness of cases and follow-up interviews verified plausibility of external introduction versus prison transmission.

Results :

There were 248 staff and 205 resident cases across all 47 prison sub-areas; overall attack-rate was 17.1%. Highest case-numbers were in admissions (n = 118, attack-rate = 29.8%). Descriptive analysis identified an index-case in a resident who contracted COVID-19 in hospital. A peak in cases was seen between 16-29th December (staff = 61, residents = 60), commensurate with community rates. A second peak in mid-January was an artefact of asymptomatic staff-testing. Network analysis combined with WGS indicated that this outbreak was seeded by multiple community importations, but also involved person-to-person transmission within the prison.

Conclusions :

Traditional descriptive methods identified an index case but did not distinguish imported cases. Our integrated mapping and WGS approach enabled us to determine the location and origin of cases and tailor control measures. Subsequent cohorting prevented infection in other areas; restricting staff to working in one location (including overtime) and socialising only with those from the same block (including break-times) controlled the spread. This maintained prison operational capacity and maximised welfare.

Poster Tour Abstracts

c. SARS-CoV-2 Immunogenicity in healthcare workers infected before and after COVID-19 vaccination: Israel, January-March 2021: Implications for vaccination policy

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Background :

Vaccination with two doses of the BNT162b2 vaccine is highly effective against SARS-CoV-2 infection. The second may not be necessary in individuals naturally infected with SARS-Co-V2. We measured Anti-spike IgG response among vaccinated healthcare workers from Ziv Medical Centre, Israel, according to their SARS-CoV2 infection status in order to inform vaccination policy.

Methods :

Pre-vaccination infection status was ascertained among study participants using an IgG assay and self-reported history. Anti SARS-CoV-2 spike IgG levels were measured around 21 days and 51 days post-dose one, using a quantitative serological assay. All workers who developed COVID19-compatible symptoms during the study period (December 2020- March 2021) were PCR tested. Antibody levels were reported using geometric mean concentration expressed in AU/ml (GMC) alongside 95%

confidence intervals (95% CI). IgG levels were compared among groups of ZMC workers according to their infection status (uninfected, infected before/after vaccination)

Results :

725/1500 staff received at least one vaccine dose and were tested at least once. Of these, 25 had evidence of pre- vaccination infection and 35 of infection post-dose 1. Compared with uninfected individuals, previously infected individuals who received a single dose had IgG titers that remained high approximately 50 days post-vaccination, more than twice higher than previously uninfected individuals who received two doses (GMC 464.7 vs 196). Fifity days post- vaccination, IgG GMC among those infected post-dose 1 was 83.8 (95%CI 60.5-115.9), comparable to those previously uninfected who received a single dose (90.2, 95%CI 4.7-17210), lower than those uninfected who received two doses (196, 95%CI 189-203.2)

Conclusions :

Pre-vaccination infection increased IgG titres but post vaccination infection did not. A single dose is likely sufficient for those infected pre-vaccination but those infected post-dose one should receive the second.

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

Keywords : COVID-19, vaccines, vaccine immunogenicity, Israel, SARS-CoV-2

ABSTRACT ID: 134

PRESENTED BY: Kamal Abu Jabal / kamalA@ziv.gov.il

d. [late breaker] Impact of national lockdown in reducing SARS-CoV-2 transmission in Portuguese municipalities

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Background :

Rapid spread of the SARS-CoV-2 infections was responsible for the rupture of health services and forced drastic lockdown measures in many countries, driving millions into a socioeconomic crisis. Understanding the impact of non- pharmacological interventions on epidemic control in different socioeconomic contexts is important to inform decision-makers. We aimed to compare the effect of nationwide lockdown on SARS-Cov-2 incidence in different municipalities, grouped by socioeconomic features.

Methods :

Based on national surveillance data on a laboratory confirmed SARS-CoV-2 cases we developed an ecological interrupted time series analysis study in 277 Portuguese municipalities grouped by socioeconomic features using two- steps cluster analysis. Change in SARS-COV-2 daily incidence after lockdown introduction on March 18, 2020 was estimated in each cluster by negative binomial regression. Two municipality clusters were considered, with cluster A characterized by younger population with lower education and purchasing power and smaller population density.

Results :

Before lockdown, incidence rates increased by 24,7% and 19,0% daily, reaching 11,42 and 14,11 per 100.000 inhabitants in cluster A and B, respectively. With lockdown introduction, rates decreased by 4,0% and 4,2% daily, reaching 2,96 and 3,50 per 100.000, in cluster A and B 42 days after restrictions implementation. Overall, lockdown measures avoided 138.676,76 and 60.404,15 cases per 100.000, in cluster A and B, respectively.

Conclusions :

Before lockdown, higher SARS-CoV-2 transmission was observed in the municipalities with lower socioeconomic status, which was expected, considering these socioeconomic features are associated with higher transmission of the virus. Lockdown prevented more cases in these municipalities. Despite the socioeconomic impact, lockdown has demonstrated to be a crucial measure to control SARS-CoV-2 transmission, particularly in municipalities with lower socioeconomic status.

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

Keywords : covid-19 public health interventions socioeconomical

ABSTRACT ID: 297

PRESENTED BY: Teresa Garcia / garcia.64629@gmail.com

e. [late breaker] Antibody levels among hospital staff diagnosed with COVID-19 and factors related with antibody levels

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Poster Tour Abstracts

Background :

At Ege University Hospital, 14% of the staff had been diagnosed with COVID-19 until December 31, 2020. The first and second doses of Sinovac were administered in mid-January and mid-February 2021. Our aim was to explore antibody levels of COVID-19 diagnosed hospital staff and associated factors.

Methods :

The study was a cross-sectional study on 850 hospital staff diagnosed with COVID-19 between March 11-December 31, 2020. All had been followed-up by the Occupational Health and Safety Unit of the hospital from where they were later invited to this study. 637 (74.9%) participated by replying a 24-question telephone survey and giving blood samples between March 22-July 27 2021. IgG antibodies to the S1 antigen of the SARS-CoV-2 virus were detected with ELISA, both qualitatively and quantitatively. Chi-square, Student t, variance, correlation analyses, logistic, Cox regression and Kaplan-Meier survival analyses were used. Ethical approval was obtained in February 2021 with no.21-2T/54.

Results :

The mean age of the participants was 37.0 ±9.7 and 63.4% were female; 32.0% were nurses, 13.2% physicians. Among participants, 35.2% had a more severe disease period than others and 34.5% had fever. Participants were included minimum 56, maximum 377 days after their COVID-19 infection. During enrolment, 137 (21.5%) were unvaccinated, 39 (6.1%) one-dose and 461 (72.4%) two-dose vaccinated. Among the 637 participants, 544 (85.4%) tested positive, 29 (4.6%) borderline, 64 (10.0%) negative for antibodies. Antibody positivity was higher among vaccinated, over 40 years and moderate disease groups. Among the unvaccinated, 97.8%, 59.4%, 38.2% and 14.3% tested positive at respectively 3rd, 6th, 9th, 12th months post-infection.

Conclusions :

Moderate disease group had higher antibody positivity than mild and severe infection groups. Vaccination is recommended between the 3rd-6th months post-infection.

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

Keywords : COVID-19, immunity, antibodies, health staff

ABSTRACT ID: 335

PRESENTED BY: Raika Durusoy / raika.durusoy@ege.edu.tr

Poster tour 13
Antimicrobial resistance

Abstracts

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a. Extended spectrum ß-lactamases in human Salmonella isolates in Spain from 2002 to 2018

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Background :

Global outbreaks of extended-spectrum β-Lactamases (ESBLs) and carbapenemase-producing bacteria lead to first choice antibiotic treatment failures. Therefore the aim of this study is to monitor the clinically relevant AMR determinants circulating in Salmonella enterica, we here describe the prevalence of ESBLs among the isolates collected in Spain from 2002 to 2018.

Methods :

Of the 22,503 human samples submitted to the National Center for Microbiology, antimicrobial susceptibility testing was performed randomly on 33% and 50% of the Salmonella isolates received between 2002-2011 and 2012-2018, respectively. WGS and cgMLST was performed on all isolates harboring resistance to ß-lactams (cefotaxime and/or ceftazidime).

Results :

Among the 258 we identified 16 ESBLs belonging to the families CMY, SHV, TEM and CTX-M as well as an ampC-type ß-lactamase. We identified isolates of the serotypes Corvallis, Rissen and Enteriditis harboring blaOXA-48 and believe this to be its first description from human samples. The most commonly identified ESBLs were blaCTX-M-9 (50%) followed by blaSHV-12(12%) and blaCMY-2(11%). We identified 32 different serotypes harboring ESBLs of which the most common were ST-34 monophasic Typhimurium (31%), ST-16 Virchow (18%) and ST-15, -19, -36, -110 and -323 Typhimurium (12 %). The ESBLs identified were most commonly associated with the plasmid replicon types IncH12a (49%) of which 95% harbor blaCTX-M-9, followed by incl1(17%) and IncFIIS(7%). 187 (72%) of the isolates in this study grouped into 21 clusters. The largest cluster was composed of 45 Salmonella Virchow (ST16) all of which harbored blaCTX-M-9.

Conclusions :

While blaOXA-48 is described in Salmonella of animal origins, its recent appearance in human Salmonella strains poses a grave threat to first-choice treatment options. National surveillance efforts should consider declaring these resistance determinants when identified in human isolates

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Subject : Microbiology

Keywords : Salmonella Enterica, Antibiotic Resistance, AMR, Extended-spectrum B-Lactamases

ABSTRACT ID: 161

Poster Tour Abstracts

PRESENTED BY: Andreas Hoefer / ahoefer@isciii.es

b. Who was given antibiotics in primary care in Northern Ireland, during 2019 and what is the role of prescribers? A cross-sectional, multi-level analysis

C. Nugent [1]

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[4] Public Health England

[5] NI Health and Social Care Board

Background :

Inappropriate use of antibiotics is a key driver of antimicrobial resistance (AMR). Northern Ireland (NI) antibiotic consumption is the highest in the UK and ~80% occurs in primary care. To effectively develop and target interventions it is necessary to understand what is driving antibiotic consumption including patient and prescriber factors.

Methods :

A cross-sectional study using a random sample of everyone registered with a GP in NI in 2019 (n=10,000) was extracted from routine health information sources in the NI Regional Data Warehouse. Multi-level logistic regression analysis was used to understand the role of sociodemographic factors, catheter status (known to increase infection risk), GP practices and GP federations (GP networks that help deliver government mandated agendas) in total antibiotic prescribing.

Results :

The association between age and being prescribed an antibiotic differed according to gender. Compared with males aged 0-10 years, the odds of receiving an antibiotic increased exponentially among males aged over 70 years and females aged over 50 years. Catheter use was significantly associated with antibiotic prescription (aOR=6.82, 95% CI= 2.50-18.64). After adjusting for other factors the effect of deprivation was not statistically significant and no difference was found between urban/rural settlements. There was significant variation in the odds of antibiotic prescribing between GP practices and between federations.

Conclusions :

This work has confirmed the profile of individuals most likely to receive an antibiotic prescription in NI primary care and identified GP practice as a significant source of variation; suggesting interventions to reduce consumption should betargeted at both the individual and GP practice levels.

Subject : Field epidemiology (e.g. outbreak investigations)
Keywords : Antimicrobial Resistance, Antimicrobial Stewardship, Primary Care, Sociodemographics, Catheters
ABSTRACT ID: 194
PRESENTED BY: Christopher Nugent / chris.nugent@hscni.net

c. Antimicrobial-resistance in human strains of Salmonella spp: data from Enter-Net surveillance system 2016-2019, Italy

G. Errico [1]

L. Villa [2], A. García-Fernández [3], S. Owczarek [4], D. Fortini [5], A. Dionisi [6], S. Arena [7], L. Busani [8], C. Lucarelli [9]

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Background :

Antimicrobial-resistance in Salmonella spp. is of concern, in particular to critically important antibiotics. In Italy, the national voluntary laboratory surveillance system, Enter-Net, coordinated by Istituto Superiore di Sanità, collects epidemiological, microbiological data and strains. We analysed antimicrobial-resistance data of Salmonella spp. human

strains during 2016-2019 in order to provide recommendations for surveillance improvement.

Methods :

Antimicrobial susceptibility tests (ASTs) with a panel of 12 antibiotics, according to ECDC protocol except for azithromycin and tigecycline, were available for 883 strains for which multidrug-resistance (MDR) was calculated. ASTs with modified panels were available for 728 additional strains. Data analysis was performed using STATA.

Results :

A high proportion of strains was resistant to sulphonamides (45.2%), ampicillin (41.3%), and tetracycline (41.3%). Third-generation cephalosporin resistance was 2.2%, and most strains were S. Infantis (71.7%). Colistin resistance was 7.7%, and 77.7% of the strains were S. Enteritidis. Fluoroquinolone resistance was observed in 11.7% and the most frequent serovar was S. Enteritidis (28.1%), followed by S. Infantis (18.7%) and S. Typhimurium monophasic variant (STYM, 12.9%). 37.7% of strains were MDR. The most frequent MDR-profiles included at least Ampicillin-Sulfamethoxazole- Tetracycline (ASuT) and Ampicillin-Chloramphenicol-Sulfamethoxazole-Tetracycline (ACSuT), representing 54.8% and 14.3% in S. Typhimurium, 91.1% and 7.8% in STYM and 46.4% and 17.9% in S. Infantis. Among MDR-S. Infantis strains, out of 14-ESBL strains, 64.3% had at least the ASuT profile.

