HYBRID

# ESCAIDE

European Scientific Conference
on Applied Infectious Disease Epidemiology

## 23-25 November 2022

📍 in Stockholm & online

ESCAIDE

ecdc
EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

#ESCAIDE 2022

ABSTRACT BOOK

# About ESCAIDE

The European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) is an annual conference which aims at strengthening the prevention and control of communicable disease through the sharing of knowledge, experience and contacts. It also provides opportunities for further professional development for fellows and students.

ESCAIDE is composed of a broad programme of sessions. The scientific content of the Conference primarily consists of plenary sessions, and oral and poster abstract presentations, which form a platform for the sharing of scientific advances.

# Foreword

**A very warm welcome to the 2022 ESCAIDE conference, which is a hybrid event held in Stockholm and online for the first time! I hope you will find attending this hybrid edition of ESCAIDE a stimulating and rewarding experience and enjoy the wide variety of sessions and in-person and online interactive opportunities on offer.**

In contrast to previous iterations of the conference, this 2022 edition of ESCAIDE was planned as a hybrid event from the outset to promote sustainability and accessibility. This hybrid approach integrates aspects of in-person and online delivery to reach a broader audience and offer complementary experiences to all conference participants. I would like to take this opportunity to invite you all to make use of the many interactive features and events available during the conference 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 2022 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 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 explore ethical considerations surrounding pandemic control (Plenary A). The protection and promotion of the health of displaced people will be discussed in Plenary B. Plenary C will consider exciting revolutions in vaccination. Challenges relating to public health communication and infodemics will be discussed in Plenary D. The conference concludes with Plenary E, with a consideration of recent developments in communicable disease surveillance following the past two year's experiences with the COVID-19 pandemic. The theme that strikes me throughout the plenary sessions this year is the importance of taking the broader view: as professionals committed to the prevention and control of infectious diseases, it is crucial to remember the broader perspectives and issues that impact our work.

Finally, I wish you a successful and enjoyable ESCAIDE 2022, and hope that you leave the conference with new insights, useful contacts, as well as a renewed enthusiasm for your role in the fight to address communicable diseases.

Mike Catchpole

Chair, ESCAIDE Scientific Committee

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# General programme

PROVISIONAL: last update: 28 October 2022

| CET time zone | DAY 1  -  23 November |
|---|---|
| 07.30-08.50 | REGISTRATION AND WELCOME COFFEE `LEVEL 1` |
| 08.50-10.00 | PLENARY SESSION A `AUDITORIUM 1 STORA HALLEN`<br>**Controlling a pandemic – what are the ethical boundaries?**<br>**Chaired by:** *Andrea Ammon (ECDC) and* **ESCAIDE Scientific Committee member** *Mike Catchpole (ECDC)*<br>**Keynote speaker:** *Alena Buyx (Technical University of Munich, Germany)* |
| 10.00-10.15 | **Message from ECDC Director and ECDC Chief Scientist**<br>`AUDITORIUM 1 STORA HALLEN` |
| 10.15-11.00 | COFFEE BREAK `LEVEL 1` |

| 11.00-12.30 | FIRESIDE SESSION 1<br>`AUDITORIUM 1 STORA HALLEN`<br>**Implementation science** | FIRESIDE SESSION 2<br>`AUDITORIUM 2 RIDDARSALEN`<br>**Sexually and community acquired infections, including HIV** |
|---|---|---|

| 12.30-14.30 | LUNCH BREAK<br>`LEVEL 7` | 12.30-13.00<br>Mindfulness session: be your own coffee or chamomile tea, with Aiga Berke<br>`ROOM TORNET` | |
|---|---|---|---|
| | | 13.00-13.30<br>ONLINE ONLY-POSTERS | 13.00-14.00<br>**Career Compass**<br>`AUDITORIUM 2 RIDDARSALEN` |
| | | 13.30-15.00<br>FIRESIDE SESSION 3<br>`AUDITORIUM 1 STORA HALLEN`<br>**Secondary public health impacts** | 14.00-15.00<br>MODELLING SESSION<br>`ROOM FOGELSTRÖM`<br>**Modelling the future of living alongside COVID-19 in Europe**<br>**Moderated by:** *Frank Sandmann*<br>**Speakers:** *Sebastian Funk (LSHTM, UK), Rebecca Borchering (US CDC), Philippe Beutels (University of Antwerp, Belgium)* |

| 15.15-16.00 | Poster tour 1 **Knowledge for policy and practice**<br>Poster tour 2 **Emerging and vector-borne diseases**<br>Poster tour 3 **Respiratory diseases**<br>Poster tour 4 **Food -and water borne diseases and zoonoses**<br>`ROOMS MÄLARSALEN & STRINDBERG` |
|---|---|
| 16.00-16.30 | COFFEE BREAK `LEVEL 1` |
| 16.30-18.00 | PLENARY SESSION B `AUDITORIUM 1 STORA HALLEN`<br>**Refugees and refuge: how to promote and protect the health of displaced people**<br>**Chaired by the ESCAIDE Scientific Committee members:** *Stine Nielsen (EAN) and Chikwe Ihekweazu (WHO)*<br>**Speakers:** *Paul Spiegel (Johns Hopkins Center, United States), Aurélie Ponthieu (Médecins Sans Frontières), Elke Jakubowski (Health Policy Europe, Germany), Apostolos Veizis (INTERSOS, Greece)* |
| 18.00-18.15 | DAILY WRAP-UP `AUDITORIUM 1 STORA HALLEN` |
| 18.30-20.30 | NETWORKING COCKTAIL `LEVEL 7` |

**#ESCAIDE 2022**  European Scientific Conference on Applied Infectious Disease Epidemiology

| CET time zone | **DAY 2** - *24 November* | | |
|---|---|---|---|
| 08.30-09.00 | WELCOME COFFEE **LEVEL 1** | | |
| 09.00-10.30 | PLENARY SESSION C **AUDITORIUM 1 STORA HALLEN**<br>**Revolutions in vaccination in the age of COVID-19**<br>Chaired by the ESCAIDE Scientiic Committee members: *Adam Roth (ECDC) and Magdalena Rosińska (National Institute of Health, Poland)*<br>**Speakers:** *Hanna Nohynek (THL, Finland), Cornelia Betsch (University of Erfurt, Germany), Jeremy Ward (INSERM, France)* | | |
| 10.30-11.00 | COFFEE BREAK **LEVEL 1** | | |
| 11.00-12.30 | FIRESIDE SESSION 4<br>**AUDITORIUM 1 STORA HALLEN**<br>**COVID-19: vaccine effectiveness** | | FIRESIDE SESSION 5<br>**AUDITORIUM 2 RIDDARSALEN**<br>**COVID-19: surveillance action** |
| 12.30-14.30 | LUNCH BREAK<br>**LEVEL 7** | 12.30-13.00<br>Vitamin groove,<br>with Irina Ljungqvist<br>**ROOM TORNET**<br><br>13.00–13.30<br>ONLINE ONLY-POSTERS<br><br>13.30-15.00<br>EUROSURVEILLANCE SEMINAR<br>**AUDITORIUM 1 STORA HALLEN**<br>**Communicating science: social media and other means**<br>*Pitfalls and benefits*<br>**Moderated by:** *Mario Fafangel (National Institute of Public Health, Slovenia)*<br>**Speakers:** *Isabella Eckerle (University of Geneva, Switzerland) and Pampa García Molina (Science Media Centre, Spain)* | 12.30-14.00<br>**ROOM FOGELSTRÖM**<br>**EAN General Assembly meeting (closed event)**<br><br>14.00-15.00<br>MEDIPIET SESSION<br>**AUDITORIUM 2 RIDDARSALEN**<br>**The role of national FETPs in strengthening countries' capacities for infectious disease prevention and response**<br>**Moderated by:** *Adam Roth (ECDC)*<br>**Speakers:** *Paata Imnadze (NCDC, Georgia), Nada Ghosn (Ministry of Public Health, Lebanon), Nissaf Bouafif ép Ben Alaya (Ministry of Health, Tunisia), Katharina Apers (RKI, Germany)* |
| 15.15-16.00 | Poster tour 5 **COVID-19: vaccination and immunity**<br>Poster tour 6 **Intervention and health promotion**<br>Poster tour 7 **Antimicrobial resistance**<br>Poster tour 8 **Surveillance: opportunities and evaluation**<br>Poster tour 9 **Late-breakers**<br>**ROOMS MÄLARSALEN & STRINDBERG** | | |
| 16.00-16.30 | COFFEE BREAK **LEVEL 1** | | |
| 16.30-18.00 | PLENARY SESSION D **AUDITORIUM 1 STORA HALLEN**<br>**Cutting through the noise: the role of Public Health experts in managing an infodemic**<br>Chaired by the ESCAIDE Scientiic Committee members: *John Kinsman (ECDC), Petronille Bogaert (Sciensano, Belgium), and Mircea Ioan Popa (Carol Davila University of Medicine and Pharmacy, Romania)*<br>**Speakers:** *Mihai Craiu (Bucharest Mother and Children Hospital, Romania), Neville Calleja (Ministry for Health, Malta), Alma Tostmann (Radboudumc, The Netherlands), Martyna Bildziukiewicz (European External Action Service)* | | |
| 18.00-18.15 | DAILY WRAP-UP **AUDITORIUM 1 STORA HALLEN** | | |
| 18.30-20.00 | BARCAMP **AUDITORIUM 2 RIDDARSALEN** | | |

*CET time zone*

# DAY 3 - *25 November*

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|---|---|
| 08.30-09.00 | **WELCOME COFFEE** `LEVEL 1` |

**09.00-10.30**

**PLENARY SESSION E** `AUDITORIUM 1 STORA HALLEN`

**The COVID-19 pandemic – a surveillance game changer?**

Chaired by the ESCAIDE Scientific Committee members: *Vicky Lefevre (ECDC), Bruno Coignard (Santé publique France) and Luísa Peixe (University of Porto, Portugal)*

Speakers: *Silke Buda (RKI, Germany), Søren Alexandersen (SSI, Denmark), Fernando Simon (Ministry of Health, Spain)*

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|---|---|
| 10.30-11.00 | **COFFEE BREAK** `LEVEL 1` |