Conclusions :

This study confirms the high level of resistance and MDR in human strains of Salmonella spp. in Italy. The third- generation cephalosporin resistance in S. Infantis is of particular concern. We recommend to continue monitoring antimicrobial-resistance and implement the surveillance with a One-Health approach to better understand AMR-trends and related risks.

Subject : Surveillance
Keywords : Salmonella,surveillance,antimicrobial-resistance,MDR,ESBL
ABSTRACT ID: 17
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d. Phylogenomic relatedness between Austrian N. gonorrhoeae strains correlates with antimicrobial resistance patterns

J. Schaeffer [1]

K. Lippert [2], S. Pleininger [3], A. Stöger [4], P. Hasenberger [5], F. Heger [6], A. Eigentler [7], A. Geusau [8], A. Indra [9], F. Allerberger [10], W. Ruppitsch [11]

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ESCAIDE

Poster Tour Abstracts

for Health and Food Safety, Vienna, Austria

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[10] Austrian Agency for Health and Food Safety, Vienna, Austria

Background :

Gonorrhoea, caused by Neisseria gonorrhoeae, is the second most common bacterial sexually transmitted infection. Due to the plasticity of its genome, N. gonorrhoeae acquires antimicrobial resistance (AMR) at a fast rate. In this study, we searched for epidemiologic and genetic factors associated with AMR.

Methods :

1,398 clinical strains isolated between 2016 and 2020 at the Austrian National Reference Center for Gonococci were included in this study. They were tested for AMR and characterized by whole genome sequencing (WGS) and core genome multilocus sequence typing (cgMLST). From WGS data, 32 genes associated with AMR were extracted. Univariate analysis was conducted on epidemiological and genetic variables.

Results :

Resistance rates were 14% for azithromycin, 16% for penicillin and 60% for ciprofloxacin. AMR against extended spectrum cephalosporin (ESC) were still rare (3% for cefixime and none for ceftriaxone). AMR rate was increasing over time for all but penicillin. Azithromycin AMR was more frequent in Asian patients (OR=7.7). Sex workers were at higher risk of ESC resistance but lower risk of penicillin resistance. Sequences were searched for AMR genes. Penicillin AMR was strongly associated with blaTEM carriage (OR=31), and ≥99% of ciprofloxacin resistant isolates carried gyrA D95 substitution. CgMLST analysis highlighted two branches with specific AMR patterns. One included most azithromycin-resistant isolates, which all carried mosaic mtr genes. The second branch contained all cefixime-resistant isolates, most possessing mtrR G45 substitution (OR=29) and penA mutations.

Conclusions :

This study showed an increasing rate of AMR among Austrian N. gonorrhoeae isolates, which is concerning. Isolates resistant to azithromycin or cefixime clustered in cgMLST, suggesting a single importation. The good correlation between genomics and AMR advocates for systematic molecular surveillance of N. gonorrhoeae.

Subject : Microbiology

Keywords : Neisseria gonorrhoeae, antimicrobial resistance, whole genome sequencing, risk factors, resistance genes

ABSTRACT ID: 81

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

e. Detection of healthcare-related infections due to multidrug-resistant microorganisms in COVID-19 patients at an Intensive Care Unit in a secondary hospital in Spain

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Background :

Rises in healthcare related infections (HRI) have been reported during the current SARS-CoV-2 pandemic. Some of these HRI are due to multidrug-resistant microorganism (MRM), whose known risk factors include previous hospital admission during the last three months, institutionalized patients, known previous infection and/or colonization by MRM, having received antibiotics for seven or more days in the last month, especially cephalosporins or carbapenems and special medical conditions, among others. Patients admitted to Intensive Care Units (ICU) are at special risk of both developing HRI and infections due to MRM. In this study, we aimed at assessing the epidemiological features and dynamics of HRI due to MRM among patients who were admitted to the ICU during the COVID-19 outbreak between February 27 and July 31, 2020 in Spain in a secondary hospital.

Methods :

Retrospective descriptive study of HRI due to MRM in confirmed COVID-19 ICU in-patients during the first wave of the SARS-CoV-2 pandemic at Infanta Sofía University Hospital, San Sebastián de los Reyes (Madrid). Patient characteristics, antimicrobial drug therapy and microbiological samples outcomes were analysed.

Results :

76 confirmed COVID-19 cases were admitted to our ICU. 30 HRI that met national HRI criteria were detected in 14 patients. The most frequently detected HRI were tracheobronchitis (57.14%, 95% CI 45.94%-68.34%, n=8), bacteriemia (50%, 95% CI 40.20%-59.80%, n=7) and ventilator-associated pneumonia (42.86%, CI 34.46%-51.26%, n=6). Positive cultures for MRM were detected in 32 samples. Extended betalactamase producing Klebsiella pneumoniae was the most frequently detected MRM (n=24).

Conclusions :

We detected 30 HRI in 14 patients, both in clinical and colonization samples. Both infection control to prevent HRI and screening for MRM are of great importance to avoid further spread.

Subject : Microbiology

Keywords : hospital acquired infection, multiresistant, intensive care, COVID

ABSTRACT ID: 242

PRESENTED BY: Christine Giesen / christine.giesen@salud.madrid.org

Poster Tour Abstracts

Poster tour 14
COVID-19: surveillance

Abstracts

a. A novel surveillance tool to estimate the serial interval, reproduction number and dispersion parameter for coronavirus disease 2019 using contact tracing data

B. Silenou [1]

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Background :

The digital surveillance outbreak response management and analysis system (SORMAS) contains a COVID-19 specific module to support countries in epidemic response. It consists of documentation, linkage and follow-up of cases, contacts and events. To allow SORMAS users to compute key surveillance indicators and estimate disease parameters from such a complex network of data in real time, we developed the SORMAS statistics (SORMAS-Stats) app based on R- Shiny framework.

Methods :

Based on review and users' requests, we included the following visualization and estimation of parameters in SORMAS- Stats: transmission network diagram, serial interval (SI), time-varying reproduction number (Rt), dispersion parameter (K) and additional surveillance indicators presented in graphs and tables. We estimated SI by fitting a Lognormal distributions to the observed serial interval data, defined as the number of days between symptoms onset dates of infector-infectee pairs. We estimated K by fitting a negative binomial distribution to the observed number of infectees per infector. We applied the Markov Chain Monte Carlo approach using the observed serial interval and incidence data to estimate Rt.

Results :

Using contact tracing data for 4724 infector-infectee pairs of confirmed cases reported between 18/02/2021 and 18/05/2021 in Bourgogne-Franche-Comté, we estimated mean SI of 4.73 (95% CI, 4.61–4.84) and K of 0.62 (95% CI, 0.61–0.63). The daily estimated Rt values ranged from 0.8 to 1.5. These estimates are in line with findings from previous studies.

Conclusions :

We provide a tool for real time estimation of parameters, which are essential to monitor an outbreak. SORMAS-Stats would greatly assist public health authorities in the countries using SORMAS or similar tools by providing extensive visualizations and computation of surveillance indicators.

Subject : Surveillance
Keywords : COVID-19,Disease Outbreak, Contact Tracing, Serial Interval, Basic Reproduction Number, Infectious Disease Incubation Period, Superspreading Events, Telemedicine, Public Health
ABSTRACT ID: 252
PRESENTED BY: Bernard Chawo Silenou /

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b. SARS-CoV-2 antibody testing in healthcare workers: a comparison of the clinical performance and retained sensitivity of three commercially available immunoassays, Ireland, 2020

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Background :

SARS-CoV-2 immunoassays can be used in seroprevalence studies to guide public health decision-making. We compared results of three assays used in a healthcare worker (HCW) seroprevalence study to learn more about retained sensitivity over time on different assays.

Methods :

Seroprevalence testing was carried out in October 2020 on 5,788 unvaccinated HCWs in two Irish hospitals. The study population were those HCW who participated in seroprevalence testing and who were previously SARS-CoV-2 positive by PCR (n=367, 6.3%). Time since PCR positivity ranged from 2-33 weeks. We analysed positivity on three SARS-CoV-2 immunoassays; one anti-nucleocapsid IgG immunoassay (Abbott) and two total antibody immunoassays (Roche anti-nucleocapsid; Wantai anti-spike). All 367 were tested on Abbott and Roche, and all those who were positive or inconclusive on Abbott (71%) were tested on Wantai. Multivariable logistic regression was carried out on Abbott results, controlling for age, sex, ethnicity/background, type of patient contact, symptom severity, and time since PCR diagnosis.

Results :

Overall, 95% (95%CI92-96) tested positive on Roche and 41% (95%CI35-46) tested positive on Abbott. All of those tested on Wantai had a positive result. Decline in Abbott positivity began at 21 weeks (150 days) after confirmed infection. Factors associated with Abbott seronegativity included sex (male OR0.30;95%CI0.15-0.60), symptom severity (OR0.19 severe symptoms;95%CI0.05-0.61), ethnicity (OR0.28 Asian ethnicity;95%CI0.12-0.60) and time since PCR diagnosis (OR2.06 for infection 6 months previously; 95%CI1.01-4.30), (P ≤0.050).

Conclusions :

Compared to Abbott, the Roche assay seems to be more appropriate for SARS-CoV-2 seroprevalence studies due to maintained antibody detection up to 33 weeks. Wantai outperformed Roche but further study is needed on an unbiased Wantai sample. Further comparative studies are required to guide most appropriate use/choice of immunoassays in

Poster Tour Abstracts

various settings/scenarios, particularly vaccinated populations.

c. A Tailored Surveillance System for COVID-19 Infections within Prisons in Wales

G. Jones [1]

F. Thomas [2], L. Fina [3], S. Perrett [4], J. Price [5], J. Salmon [6], C. Smith [7], M. Eveleigh [8], D. Beynon [9], J. Gough [10], M. Rennocks [11], A. Davies [12]

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Background :

Prisons are high-risk settings for large-scale outbreaks of COVID-19 that involve higher rates of infection, hospitalization and mortality compared to the general population after adjusting for age. During the second wave (defined as 1st October 2020 – 1st March 2021), despite stringent control measures, all prisons in Wales experienced complex outbreaks. In partnership with HM Prison and Probation Service, Public Health Wales developed a tailored, standardized surveillance system to monitor COVID-19 within prisons, which supported Outbreak Control Teams (OCTs) with invaluable, timely detection of cases, the ability to assess spread in a multifaceted environment and recommend effective control measures.

Methods :

We defined a minimum surveillance dataset and designed a standardised, live, line-list held within MS Teams. Alongside the standard data fields (Name, Demographics, Staff/Prison Resident, Onset/Specimen Date, Symptomatic Status), the dataset was continuously refined and expanded throughout the period to include resident/staff roles, external movement, cell locations, site movement and outcomes in terms of hospitalisations and mortality.

Results :

There were 1,280 cases reported (609 prison residents, 649 prison staff and 22 unknowns). Data was used by OCTs to inform outbreak management and the impact of system changes, and was summarised within a weekly report for key stakeholders.

Conclusions :

A tailored surveillance system with fields relevant to the prison environment enabled timely detection and assessment of cases, trends and outbreaks, and helped support policy decisions and the evaluation of control measures. Recommendations: Prison surveillance systems require fields unique to prison settings to accurately assess risk, improve formal agreements surrounding routine data-sharing across health and justice to improve analytical capability.

d. Calculating the serial interval of SARS-CoV-2 in Lebanon using 2020 contact-tracing data

N. Haddad [1]

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[8] London School of Hygiene and Tropical Medicine, Department of Global Health and Development; National University of Singapore, Saw Swee Hock School of Public Health

Background :

The first detected COVID-19 case in Lebanon on 21 February 2020 engendered implementation of a nationwide lockdown alongside timely contact-tracing and testing. Our study aims to calculate the serial interval of SARS-CoV-2 using contact tracing data collected from 21 February to 30 June 2020 in Lebanon to guide testing strategies.

Methods :

rRT-PCR positive COVID-19 cases reported to the Ministry of Public Health Epidemiological Surveillance Program (ESU- MOH) are rapidly investigated and identified contacts tested. Positive cases and contacts assigned into chains of transmission during the study time-period were verified to identify those symptomatic, with non-missing date-of-onset and reported source of exposure. Selected cases were classified in infector-infectee pairs. We calculated mean and standard deviation for the serial interval and best distribution fit using AIC criterion.

Results :

Of a total 1,788 positive reported cases, we included 103 pairs belonging to 24 chains of transmissions. Most cases were Lebanese (98%) and males (63%). All infectees acquired infection locally. Mean serial interval was 5.24 days, with a standard deviation of 3.96 and a range of -4 to 16 days. Normal distribution was an acceptable fit for our non-truncated data.

Conclusions :

Timely investigation and social restriction measures limited recall and reporting biases. Pre-symptomatic transmission up to 4 days prior to symptoms onset was documented among close contacts. Our SI estimates, in line with international literature, provided crucial information that fed into national contact tracing measures. Our study, demonstrating the value of contact-tracing data for evidence-based response planning, can help inform national responses in other countries.

Poster Tour Abstracts

e. A cohort study describing COVID-19 transmission in named contacts over time and across settings and population groups in England

C. Turner [1]

C. Chen [2], M. Vabistsevits [3], P. Blomquist [4], H. Moore [5], S. Packer [6], C. Anderson [7], G. Hughes [8], PHE CTC Data team

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Background :

Population-level contact tracing by NHS Test and Trace in England provides an opportunity to compare transmission risk to contacts identified. Secondary attack rates provide a standard measure of risk allowing comparison across time and populations.

Methods :

All COVID-19 cases in England in NHS Test and Trace between 2020-08-01 and 2021-01-31 were included. Cases named recent close contacts during contact tracing, including the setting/type of activity where contact occurred. Case and contact episodes were matched into persons and cases named as a contact 2-14 days prior to symptom onset were considered secondary cases; the most recent exposure (preferring household) within the window was considered effective. Secondary attack rates were computed by characteristics of interest of the index case and the transmission event.

Results :

Of 3,306,696 cases reported, 609,895 (18.4%) had a known exposure. Secondary attack rates (SAR) increased from 6-7% in August 2020 to 12-14% in December and fell to 11% in January 2021. The overall SAR over 6,474,126 contacts was 9.7%, highest (10.5%) among household members and household visitors (8.1%), and lowest in workplace/ education settings (4.4%). SARs increased with age of contact: 6.1% in those under-10, 12.9% in 40-49 year olds and 15.4% in the 80+ group. Direct contacts had much higher SAR (10.1%) than close contacts (5.7%) as did contacts of symptomatic (10.4%) than asymptomatic cases (3.5%).

Conclusions :

Secondary attack rates can measure the effects of behavioural or environmental factors, interventions and viral variants and monitor trends over time. We identified significant variation over time and between settings. These national scale contact tracing data can be used to identify subpopulations or settings at increased risk of transmission and direct public health actions.

Subject : Modelling, bioinformatics and other biostatistical methods
Keywords: COVID-19, Close-Contact Transmission, Contact Tracing, Secondary Attack Rate, Transmission
ABSTRACT ID: 248
PRESENTED BY: Charlie Turner / charlie.turner@phe.gov.uk

Poster tour 15
COVID-19: vaccines

Abstracts

a. Preliminary results from a pilot study evaluating the time of viral clearance in asymptomatic COVID-19 vaccinated and unvaccinated patients

L. Bubba [1]

C. Galli [2], L. Pellegrinelli [3], V. Primache [4], S. Delbue [5], L. Signorini [6], M. Dolci [7], S. Binda [8], E. Pariani [9]

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Background :

COVID-19 vaccines demonstrated to reduce the number of hospitalised cases; however, vaccinated subjects can be still infected by SARS-CoV-2. We present the preliminary results of a pilot study investigating the time of clearance of SARS-CoV-2 infection in asymptomatic individuals by using real-time RT-PCR cycle threshold (Ct) value as a proxy parameter of viral shedding.

Methods :

33 asymptomatic individuals (median age: 58.6 yrs, IQR: 23.9 yrs) who resulted SARS-CoV-2-positive during screening programs were included in the study. Six (18.2%) of them (median age: 52.6 yrs, IQR: 8.4 yrs) had received the second dose of COVID-19 vaccine at least 15 days before the first positivity detection (index episode). One hundred-six nasal-pharyngeal swabs were collected and analysed by real-time RT-PCR for SARS-CoV-2 detection.

Results :

At the index episode the mean Ct value was 27.7 (range: 13.6-36.2) and the average time for viral clearance (i.e. Ct=undetected) was 36 days. No differences were observed in terms of Ct at the index episode between vaccinated and unvaccinated ($p>0.05$). Vaccinated individuals cleared the infection in a shorter time than unvaccinated ones (mean: 27 days vs. 40 days, p=0.02). From the index episode, the mean time to reach a Ct>32 (considered as potential cut-off for infectivity) was 12 days, with no difference between unvaccinated and vaccinated (mean: 12.3 vs. 11.3, $p>0.05$).

Conclusions :

These preliminary findings indicate that irrespective to vaccination status, a Ct value >32 is achieved in 12 days on average; vaccinated individuals showed a significantly shorter time of viral clearance. Investigating SARS-CoV-2 shedding and potential infectivity of vaccinated individuals is a public health key action to identify proper control measures to prevent SARS-CoV-2 spread and to inform authorities.

Subject : Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)
Keywords : COVID-19 vaccine; asymptomatic; viral clearance; SARS-CoV-2; control measures
ABSTRACT ID: 144
PRESENTED BY: Laura Bubba / laura.bubba@unimi.it

Poster Tour Abstracts

b. COVID-19 vaccine effectiveness in Malta in SARI hospitalised patients: preliminary results February – April 2021, Joaquin Baruch

J. Baruch [1]

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[2,3,4,5] Infectious Disease prevention and Control unit

Background :

As COVID-19 vaccination began in Europe, ECDC funded a multicountry test-negative design study to measure product- specific COVID-19 vaccine effectiveness (VE). This study measured Pfizer/BioNTech VE against COVID-19 severe acute respiratory illness (SARI; case definition: cough, fever, onset of symptoms within 10 days, and hospitalisation) among hospitalised patients in Malta.

Methods :

The hospital team recruited all SARI cases eligible for vaccination. Cases were SARS-CoV-2 PCR-positive patients, and controls were those PCR-negative. We collected vaccination status (at least one dose vs. not vaccinated), sex, chronic conditions, admission month, and age group. Using logistic regression, we measured VE as (1 - odds ratio)*100 adjusted by sex and month, and stratified by age (‹75, ›=75). We measured VE by days between vaccination and hospitalisation: ›14 days (VE›14 days) or ›7 days (VE›7days).

Results :

From February 1st to April 30th 2021, we identified and enrolled 164 SARI cases that were eligible for vaccination with confirmed SARS-CoV-2 PCR status: 40 controls and 124 cases. VE›7days was 81.6% (95% CI: 41.5 - 94.7%) and 93.3% (71.7 - 98.6%) for ›=75 and ‹75 years, respectively. VE›14 days was 85.8% (47.6 -96.6%) and 96.7% (81.5 - 99.9%) for ›=75 and ‹75 years, respectively.

Conclusions :

These preliminary results suggest that the Pfizer/BioNTech vaccine confers high protection against SARI laboratory- confirmed as SARS-CoV-2. VE seems higher for the ‹75 age category than the ›=75 category and appears optimal at more than 14 days since vaccination. These findings are promising and adjustment for other potential risk factors and vaccination brands will be performed as more data are collected. Obtaining VE estimates for specific age groups and risk profiles for each vaccine brand is key to successfully controlling this pandemic.

Subject : Surveillance
Keywords : Vaccine effectivness,COVID-19,Malta,SARI,Vaccine
ABSTRACT ID: 131
PRESENTED BY: Joaquin Baruch / joaquinbaruch2@gmail.com

c. Surveillance of adverse events following immunization against covid-19: first four months of immunization campaign in Slovenia, Veronika Učakar

V. U?akar [1]
K. Krnc [2]

[1] Specialist in public health
[2] Surveillance officer

Background :

Monitoring adverse events following immunization (AEFI) is important in maintaining public confidence needed to reach sufficient vaccination coverage for disease control. The Slovenian AEFI Registry at the National PH Institute collates mandatory reports about AEFI from health care provides. Our aim was to analyse AEFI surveillance data for three covid-19 vaccines (Pfizer/Biontec, Moderna, AstraZeneca) used in Slovenia from 27/12/2021 to 2/5/2021 in order to monitor vaccine safety.

Methods :

Dose-based AEFI reporting rates were calculated using number of vaccine doses administered as the denominator. All AEFI were classified according to System Organ Class (SOC). Definition for serious AEFI included death, life- threatening illness, hospitalization, or prolongation of hospitalization, permanent disability and other clinical relevant conditions.

Results :

Alltogether 640,683 doses of covid-19 vaccines were administreted in Slovenia. The AEFI Registry received 2,525 reports for Pfizer/Biontec vaccine (dose-based reporting rate 596.6/100,000), 1,883 for AztraZeneca (1,456.5/100,000) and 94 for Moderna (138.0/100,000), containing predominantly non-serious and expected AEFI. Overall, the most reported AEFI were general disorders and administration site conditions (Pfizer/Biontec: 59.2%, AstraZeneca: 53.4% and Moderna: 56.4%). Forty-one reports for Pfizer/Biontec (1.6%) included serious AEFI with dose-based reporting rate of 9.2/100,000, 21 (1.1%) for AstraZeneca (16.2/100.000) and 3 (3.2%) for Moderna (4.4/100,000). Altogether there were 20 deaths reported (Pfizer/Biontec: 15, AstraZeneca 3 and Moderna 2), of those seven were assessed as unlikely related to vaccination, the rest are under investigation.

Conclusions :

The type and frequency of AEFI detected are comparable to the results from other surveillance systems. The benefit-risk balance for covid-19 vaccines used in Slovenia remains positive. Sustaining AEFI surveillance will be also important in the future because of availability of new vaccines and implementation of expanded vaccine recommendations.

Subject : Surveillance
Keywords : adverse events following immunization, surveillance, covid-19 vaccines, Slovenia
ABSTRACT ID: 105
PRESENTED BY: Veronika Učakar / veronika.ucakar@nijz.si

d. COVID-19 vaccine effectiveness at outpatient level in Europe: 2021 pooled results from 11 countries

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Poster Tour Abstracts

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Background :

The I-MOVE-COVID-19 and ECDC COVID-19 vaccine effectiveness (VE) networks at primary care level include 13 study sites in 11 European countries. These networks aim to measure VE against COVID-19 in vaccination target groups overall, by age group and vaccine brand.

Methods :

Twelve study sites adapted influenza sentinel physician networks, although not all swabbing occurs on site. One study site is exclusively based around COVID-19 testing centres. We conducted a multicentre study, pooling individual data from the I-MOVE-COVID-19 and ECDC networks among those aged 30 years and over between 14 December 2020 and 31 August 2021. Patients with COVID-19-like symptoms were swabbed: those testing SARS-CoV-2 PCR positive were cases and those testing negative were controls. We estimated VE using logistic regression adjusted for study site, age and swab date, with chronic condition and sex as potential confounders.

Results :

We included 25,096 outpatients (4,018 cases and 21,077 controls) from 11 study sites. Adjusted overall complete dose VE was 74% (95%CI: 69–78), 72% (95%CI: 65–77), 82% (95%CI: 69–89), and 81% (95%CI: 68–89) for 30–49, 50–64, 65–74 and 75+ year-olds, respectively. The VE for 30–64 and 65+ year-olds was 77% (95% CI: 74–80) and 82% (95%CI: 74–87), 65% (95%CI: 57–72) and 68 (95%CI: 38–84), and 91% (95%CI: 86–94) and 88% (95%CI: 76–94) for Comirnaty, Vaxzevria, and Spikevax vaccines, respectively.

Conclusions :

Our results suggest good protection against COVID-19 at outpatient level, among those aged 30 years and over who are completely vaccinated, overall, and for Comirnaty, Vaxzevria, and Spikevax vaccines. Differences between VE by brand may also be explained by circulating variants, specific populations targeted, delays between doses and chance.

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

e. Two doses of the mRNA vaccine Comirnaty effectively reduced transmission of SARS-CoV-2: evidence from a SARS-CoV-2 B.1.1.7 outbreak in a nursing home, Osnabrück, Germany, January-March 2021

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Background :

Shortly after completing vaccination with Comirnaty (BioNTech/Pfizer), an outbreak of SARS-CoV-2 infections occurred in a nursing home in Osnabrück, Germany. We assessed vaccine effectiveness (VE) and compared viral load and secondary attack rates (AR) in vaccinated and unvaccinated cases.

Methods :

Cases were residents (living at the nursing home or receiving day-care) and staff testing PCR-positive between 03 January 2021 and 18 March 2021. Data on vaccination status, disease severity and SARS-CoV-2 testing was obtained for all cases, while the infection status of household members was assessed for SARS-CoV-2-positive staff only. We estimated VE as [1-RR], using Poisson regression models. For investigating vaccine effects, we analysed Ct-values as a proxy for viral load using linear regression models.

Results :

In this cohort, 95/124 (77%) residents and 72/128 (56%) staff were vaccinated twice with Comirnaty. AR among vaccinated and unvaccinated residents [24/95 (25%) vs. 10/29 (34%); p=0.46, Chi-squared test] and staff [5/72 (7%) vs. 11/56 (20%); p=0.06] were comparable. Of 50 cases, four were hospitalised [1/4 (25%) vaccinated] and five [2/5 (40%) vaccinated] died of COVID-19 (all residents). Variant B.1.1.7 was detected in 27/28 of typed cases. Age-adjusted VE was 88% [95%CI:37-98%; p=0.04] against hospitalization or death and 68% [95%CI:36-84%; p<0.01] against symptomatic SARS-CoV-2 infection. With increasing duration between the second vaccine dose and first PCR, the Ct- value was significantly higher [0.25 units/day;95%CI:0.04-0.47; p=0.02]. The secondary AR was lower in households of vaccinated [2/9 (22.2%)] than of unvaccinated SARS-CoV-2-positive staff [12/18 (66.7%); p=0.05, Fisher's exact test].

Conclusions :

While two doses of Comirnaty significantly reduced SARS-CoV-2 infections, severe outcomes, viral load and secondary transmission in households, they did not do so entirely, hence emphasizing the role of non-pharmaceutical interventions after completed vaccination.

Poster Tour Abstracts

Poster tour 16
Healthcare-associated infections

Abstracts

a. Factors influencing infection rate among tested positive residents for SARS-CoV-2 in Flemish nursing homes during the first wave of COVID-19 pandemic, Laurene Peckeu

L. Peckeu [1]

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Background :

In April-May 2020, Belgium experienced high numbers of fatal COVID-19 cases among nursing homes (NH) residents. In response, a mass testing campaign was organized testing all residents and staff of all NHs. It is unclear which factors predispose NH to SARS-CoV-2 outbreaks. We analysed data collected during the mass testing campaign to understand which institutional factors were associated with increased infection rate of SARS-CoV-2 among residents in the Flanders region.