**11.00-12.30**

| **FIRESIDE SESSION 6** `AUDITORIUM 1 STORA HALLEN` | **FIRESIDE SESSION 7** `AUDITORIUM 2 RIDDARSALEN` |
|---|---|
| **COVID-19: intervention and health promotion** | **Food and water-borne and vector diseases** |

**12.30-14.30**

**LUNCH BREAK** `LEVEL 7`

**12.30–13.00**
Yoga for body and mind stretching, with Maria Keramarou `ROOM TORNET`

**13.00–13.30**
ONLINE ONLY-POSTERS

**14.00–15.00**
SOCIAL SCIENCES SESSION

`ROOM FOGELSTRÖM`

**Use of social science methods to support the prevention and control of infectious diseases in Europe**

**Moderated by:** *John Paget (Nivel, Netherlands)*
**Speakers:** *Tamara Giles-Vernick (Institut Pasteur, France), Jens Seeberg (Aarhus University, Denmark), Danny de Vries (Amsterdam Institute for Global Health and Development, the Netherlands), Alice Desclaux (Fann Research Center, Senegal) and John Kinsman (ECDC)*

| **13.30-15.00**<br>**FIRESIDE SESSION 8**<br>`AUDITORIUM 1 STORA HALLEN`<br>**COVID-19: Surveillance approaches** | **13.30-15.00**<br>**FIRESIDE SESSION 9**<br>`AUDITORIUM 2 RIDDARSALEN`<br>**Late breakers** |
|---|---|

**15.15-16.00**

Poster tour 10 **Surveillance approaches**
Poster tour 11 **Food and water-borne diseases and zoonoses: outbreaks**
Poster tour 12 **COVID-19: burden of disease**
Poster tour 13 **COVID-19: vaccine effectiveness**
`ROOMS MÄLARSALEN & STRINDBERG`

| | |
|---|---|
| 16.00-16.30 | **COFFEE BREAK** `LEVEL 1` |
| 16.30-17.00 | **FINAL WRAP-UP**<br>`AUDITORIUM 1 STORA HALLEN` |
| 17.00-17.15 | **CLOSING CEREMONY AND AWARDS** `AUDITORIUM 1 STORA HALLEN` |

# FIRESIDE SESSIONS PROGRAMME

PROVISIONAL : last update: 31 August 2022

*CET time zone* **DAY 1** - *23 November*

**11.00-12.30**

### FIRESIDE SESSION 1
*moderated by Howard Needham*

#### Implementation science

a. Enhanced event-based surveillance: monitoring events during the Ukraine crisis, 2022, *Jon Bilbatua*

b. Collaborative modelling of the future dynamics of COVID-19: the European Forecasting and Scenario Hubs, *Katharine Sherratt*

c. Endemic Zika Virus in Brazil, *Laith Yakob*

d. Effectiveness of Four Vaccines in Preventing SARS-CoV-2 Infection in Kazakhstan, *Dilyara Nabirova*

e. An Approach to Developing One Health Field Epidemiology Competencies, *Marion Muehlen*

f. *Community-based One Health Approach to* Prevent, Detect and Respond to Disease Outbreaks, *Muhammad Abdi Haryono*

### FIRESIDE SESSION 2
*moderated by Aura Georgina Aguirre-Beltran*

#### Sexually and community acquired infections, including HIV

a. Invasive beta-hemolytic streptococcal infections in Finland, 2006-2020: The rise of Lancefield group C/G infections, *Dafni Katerina Paspaliari*

b. Investigating the sociodemographic and behavioural factors associated with hepatitis C virus testing amongst people who inject drugs in England, Wales and Northern Ireland, *Jin-Min Yuan*

c. Neisseria gonorrhoeae antimicrobial resistance surveillance in the Netherlands: a 10-year overview, *Maartje Visser*

d. Contribution of Sexual Health Centres in hepatitis B detection and control in the Netherlands, *Stijn Raven*

e. Effects of Improving Partner Notification on HIV and gonorrhea transmission among men who have sex with men in the Netherlands, *Maarten Reitsema*

f. (late breaker) Questionnaire data identifies monkeypox common exposure events at sex-on-premise venues and festivals, England, *Alessandra Løchen*

**13.30-15.00**

### FIRESIDE SESSION 3
*moderated by Julien Beaute*

#### Secondary public health impacts

a. How COVID-19 fast-tracked the development of a national microbiology laboratory database for surveillance in Norway: Success factors, *Nina Aasand*

b. Impact of universal Tuberculosis (TB) vaccination cessation on the epidemiology of paediatric TB cases in Ireland, 2011-2021, *Sarah Jackson*

c. A systematic review on the impact of COVID-19 on cervical cancer prevention, diagnosis and treatment, *Giulia Dallagiacoma*

d. The impact of the COVID-19 pandemic and non-pharmaceutical interventions on infectious diseases under national surveillance in the Netherlands from 2020 to Q1 2022, *Gijs Klous*

e. The impact of the COVID-19 pandemic on the transmission of hepatitis B virus among men who have sex with men: a mathematical modelling study, *Maria Xiridou*

f. (late breaker) Estimated averted COVID-19 hospitalisations by the COVID-19 vaccination campaign in the Netherlands, 2 August 2021 through 30 August 2022, *Senna van Iersel*

**11.00-12.30**

## COVID-19: vaccine effectiveness

a.  Vaccine effectiveness against COVID-19 and associated death in Alpha and Delta variant outbreaks in long-term care facilities in Germany, *Mirco Sandfort*

b.  Primary course and booster vaccine effectiveness against Omicron: Results from a European multicentre study at primary care/ambulatory level, *Charlotte Lanièce Delaunay*

c.  COVID-19 vaccine effectiveness against SARS-CoV-2 infection during the Delta period in the Netherlands: A nationwide study adjusting for chance of exposure, *Katja van Ewijk*

d.  Covid-19 vaccination programme effectiveness against SARS-CoV-2 related infections, hospital admissions and deaths in the Apulia region of Italy: a one-year retrospective cohort study, *Tobias Homan*

e.  Estimation of COVID-19 vaccine effectiveness against hospitalisation in individuals aged 65+ years using electronic health registries; pilot study in four EU/EEA countries, January-February 2022, *Alexis Sentís Fuster*

f.  A new challenge for control selection in influenza vaccine effectiveness test-negative design studies in the COVID-19 context: Results from the European I-MOVE multicentre study at primary care level, *Esther Kissling*

## COVID-19: surveillance action

a.  Comparative risk of cerebral venous sinus thrombosis (CVST) following SARS-CoV-2 vaccination or infection: A national cohort study using linked electronic health records, *Columbus Ohaeri*

b.  Risk of SARS-CoV-2 infection among members of a fitness centre chain in Stockholm, Sweden 2020: Is going to the gym risky?, *Anine Kongelf*

c.  Bus riding as amplification mechanism for an explosive COVID-19 outbreak after import of SARS-CoV-2 by air travellers, Germany, 2021, *Meike Schöll*

d.  Disease severity and outcomes of COVID-19 in cases infected with SARS-CoV-2 Delta and Omicron variants, Skåne region, Sweden, December 2021 - January 2022, *Anine Kongelf*

e.  A comparison of COVID-19 critical care admission incidence in Wales by vaccine status, *Mai Barry*

f.  Estimate of school-specific reproductive number during weekly screening in the Auvergne-Rhône-Alpes region, France, week 47 to 50, 2021, *Elisabetta Colosi*

# DAY 3 - *25 November*

**11.00-12.30**

### FIRESIDE SESSION 6
*moderated by Harold Noël*

## COVID-19: intervention and health promotion

a. Nosocomial acquisition not associated with increased mortality amongst hospitalised COVID-19 cases in Wales, Feb 2020-Mar 2022, *Rubeshkumar Polani*

b. Incidence rate and risk factors associated with SARS-CoV-2 infection in healthcare workers from three European hospitals, July 2021-April 2022, *Camelia Savulescu*

c. Determinants of healthcare workers' self-reported compliance to infection prevention and control during the COVID-19 pandemic: a cross-sectional study in Dutch residential care facilities, *Famke Houben*

d. Assessing the robustness of SARS-CoV-2 vaccine trial results: systematic review and meta-analysis, *Ngoc-Anh Hoang*

e. Socioeconomic patterns of COVID-19 vaccine uptake in children aged 5-11 in Italy (January - April 2022), *Alberto Mateo Urdiales*

f. The association between SARS-CoV-2 sero-prevalence and cross-border mobility for visiting family or friends among Dutch residents of a border province, *Demi ME Pagen*

### FIRESIDE SESSION 7
*moderated by Moa Rehn*

## Food -and water borne and vector diseases

a. Regional shift in Pogosta disease incidence during 2021 epidemic in Finland, *Eveline Otte im Kampe*

b. Risk of lymphoma increased after Puumala virus infection in Finland, 2009-2019: a retrospective register-based study, *Sohvi Kääriäinen*

c. An Easter Surprise: Salmonella Typhimurium outbreak linked to chocolate products in the United Kingdom, 2022; a case control study, *Amoolya Vusirikala*

d. International outbreak of Salmonella Typhimurium linked to a chocolate factory in 2022: Belgian findings, *Valeska Laisnez*

e. Whole Genome Sequencing identified a prolonged Salmonella Poona nursery outbreak (2016-2021) in North West England, UK, *Joanna Garner*

f. Climate Warming and increasing Vibrio vulnificus infections in North America, *Elizabeth Archer*

**13.30-15.00**

### FIRESIDE SESSION 8
*moderated by Carlos Carvalho*

## COVID-19: Surveillance approaches

a. Linkage of SARS-CoV-2 sequencing results to the Bavarian surveillance system from January 2021 through February 2022, Germany, *Liza Coyer*

b. Using a novel 'difference-in-differences' method and syndromic surveillance to estimate the impact of media reporting on local health-care utilisation during an early stage of the COVID-19 pandemic, *Aryan Nikhab*

c. Wastewater surveillance for SARS-CoV-2 closely mirrors incidence data: results from national surveillance in Denmark, October 2021 – May 2022, *Oliver McManus*

d. SARS-CoV-2 Genomic Surveillance: Lessons Learned from the EMERGEN Consortium, France, 2021-2022, *Justine Schaeffer*

e. How do we keep a cohort engaged? Lessons from one year of following up over 44,000 SIREN study participants, UK, *Sarah Foulkes*

f. (late breaker) Surveillance of vaccine effectiveness against mortality from different SARS-CoV-2 variants in southern Sweden between December 2020 and June 2022, *Dominik Dietler*

### FIRESIDE SESSION 9
*moderated by Eleanor McNamara*

## Late breakers

a. Exploring non-viral exposures causatively or contributorily associated with paediatric cases of acute hepatitis of unknown aetiology in the United Kingdom, 2022, *Hannah Taylor*

b. Monkeypox vaccination acceptance among male users of gay dating apps in Europe, *Juliana Reyes*

c. Monkeypox cases in women in England: Characterising transmission routes and monitoring spread outside of GBMSM, *Katie Wrenn*

d. Decreasing mortality linked to SARS-CoV-2 infections in long-term care facilities in Luxembourg: results from national surveillance March 2020-September 2022, *Corinna Ernst*

e. Primary series and booster vaccine effectiveness against the SARS-CoV-2 Omicron variant in a cohort of healthcare workers in Albania, January – May 2022, *Iris Finci*

f. (late breaker) High vaccine effectiveness against severe COVID-19 outcomes during the Omicron era in Luxembourg, December 2021-August 2022, *Dritan Bejko*

# POSTER TOURS PROGRAMME

PROVISIONAL : last update: 31 August 2022

CET time zone | **DAY 1** - *23 November*

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**15.15-16.00**

POSTER TOURS 1   *moderated by Gabrielle Schittecatte*

## Knowledge for policy and practice

a. The COVID-19 pandemic impacted syphilis testing at anonymous consultation clinics in North-Rhine Westphalia state, Germany, 2019-2021, *Katja Siling*

b. Translating the COVID-19 epidemiological situation into policies and measures: the Belgian experience, *Geraldine De Muylder*

c. One Health in policy and practice: A UK case study of Corynebacterium ulcerans in a pet and challenges managing human health risk for zoonotic disease where guidance is focused on human cases, *Penelope Cresswell-Jones*

d. Importance of regional networking in building national FETP: Experience of Lebanon, *Zeina Farah*

e. Assessment of infection prevention and control in hospitals providing medical care for coronavirus infection (COVID-19) in Bishkek, Osh cities and Chui region, Kyrgyzstan, 2020, *Altynai Dzhalimbekova*

f. Activation of crisis management structures at the Robert Koch Institute during the COVID-19 pandemic, *Ulrike Grote*

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**15.15-16.00**

POSTER TOURS 2   *moderated by Patrizio Pezzotti*

## Emerging and vector-borne diseases

a. Modelling the human force of infection of West Nile virus in Europe, *Giovanni Marini*

b. Risk assessment and preparedness plan development for West Nile Virus (WNV) transmission in the State of Baden-Wuerttemberg, Germany, 2022, *Sabrina Nothdurfter*

c. Predictors of Lassa fever diagnosis in suspected cases reporting in health facilities: A secondary data analysis of Nigerian surveillance data, 2018-2021, *Sandra Mba*

d. Spatiotemporal spread of tick-borne encephalitis in the EU/EEA, 2012-2020, *Jasper Van Heuverswyn*

e. Elevated tick borne encephalitis seroprevalence in blood donors in regions classified as moderately-affected or low -risk in Poland, 2022, *Katarzyna Pancer*

f. (late breaker) Once more unto the breach: The public health response of an Australian state to the global Monkeypox outbreak 2022, *Justine Marshall*

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**15.15-16.00**

POSTER TOURS 3   *moderated by Katie Palmer*

## Respiratory diseases

a. Integrated surveillance of SARS-CoV-2 and other human respiratory viruses in a public testing facility in Utrecht, the Netherlands to monitor co-circulation in a susceptible population, *Stijn Raven*

b. Feasibility to estimate real-time influenza vaccine effectiveness: a pilot study across five European study sites, *Marine Maurel*

c. The epidemiology of respiratory syncytial virus in children during the COVID-19 pandemic measured by laboratory, clinical and syndromic surveillance in England: a retrospective observational study, *Megan Bardsley*

d. Differences found in the epidemiology of Tuberculosis (TB) among migrants versus non-migrants in Ireland, 2011-2020, *Sarah Jackson*

e. A SARS-CoV-2 Omicron outbreak among crew members on a cruise ship in Germany in early 2022, *Silja Bühler*

f. COVID-19 outbreak in an elderly care home: very low vaccine effectiveness and late impact of booster vaccination campaign, *Katja van Ewijk*

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**15.15-16.00**

POSTER TOURS 4   *moderated by Steen Ethelberg*

## Food -and water borne diseases and zoonoses

a. Timely and reliable outbreak investigation using a non-probabilistic online panel as a source of controls - two parallel case-control studies investigating a Salmonella Braenderup outbreak in Germany, *Anna Luczynska*

b. An outbreak of Escherichia coli-associated haemolytic uremic syndrome linked to consumption of an unexpected food vehicle, France 2022, *Catarina Krug*

c. Outbreak investigation of cholera in a peri-urban village of Panchkula district, Haryana, India, 2021, *Shivani Gupta*

d. Cholera Outbreak Investigation, Ballo Adda Mohalla, Lucknow District, Uttar Pradesh 2021, *Surabhi Tripathi*

e. Norovirus GII.3[P12] outbreak associated with the drinking-water supply in a rural area in Galicia, Spain, 2021, *Camille Jacqueline*

f. Impact of COVID-19 restrictions on the epidemiology of Cryptosporidium spp. in England and Wales, *James Adamson*

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*CET time zone* **DAY 2** - *24 November*

**15.15-16.00**

POSTER TOURS 5 *moderated by Nathalie Nicolay*

## COVID-19: vaccination and immunity

a. Seroprevalence of SARS-CoV-2 IgG antibodies and factors associated with neutralizing activity among primary health care workers six months after vaccination rollout in France, *Marie Pouquet*

b. Direct and indirect vaccination effects on SARS-CoV-2 infection in day-care centers: evaluating the policy for early vaccination of day-care staff in Germany, 2021, *Anja Schoeps*

c. Impaired immunity and high attack rates caused by SARS-CoV-2 variants among vaccinated long term care facility residents, *Dorothée Obach*

d. The effect of hybrid immunity during Omicron variant wave in a European healthcare worker cohort, December 2021 - April 2022, *Camelia Savulescu*

e. B cell mediated immunogenicity following boosting with the BNT162b2 SARS-CoV-2 vaccine in dialysis patients, Israel, 2021-22, *Neta Tuvia*

f. Estimating COVID-19 and influenza vaccination coverage in homeless populations; Wales, UK, *Gethin Jones*

**15.15-16.00**

POSTER TOURS 6 *moderated by Frantiska Hruba*

## Intervention and health promotion

a. Deciding about maternal pertussis vaccination: associations between intention, and needs and values in a vaccine-hesitant religious group, *Anne de Munter*

b. Advocacy and community engagement in TB control: the Kano wellness on wheels (WoW) experience, *Mustapha Musa Tukur*

c. Hantavirus and Leptospira spp.: Seroprevalence, knowledge and preventive behaviour in seasonal harvesters in Lower Saxony, Germany, 2021, *Saskia Schmitz*

d. Considerable doubt about rubella screening and vaccination intention among unvaccinated orthodox Protestant women, *Anne de Munter*

e. Lessons from a protracted iGAS outbreak with added complexity of concurrent scabies outbreak, in a UK residential nursing care facility 2020-2021, *Philippa Williams*

f. Vaccine confidence among the adult population of Bishkek and Naryn, Kyrgyz Republic, 2021, *Marina Malisheva*

**15.15-16.00**

POSTER TOURS 7 *moderated by Annick Lenglet*

## Antimicrobial resistance

a. International patient transfers causing healthcare associated outbreaks of carbapenem-resistant Acinetobacter baumannii in Germany, August – September 2021, *Jonathan Baum*

b. Emergence of carbapenemase-producing Enterobacterales causing infection in companion animals, *Joana Moreira Da Silva*

c. Trends in antibiotic resistance in Portugal: analysis of surveillance data from 2015 to 2020, *Vera Manageiro*

d. Increasing trends in extended-spectrum β-lactamase production in urine and blood Escherichia coli isolates in Finland in 2008–2019: a retrospective nationwide study, *Heikki Ilmavirta*

e. Increase in extensively-drug resistant Shigella sonnei infections in Spain, 2021-2022, *Camille Jacqueline*

f. Failure of scabies treatment: a systematic review and meta-analysis, *Felix Reichert*

**15.15-16.00**

POSTER TOURS 8 *moderated by Amelie Plymoth*

## Surveillance: opportunities and evaluation

a. Candida auris in Attica hospitals, Greece: yet another Hospital Acquired Infection, *Lida Politi*

b. Clostridioides difficile infection surveillance system in Norway: evaluation of the data completeness, 2019-2021, *Lea Franconeri*

c. Wastewater-based surveillance of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae in Finland: Informed selection of sites for sampling, *Dafni Katerina Paspaliari*

d. Evaluation of random-digit-dialing (RDD) recruitment to invite participants for serological tests as a method to obtain a representative sample for general population seroepidemiological surveys, *Magdalena Rosinska*

e. Evaluation of 17 years of MERIN (Meningitis and Encephalitis register in Lower Saxony, Germany) surveillance program: acceptability survey and data quality assessment, *Anna Luczynska*

f. Evaluation and comparison of statistical algorithms for monitoring COVID-19 case and death trends in EU/EEA Member States, *Chiara Entradi*

**15.15-16.00**

POSTER TOURS 9 *moderated by Iro Evlampidou*

## Late breakers

a. Association between Paediatric Hepatitis Cases of Unknown Aetiology and Adenovirus in Wales, July 2022, *Frances Rowley*

b. Largest reported outbreak of Crimean-Congo Hemorrhagic Fever (CCHF) in Georgia, 2022, *Levan Liluashvili*

c. Assessing the short- and long-term impact of behavioural changes and vaccination on the size of a future monkeypox outbreak: A modelling study among men who have sex with men in Belgium, *Achilleas Tsoumanis*

d. Use of network diagrams to support dynamic assessment of monkeypox transmission patterns in Wales, United Kingdom, 2022, *Albert Yung*

e. Should we use the 4CMenB (Bexsero®) meningitis vaccine to protect men who have sex with men (MSM) in England against gonorrhoea? A model-based analysis of impact and cost-effectiveness, *Dariya Nikitin*

f. Feasibility of an ad-hoc participatory daily antigen rapid testing surveillance (DARTS) system for COVID-19 infection in Hong Kong, *Nicole Ngai Yung Tsang*