Methods :

Data were collected on demographics, group category (staff or resident), name of the NH, symptoms status and test result. We retrieved additional data on the number of beds and staff, type of beds (level of dependency of the residents) and status (public, private for profit/non-profit institutions) of each NH. Risk factors were assessed using negative binomial regression.

Results :

In total, 695 NHs were included, 282 (41%) had at least one resident tested positive. Higher infection rate among residents was associated with higher fraction of RVT beds (more dependent ones) (IRR: 2.43; 95%CI: 1.12-5.24) and higher infection rate among staff (IRR: 377.08; 95%CI: 77.69-2025.55), albeit with large uncertainty. No other NH characteristics: mean age of staff and resident, ratio staff/residents, proportion of asymptomatic tested positive and status of the NH, were found associated with an increased infection rate among residents.

Conclusions :

This study confirms that staff-resident interactions play a key role in SARS-CoV-2 transmission dynamics during the first COVID-19 wave in Flemish NHs. Staff infection rate may reflect infection rates in the general community, hence may represent a proxy for introduction and subsequent transmission. Regular staff testing, vaccination, assessment of infection prevention and control strategies and preparedness plan is needed to face future SARS-CoV-2 epidemics in these settings.

Poster Tour Abstracts

E. Marchant [1]

J. Coelho [2], M. Bardsley [3], K. Chandler [4], M. Cox [5], M. Cliff [6], C. Giljohann [7], M. Harrison [8], N. Love [9], A. Wright [10], B. Pichon [11], S. Balasegaram [12], C. Humphreys [13], A. Phillips [14], D. Ready [15], D. Todkill [16], C. Brown [17], T. Lamagni [18], V. Decraene [19]

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Background :

Due to observations suggesting a change in the epidemiology of invasive group A Streptococcus (iGAS) clusters, we conducted a review to investigate and quantify changes.

Methods :

We extracted data including onset dates, population affected, setting, and emm type from public health management records for clusters of iGAS (≥2 cases of confirmed or probable infection linked in time and place) and national reference laboratory data from 2015-2019.

Results :

232 clusters were identified with increasing annual incidence (21 in 2015 to 69 in 2019). The most common settings were hospital/maternity (n=66), care homes (n=61), and homeless shelters (n=32). A yearly increase was seen in all settings apart from hospital/maternity which remained stable. Cluster incidence increased notably in care homes (5 in 2015; 20 in 2019), homeless shelters (1 in 2015; 12 in 2019), and patients receiving home nursing care (0 in 2015; 6 in 2019). The most common emm types were emm 89.0, 1.0, and 66.0. emm 108.1 emerged in 2017 and was the most common by 2019, predominantly affecting people who use drugs and the homeless. The median cluster size was 2 confirmed iGAS cases but extended to 36 cases, with cluster duration ranging 1-170 weeks (median 6). Maximum cluster size and duration increased between 2015 and 2019.

Conclusions :

Whilst further assessment is needed to determine if increased ascertainment played a role, our study suggests a marked increase in iGAS cluster incidence in England. Timely identification to initiate prompt public health management has become increasing challenging given the complex and dispersed populations affected, reflected in increased size and duration of clusters. Routine adoption of whole genome sequencing will facilitate early detection and response to clusters of these life-threatening infections.

Subject : Burden of disease
Keywords : Group A Streptococcus, England, Incidence, Clusters
ABSTRACT ID: 53
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Background :

The unique characteristics of psychiatric institutions, i.e., host factors and living conditions, contribute to the onset and spread of infectious agents. Infection prevention and control (IPC) is essential to minimse transmission. Despite abundant studies regarding IPC conducted in hospitals, few studies focused on mental health care settings. Yet, the general low IPC compliance in psychiatric institutions is recognised as serious concern. Therefore, we determined perceived facilitators and barriers to IPC among professionals from psychiatric institutions, as well as to identify professional-reported recommendations to promote IPC.

Methods :

A qualitative study involving sixteen semi-structured interviews was conducted (before covid-19) among professionals from four Dutch psychiatric institutions. Data analysis comprised thematic analysis (conducted by two researchers independently), following a pre-existing integrated theoretical framework for implementing change.

Results :

Our findings indicated patients' unwillingness to comply with IPC and risk behaviour (both related to mental illness), professionals' negative attitude and lack of knowledge, lack of organisational priority and financial resources, and the dominant sectoral norm in which IPC and somatic aspects are inferior to mental aspects as main barriers. The main facilitators comprised mutual professional feedback, structural education, and clear task division between professionals regarding IPC responsibility ('role clarity'). The main recommendations included: (1) increase awareness towards IPC among all staff, by education and information provision, and development of formal agreements (i.e., IPC guidelines); (2) make room for and facilitate IPC at the organisational level, by appointing a professional responsible for IPC, reduction of work demands, and provision of adequate IPC equipment and facilities.

Conclusions :

Promoting IPC in mental health care settings is best achieved by multifaceted and mutlilevel (e.g., professional and organisational level) approaches, while balancing IPC needs and mental health care.

Subject :

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

Keywords : Infection Control , Healthcare Associated Infections , Mental Health Services , Psychiatry , Qualitative Research
ABSTRACT ID: 73
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Poster Tour Abstracts

d. 'Scanning for a source': A national nosocomial outbreak of Burkholderia cepacia complex associated with ultrasound gel, United Kingdom, 2020-2021

J. Doran [1]

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Background :

In December 2020, Public Health England identified and investigated a cluster of Burkholderia contaminans cases from hospitals across England. Another cluster ongoing since 2010, B.cepacia-genomovar-1, had an increase in cases and was subsequently incorporated into the investigation. Both organisms are members of Burkholderia cepacia complex (Bcc), gram-negative betaproteobacteria, ubiquitous in the environment.

Methods :

Confirmed outbreak cases of B.contaminans or B.cepacia-genomovar-1 were defined as any UK clinical isolates with common pulsed-field gel electrophoresis profiles since July 2020 or January 2010, respectively. For B.contaminans, we implemented an analytical study with conditional logistic regression (case-crossover design with 10-day case/control periods). Hospitals provided exposure information through online questionnaires and submitted products for testing. For B.cepacia-genomovar-1, as a microbiological link was quickly identified, only descriptive epidemiology was performed. For both clusters, whole genome sequencing (WGS) was performed on relevant case and product isolates.

Results :

We identified 61 B.contaminans and 136 B.cepacia-genomovar-1 confirmed cases. For both clusters, 70% of isolates were invasive and had similar demographics (52% male; median age: 56). A definitive microbiological link (WGS within 1-31 SNPs) with B.cepacia-genomovar-1 cases was identified with a single brand of 28 ultrasound gel samples submitted by eight hospitals. An independent epidemiological association was identified between B.contaminans and

exposure to ultrasound gel during the case period (aOR: 5.7, 95% CI: 1.6-20.9), although not microbiologically confirmed. Practice issues surrounding ultrasound gel, including refiling bottles, were identified.

Conclusions :

A link between two Bcc outbreaks and exposure to ultrasound gel in the UK was identified. Product-suspension and implementation of guidance on safe use of ultrasound gel was followed by a decrease in cases. We recommend that refilling of ultrasound gel bottles shouldn't occur.

e. Staphylococcus aureus (SA): a real increase of invasive infections in Finland in 2020? A time-series analysis of reported invasive SA cases in Finland, 2016-2020, Dorothée Obach

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Background :

From 30% to 50% of the human population are healthy carriers of Staphylococcus Aureus (SA). For invasive SA infection, fatality rate can reach 20%. In summer 2020, four physicians observed small clusters of invasive SA infections without a clear source of infection in Helsinki-Uusima, Tampere, Seinäjoki, and Jyväskylä hospitals. An increase of SA infections related to increasing swabbing capacities due to COVID-19 pandemic was suspected. We performed a time series analysis of invasive SA infections in Finland from 2016-2020 to determine if this increase was real and of concern.

Methods :

We collected monthly numbers of invasive SA cases by age-group and health district (HD) from two national registers from 01/01/2016-31/12/2020. We described invasive SA incidence count at country level and analysed invasive SA cases using Poisson regression to characterize trends. A p-value <0.05 was considered significant.

Results :

We observed underreporting in the Keski-Suomi HD in 2020 (37 cases versus a mean of 111/year from 2016-2019) and excluded it from the analyses. Median annual number of cases was 2,156 (range: 2,032-2,233) from 2016-2019 compared to a total of 2,206 cases in 2020. The 0-15 age group represented 3.7% of all reported cases compared to 4.7% in 2020. Number of cases increased monthly (IRR=1.0014 adjusted on a 3-month periodicity, p-value=0.010). However, the monthly trend observed in 2020 (IRR=0.9967, 95%CI [0.9843-1.0091]) and 2016-2019 (IRR=1.0020, 95%CI [1.0005-1.0035]) did not differ significantly. We observed a similar pattern when restricting our analysis to cases aged <15 years.

Conclusions :

There was no unusual increase of invasive SA infections in Finland in 2020. With limited data on nasopharyngeal swab related complications in the pandemic context, enhanced surveillance and investigation of SA infections are necessary.

Poster Tour Abstracts

Poster tour 17
Late breakers

Abstracts

a. Surveillance during a pandemic: COVID-19 cross-border contact-tracing in Germany, April-October 2020

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Background :

Statutory surveillance for SARS-CoV-2 in Germany includes demographical data and information on cases. Information on cross-border events is not systematically collected and analysed. The Emergency Operations Centre (EOC) at the Robert Koch Institute (RKI) coordinates cross-border contact-tracing for COVID-19 on national level and collects and shares data with subnational public health authorities and foreign countries. Our aim is to evaluate the collected information on cross-border events over time and assess if it provides additional value to the routine surveillance data.

Methods :

COVID-19 cross-border contact-tracing events were recorded using unique identifiers. We extracted data on cases, contacts, date and setting of exposure. We performed a descriptive analysis of events extracted from the time period April-October 2020.

Results :

To date, 2927 registered events have been analysed. Germany initiated communication 1,959 times, and other countries 962 times (Missing: N=5). In 1,938 events, 9,009 contacts and in 989 events 1,677 cases were communicated. In 885 events (45.7%) one contact was communicated, and 1053 events (54.3%) included two or more contacts (median 3, range: 2-1872). The exposure context was known for 1,405 events, and overall most frequently included private gatherings (34.5%) and flights (33.5%). This varied however over the given time period, with flights being the predominant exposure context during summer (July-August). Most frequent countries of exposure were Germany (N=661) and Austria (N= 249). Time delay between date of exposure and notification contacts to RKI was 6 days (median).

Conclusions :

The analysis of cross-border contact-tracing data has demonstrated added value and fosters timely communication on contacts and exposure context. This data has potential to complement the statutory surveillance for COVID-19 in Germany to supplement control strategies and maximize impact on the COVID-19 response.

Subject : Surveillance
Keywords : COVID-19, contact-tracing, surveillance, Germany
ABSTRACT ID: 314
PRESENTED BY: Ida Sperle / sperle-heupeli@rki.de

b. Seroprevalence of SARS-CoV-2 in Sweden, April 26 to May 9, 2021

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Background :

Sweden experienced a third wave of COVID-19 in the beginning of April 2021. Vaccination against COVID-19 started in December 2020. By the end of April 2021, 9% of the Swedish population as whole and 27% of persons 65 years and older were fully vaccinated. We conducted a point seroprevalence study of SARS-CoV-2 in April/May 2021 in order to estimate seroprevalence at a national level at this time point.

Methods :

In total, 2860 individuals from a probability-based web panel, between the ages of 3 and 90, participated. Participants took themselves blood samples and sent by post to the laboratory for processing of dried blood spot (DBS) and subsequent IgG antibody analysis against the SARS-CoV-2 spike-protein. Participants' vaccine status was collected from the national vaccination register, and previously reported cases were identified in the national notification system. In addition, background variables from the population register were analyzed in order to determine if they were associated with risk of contracting the infection.

Results :

In total, 32.8% (95%CI:30.6-35.1) had detectable antibodies against SARS-CoV-2. There was no statistical difference between genders. There was a higher proportion (p-value<0.05) of participants with antibodies in the age group 65+ years as compared to the other age groups, as expected since they have been a prioritized group for vaccination. Among non-vaccinated, 20.1% (95%CI:17.6-22.7) had detectable antibodies, with a higher proportion in the age group 11-19 years compared to 20-64 years (p-value<0.05). All participants that were fully vaccinated had detectable antibodies. The vast majority of participants with previously confirmed COVID-19, ranging from 81.7-97.8% (depending on the time from infection), had detectable antibodies.

Conclusions :

The study showed that approximately 33% of the population had detectable antibodies against SARS-CoV-2.

Subject : Surveillance
Keywords : seroprevalence, IgG antibody, surveillance, risk factors, COVID-19, population study
ABSTRACT ID: 331
PRESENTED BY: Jessica Beser / jessica.beser@folkhalsomyndigheten.se

c. Improving public health surveillance using automatic summarization

P. Fung [1]

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ESCAIDE

Poster Tour Abstracts

7,8,9 Center for Artificial Intelligence Research (CAiRE), The Hong Kong University of Science and Technology

Background :

The COVID-19 pandemic has been accompanied by an 'infodemic' posing unprecedented challenges and opportunities to health surveillance systems like that of the Epidemic Intelligence from Open Sources (EIOS) initiative. The volume of news articles processed by the system increased by nearly an order of magnitude, precluding human analysts from manually analyzing and assessing content. Automatic tools to assist public health analysts are urgently needed to make the workload more manageable. One such tool is automatic summarization, which can condense individual articles, as well as clusters of articles, into concise summaries.