CET time zone **DAY 3** - *25 November*

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**15.15-16.00** POSTER TOURS 10 *moderated by Raquel Medialdea Carrera*

### Surveillance approaches

a. SARS-CoV-2 in schoolchildren during the Delta variant wave August to December 2021– finding from the Danish comprehensive register-based surveillance system, *Tjede Funk*

b. Rapid establishment of a prospective surveillance system for child mortality and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection in England, *Gemma Smith*

c. Repeated nationwide serosurveillance of SARS-CoV-2 in the Netherlands during the second year of the pandemic: a prospective population-based cohort, *Eric Vos*

d. Investigating opportunities for surveillance of long term chlamydia complications in the Netherlands: a qualitative study, *Elke Den Boogert*

e. Characterisation of measles transmission chains in three outbreaks in the post-elimination phase. Spain 2017-2019, *Kevin Bliek-Bueno*

f. Evaluating severity parameters for scaling up and down public health and social measures during the COVID-19 pandemic in select WHO Member States, *Holly Sadler*

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**15.15-16.00** POSTER TOURS 11 *moderated by Aine Collins*

### Food and water-borne diseases and zoonoses: outbreaks

a. Monophasic Salmonella Typhimurium outbreak linked to chocolate products, Ireland, 2022, *Charlotte Salgaard Nielsen*

b. Successful containment of a Listeria monocytogenes outbreak caused by shredded vegetables, Hesse/Germany, 2021-2022, *Laura Becker*

c. Outbreak of monophasic Salmonella Typhimurium linked to fresh small tomatoes, Sweden, 2021, *Karolina Fischerström*

d. Cluster of dog bite injuries and rabies exposures - Tajikistan, 2022, *Rajabali Sharifov*

e. High fatality rate from probable botulism linked to home canning - Tajikistan, 2021, *Sakina Shoeva*

f. Lassa fever in the East of England: the multiagency response, *Eleanor Turner-Moss*

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**15.15-16.00** POSTER TOURS 12 *moderated by Lynn Meurs*

### COVID-19: burden of disease

a. Occupational risk factors for SARS-CoV-2 infection amongst healthcare workers in England during the second wave: the SIREN prospective cohort study, September 2020 - April 2021, *Edward Monk*

b. Milder disease trajectory among COVID-19 patients hospitalised with the SARS-CoV-2 Omicron variant compared with the Delta variant in Norway, *Jeanette Stålcrantz*

c. The impact of the COVID-19 pandemic on health-related quality of life in the Dutch population: a preliminary analysis, *Cheyenne C.E. van Hagen*

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**15.15-16.00** POSTER TOURS 13 *moderated by Alexis Sentis*

### COVID-19: vaccine effectiveness

a. Effectiveness of BNT162b2 vaccine against SARS-CoV-2 infection and severe COVID-19 in children 5-11 years old in Italy (January-April 2022), *Chiara Sacco*

b. Monitoring vaccine effectiveness against SARS-CoV-2 infection in a Dutch cohort – The VAccine Study COvid-19 (VASCO), *Anne Huiberts*

c. Vaccine effectiveness of mRNA vaccines against COVID-19 hospitalisation during Omicron circulation in Europe in adults ≥20 years: I-MOVE-COVID-19 and ECDC hospital networks, 27 Dec 2021–31 Mar 2022, *Angela Mary C. Rose*

d. Vaccine effectiveness of BNT162b2 COVID-19 in adolescents: results of a Portuguese population-based cohort study based on electronic health records linkage, *Baltazar Nunes*

e. Relative effectiveness of COVID-19 vaccine booster dose against Delta and Omicron SARS-CoV-2 infection in a European healthcare worker cohort, June 2021- April 2022, *Camelia Savulescu*

f. Effectiveness of BNT162b2 mRNA booster doses and hybrid-immunity against SARS-CoV-2 infections during the Delta and Omicron variant waves; the UK SIREN study September 2021 to February 2022, *Victoria Hall*

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# PLENARY SESSIONS

Plenary sessions at ESCAIDE aim to 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 discuss and tackle topics of significant current importance in infectious disease and public health, deliver inspiring presentations and address questions from the audience. There are five plenary sessions at ESCAIDE 2022, chaired by the ESCAIDE Scientific Committee. The format of each varies from panel discussions, interviews and debates.

# Scientific committee



## Mike Catchpole
**Sweden**
*Chief Scientist at ECDC, Chair of ESCAIDE Scientific Committee, ECDC*

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.



## Bruno Coignard
**France**
*Director, Infectious Diseases Division, Santé publique France*

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.

## Vicky Lefevre
**Sweden**

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

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

## Magdalena Rosińska
**Poland**

*National Institute of Public Health-National Institute*
*of Hygiene (NIPH-NIH)*

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.

# Mircea Ioan Popa
**Romania**

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

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.



# Petronille Bogaert
**Belgium**

*Head of Unit, EU Health Information Systems, Sciensano*

Petronille Bogaert is head of unit EU health information systems at Sciensano, Belgium. Her work primarily focusses on European research projects in the area of population health information. She is Principle Investigator of the Population Health Information Research Infrastructure for COVID-19 and is heavily involved in the Joint Action Towards the European Health Data Space (TEHDAS) and other European projects such as HealthyCloud and BY-COVID. She is a graduate from a double European Master of Public Health. Additionally, she also holds a Bsc and Msc in Biomedical Sciences and is PhD candidate at Tilburg University specializing in European Health Information Systems. She is president of the EUPHA section on Public Health.

## Adam Roth
**Sweden**
*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
**Spain**
*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.

## John Kinsman
**Sweden**
*Expert Social and Behaviour Change, European Centre for Disease*
*Prevention and Control (ECDC)*

John Kinsman has conducted social and behaviour change research since 1996, including on the social determinants of health, health system strengthening, public health emergency preparedness, and the prevention and control of specific diseases such as HIV/AIDS, Ebola, Zika and poliomyelitis. He joined ECDC in 2019, working initially on promoting vaccination acceptance and the prevention of antibiotic resistance in the EU, but since the emergence of the COVID-19 pandemic, his work has focused exclusively on the response. Projects have included addressing pandemic fatigue, supporting socially vulnerable populations, promoting COVID-19 vaccination, and countering online vaccination misinformation. John gained his PhD in medical anthropology at the University of Amsterdam in 2008, and was Associate Professor in Global Health at Umeå University in Sweden from 2013 until he joined ECDC.

**Plenary sessions** - Scientific committee

## Luísa Peixe
**Portugal**
*Professor of Bacteriology, University of Porto*

Luísa Peixe has a degree in Pharmaceutical Sciences and doctorate in Microbiology. During her career as Professor of Bacteriology at the Faculty of Pharmacy of the University of Porto (FFUP), Portugal (1987- present) she has conducted research on antimicrobial resistance on different clinically relevant bacteria, with a One Health approach. This is done to understand the ecology, drivers and evolution of bacteria, as well as to help improve their detection and control. As the effectiveness of standard antimicrobial treatments in urinary tract infections has vastly diminished, her research team has been investigating the role of the urinary microbiome in urinary tract health and disease. Currently, she is Director of Department of Biological Sciences at FFUP and has published over 200 publications in international peer-reviewed journals. She holds several positions in national and international institutions in connection with her expertise in clinical bacteriology and antimicrobial resistance. These include the Biological Hazards Panel at the European Food Safety Authority (EFSA), the Qualitative Presumption of Safety Working Group at EFSA and the Joint Programming Initiative on Antimicrobial Resistance (JPIAMR) Scientific Board.

## Chikwe Ihekweazu
**Germany**
*Assistant Director-General, Health Emergency Intelligence, WHO*

Dr Chikwe Ihekweazu is the Assistant Director General at the World Health Organization (WHO) for Surveillance and Health Emergency Intelligence and leads the WHO Hub for Pandemic and Epidemic Intelligence, based in Berlin, Germany.

Previously, Dr Ihekweazu was the first Director General of the Nigeria Centre for Disease Control (NCDC), which he led July 2016 - October 2021, building it from a small unit to a leading public health agency in Africa. He acted as Interim Director of the West Africa Regional Centre for Surveillance and Disease Control through 2017.

Dr Ihekweazu trained as an infectious disease epidemiologist and has over 25 years' experience working in senior public health and leadership positions in national public health institutes including NCDC, South African National Institute for Communicable Diseases, the UK's Health Protection Agency, and Germany's Robert Koch Institute. Dr Ihekweazu has led several short-term engagements for WHO, mainly building surveillance systems and responding to major infectious disease outbreaks. He was part of the first WHO COVID-19 international mission to China.

Dr Ihekweazu is a graduate of the College of Medicine, University of Nigeria and has a Masters in Public Health from the Heinrich-Heine University, Dusseldorf, Germany. In 2003, he was awarded a Fellowship for the European Programme for Intervention Epidemiology Training and subsequently completed his Public Health specialisation in the UK. He has over one hundred publications in medical peer review journals, mostly focused on the epidemiology of infectious diseases. Dr Ihekweazu is on the board of the NGOs: African Society of Laboratory Medicine, Child Health and Mortality Prevention Surveillance, Public Health Foundation of Nigeria, Health Watch Foundation, Society for Family Health, Education as a Vaccine, and the Africa Policy Advisory Board of ONE. He was a TED Fellow and co-founded and delivered the TEDxEuston event from 2009 to 2019.

# Plenary speakers

## Plenary A:
## Controlling a pandemic
## – what are the ethical boundaries?



### Alena Buyx
**Germany**

*Professor, Institute for the History and Ethics of Medicine, Technical University of Munich*

Alena Buyx is Professor and Director of the Institute for the History and Ethics of Medicine at the Technical University of Munich. Previously, she held positions at Münster University, Harvard University, Kiel University and the Nuffield Council on Bioethics in London. A medical doctor with degrees in philosophy and sociology, Buyx regularly advises large international research consortia or institutions such as WHO on issues of biomedical and research ethics. She has been a member of the German Ethics Council since 2016 and was elected its chair since 2020. In 2021, she was appointed a member of the German Government's Covid-19 Expert Advisory Council. In these latter roles and during the Covid 19 pandemic, she provided various policy advice to government and other institutions and engaged in public debate.
*Photo copyright: Klaus Ranger*

## Plenary B:
## Refugees and refuge: how to promote and
## protect the health of displaced people



### Paul Spiegel
**United States**

*Director, Johns Hopkins Center for Humanitarian Health*

Dr Spiegel, a Canadian physician and epidemiologist by training, is one of the few humanitarians in the world that both responds to and researches humanitarian emergencies. He is internationally recognised for his research on preventing and responding to humanitarian emergencies, and more recently broader issues of migration. Beginning in 1992 as a Medical Coordinator responding to the refugee crisis for the "lost boys of Sudan" in Kenya, Dr. Spiegel has responded to and managed numerous humanitarian crises in Africa, Asia, Europe and the Middle East for over 30 years. Most recently he managed the emergency response for WHO in Afghanistan (Nov/Dec 2021) and in Europe for the Ukrainian refugees (Mar/Apr 2022).

Dr Spiegel is the Director of the Johns Hopkins Center for Humanitarian Health and Professor of the Practice in the Department of International Health at the Johns Hopkins Bloomberg School of Public Health (JHSPH). Before JHSPH, Dr. Spiegel was the Deputy Director of Program Support and Management and the Chief of Public Health at the United Nations High Commissioner for Refugees. He previously worked as a Medical Epidemiologist in the International Emergency and Refugee Health Branch at the Centers for Disease Control and Prevention in the United States, a Medical Coordinator with Médecins Sans Frontières and Médecins du Monde in refugee emergencies, and has been a consultant for numerous international organizations including the Canadian Red Cross and WHO. Dr Spiegel was the first Chair of the Funding Committee for Research for Health in Humanitarian Crises (2013-2018). He has published over 130 peer-reviewed articles on humanitarian health and migration. He has served as a Commissioner on the Lancet Commission for Migration and Health and the Lancet Commission on Syria. He is currently co-chair of Lancet Migration.

## Aurélie Ponthieu
**Belgium**
*Director, Analysis Department, Médecins Sans Frontières*

Aurélie Ponthieu has been working for the international medical humanitarian organisation Médecins Sans Frontières (MSF) since 2006. She is currently Director of the Analysis Department at MSF in Brussels where she manages a team composed of humanitarian specialists in the areas of health politics, forced migration, conflict and humanitarianism and negotiated access. Her area of expertise includes forced migration and the humanitarian impact of asylum and migration policies. She provides support to MSF operations in terms of context analysis, positioning and advocacy strategies.
Before working at MSF Headquarters in Brussels, she has worked in MSF Operations for several years in Niger (2006), Sudan (2007-2008), Chad (2008), Colombia (2009) and Haiti (2010). She also been sent to support emergency interventions during Ebola outbreaks in Liberia (2014) and the DRC (2019). In 2020 she worked on the covid-19 pandemic, advising the MSF emergency response in Brussels and as an Emergency Coordinator in Ecuador.
She has a Master's degree in International and European Law from the University of Toulouse (exchange program with McGill University in Montreal) and a Post-Graduate degree in Humanitarian Action/International Field Legal Assistance from the University of Aix-Marseille (NOHA).

## Elke Jakuboswki
**Germany**
*Director of Medical Department of Public Health Services and Infectious Diseases, Ministry of Social Affairs, Hamburg, Germany*

Elke Jakubowski is a Medical Doctor who specialized in comparative public health systems and health policies. Elke has been working for the World Health Organization in the European Region for about two decades. During her time in WHO, Elke has worked intensively with many Member States of the European Region, providing policy advice on strengthening health systems and improving access to health services. She moved back to Hamburg, Germany, four years ago in order to gain practical experience in policy making. In Germany, Elke was responsible for preventing and managing infectious diseases in the Free and Hanseatic City of Hamburg, working in the ministry of social affairs. She also coordinated the medical aspects of the Corona pandemic at the regional level since 2020. In early 2022, Elke additionally took over responsibility for setting up structures and processes to improve access to public health and medical services for the growing number of displaced people in Hamburg. Elke is currently reengaging in international health work, which is the passion of her professional life.

## Apostolos Veizis
**Greece**
*Executive Director, INTERSOS*

Dr. Apostolos Veizis is currently the Executive Director of INTERSOS in Greece. He has worked at the headquarters of Medecins Sans Frontieres-Greece as Director of Medical Operational Support Unit (SOMA), Programs and Institutional relations Director and Medical Director. Prior to that he worked as Head of Mission and Medical Coordinator for Medecins Sans Frontieres and Medecins Du Monde in Afghanistan, Azerbaijan, Russian Federation, Albania, Egypt, Georgia, Greece, Turkey. He also participated in assessment, emergency assignments and evaluations in Kyrgyzstan, Morocco, Armenia, Lebanon, Syria, Ukraine, Turkmenistan, Zambia, Malawi, Uzbekistan, North Macedonia, Cyprus, Moldova, Poland and Tajikistan. He is Advisory board member of the Lancet Migration European Regional Hub. He also participated and had announcements in international and national congresses and contributed to publications of relevant articles.

## Plenary C:
## Revolutions in vaccination in the age of COVID-19



## Hanna Nohynek
**Finland**
*Chief Physician, Unit Vaccines and Immune Protection, THL*

Hanna Nohynek is a Chief Physician of the Infectious Diseases Control and Vaccines Unit at the Finnish Institute for Health and Welfare (THL). Her research interests are register-based vaccine impact studies, evidence-based policy and decision making, vaccine uptake, vaccine safety, hesitancy, RSV, influenza, and pneumococcus. She was instrumental in designing the HPV vaccine introduction to the Finnish national immunisation programme. She has served on expert committees evaluating HBV, PCV, and rotavirus vaccine in Finland, and as an advisor to organisations including the EU, WHO and GAVI. She presently is a member of the WHO SAGE, chair of the WHO SAGE working group on COVID-19 vaccines, and a member of subgroup Influenza Vaccines, a member of the ECDC NITAG coordinating committee, and Vice-Chair and Board Member of the International Vaccine Institute. She also serves as secretary of the Finnish NITAG.

# Cornelia Betsch
**Germany**

*Heisenberg Professor for Health Communication,*
*University of Erfurt*

Cornelia Betsch is a psychologist and appointed Heisenberg Professor for "Health Communication" at the University of Erfurt. There she created the master's degree programme of the same name, a mix of psychology, communication science, medicine and public health. She also heads the Health Communication working group at the Bernhard Nocht Institute for Tropical Medicine in Hamburg. Even before the Corona pandemic, she was doing research in the field of psychology and infectious diseases control. Since the beginning of the pandemic, she and her team have regularly carried out the COVID19 Snapshot Monitoring (COSMO), a recording of the psychological corona situation. For this work she received the German Psychology Prize in 2021 and the Thuringian Research Prize in 2022. She presently is a member of the German government's COVID-19 Expert Advisory Council, of the WHO Technical Advisory Group on Behavioral and Cultural Insights, and of the Interdisciplinary Commission for Pandemic Research by the German Research Foundation (DFG). She is currently setting up an interdisciplinary research institute on Planetary Health Behaviour.
*Photo copyright: Marco Borggreve*



# Jeremy Ward
**France**

*Associate Researcher, INSERM*

Dr Jeremy Ward is a sociologist and associate researcher at the French National Institute for Health and Medical Research (INSERM). His work has mainly been focused on vaccine-related controversies in France and their effect on the French public. His focus is on the interface of sociology of public controversies, sociology of science and of cognition and representations. He has published in a variety of journals (Nature Immunology, Lancet Infectious diseases, Social Science and Medicine, Revue Française de Sociologie), and has numerous publications on vaccine mandates, including for COVID-19 vaccination.

## Plenary D:
## Cutting through the noise: the role of public health experts in managing an infodemic



### Mihai Craiu
**Romania**
*Professor of Paediatrics, Carol Davila University of Medicine*

Mihai Craiu is a Professor of Paediatrics at the Carol Davila University of Medicine in Romania. He has worked as a paediatrician for almost 30 years at the National Institute for Mother and Child Health of Romania (IMCHR). He has also served as a board member on national councils (the National Society of Paediatrics-SRPed and the National Society of Paediatric Respiratory Diseases) and is currently leading the Romanian NITAG. He is the founder of a social media educational project, 'Spitalul Virtual pentru Copii' ('The Virtual Children's Hospital'), which has contributed to changing the landscape of communication and education in Romanian language to parents.



### Neville Calleja
**Malta**
*Director, Health information and research, Ministry for Health*

Professor Neville Calleja is a medical doctor and public health specialist leading the Directorate for Health Information and Statistics within the Ministry for Health in Malta. He lectures medical statistics, epidemiology and public health to health care professionals, together with ethical and scientific review of projects, both at the local and international level. He has also been involved with collaborative research projects on health information, on developing statistical frameworks at the national level, and on piloting a WHO-designed peer-review health information system assessment methodology and also chairing a number of fora on the subject for WHO in Europe. Since 2020, he has been working with WHO to set up an infodemic management strategy and has been actively involved in the training of infodemic managers globally since.

## Alma Tostmann
**Netherlands**
*Epidemiologist and Deputy Head, Infection Prevention and Control Unit,
Dept Medical Microbiology, Radboud University Medical Centre*

Alma Tostmann works as an infectious disease epidemiologist and assistant professor at Radboud University Medical Centre in the Netherlands. She is Deputy Head of the Infection Prevention and Control Unit responsible for the surveillance of hospital acquired infections and the detection of outbreaks. Her research and teaching interests include global public health, infectious disease prevention, outbreak detection and control. She received the Dutch Women in Media award in 2022 for her active role in explaining epidemiological concepts and providing updates on the COVID pandemic in the media. She has also served as regional epidemiologist for the Antimicrobial and Infection Prevention Regional Healthcare Network of the province Gelderland (GAIN) and is affiliated to the National Institute for Public Health and the Environment (RIVM) as Regional Epidemiology Consultant for AMR. She is also a previous EPIET fellow and has previously served as the vice president of the EPIET Alumni Network.