Methods :

Abstractive summarization models (which involve paraphrasing the corpus using novel sentences) based on BART (a '...denoising autoencoder for pretraining sequence-to-sequence models...') were developed, tested and fine-tuned on single articles using a CNN/DailyMail dataset and on clusters of articles using a MultiNews dataset. The latter model underwent pre- and post-processing to better tailor it to the EIOS system.

Results :

The model was fine-tuned using 286,817 individual articles and 44,972 clusters of articles, together with their corresponding human-written summaries. F1 scores were around 44%, close to current state-of-the-art models indicating good performance and usability.

Conclusions :

Automatic summarization has been successfully integrated into the EIOS system, supporting public health analysts who are currently overwhelmed by the amount of information being published. This is one of the first applications of a state-of- the-art machine learning algorithm used for automated summarization in the domain of public health intelligence. The algorithm is being further tuned and additional use cases will be identified, based on the feedback from the analysts.

Subject : Surveillance
Keywords : Public Health , Machine Learning,Intelligence, Algorithms, Epidemics
ABSTRACT ID: 330
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d. Delta variant and mRNA Covid-19 vaccines effectiveness: higher odds of vaccine infection breakthroughs

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[5,6,7] Unilabs

Background :

Information on COVID-19 vaccines' effectiveness and viral loads in vaccine infection breakthrough cases are critical to inform decision-makers. Few studies have compared the effectiveness of mRNA vaccines against Delta versus Alpha variant of concern (VOC) and estimated variant-specific viral loads in vaccine infection breakthroughs cases.

Methods :

We developed a case-case study to compare mRNA vaccines' effectiveness against Delta versus Alpha variant using data on RT-PCR SARS-CoV-2 positive cases notified in Portugal during May-July 2021. The odds of vaccine infection breakthrough in Delta compared to Alpha cases were estimated by conditional logistic regression adjusted for age group, sex, matched by the week of diagnosis. RT-PCR cycle threshold values (Ct values) were compared by vaccination status and variant as an indirect measure of viral load and infectiousness.

Results :

We report a statistically significant higher odds of vaccine infection breakthrough complete vaccination (OR=1.96; CI95% 1.22 to 3.14) in the Delta cases when compared to the Alpha cases. We observed that Delta variant cases revealed a Ct-value mean increase of 2.24 (CI95% 0.85 to 3.64) between unvaccinated and fully vaccinated breakthrough cases contrasting with 4.49 (CI95% 2.07 to 6.91) in the Alpha VOC.

Conclusions :

We found significantly higher odds of vaccine infection breakthrough in Delta when compared to Alpha cases, suggesting lower effectiveness of the mRNA vaccines in preventing Delta variant infections. Additionally, the vaccine breakthrough cases are estimated to be of higher mean Ct values, suggesting higher infectiousness with the Delta variant infection. These findings can help decision-makers weigh on the application or lifting of control measures and adjusting vaccine roll-out depending on the predominance of the Delta variant and the coverage of partial and complete mRNA vaccination.

Subject : Surveillance
Keywords : Severe acute respiratory syndrome coronavirus 2, B.1.1.7 variant, B.1.617.2 variant, vaccine effectiveness
ABSTRACT ID: 309
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e. [late breaker] SARS-CoV-2 attack rate during air travel: results from 46 flights traced by the German health authorities, January - March and June - August 2020

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Background :

Evidence on the risk of SARS-CoV-2 transmission during air travel is scarce. We aimed to estimate the attack rate for wild-type SARS-CoV-2 to improve the evidence base for the adaptation of non-pharmaceutical intervention (NPI) strategies aboard airplanes.

Methods :

In collaboration with German Public Health Authorities (PHA), we conducted a follow-up on on-flight SARS-CoV-2 contact persons that the Emergency Operations Centre at the Robert Koch-Institute had forwarded to the PHA between January to March 2020 (before masking on flights became mandatory) and June to August 2020 (after mandatory masking). We retrospectively collected data on whether these contact persons had been successfully contacted, become symptomatic, tested for SARS-CoV-2 and whether alternative exposures other than the flight were

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known.

Results :

Complete data that allowed for the calculation of attack rates were available for 108 contact persons (median age of 36 (IQR 24-53), 40% female), traveling on 46 flights with a median flight duration of 3 hours (IQR 2-3.5). 62 of these persons travelled after masking on flights became mandatory. 13/87 developed symptoms, 44/77 were tested (no data for 21 and 31 respectively). 13 persons (9 SARS-CoV-2 test positives) were excluded from analysis due to a likely alternative exposure. We thus identified 4 probable on-flight transmissions (2 after mandatory masking). The overall attack rate resulted in 4.2% (4/95; 95% CI: 1.4% - 11.0%). Considering only flights after mandatory masking, the attack rate was 3.6% (2/56, 95%CI 0.6% - 13.4%).

Conclusions :

Risk of wild-type SARS-CoV-2 transmission during air travel seemed low, but not negligible. In order to formulate an effective, evidence-based NPI protocol for air travel, further studies considering SARS-CoV-2 variants of concern and vaccination status are needed.

Subject : International health and migration

Keywords : SARS-CoV-2, attack rate, flight, COVID-19, air travel

ABSTRACT ID: 304

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f. [late breaker] LongCOVID Kids study: long-term effects of COVID-19 in children in the Netherlands

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Background :

Long-term effects of COVID-19 in children remain unclear and pediatric studies are scarce. This study assesses characteristics and impact of persistent symptoms after acute COVID-19 (long COVID) in children aged 5-18 in the Netherlands.

Methods :

In this ongoing cohort study, children with existing long COVID symptoms are retrospectively included from 24 June 2021 via self-registration on the LongCOVID study website. Characteristics and impact of long COVID symptoms are assessed by validated questionnaires, mainly focusing on fatigue, pain, shortness of breath, cognitive functioning and impact on daily life and school attendance.

Results :

Until 13 September 2021, 69 children reporting long COVID symptoms (median age 14 (range 5-17; 62% female) were included, among which fatigue (74%), headache (55%), concentration difficulties (33%) and difficulties in busy places (33%) were most frequent, with a median duration of symptoms of 6 months at inclusion time (range 0.4-16). None were hospitalised during the acute phase of infection. The majority of children aged ›10 (39/50;78%) indicate these symptoms have large impact on their lives, and 51% of all children are absent from school at times, or are not able to go to school at all (7%) because of their symptoms. In 4 weeks prior to inclusion, these children have missed on average 8 full school days (range 0-20) and missed classes on another 10 days (range 1-20).

Conclusions :

Even after relatively mild acute infection, children report long COVID symptoms that have great impact to their daily life and school attendance. To improve our insight into prognosis and burden of disease related to COVID-19 in children, prospective cases with acute COVID-19 will be also assessed for development of long COVID symptoms, which is key for policy-making.

Subject : Burden of disease

Keywords : long COVID, COVID-19, SARS-CoV-2, Children, Persistent symptoms

ABSTRACT ID: 313

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ESCAIDE

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Poster tour 18
HIV, sexually transmitted infections and viral hepatitis

Abstracts

a. Drop in prescriptions for treating hepatitis C in Germany during the early phases of the COVID-19 pandemic in 2020

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Background :

Early treatment of hepatitis C (HCV) prevents severe sequels and transmission. In Germany HCV drug prescriptions decline since 2015. During the COVID-19 pandemic, temporary closures of HCV treatment facilities could have further reduced HCV treatment, impacting negatively HCV morbidity and mortality. Therefore, we assess if a HCV treatment gap occurred in Germany in 2020.

Methods :

Monthly HCV drug prescription data from pharmacies for patients with statutory health insurance (approx. 90% of population) was assessed. Log-linear models were built with data from 01/2018-02/2020 (=pre-pandemic) to calculate 95%CI for expected prescriptions for 01/03/2020-31/12/2020 and the pandemic phases (first wave: calendar months(CM) 3-5; summer:CM6-9; second wave: CM>9), with all data and stratified for the prescriber's specialisation.

Results :

In Germany, 13,394 monthly HCV treatment regimens were prescribed 01/03/2020-31/12/2020, as expected (13,227-15,070) based on a monthly 2% reduction (p<0.001) since 01/2018. These were 4,368 regimens less than in 2019, just as predicted (2,547-4,684). Regimens were mainly prescribed by internists (n=8,818;66%), outpatient clinics (n=2,233;16%) and general practitioners (GPs, n=2,094;16%). While they all prescribed less than expected during the first wave (total: 4,065 vs. 4,229-4,720; internists:2,749 vs. 3,656-3,889; outpatient clinic:571 vs. 964-1,105; GP:660 vs 762-826) and in summer (total:5,214 vs. 5,285-6,024; internists:3,386 vs. 4,062-4,300; outpatient clinic: 933 vs. 1,043-1,183; GP:798 vs. 901-971), they prescribed at expected levels during the second wave (total: 4,115 vs. 3,713-4,326; internists:2,683 vs. 2,489-2,719; outpatient clinic:729 vs. 609-740; GP:636 vs. 585-657).

Conclusions :

HCV prescriptions in 2020 fell within the lower realm of expected counts. However, all specialties prescribed less during the first wave and summer, indicating a ubiquitous HCV treatment gap. Later, prescriptions met expectations, indicating that services adapted. In future pandemics, services need to adopt sooner to maintain continuous care.

Subject : Burden of disease
Keywords : Hepatitis C, COVID-19, Anti-retroviral agents, Delivery of Health Care
ABSTRACT ID: 34

b. The STI re-emergence in Catalonia (2017-2019): epidemic characterization, socio-epidemiological clustering approach, and HIV co-infection associated factors

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Background :

The objectives of this study were to describe the epidemiological characteristics of the STI-cases, to identify STI-HIV coinfection associated factors, and to identify and characterize STI socio-epidemiological clusters in Catalonia from 2017 to 2019.

Methods :

We performed a descriptive analysis of STI-confirmed cases (chlamydia,

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gonorrhea, syphilis, and LGV) using all notified STI and HIV cases. Factors associated with HIV coinfection were determined using logistic regression. We identified and characterized STI socio-epidemiological clusters by basic health area (ABS) using K-means clustering methodology.

Results :

The STI cases were doubled, primarily due to the increase in chlamydia and gonorrhea in women and people younger than 30 years of age, 11% were reinfections, and 6% coinfected with HIV. Men, aged 30-60, living in urban and less deprived ABS, and having multiple STI episodes were associated with an increased risk of HIV coinfection. When comparing the distribution of proportions of socio-epidemiological characteristics' in the overall STI-cases with those within the three clusters of ABS identified (A, B, and C), we found in A) similar distribution-values; B) a higher proportion of chlamydia, women, younger people, heterosexuals, and people living in rural and more deprived areas; and C) higher incidence rates for all STI, higher proportion of MSM, multiple episodes, HIV coinfection, and higher proportions of people living in urban and less deprived areas.

Conclusions :

STI increased dramatically in Catalonia from 2017 to 2019, mostly in women and young people. We identified and characterized three socio-epidemiological clusters, which, along with the associated HIV confection factors, provides a characterization of key populations at a small area level that may allow designing effective measures to enhance STI/HIV prevention and control.

Subject : Surveillance

Keywords : Communicable Disease Control, Epidemiological Monitoring, Cluster Analysis, Sexually Transmitted Diseases, HIV Coinfection

ABSTRACT ID: 143

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c. Trends in Shigella among men who have sex with men following COVID-19 restrictions

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Background :

Shigella spp. is an enteric bacterial pathogen transmitted via the faecal-oral route, causing dysentery. Cases are often travel associated but a high proportion of domestically acquired cases are sexually transmitted among men who have sex with men (MSM), with Shigella flexneri and Shigella sonnei alternating as the most reported species. The study objective was to examine data on Shigella spp., exploring the impact of UK-wide COVID-19 restrictions, and which species and genotypic clusters have continued to circulate among MSM.

Methods :

We analysed data on Shigella spp. isolates referred to the national reference laboratory, between 2019 and 2020. We included adult men (≥16 years) without a recent history of foreign travel as a proxy for presumptive MSM transmission. A genotypic cluster was defined as two or more cases whose isolates varied by 10 single nucleotide polymorphisms or fewer.

Results :

There was a 40% decrease in reported Shigella diagnoses among presumptive MSM in 2020 compared to 2019 (379 vs 628). A decline was seen in both S.sonnei and S.flexneri, but the decrease was more marked in S.sonnei (-90%, from 51 in Q1 2020 to 5 in Q3 2020, compared to -30%, from 86 to 60 in S.flexneri). Three dominant serotypes of S.flexneri (1b, 2a and 3a) emerged as genotypic clusters and persisted throughout 2020.

Conclusions :

The implementation of COVID-19 control measures corresponded with a decrease in Shigella diagnoses in 2020, yet three clusters of S.flexneri remained in circulation. The reduction in diagnoses likely reflects compliance to social distancing measures leading to fewer infections, alongside fewer accessing services. However, further research is required to explore the characteristics of the three S.flexneri clusters to understand why they have prevailed among MSM.

Subject : Surveillance

Keywords : Shigella, Sexually Transmitted Diseases, Epidemiologic Surveillance, Shigella flexneri, Shigella sonnei

ABSTRACT ID: 82

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d. Impact of COVID-19 control measures on testing and notification trends of syphilis and gonorrhoea in New Zealand

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Background :

As COVID-19 reached New Zealand (NZ), the government became aware that testing and contact tracing capacity was low to mitigate the virus. A strict nationwide lockdown on March 26th was implemented; after 5 weeks NZ eased lockdown measures, and after 7 weeks the de-facto national stay-at-home order was lifted. During lockdown, community-transmission control measures were introduced including cancelling public events, restricting gatherings, stay-at-home policies, restricting internal movements, and reprioritising health services. Most primary care interactions were remote, and lab testing (including for sexually transmitted infections) was reduced to allow for increased SARS- CoV2 testing. Our objective was to quantify testing and case-positivity temporal trends by demographics and risk groups, and to highlight the impact COVID-19 control measures have had on these trends.