## Martyna Bildziukiewicz
**Poland**
*Head, East Strategic Communications Task Force,
European External Action Service*

Dr Bildziukiewicz is a strategic communications and disinformation expert. Since 2018, she has been part of the EU East StratCom Task Force, of which she became the head in May 2021. The task force, based in the European External Action Service, runs the EUvsDisinfo project – the European Union's flagship initiative that monitors, responds to, and raises public awareness about pro-Kremlin disinformation. Dr Bildziukiewicz is also engaged in EU strategic communications in the Eastern Neighbourhood. Before she started to explore the dark side of words and messages, she was a career diplomat, spokesperson of the Polish Permanent Representation to the EU, journalist, and analyst. She holds a PhD in political science.

# Plenary E:
## The COVID-19 pandemic – a surveillance game changer?



## Silke Buda
**Germany**

*Deputy Head, Respiratory Infections Unit, Robert Koch Institute (RKI)*

Silke Buda is the Deputy Head of the Respiratory Infections Unit at the Robert Koch Institut, which is responsible for the surveillance, monitoring, epidemiological research and development of preventive concepts for respiratory infections. She has been working for some years on the use of ICD-10 codes for surveillance of viral respiratory diseases, including COVID-19, influenza and RSV. She has extensive experience in the use of electronic health records and surveillance of respiratory pathogens.



## Søren Alexandersen
**Denmark**

*Executive Vice President, Diagnostic Preparedness, Statens Serum Institut (SSI)*

Søren Alexandersen is the Executive Vice President for Diagnostic Preparedness at Statens Serum Institut. This is part of an integrated One Health collaboration, which involves the laboratory diagnosis of infections in humans and animals. His research interests include the development and use of molecular biology methods, including sequencing and metagenomics, as well as virus detection, characterisation and pathobiology, molecular epidemiology, and One Health. He is also an Affiliate Professor at Deakin University, in Victoria, Australia.
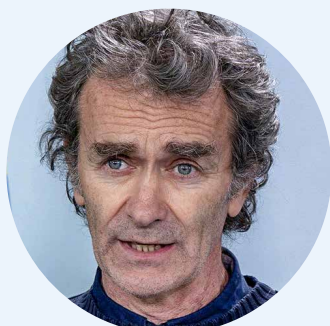


## Fernando Simon
**Spain**

*Director, Coordination Centre for Health Alerts and Emergencies, Ministry of Health*

Fernando Simón Soria is a Spanish epidemiologist serving as Director of the Coordination Centre for Health Alerts and Emergencies of the Ministry of Health. He came to public prominence as spokesman for the special committee on Ebola virus disease in Spain in 2014, and a similar role during the COVID-19 pandemic. He graduated in Medicine at the University of Zaragoza and specialized in Public Health and Epidemiology at the London School of Hygiene & Tropical Medicine. Simón trained in the European Training Program in Intervention Epidemiology (EPIET) at the European Centre for Disease Prevention and Control.

# Plenary summaries

## Plenary A:
## Controlling a pandemic
## – what are the ethical boundaries?

Day 1 - Wednesday 23 November, 8:50-10:00

**Keynote session**
From an ethicist's perspective, how can the public health objective of bringing a pandemic under control be reconciled with the societal needs for freedom of choice and a functioning economy? Experience from the last two years with lockdowns and vaccination and face mask mandates has raised questions about how to balance the need to protect lives with the need to protect livelihoods. The session will include reflections on how ethical aspects should be taken into account when preparing for a public health crisis, and how ethicists and public health experts/policymakers can work together better to integrate ethics into decision making regarding public health measures.

**Chairs:** Andrea Ammon (ECDC) and Mike Catchpole (ECDC)
**Keynote speaker:** Alena Buyx (Technical University of Munich, Germany)


## Plenary B:
## Refugees and refuge: how to promote and protect the health of displaced people

Day 1 - Wednesday 23 November, 16:30-18:00

The challenges of protecting and promoting the health of people displaced by war or other events are manifold. Those responsible for providing support need to take into account the conditions that displaced people experienced prior to their flight, the conditions encountered during flight, and the conditions under which they will be accommodated in the receiving country. The assessment of needs and provision of support need to be culturally sensitive, avoid unwarranted stigmatisation and cope with the challenges of working with a mobile population. In this session the audience will hear from, and have the opportunity to engage in discussion with, experts with frontline practical experience and policy expertise of responding to refugee needs.

**Chairs:** Stine Nielsen (EAN) and Chikwe Ihekweazu (WHO)
**Speakers:** Paul Spiegel (Johns Hopkins Center, USA), Aurélie Ponthieu (Médecins Sans Frontières), Elke Jakubowski (Health Policy Europe, Germany), Apostolos Veizis (INTERSOS, Greece)

## Plenary C:
## Revolutions in vaccination in the age of COVID-19

Day 2 - Thursday 24 November, 9:00-10:30

Throughout the COVID-19 pandemic, we have seen major developments in vaccination. These developments have raised important questions which will impact future vaccination programmes - including regarding the implications that COVID-19 vaccine incentives, certificates and mandates might have on the future of routine vaccination and uptake; regarding how mRNA vaccines have transformed vaccination; and regarding the progress in evidence-based public communication about vaccines. This session will explore how the attitudes and drivers, especially those related to new vaccine technologies and to vaccine mandates, should be monitored and how the information derived from such monitoring could and should be used by governments and institutions to design successful campaigns aimed at promoting vaccination acceptance and uptake.

**Chairs:** Adam Roth (ECDC) and Magdalena Rosińska (National Institute of Health, Poland)
**Speakers:** Hanna Nohynek (THL, Finland), Cornelia Betsch (University of Erfurt, Germany), Jeremy Ward (INSERM, France)

## Plenary D:
## Cutting through the noise: the role of public health experts in managing an infodemic

Day 2 - Thursday 24 November, 16:30-18:00

Experiences from the COVID-19 pandemic highlight challenges for public health communicators in the rapidly changing environment of public communication, including the influence of social media and the increasing polarisation of public perception and debate. This session explores how public health communicators and institutions can best contribute to building public trust and promoting scientific literacy by identifying skills and systems needed to effectively respond to and prepare for infodemics and handling misinformation.

**Chairs:** John Kinsman (ECDC), Petronille Bogaert (Sciensano, Belgium), and Mircea Ioan Popa (Carol Davila University of Medicine and Pharmacy, Romania)
**Speakers:** Mihai Craiu (Mother and Children Hospital Bucharest, Romania), Neville Calleja (Ministry for Health, Malta), Alma Tostmann (Radboud University Medical Centre, Netherlands), Martyna Bildziukiewicz (European External Action Service)

**Plenary sessions** - Plenary session summaries

# Plenary E:
# The COVID-19 pandemic
# – a surveillance game changer?

Day 3 - Friday 25 November, 9:00-10:30

The past two year's experiences with the COVID-19 pandemic have offered new perspectives on communicable disease surveillance. This session will explore how data from electronic health records can contribute to communicable disease surveillance, how genome sequencing has contributed to our assessment and response activities relating to COVID-19, and what the implications are for future surveillance of acute respiratory infections.

**Chairs:** Vicky Lefevre (ECDC), Bruno Coignard (Santé publique France), and Luísa Peixe (University of Porto, Portugal)
**Speakers:** Silke Buda (RKI, Germany), Søren Alexandersen (SSI, Denmark), Fernando Simon (Ministry of Health, Spain)

# Abstract presentations

**Abstract presentations form a key part of the scientific programme at ESCAIDE. Abstracts are presented at ESCAIDE as either oral presentations or posters.**

**This year, over 430 abstracts were submitted to the standard call for abstracts, and over 90 to the late breaker abstract call. Of these, 170 standard call abstracts, and 21 late breakers, were selected to be presented as posters or oral presentations, covering a diverse spectrum of topics within applied infectious disease research and epidemiology. Poster tours and oral presentations are organised by topic and dispersed throughout the conference programme.**

## Oral presentations – fireside sessions

A *fireside session* is a moderated Q&A where the presenters are given the opportunity to discuss their work and answer questions from the audience. Presentations are be grouped by theme into sessions.

During the session, each presenter has 15 minutes to discuss their work, which includes a short presentation by the speaker (~7 min), a moderator-led discussion (~5 min) and questions from the audience (~2 min).

## Poster presentations – poster tours

Each can be viewed on the conference online platform, and throughout the conference days, in e-poster terminals spread in the venue and in the e-poster area. The details of the poster and presenter will be available, and participants can directly message presenters about their work.

At ESCAIDE 2022 we are also hosting *poster tours* in a hybrid format for many of the poster abstracts. These give presenters and participants an opportunity to delve deeper into their content. In each 45-minute session, presenters have 2 minutes to introduce their work, which is 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 contact the authors to further discuss the research.

The posters are available on the online conference 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.

## Online-only posters

Online-only posters will be displayed in the virtual poster exhibition on the online conference platform, and the abstracts will be listed in the abstract book. However, due to time and venue capacity limitations, there will not be the opportunity to give a verbal presentation of the poster, but participants will be encouraged to view the posters online and can post comments and questions for you to respond to.

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# Abstract reviewers

*The Scientific Committee warmly thanks the reviewers of the abstracts submitted for ESCAIDE 2022.*

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# Fireside sessions

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## FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 − 12:30

## Implementation science

**MODERATOR**
Howard Needham

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## Abstract

### Enhanced event-based surveillance: monitoring events during the Ukraine crisis, 2022

**J. Bilbatua** [1]

X. Andrianou [2], H. Tareq [3], G. Mirinaviciute [4], L. Alexakis [5], N. Rachwal [6], L. Lucena Baeza [7], G. Spiteri [8]

[1-8] European Centre for Disease Prevention and Control

**BACKGROUND**
The Ukraine crisis led to large and sudden population movements to various EU/EEA countries, resulting in a possible increased communicable disease risk. This prompted ECDC to enhance its event-based surveillance (EBS) activities to rapidly detect, assess, and communicate possible infectious disease threats.

**METHODS**
ECDC monitored official and non-official open sources using web-aggregators and social media for events with potential public health impact primarily on infectious diseases and on size and direction of population movements, impact on healthcare/infrastructure/supplies and other hazards. We extracted information on signals collected between 3 March and 15 May 2022 and describe them quantitatively and qualitatively.

**RESULTS**
Overall, 233 signals were detected from media (73%) and official sources (27%). Of these, 37.3% related to population movements and 32.2% (n=75) to infectious diseases. The latter mostly related to prevention activities in receiving countries (n=57). There have been only few and sporadic cases of infectious diseases detected, and mostly by teams in the field rather than by population-based or targeted surveillance systems.

**CONCLUSIONS**
No major communicable diseases events  have been detected so far, possibly due to the rapid dispersion and integration of displaced people in the communities, rather than residing in crowded temporary settings. Information from the field was relevant and timely, suggesting that multiple information sources are pivotal in similar events. In the absence of strong syndromic or laboratory-based surveillance systems, enhanced EBS enabled health monitoring and could support preparedness and response actions.

**Keywords:** Event-based Surveillance, Epidemic intelligence, Crisis, Threats
**ABSTRACT ID:** 411
**PRESENTED BY:** Jon Bilbatua / jon.bilbatua@ecdc.europa.eu

# FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 − 12:30

## Implementation science

**MODERATOR**
Howard Needham

## Abstract

### Collaborative modelling of the future dynamics of COVID-19: the European Forecasting and Scenario Hubs

**K. Sherratt** [1]

H. Gruson [2], J. Bracher [3], S. Funk [4]

[1, 2, 4] London School of Hygiene and Tropical Medicine (LSHTM)
[3] Karlsruhe Institute of Technology

**BACKGROUND**
Modelling future epidemic dynamics involves short-term forecasts for situational awareness as well as longer term scenarios for broader insights and planning. Differences in underlying assumptions, methodologies and model structures can lead to different modelled outcomes, limiting the utility of any single model in informing policy. We aimed to create a public, collaborative platform with standardised reporting of results for modelling COVID-19 outcomes across 32 European countries.

**METHODS**
We created the European COVID-19 Forecasting and Scenario Hubs. From March 2021, we combined weekly short-term forecasts of cases, hospitalisations, and deaths from up to 30 teams, and assessed predictions by later comparing them to observed outcomes. From March 2022, we further collated multiple rounds of 9-12 month scenario simulations, exploring the interaction of waning immunity with new variants and vaccinations. We evaluated projections by the extent of variation between models, scenarios, and countries.

**RESULTS**
Forecast models competently predicted stable epidemic behaviour, but varied in their ability to account for inflection points, for example due to new variant introductions or population-level behaviour change. Relative to individual models, an ensemble improved performance 1-4 weeks ahead, outperforming them for 84% of case forecasts (N=862) and 92% of death forecasts (N=746). In scenario comparisons, we found the speed of waning immunity crucial in the seasonal timing of COVID-19 outbreaks, while we observed greater variation between models, compared to between countries, in the frequency and magnitude of outbreaks.

**CONCLUSIONS**
No major communicable diseases events have been detected so far, possibly due to the rapid dispersion and integration of displaced people in the communities, rather than residing in crowded temporary settings. Information from the field was relevant and timely, suggesting that multiple information sources are pivotal in similar events. In the absence of strong syndromic or laboratory-based surveillance systems, enhanced EBS enabled health monitoring and could support preparedness and response actions.

# FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 − 12:30

## Implementation science

**MODERATOR**
Howard Needham

## Abstract

### Endemic Zika Virus in Brazil

**L. Yakob** [1]
[1] London School of Hygiene & Tropical Medicine

**BACKGROUND**
Following a cluster of associated neurological disorders and neonatal malformations, WHO declared the Zika virus (ZIKV) outbreak in Latin America and the Caribbean a Public Health Emergency of International Concern (PHEIC) in 2016. By 2017, new cases in the region had declined and the epidemic was widely considered to be over by 2018. Although subsequent large outbreaks have not occurred, low-level ZIKV transmission persists. Study objectives were to identify Brazilian states with consistent, ongoing transmission, and, to forecast future cases at the regional level.

**METHODS**
Post-PHEIC data on confirmed and suspected cases (years 2017-2020) were used to train and validate Seasonal Autoregressive Integrated Moving Average (SARIMA) models for Brazil at the regional level. Consistency scores were generated for post-PHEIC, population-standardized cases at the municipality level (n=5,570). These were then used to weight kernel density estimates to map hotspots. Clustering was estimated using Moran's I.

**RESULTS**
The SARIMA models provided adequate fits as indicated by diagnostic plots and low Root Mean Square Errors. 8,476 new cases were forecasted for 2021-2022 (95%CI 279–54,732 new cases) mostly in the northeast and southeast regions. Hotspot municipalities with consistent ZIKV transmission were identified for all five Brazilian regions. Monte Carlo simulation indicated significant spatial clustering (p=0.047) and Moran's I statistics estimated per calendar month demonstrated clear seasonality in clustering.

**CONCLUSIONS**
This study provides spatiotemporal targets for more intensive vector control efforts to ameliorate disease burden among the worst-affected populations. It also informs site selection for seroprevalence studies and intervention trials.

**Keywords:** Zika virus, Endemic, Transmission, Clusters, Mosquito
**ABSTRACT ID:** 9
**PRESENTED BY:** Laith Yakob / laith.yakob@lshtm.ac.uk

# FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Implementation science

**MODERATOR**
Howard Needham

## Abstract

### Effectiveness of Four Vaccines in Preventing SARS-CoV-2 Infection in Kazakhstan

**D. Nabirova** [1]
R. Horth [2], M. Smagul [3], G. Nukenova [4], A. Yesmagambetova [5], D. Singer [6], A. Henderson [7], A. Tsoy [8]

[1] Senior Advisor for Central Asia FETP - U.S. Centers for Disease Control and Prevention, Central Asia Regional Office, Almaty, Kazakhstan
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[5, 8] Ministry of Healthcare, Nur-Sultan, Kazakhstan
[7] U.S. Centers for Disease Control and Prevention, Atlanta, USA

**BACKGROUND**
In February 2021 Kazakhstan began offering COVID-19 vaccines to adults. Breakthrough SARS-CoV-2 infections raised concerns about real-world vaccine effectiveness. We aimed to evaluate effectiveness of four vaccines against SARS-CoV-2 infection.

**METHODS**
We conducted a retrospective cohort analysis among adults in Almaty using aggregated vaccination data and individual-level breakthrough COVID-19 cases (≥14 days from 2$^{nd}$ dose) using national surveillance data. We ran time-adjusted Cox-proportional-hazards model with sensitivity analysis accounting for varying entry into vaccinated cohort to assess vaccine effectiveness for each vaccine (measured as 1-adjusted hazard ratios) using the unvaccinated population as reference (N=565,390). We separately calculated daily cumulative hazards for COVID-19 breakthrough among vaccinated persons by age and vaccine month

**RESULTS**
From February 22 to Sept 1, 2021 in Almaty, 747,558 (57%) adults were fully vaccinated (received 2 doses) and 108,324 COVID-19 cases (11,472 breakthrough) were registered. Vaccine effectiveness against infection was 78% (sensitivity estimates: 74–82%) for QazVac, 77% (72–81%) for Sputnik V, 71% (69–72%) for Hayat-Vax, and 69% (64–72%) for CoronaVac. Among vaccinated persons, the 90-day follow-up cumulative hazard for breakthrough infection was 2.2%. Cumulative hazard was 2.9% among people aged ≥60 years versus 1.9% among persons aged 18–39 years (p<0.001), and 1.2% for people vaccinated in February–May versus 3.3% in June–August (p<0.001).

**CONCLUSIONS**
Our analysis demonstrates high effectiveness of COVID-19 vaccines against infection in Almaty similar to other observational studies. Higher cumulative hazard of breakthrough among people >60 years of age and during variant surges warrants targeted booster vaccination campaigns.

**Keywords:** SARS-CoV-2 infection, Vaccine effectiveness, Kazakhstan, QazVac vaccine
**ABSTRACT ID:** 229
**PRESENTED BY:** Dilyara Nabirova / dnabirova@gmail.com

# FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Implementation science

**MODERATOR**
Howard Needham

## Abstract

### An Approach to Developing One Health Field Epidemiology Competencies

**M. Muehlen [1]**
B. Alessandrini [2], C. David [3], S. D'albenzio [4], R. Dissanayake [5], S. Dunkle [6], J. Pinto [7], H. Simmons [8],
A. Zaghloul [9], K. Schenkel [10]

[1, 9, 10] WHO
[2, 3, 4, 8] OIE
[5, 6, 7] FAO

**BACKGROUND**
Recent epidemics and pandemics have shown the need for a multi-sectoral, interdisciplinary epidemiology workforce with a wide range of competencies. Field epidemiologists play a vital role in surveillance, field investigation, preparedness and response to biothreats. This project defined One Health field epidemiology competencies for the public, animal, and environment health sectors at the frontline, intermediate, and advanced levels.

**METHODS**
A joint tripartite (FAO, OIE, WHO) working group conducted desk top reviews of existing competencies and curricula for field epidemiology training programs (FETPs) and FETPs for veterinarians (FETPVs) and met weekly from March-September 2021 to organize them into domains and subdomains. An online survey among existing FETP(V)s was conducted to identify current competencies. A technical advisory group (TAG) of international stakeholders and experts was convened to review and validate proposed competencies and define them as core (mandatory) or optional at all three levels.

**RESULTS**
More than 300 field epidemiology competencies were identified for the frontline level, an additional 280 for the intermediate, and 324 for the advanced levels. During the review process, the TAG proposed merging Data Analysis and Bioinformatics and suggested Ecosystem Health as an additional domain. Competencies were grouped into 14 domains with 75 subdomains and considered core when at least 90% of the TAG survey respondents prioritized them.

**CONCLUSIONS**
Given the importance of a multisectoral workforce that is competent in epidemiological skills and methods and capable of conducting a full range of activities in the field, it is essential to ensure they receive competency-based training associated with their position. The domains and core competencies identified through this collaborative review will be used to propose a progressive one health field epidemiology curricular pathway for all three levels.