Methods :

NZ collects all laboratory results for gonorrhoea and relies on clinician notification for syphilis. We analysed all notifications of gonorrhoea and syphilis from 2013-20 using R.

Results :

Syphilis notifications peaked in early-2019, and have significantly declined every quarter since (p<0.05), with COVID-19 having little impact. While gonorrhoea notifications increased by 30% in Jan/Feb 2020 compared to 2019, during the lockdown month of April, notifications decreased by 48% compared to 2019. The case-positivity rate for gonorrhoea doubled during lockdown (>8%), before returning to 4-5%. The decrease in testing and notifications was proportional by sex, age and ethnicity; some differences were noted by region.

Conclusions :

Syphilis notifications were not impacted by COVID control measures; clinical care was maintained throughout. Gonorrhoea testing and case-positivity were markedly affected during lockdown, but returned as expected post- lockdown. No additional concerns in equity of care were identified as a result of the COVID-19 lockdown.

Subject : Surveillance

Keywords : COVID-19, Gonorrhoea, Syphilis, notification, laboratory

Poster Tour Abstracts

testing, lockdown
ABSTRACT ID: 20
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e. A pilot sentinel surveillance to monitor the treatment of chronic hepatitis B and C infections in European centres in 2019

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Background :

Chronic hepatitis B (HBV) and hepatitis C (HCV) infections cause approximately 64,000 deaths annually within the European Union and Economic Area. Targets for hepatitis elimination by 2030 require 75% of eligible patients to be treated and 90% to have achieved viral suppression. We report on a pilot sentinel surveillance system to monitor progress in achieving treatment targets of individuals with chronic HBV and HCV infections.

Methods :

The sentinel surveillance required retrospective enhanced reporting of patients presenting at seven pilot clinics in three countries (Croatia, Romania and Spain). Clinical records of patients with a confirmed diagnosis of chronic HBV and/or HCV who presented for the first time between 1 January 2019 and 30 June 2019 were reviewed from date of first attendance through to 31 December 2019. Data were collected on socio-demography, clinical history, diagnostic and virological results, and treatment and treatment outcomes.

Results :

Of the 206 chronic HBV infections, treatment information was reported for 174 (84%) of whom 75 were reported as eligible for treatment and 37 were treated. The majority were reported as achieving viral suppression (84%; 31/37) and all were continuing treatment. Of the 316 chronic HCV infections, treatment information was reported for 298 of whom 184 (62%) were reported as being treated. The majority (177; 96%) were treated with Direct Acting Antivirals and nearly all (180; 97%) had ended treatment and had achieved (167; 91%) sustained virological response.

Conclusions :

Targets were missed for the initiation of treatment but were met for viral suppression of HCV but not HBV. The insights gained from this pilot justify its future expansion to monitor the progress in achieving hepatitis control targets which were not currently available nationally.

Subject : Surveillance
Keywords : Hepatitis B, Hepatitis C, Treatment, Sentinel surveillance
ABSTRACT ID: 132
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Poster tour 19
Vaccine preventable diseases: surveillance

Abstracts

a. First evaluation of completeness and sensitivity of the measles surveillance system in the Czech Republic from January 2018 to June 2019

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Background :

We evaluated completeness and estimated sensitivity of the measles surveillance using the new electronic version of the national notification system of infectious diseases (ISIN) in order to assess ISIN performance.

Methods :

We assessed the internal completeness of measles reporting in ISIN for demographic characteristics (week and region of reporting, age and gender), date of onset, complications, hospitalisations, vaccination status, used laboratory methods and country of import from January 2018 to June 2019. We used capture-recapture method (CRM) comparing datasets from National Reference Laboratory (NRL) and ISIN. Unique personal identifier was used to match the cases. The total number of measles cases in the population was assessed using the Chapman's formula. Sensitivity of reporting was assessed by dividing the number of reported cases by CRM estimated true number of cases.

Results :

In ISIN we found 100% completeness of many variables. The most missing data were on vaccination status (20%), serology results (55%) and laboratory methods (8%). ISIN had 765 measles cases registered. NRL confirmed 653 patient samples. In both systems 612 cases were matched. The CRM estimated total number of cases was 816 (95% CI: 809-823) compared to 806 reported cases. The estimated surveillance system sensitivity was 98.8%. Five percent (n=41) of cases positively tested in NRL were not reported to ISIN. Sources of data are not fully independent.

Conclusions :

We found high level of data completeness for many variables. We recommend technical changes (more mandatory fields and more logical syntax to check data) in ISIN to improve data completeness. Data providers will be reminded to report all measles cases into ISIN and send samples to NRL.

Subject : Surveillance
Keywords : Epidemiology, Surveillance, Public Health Surveillance, Measles
ABSTRACT ID: 74
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Poster Tour Abstracts

b. A simple tool for guiding decisions on roll-out and capacity management for the Danish COVID-19 vaccination programme

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Background :

The Danish Health Authority manages the Danish vaccination programme. When the first COVID-19 vaccines arrived in Denmark in week 52/2020, we needed an easy-to-develop and flexible tool to guide decisions on vaccine rollout, estimate how many persons to invite for vaccination and produce a weekly calendar with estimated vaccination week for each priority group defined in the national vaccination programme.

Methods :

Vaccine delivery schedules and number of vaccinated persons were obtained from Statens Serum Institute. Number of persons in each priority group was obtained from Statistics Denmark (age cohorts) or estimated based on three national registries (patient, income and healthcare authorization). Utilization rate and vaccine uptake was estimated for each vaccine. A tool was developed using Excel and data was collected daily. For quality control, similarity between Area Under the Curve (AUC) for estimated and actual first-dose vaccinations was monitored.

Results :

On 08/01/2021, we published a national vaccination calendar which has since been modified due to policy decisions, delivery schedule changes and inaccurate priority group estimates. Our tool was used for scenario planning and policy- making e.g. discontinuing the Vaxzevria® vaccine. From week 52/2020-week 13/2021, our tool also provided data for weekly announcements to the five Danish regions regarding the number of persons to invite for vaccination among priority groups. By week 13/2021, 85,810 persons had received at least one dose, and estimations were similar to the actual number of persons vaccinated per week (0.52% difference between AUCs).

Conclusions :

A simple and flexible Excel-based tool was useful to guide essential decisions on vaccine rollout at national and regional level and provided accurate estimates for the number of persons to invite for first dose vaccinations among priority groups in Denmark.

Subject : Surveillance
Keywords : COVID-19, vaccination, capacity management, surveillance, estimates
ABSTRACT ID: 142
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c. Vaccines protect from severe COVID-19 – results of case-case comparison in Bavaria, Germany, between January and March 2021

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Background :

In Bavaria, COVID-19 vaccination started late December 2020, prioritizing according to Standing Committee on Vaccination (STIKO) recommendations. Efficacy of STIKO-recommended vaccines was 63% to 95% in protecting against any clinical, laboratory-confirmed COVID-19 disease according to phase III clinical trials. We aimed to assess vaccine effectiveness, comparing disease outcomes between fully and incompletely vaccinated SARS-CoV-2 cases. Incompletely vaccinated cases served as comparison group as they are similar to fully vaccinated cases in terms of vaccination eligibility criteria while they are not fully protected from disease yet.

Methods :

We included PCR-confirmed SARS-CoV-2 cases, notified to the Bavarian Health and Food Safety Authority between 26.12.2020-01.04.2021. We compared odds of severe disease (dyspnea, pneumonia or acute respiratory distress syndrome), all-cause hospitalization and death in fully vaccinated cases (diagnosis ≥14 days after second vaccination) and incompletely vaccinated cases (diagnosis ‹10 days after first vaccination) using multivariable logistic regression, adjusting for age group, sex and infection with a variant of concern (VoC).

Results :

Among 167,127 notified SARS-CoV-2 cases ≥18 years of age, 461 were fully and 1,024 incompletely vaccinated. The median age was 76 (IQR:49-87) and 57 (IQR:42-81) years, respectively. Among fully vaccinated, 16/362 (4.4%) had severe disease, 56/386 (14.5%) were hospitalized, 25/461 (5.4%) died; among incompletely vaccinated, 65/898 (7.2%), 120/937 (12.8%) and 87/1024 (8.5%), respectively. The adjusted odds of severe disease, hospitalization and death were lower for fully compared to incompletely vaccinated cases (OR=0.32 (95%CI: 0.17-0.57), OR=0.70 (95%CI: 0.47-1.03) and OR=0.47 (95%CI: 0.26-0.74)).

Conclusions :

These results suggest that full vaccination is effective in reducing the risk of severe COVID-19. Nevertheless, temporal effects due to vaccination prioritization and emergence of VoC during the study period still have to be considered.

Subject : Surveillance
Keywords : SARS-CoV-2,COVID-19,Vaccines,Vaccination
ABSTRACT ID: 103
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d. High influenza vaccination coverage among healthcare workers in acute care hospitals in Finland, 2017-2020

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Background :

Despite the public health relevance of influenza vaccination for healthcare workers (HCWs) coverage isn t high enough in most European countries. In Finland a new act was introduced in 2017, according to which it is the employer's responsibility to use only vaccinated HCWs for servicing vulnerable patients. Only one national survey on this issue has previously

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been conducted in 2014 showing also low coverage (41%; range 18-86) although only one third of acute care hospitals monitored coverage at the time. We determined the influenza vaccination coverage among HCWs in Finnish acute care hospitals in the three seasons following the introduction of this act, 2017/18, 2018/19 and 2019/20.

Methods :

We analyzed data collected by a web-based survey sent annually to all Finnish acute care hospitals and described the influenza vaccination coverage among HCWs during these seasons. We calculated mean coverage per health care district and season.

Results :

In season 2017/2018, 38/39 hospitals, in 2018/19, 35/36 hospitals and in 2018/2019 31/33 hospitals provided data. The mean coverage was 83.7% (range: 65.5-95.0) in season 2017/18, 90.8% (range: 57.0-98.0) in 2018/19, and 87.6% (range: 72.0-99.3) in season 2019/20. There was no significant increase or decrease of mean coverage across the three seasons. The differences between districts were only significant in 2018/19 (p<0.005).

Conclusions :

The coverage of influenza vaccinated HCWs in Finnish hospitals was high in all three seasons and the current legal situation in Finland seems to provide a good background for this, as coverage clearly increased between 2014 (before the introduction of the law) and 2017/18 (after the introduction of the law) and has remained high thereafter. HCW influenza vaccination coverage surveillance remains important and should be continued.

Subject : Surveillance

Keywords : influenza, surveillance, vaccination, vaccination coverage, healthcare workers

ABSTRACT ID: 28

PRESENTED BY: Charlotte Hammer / charlotte.hammer@thl.fi

e. Does Health Care Workers' Reluctance for Vaccines extend to COVID-19 Vaccines? - A cross-sectional Survey among Health Care Workers from Hospitals in Germany in March 2021

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Background :

Health Care Workers (HCWs) are central to the success of the COVID-19 vaccination efforts. However, research consistently showed that a substantial fraction of HCWs refuses vaccinations in general. Even in an emergency, during the 2009 H1N1 pandemic, vaccination intention among HCWs was very low. Will HCWs accept COVID-19 vaccines?

Methods :

In March 2021, we conducted a cross-sectional online survey with HCWs from 123 hospitals in Germany. Beyond information on vaccination status and intention to be vaccinated against COVID-19, we collected reasons pro/contra vaccination and utilized the 5C-scale to assess psychological antecedents of vaccination. We weighted the sample based on the 2019 government HCWs census and analyzed the data descriptively.

Results :

Of the 26,080 participants, 83.2% [82.7-83.6%] had already received at least one vaccine dose and 9.8% [9.5 – 10.2%] were not vaccinated but reported strong intention to be vaccinated. However, 7.0% [6.7-7.3%] refused vaccination or were hesitant. This group stated 'wanting to wait' (58.1% [55.8 – 60.0%]), fear of 'lasting health damage' (53.0% [50.7 – 55.0%]) and 'strong side effects' (49.4% [47.1 – 51.7%]), and distrust in 'new vaccination-technologies' (49.0% [46.7 – 51.2%]) as reasons. Compared to the vaccinated, they also scored higher in complacency (median 2 vs 1) and lower in confidence (2 vs 6) [Mann-Whitney-U, p

Conclusions :

Unlike in previous crises, overall, COVID-19 vaccines were well accepted among HCWs and the majority of HCWs in German hospitals were already vaccinated. However, a considerable fraction refused or hesitated to be vaccinated. Because HCWs serve as role models for health behavior for the general population, this may have a lasting negative impact on the pandemic response. Addressing distrust and fear in HCW may be key to ensure long-term success of COVID-19 vaccination campaigns.

Subject : Surveillance

Keywords : Covid-19,Health Care Worker, HCW, Vaccine hesitancy, vaccination, pandemic response

ABSTRACT ID: 106

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Poster Tour Abstracts

Poster tour 20
Preparedness

Abstracts

a. Meteorological conditions and Legionnaires' disease - a systematic review

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Background :

A number of studies suggest that meteorological conditions are related to the risk of Legionnaires' disease (LD) but the findings are not consistent. Identifying which conditions influence disease occurrence can improve differential diagnosis for community-acquired pneumonia and surveillance of LD. A systematic review was conducted to describe the evidence on the association of weather with sporadic LD and highlight the key meteorological conditions related to this outcome.

Methods :

PubMed, EMBASE, The Cochrane Library and OpenGrey were searched on 26-27 March 2020 without date, language or location restrictions. Key words included "legionellosis", "legionnaires' disease", combined with "meteorological conditions", "weather", "temperature", "humidity", "rain", "ultraviolet rays", "wind speed", etc. The study was conducted according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines and it was registered in PROSPERO (#CRD42020168869).

Results :

811 articles were identified, of which 17 were included in the qualitative synthesis. The studies investigated different meteorological variables and most of them examined the combined effect of several meteorological variables. The most commonly examined factors were precipitation (15/17) and temperature (15/17), followed by relative humidity (12/17). The studies suggested that increased precipitation, temperature and relative humidity were positively associated with the incidence of LD. There was weak evidence that higher wind speed, UV radiation and longer sunshine duration were inversely linked with the occurence of LD.

Conclusions :

A period of increased but not very high temperatures, followed by a period of increased precipitation, favour the occurrence of LD. Taking weather conditions into account helped explain the epidemiological patterns of LD sporadic cases. Increased awareness on the contribution of weather conditions among clinicians and public health professionals can improve diagnosis and enhance surveillance of LD.

Subject : Preparedness (e.g. preparedness planning, simulation exercises, after action reviews)
Keywords : Legionnaires' Disease,Legionellosis,Weather,Meteorological Factors,Systematic Reviews
ABSTRACT ID: 63
PRESENTED BY: Despina Pampaka / d.pampaka@gmail.com

b. Experiences from the first state-run quarantine for SARS CoV-2 in 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, February 2020. Main stakeholders involved in the management of the quarantine were local district, local public health authority, German Red Cross and the Bundeswehr. This study aims at improving state-run quarantines by providing lessons learnt.

Methods :

By applying grounded theory, the first author provided input through observation and conducted six semi-structured interviews between April 2020-March 2021, to understand stakeholders' perceptions and experiences. Through open and axial coding, themes were identified such as hygiene and health management, communication at and between different levels, waste management, infrastructure, governance, professional qualifications needed and legal aspects.

Results :

The legal jurisdiction to manage and implement the quarantine was identified as a major problem, since responsibilities were not clear between the stakeholders. Initial challenges were lack of hygiene and waste management plans. All stakeholders felt that they had insufficient experience with the emergency management of biological threats in the given setting. Communication was perceived as challenging and often parallel in a situation with a lot of pressure from outside, different working cultures, and non-defined responsibilities. Established personal relationships and professional networks were advantageous in managing the quarantine.

Conclusions :

Globally, state-run quarantines have been regularly used to prevent transmission from travellers or to avoid household infections if isolation is not feasible at home. Legal jurisdiction and responsibilities in state-run quarantines need to be clarified in Germany. Training of stakeholders in emergency management of biological threats is necessary. Standard operating procedures for the implementation of a state-run quarantine including hygiene and waste management should be defined.

Subject : Preparedness (e.g. preparedness planning, simulation exercises, after action reviews)
Keywords : Quarantine, repatriation, SARS-COV-2, evacuation, pandemic
ABSTRACT ID: 180
PRESENTED BY: Kathrin Schaten / schatenk@gmail.com

Poster Tour Abstracts

c. Mapping the risk of dengue in Spain

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Background :

The establishment of Aedes albopictus in Spain, its spread into new areas and the presence of dengue imported viraemic cases, pose an increasing risk of local dengue transmission. Mapping the risk of local dengue transmission can guide future preparedness measures for controlling the disease.

Methods :

Environmental, entomological, epidemiological, demographic, tourism and travel data were analysed to produce a series of maps to represent: (i) the distribution of Ae. albopictus across municipalities; (ii) the risk of expansion of Ae. albopictus; (iii) the calculated index of travelers from dengue-endemic areas (IDVZE) per province; (iv) and the percentage contribution of each municipality to the total number of cases in Spain. Using algebra map tools, a final map was plotted to present the risk of autochthonous dengue in Spain at a municipal level from 2016 to 2018.

Results :

Ae. albopictus was detected in 983 municipalities, distributed mostly in the Mediterranean area. Municipalities in Madrid and Barcelona contributed the most to the total number of notified imported dengue cases. The highest IDVZE was observed in Madrid. The overall risk of autochthonous cases was higher in the Mediterranean region, mainly in the Levantine coast and some parts of the Balearic Islands. Most of the interior of the peninsula was characterised as low risk.

Conclusions :

Preparedness and response plans integrating all sectors and stratifying risk areas to mitigate the risk of autochthonous dengue should be established, prioritising early detection and follow-up of imported dengue cases and vector control measures, especially in higher risk areas such as the Mediterranean coast of Spain.

Subject : Modelling, bioinformatics and other biostatistical methods

Keywords : Dengue, Dengue virus, Travel-Related Illness, Geographic Mapping, Spain

ABSTRACT ID: 65

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d. Identifying the sectors involved in public health emergency preparedness and response: a systematic review

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Background :

The COVID-19 pandemic has highlighted the need for a multisectoral approach to public health emergency preparedness and response (PHEPR). Although the International Health Regulations (2005) and the EU Decision 1082/2013/EU have called for integration of multisectoral collaboration in all hazard PHEPR plans, literature on this is limited. Hence, this review aims to identify sectors that have been involved and/ or should be involved in collaboration during past PHEPR, as well as the domains within which collaboration occurred.

Methods :

For this systematic review, a detailed search was done in EMBASE and Scopus databases in March 2020, while using a combination of MeSH terms referring to public health emergencies, collaboration, preparedness and response. Articles published between the 1st of January 2005 and the 1st of January 2020, focusing on preparedness for, and/or response to public health emergencies of different origins affecting human health were included. The frequency with which sectors were named when describing PHEPR activities and collaboration was determined.

Results :

An analysis of the 94 included articles showed that four of the 28 sectors 'Governmental institutions', 'Human health industry', 'Experts' and 'Civil society' were named most frequently when describing both PHEPR in general, and collaboration during PHEPR. Furthermore, collaborations were named most frequently when describing activities within the PHEPR domains 'Risk and crisis management', 'Pre-event preparations and governance', and 'Surveillance'.

Conclusions :

Only a limited amount of sectors are frequently named when describing collaboration during PHEPR. Furthermore, sectors collaborate in a limited number of preparedness and response domains. The COVID-19 pandemic has shown that current practices require re-evaluation. Hence, when designing and implementing multisectoral collaboration in PHEPR plans, a more systematic approach is necessary to evaluate the involvement of relevant sectors.

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

Keywords : all hazard,public health emergency ,collaboration,preparedness,response

ABSTRACT ID: 126

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e. [late breaker] WHO's role in enhanced public health intelligence for the Tokyo 2020 Olympic and Paralympic Games during the COVID-19 pandemic, July to September 2021

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Poster Tour Abstracts

Mahran [7], M. Yanagawa [8], J. Lorenzo [9], A. Awofisayo-Okuyelu [10], R. Mizushima [11], E. Peron [12], M. Borodina [13], A. Artazcoz Glaria [14], A. Gabrielli [15], A. Takemi- Matsuura [16], J. Fontaine [17], P. Abdelmalik [18], M. Barbeschi [19], E. Hamblion [20], B. Olowokure [21]

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Background :

Mass gatherings present significant challenges for the health sector. Robust disease surveillance is essential for early detection, assessment and response to health-related events particularly during a pandemic when global events, such as the Olympics, may contribute to increased transmission, strain on healthcare capacity, and seeding of outbreaks globally. WHO's role in supplementing Japan's public health intelligence (PHI) activities through event-based surveillance (EBS) during the Tokyo 2020 Olympic and Paralympic Games is described below.

Methods :

WHO conducted EBS for public health threats including COVID-19 across WHO/UN member states, territories and areas employing an all-hazards approach. The Epidemic Intelligence from Open Sources (EIOS) system was used to detect signals of public health concern, which were assessed for impact on the Games and need for response in line with the International Health Regulations.

Results :

Between 30 June and 6 September 2021, 43,160 COVID-19-related articles and 96,000 non-COVID-19-related articles were screened from which we identified 134 and 587 signals, respectively. While most signals described COVID-19 cases within the Olympics "bubble", one signal was detected reporting three exported COVID-19 cases linked to the Games, and one alert on tropical storm Nepartak, resulting in some rescheduled games. Most signals carried moderate risk of impact on the Games and none required IHR notification. Findings were shared daily through 56 reports.

Conclusions :

The Tokyo 2020 Games was the first global, large-scale sporting event during a pandemic, and necessitated strong communication and coordination between host-country government and WHO including early planning for EBS and identification of signal scope. EIOS was found to be a useful tool for enhanced PHI and enables effective preparedness and response planning for mass gatherings, like the Olympics, during health emergencies.

Subject : Surveillance
Keywords : Public health, emergencies, World Health Organization, International Health Regulations, pandemics, intelligence
ABSTRACT ID: 337
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Poster tour 21
COVID-19: surveillance

Abstracts

a. Analysis of COVID-19 outbreak alerts generated in school settings in Slovenia, February-April 2021

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Background :

Spread of SARS-CoV-2 in the local community in Slovenia has led to outbreaks in school settings. The purpose of this study is to analyze outbreak alerts in school settings by level education in order to advice control measures.

Methods :

We analyzed data from the comprehensive covid-19 outbreaks surveillance system in Slovenian schools from February- April 2021 when kindergartens were normally open, and students returned to primary and secondary school gradually. Schools are required to notify the National Institute of Public Health of an outbreak when within 14 days: (A1) ≥15% of students in bubble have a confirmed infection; (A2) ≥10% of employees have a confirmed infection; (A3) confirmed cases occurred in ≥3 bubbles (fixed children groups). Outbreak alerts were considered as new if at least 14 days had elapsed from the previous alert.

Results :

Outbreaks were detected in 42/400 kindergartens, 71/454 primary schools and 16/155 secondary schools. The most common outbreak alert was A3, 35%, 60% and 71% in kindergartens, primary and secondary school, respectively. For A1 alerts: 12%, 21% and 29% and for A2 alerts: 54%, 19% and 0%.

Conclusions :

Most commonly outbreaks in schools were due to multiple external introductions of the pathogen. Spread in a single bubble was most common in secondary school were socialization patterns go beyond the contacts in the school setting. Due to the close contact of teachers in lower level of education spread among staff was more common. In secondary schools additional control measures should be considered to prevent spread inside a bubble. As socialization inside and outside school setting in paramount novel approaches such as self-testing could be considered to improve safety.

Subject : Surveillance
Keywords : covid-19,outbreaks,surveillance,schools,education
ABSTRACT ID: 258
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b. Detection and investigation of potential SARS-CoV-2 reinfections within the SIREN study

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Poster Tour Abstracts

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Background :

Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) reinfection cases have been reported internationally but remain rare. Large longitudinal cohort studies, such as the SARS-CoV-2 Immunity and Reinfection Evaluation (SIREN) multicentre study, which is following over 44,000 healthcare workers for a year, will provide valuable insight into characteristics of reinfections. We describe the protocol for investigating reinfections within SIREN.

Methods :

Participants undergo fortnightly nucleic acid amplification testing and monthly antibody testing at their site of enrolment and complete fortnightly questionnaires on symptoms and exposures. Test results are reported to the national surveillance system. Personal identifiable data collected at enrolment links participants to the national SARS-CoV-2 testing dataset, including historical results. A daily query identifies potential reinfections meeting the following criteria: two positive RT-PCR tests at least 90 days apart or a new RT-PCR positive test at least four weeks after a positive SARS-CoV-2 antibody test. Additionally, SIREN sites must report potential reinfections detected locally. Further details on testing and symptoms are collected, and a self-swab is obtained from the participant, for sequencing and viral culture. Quantitative antibodies testing against SARS-CoV-2 is performed on sequential serum samples. Cases are then allocated as possible, probable, confirmed or excluded, dependent on the hierarchy of evidence after clinical review.

Results :

As of 04 May 2021, among 338 potential reinfections detected within SIREN, 67 were excluded at initial screening. 215 cases had at least one quantitative serology result and were further classified as the following: 6 confirmed cases, 21 probable cases, 165 possible cases (including 97 where analysis is still on-going) and 23 cases excluded.

Conclusions :

SIREN has enabled the detection and systematic characterisation of the largest cohort of reinfections yet reported.

Subject : Surveillance
Keywords : SARS-CoV-2, Reinfection, Surveillance, Cohort Studies
ABSTRACT ID: 215
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c. SARS-CoV-2 seroprevalence in Portugal after the 3rd COVID-19 epidemic wave

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Background :

Serological surveys represent a crucial tool for monitoring COVID-19 pandemic burden and an insight on the level of immunity of the population. The Second Nationwide COVID-19 Serological Survey (ISN-COVID-19) in Portugal was conducted between February-March 2021, after the peak of the 3rd epidemic wave, and aimed to characterize the extent of SARS-CoV-2 infection and vaccine-induced humoral response within the Portuguese population, providing information to guide health interventions.

Methods :

The ISN-COVID-19 is a cross-sectional study. A non-probabilistic sample of 8,463 Portuguese residents aged 1-79 years was recruited among users of laboratories and hospitals. Sociodemographic, epidemiological and clinical data, and serum samples, were collected from each participant. Detection of SARS-CoV-2 specific IgM (anti-spike protein) and IgG (anti-nucleocapside protein) was performed with commercial chemiluminescent microparticle assay. SARS- CoV-2 specific IgG (anti-spike protein) antibody levels were quantified in positive IgM and/or IgG and vaccinated participants.

Results :

National seroprevalence was 15.5% (14.6–16.5%), being 13.5% (12.6–14.4 %) attributed to previous infection. The lowest seroprevalences were estimated for Algarve (7.7%), Madeira (6.2%) and Azores (5.8%) and among people aged 70-79 years (8.9%). IgG levels were higher among vaccinated individuals (2 doses) compared with those partially vaccinated or previously infected. Among unvaccinated individuals, IgG levels were higher if a symptomatic infection was reported and if it occurred 31-90 days before recruitment.

Conclusions :

Estimated SARS-CoV-2 seroprevalence was consistent with the intense COVID-19 epidemic observed in Portugal after October 2020. Considering the waning of antibodies after 90 days, this seroprevalence might underestimate the real COVID-19 attack rate. Nevertheless, it was 1.7-fold higher than COVID-19 incidence rate. Considering the elevated proportion of seroconversion after 2 doses of the vaccine, SARS-CoV-2 seroprevalence at population level may increase in the forthcoming months.

Subject : Surveillance
Keywords : Seroprevalence, SARS-CoV-2, Immunity, Portugal
ABSTRACT ID: 149
PRESENTED BY: Ana Paula Rodrigues / ana.rodrigues@insa.min-saude.pt

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d. Monitoring the introduction and spread of SARS-CoV-2 variants of concern in Lombardy (northern Italy) in 2021

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Poster Tour Abstracts

Romagna (I.Z.S.L.E.R.)_Brescia

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Background :

Implementation of genome sequencing of SARS-COV-2 in surveillance schemes, is essential to monitor variants circulation and to inform on adequate public health measures. We present the results of the sequencing activities to monitor the introduction of SARS-CoV-2 Variant of Concern (VOC) and Variants of Interests (VOI) in Lombardy region (northern Italy) from February to April 2021.

Methods :

A consortium of virological laboratories was set up in Lombardy for SARS-CoV-2 sequencing. Four surveys, coordinated by the Italian National Public Health Institute, aimed at estimating the point prevalence of VOC (B.1.1.7, P.1, and B.1.351 lineages) and other VOI were conducted on 10 February (Survey#1), 18 February (Survey#2), 18 March (Survey#3), 20 April (Survey#4). SARS-CoV-2-positive samples were selected randomly according to geographical representativeness.

Results :

1,050 SARS-CoV-2 positive samples were successfully sequenced. Overall, B.1.1.7 lineage predominated over the others (72%). On Survey#1, B.1.1.7 lineage accounted for 34.5% sequences, increasing up to 89% (P<0.0001) on Survey#3 and #4. On Survey#1, B.1.1.7 lineage point prevalence was higher in eastern (Brescia, 57%) and north- western (Varese, 36.4%) areas; it then increased significantly on Survey#3, with an east-to-west spread. B.1.351 lineage was detected during Survey#2 (2.2%% Milan and 1.9% Brescia) and Survey#3 (0.8%, Milan). P.1 lineage was identified on Survey#4 only (point prevalence=2%). Lineage B.1.525 was detected in Survey#3 and Survey#4 with a point prevalence of 0.9% and 1.3%, respectively.

Conclusions :

These four point prevalence surveys demonstrated the dissemination and massive spread from east to west of B.1.1.7 lineage, besides other SARS-CoV-2 VOC/VOVIs circulation. Surveillance of VOC/VOI based on high-qualified virological laboratories network should be endorsed as a powerful tool to monitor closely their introduction and spread, identifying any escalation of potential vaccine-escape mutants.

Subject : Surveillance
Keywords : SARS-CoV-2; survey; point prevalence; VOC; VOI; sequencing; lineage B.1.1.7
ABSTRACT ID: 154
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e. Completeness, timeliness and acceptability of COVID-19 surveillance in the German state of North-Rhine Westphalia, 19 February 2020 to 11 May 2021

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Background :

Good quality and timely infectious disease surveillance is essential for public health action and policy. We evaluated surveillance of COVID-19 in North-Rhine Westphalia (NRW) state, the most populous state in Germany, to assess whether surveillance meets its main objective to monitor trends and patterns of disease in population.

Methods :

We extracted data from 19 February 2020 to 11 May 2021: internal completeness for key variables was calculated as the proportion of observations with any value and timeliness as delay between diagnosis and notification to the local health authorities (LHAs) and to the regional public health institute (LZG). Data quality by LHA was used as a proxy of acceptability.

Results :

We extracted 774,401 records. Median completeness ranged from 44.7% for information on recent contact to a COVID-19 case (contact status), 88% for date of illness onset, to >99% for variables age and sex. Median time from date of diagnosis to notification to the LHA was 0 days (10th-90th percentile 0-1 days). 86.9% of SARS-CoV-2 infections were reported to LZG within two days of diagnosis. Acceptability among 53 LHAs in NRW varied greatly: median completeness for contact status was 51.6% (0.7-97.1%) and for date of illness onset 92% (8.6-99.5%). Cases were reported to LHA within 0-1 days from diagnosis (range of 10th-90th percentiles 0-4 days). Between 77.1 and 99.9% (median 97.9%) of cases were reported to LZG within two days of diagnosis.

Conclusions :

Surveillance data quality and notification timeliness for COVID-19 vary overall and among LHAs in NRW. To improve COVID-19 surveillance in NRW, we recommend further research to explore possible reasons for varying levels of acceptability among LHAs and to assess whether targeted capacity strengthening support is needed.

Subject : Surveillance

Poster Tour Abstracts

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Poster tour 22
Vaccines

Abstracts

a. COVID-19 Vaccine second dose uptake is essential to induce strong humoral response in susceptible Health Care Workers

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Background :

Vaccination against COVID-19 is a crucial tool to control the current SARS-CoV-2 pandemic, however there is still insufficient information on the humoral response after vaccine uptake and its duration.

Methods :

As part of a longitudinal cohort vaccine effectiveness study in healthcare workers, we report results on the quantification throughout time of the serological response to one and two doses of COVID-19 mRNA vaccines. Quantitative determination of IgG (anti-Spike) against SARS-CoV-2 was performed on serum samples using a chemiluminescent microparticle immunoassay (Abbott Diagnostics, IL,USA). To investigate changes in antibody concentration after the first dose and the second dose uptake were estimated the geometric mean titres (GMT) of IgG, compared using matched- pairs Wilcoxon test. Mann-Whitney tests were used to compare GMT by sex and age group at each observation moment.

Results :

The cohort includes 204 individuals (81 vaccinated and 123 non-vaccinated of which 13 had previous COVID-19 infection). After the first dose uptake all participants seroconverted. The GMT of anti-spike IgG concentration (assessed between 20 -22 days after the 1st dose) was 775 UA/ml (CI95: 611-983) while 28 days after the 2nd dose GMT was almost 12 times higher (p<0.001, GMT= 9130 UA/ml (CI95: 7580-10997). No statistical differences (P>0.05) in IgG titters were observed between sex or age groups (20-39, 40-70 years) in either moment.

Conclusions :

The results indicate that after the first vaccine dose, titres of antibodies were detected, although after the second dose was observed a "boost" in IgG titters. Follow up at 6 and 12 months is planned and will contribute to further understand the duration of vaccine and natural infection immune response.

Subject : Implementation science (e.g. integration of research findings

Poster Tour Abstracts

and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords : COVID-19 Vaccine, antibodies, Healthcare workers

ABSTRACT ID: 147

PRESENTED BY: Raquel Guiomar / raquel.guiomar@insa.min-saude.pt

b. Trust in institutions is important for vaccine acceptance - results of the longitudinal survey on COVID-19 in Lower Saxony, Germany, 2020

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Background :

A comprehensive understanding of the population's knowledge, attitudes and practice (KAP) towards COVID-19 and their relationships is essential for effective pandemic management. This study aimed to investigate KAP regarding COVID-19 over time in Lower Saxony, Germany.

Methods :

We conducted an online-based longitudinal survey among participants of a non-probabilistic panel in May (period 1) and December (period 2) 2020 to investigate acceptance of preventive measures, risk perception, concerns, trust, and attitude towards COVID-19 vaccination. Differences between the two periods and association of COVID-19 vaccine confidence with potential predictors were investigated using paired Wilcoxon signed-rank tests and multivariable logistic regression, respectively.

Results :

Of 271 participants, 162 (60%) participated in both periods. Among those, the median age was 56 [IQR 46-64]; 100 (62%) were women. The majority deemed the implemented measures relevant for containing the pandemic (80-98% for different measures in period 1 vs 73-99% period 2) but stated feeling emotionally affected by them. Trust in public health, political and scientific institutions was generally high (ranging 77-94% for different institutions, period 1), but decreased over time (67-92%, period 2, p<0.01). Participants willing to get vaccinated against COVID-19 (79%) reported higher confidence in institutions (OR: 4.17; 95%CI: 1.87-9.68) and were more likely to have been vaccinated against influenza before (OR: 5.24; 95%CI: 2.39-11.8). Concerns about possible side effects were given as the main reason for vaccine hesitancy.

Conclusions :

The study shows a general endorsement of the preventive measures and high vaccination acceptance, particularly among those with higher trust in institutions. Monitoring of KAP regarding COVID-19 allows better understanding of the public perspective over time which is crucial to guide and adapt interventions and communication to build and maintain trust among the population.

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

Keywords : COVID-19,Knowledge Attitudes Practice,Longitudinal survey,Germany,Public Health

ABSTRACT ID: 86

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c. COVID-19 vaccine hesitancy among healthcare workers in Palestine: A call for action

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Background :

With the planned COVID-19 vaccine, vaccine hesitation is one of the great challenges, particularly for health care professionals who are the key drivers for vaccine acceptance among the community. In this study, we examined the acceptance of the COVID-19 vaccine by health care workers, their concerns about it, and the reasons that might prevent them from getting vaccinated.

Methods :

We conducted a cross-sectional study using an anonymous online survey available from December 25, 2020, to January 6, 2021. The questionnaire consisted of demographic characteristics (age, gender, profession, sector, medical history, and general health), COVID-19 related knowledge, and personal history of influenza vaccination. The intention to get the vaccine once it is available was directly asked, and attitudes toward the diseases and the vaccine were studied using a four-point Likert scale statement based on the health belief model's constructs.

Results :

Of the total responders, 62.9% were females, and 52.5% were between the ages of 30-49 years. The intention to get vaccinated was only 37.8% [95%CI: 35.0%-40.6%], while 31.5% were hesitant, and 30.7% planned to refuse it. Higher levels of intention were reported among males (OR; 2.7, 95%CI: 2.0-3.7), younger ages (OR 1.7, 95%CI: 1.1-2.8), physicians (OR; 2.9, 95%CI: 2.0-4.0), HCWs at non-governmental settings (OR; 1.4, 95%CI: 1.1-1.9), those who previously received the influenza vaccine (OR 4.0, 95%CI: 2.3-7.1), and those who had higher COVID-19 related knowledge (OR; 1.7, 95%CI: 2.3-7.1).

Conclusions :

Vaccine acceptance among HCWs was much lower than expected, which would greatly diminish the role of vaccination in diminishing the burden of the COVID-19 pandemic throughout the community

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

Keywords : COVID-19 Vaccine; Vaccine hesitancy; Attitudes; Healthcare workers; Palestine

ABSTRACT ID: 62

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d. Immunity to Varicella-Zoster-Virus in women of childbearing age seeking asylum in Rhineland-Palatinate, 2015-2020

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ESCAIDE

Poster Tour Abstracts

Postgraduate Training for Applied Epidemiology (PAE)

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Background :

An infection with Varicella-Zoster-Virus (VZV) during pregnancy can have detrimental effects on the offspring. Based on different vaccination programs and differential transmission patterns, protection against VZV differs between countries. This study explores whether women of childbearing age who seek asylum in Germany are sufficiently protected against infection with VZV.

Methods :

We used results from mandatory blood testing for IgG against VZV in asylum seekers newly arriving in Rhineland- Palatinate (RP) between June 2015-December 2020. Primary outcome measure was IgG-seropositivity as determined by commercial ELISA. We analyzed the proportion of women of childbearing age with sufficient protection from varizella infection by IgG in all asylum seekers and by country. For external comparison, we used a convenience sample from the resident population in RP, analyzed in the same laboratory.

Results :

From a total of 9,081 asylum seekers with IgG VZV result, 2,765 were women of childbearing age, showing overall lower IgG-VZV-seropositivity (87% (2394/2765); 95% CI 85-88) than women residing in RP (96% (17,199/17,871); 95% CI 96-97). The IgG-seropositivity to VZV differed by place of origin and was lowest in women from Nigeria (68% (267/393); 95% CI 63-73) and from Sub-Saharan Africa overall (80% (769/959); 95% CI 78-83). Even within women of childbearing age, increasing age was found to be a significant predictor for IgG-seropositivity in both asylum seekers (p<0.001) and

the resident population in RP (p<0.001).

Conclusions :

VZV seropositivity is significantly lower in some countries of origin. A targeted vaccination program against VZV for refugees arriving in RP should secure vaccination especially in women of childbearing age from these countries. This is particularly relevant to prevent the congenital varicella syndrome, which poses a high risk to the unborn child and mother.

Subject : Surveillance

Keywords : Varicella, chickenpox, varicella-zoster-virus, refugees, asylum, Germany, seropositivity, serostatus

ABSTRACT ID: 179

PRESENTED BY: Kathrin Schaten / schatenk@gmail.com

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