**Keywords:** Field epidemiology, One Health, Workforce Development, Competency, Training
**ABSTRACT ID:** 241
**PRESENTED BY:** Marion Muehlen / muehlenm@who.int

**Abstract presentations** - Fireside sessions

# FIRESIDE SESSION 1
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Implementation science

**MODERATOR**
Howard Needham

## Abstract

### Community-based One Health Approach to Prevent, Detect and Respond to Disease Outbreaks

**S. Gabriela** [1]

M. Haryono [2], D. Handayani [3], E. Cahya [4], A. Rangkuti [5], M. Latuihamallo [6]

[1, 2, 3] The International Federation of Red Cross and Red Crescent Societies Country Cluster Delegation for Indonesia and Timor Leste
[4] The Indonesian Red Cross
[5, 6] The United States Agency for International Development

**BACKGROUND**
Recent large-scale epidemics and pandemics such as Covid-19 have demonstrated that it takes an inclusive and collaborative effort engaging communities as full-fledged partners to effectively prevent, detect, and respond to disease threats and minimize their impacts. Community members are the first responders when unusual health events of human and animal cases occur in their community.

**METHODS**
The IFRC in close collaboration with the Indonesian Red Cross Society (PMI) and the Government of Indonesia through the support of the USAID has been implementing community-based surveillance (CBS) using One Health approach. CBS utilizes community case definition to identify and report signs and symptoms of potential health risks and unusual events on animal and humans.

**RESULTS**
In 2020, a total of 234 village volunteers in four pilot districts were able to report more than 61 animal and human cases preventing outbreaks to over 80,000 community members. From the reported alerts, the Public Health Office and the Animal Health Office were able to respond to over 80 percent of confirmed cases such as leptospirosis, rabies, avian influenza, anthrax, Diphtheria, measles, dengue, tuberculosis, and Covid-19 within 24 hours.

**CONCLUSIONS**
CBS model has strengthened public health and animal health surveillance with higher community engagement, resulting in early detection, early report, and timely response. In conclusion, people at the grassroots level are vital contributors and important change agents to sustainably detect, control and contain disease spread, thus helping to save lives, increase community resilience for pandemic preparedness. The community-based One Health approach proved that a multistakeholder collaboration between Government, media, academia, private sector, and communities is workable through strategic investment and early stakeholders engagement.

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Invasive beta-hemolytic streptococcal infections in Finland, 2006-2020: The rise of Lancefield group C/G infections

**D. Paspaliari [1],**

E. Savikivi [2], J. Ollgren [3], J. Vuopio [4]

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

[1] EUPHEM

#### BACKGROUND
Beta-hemolytic streptococci are a major cause of morbidity and mortality, especially in conjunction with invasive infections. The main human pathogens belong to three Lancefield groups: A (GAS), B (GBS) and C/G (GCGS). Despite their significance, invasive streptococcal infections are notifiable in only few countries. We studied the incidence of invasive beta-hemolytic streptococcal infections in Finland in 2006-2020, focusing on GCGS, for which surveillance is particularly lacking.

#### METHODS
Case notifications were retrieved from the National Infectious Disease Register, where all invasive cases are mandatorily notified. Cases were defined as isolations from blood and/or cerebrospinal fluid. To examine the effects of age and sex, we used negative binomial regression, with age, sex and year as dependent variables.

#### RESULTS
Between 2006-2020, 3352 GAS, 4190 GBS and 8239 GCGS invasive infections were reported in Finland. The average annual incidence was 4.1 (range:2.1-6.7), 5.2 (4.0-6.3) and 10.1 (5.4-17.6) per 100,000 population, respectively, peaking in 2018-2019. For GCGS, the incidence has increased sharply (8% annual relative increase vs. 3% for GAS and 2% for GBS). The median age of cases was 56y for GAS,66y for GBS and 73y for GCGS. Male sex was overall a risk factor for GCGS (adjIRR=1.6, 95%CI=1.5-1.8) and GAS (adjIRR=1.2, 95%CI=1.1-1.4); for GBS, the association was age-group-dependent. In adults, GCGS incidence increased significantly with age, especially for age>55y.

#### CONCLUSIONS
The incidence of invasive beta-hemolytic streptococcal infections in Finland has been rising, especially for GCGS. However, national surveillance still focuses on GAS and GBS, while EU-wide surveillance is lacking. We recommend that surveillance of GCGS be enhanced, including the study of disease burden and risk factors, as well as the systematic collection and typing of isolates, to guide infection prevention strategies.

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Investigating the sociodemographic and behavioural factors associated with hepatitis C virus testing amongst people who inject drugs in England, Wales and Northern Ireland

**J. Yuan** [1]
S. Croxford [2], L. Viviani [3], E. Emanuel [4], E. Phipps [5], M. Desai [6]

[1, 2, 4, 5, 6] UK Health Security Agency (UKHSA)
[3] London School of Hygiene and Tropical Medicine (LSHTM)

#### BACKGROUND
Hepatitis C virus (HCV) transmission in the UK is driven by injecting drug use. We explore HCV testing uptake amongst people who inject drugs (PWID) in England, Wales and Northern Ireland, and identify factors associated with i) ever having an HCV test amongst people who have ever injected drugs, and ii) recently having an HCV test (within the current/previous year) amongst people who currently inject drugs (reported injecting drugs within the last year).

#### METHODS
We analysed data from the 2019 'Unlinked Anonymous Monitoring Survey' of PWID, using logistic regression.

#### RESULTS
Of 3,127 PWID, 2,065 reported injecting drugs within the last year.
Most (86.7%) PWID had lifetime histories of HCV testing. In multivariable analysis, higher odds of ever testing were associated with: female sex (aOR=1.54; 95%CI=1.11-2.14), injecting duration ≥3 years (aOR=2.94; 95%CI=2.13-4.05), ever receiving used needles/syringes (aOR=1.74; 95%CI=1.29-2.36), ever receiving opioid-agonist treatment (aOR=2.91; 95%CI=2.01-4.21), ever imprisonment (aOR=1.86; 95%CI=1.40-2.48) and ever homelessness (aOR=1.54; 95%CI=1.14-2.07).
Amongst PWID who had injected drugs within the last year, 49.9% had recently undertaken HCV testing. After adjustment, higher odds of recent HCV testing were associated with: injecting crack in the last year (aOR=1.29; 95%CI=1.03-1.61), experiencing a non-fatal overdose in the last year (aOR=1.39; 95%CI=1.05-1.85), ever receiving opioid-agonist treatment (aOR=1.48; 95%CI=0.97-2.25), receiving HCV information in the last year (aOR=1.99; 95%CI=1.49-2.65) and using a healthcare service in the last year (aOR=1.80; 95%CI=1.21-2.67).

#### CONCLUSIONS
Results suggest PWID who have experienced homelessness and incarceration – amongst the most vulnerable and marginalised in the PWID population – are engaging with HCV testing, but overall there remain missed testing opportunities. Recent initiates to injecting have highest HCV infection risk but lower odds of testing, and peer-education may help target this group.

**Keywords:** Hepatitis C, Drug users, Routine Diagnostic Test, Multivariate analysis
**ABSTRACT ID:** 253
**PRESENTED BY:** Jin-Min Yuan / jmyuan26@gmail.com

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022

11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Neisseria gonorrhoeae antimicrobial resistance surveillance in the Netherlands: a 10-year overview

**M. Visser** [1]

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[1, 3] National Institute for public health and the environment (RIVM)

[2] Public Health Laboratory, Public Health Service of Amsterdam - Amsterdam UMC, University of Amsterdam, Amsterdam Institute for Infection and Immunity (AII)

**BACKGROUND**

Antimicrobial resistance in *Neisseria gonorrhoeae* (NG-AMR) is emerging worldwide and poses a threat for effective treatment of gonorrhoea. In the Netherlands, NG-AMR is monitored in the Gonococcal Resistance to Antimicrobials Surveillance (GRAS) programme. Here, we present the main results from the last 10 years of GRAS.

**METHODS**

An average of 15 out of 24 Sexual Health Centres (SHCs) participated in GRAS between 2012 and 2021. These SHCs perform additional culturing for gonorrhoea patients and test susceptibility for ceftriaxone (first-line treatment in the Netherlands), cefotaxime, azithromycin, and ciprofloxacin using Etest. MIC-values and patient characteristics are reported in GRAS. Resistance levels were calculated using EUCAST breakpoints.

**RESULTS**

In the past 10 years, SHCs participating in GRAS reported 50,555 gonorrhoea diagnoses, of which 39.6% (n=20,031) included susceptibility tests. 80% of diagnoses were among men who have sex with men. The proportion of included pharyngeal and anorectal isolates increased from 11.7% in 2012 to 62.0% in 2021.

Between 2012 and 2021, resistance to ciprofloxacin increased from 27.7% to 52.9%. Azithromycin resistance increased from 2.1% to 18.0%, and cefotaxime resistance decreased from 4.5% to 0.1%. No resistance to ceftriaxone was reported and the proportion of strains with an MIC-value near breakpoint (0.032-0.125 mg/L) is decreasing. However, also a decrease of isolates with an MIC ≤0.002 mg/L is observed for ceftriaxone and cefixime, while the proportion of isolates with an MIC between 0.003 and 0.016 mg/L is increasing since 2017.

**CONCLUSIONS**

No resistance to ceftriaxone has been reported. However, trends of decreasing susceptibility are observed for all antimicrobials monitored in GRAS. Therefore, continued monitoring of NG-AMR is important to ensure timely detection of emerging resistance and to inform treatment and prevention guidelines.

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Contribution of Sexual Health Centres in hepatitis B detection and control in the Netherlands

**S. Raven** [1]

J. Hautvast [2], W. Yiek [3], I. Veldhuijzen [4], F. van Aar [5], J. van Steenbergen [6], C. Hoebe [7]

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[6] Centre for Infectious Diseases, Leiden University Medical Centre, Leiden, The Netherlands
[7] Department of Sexual Health, Infectious Diseases and Environmental Health, South Limburg Public Health Service, The Netherlands

**BACKGROUND**
Case finding is one of the priority actions to reduce the disease burden of chronic hepatitis B (CHB). We estimated the contribution of CBH case finding at Sexual Health Centres (SHCs) to the total national number of newly diagnosed CHB cases in the Netherlands and determined the characteristics of CHB cases detected at SHCs.

**METHODS**
We used surveillance data from all outpatient SHCs in the Netherlands and national notification data from 2008-2016. The proportion of CHB notifications detected at SHCs was calculated. Consultations without hepatitis B virus (HBV) testing (n=669,308), with acute hepatitis B diagnosis (n=73) or with HBV vaccination only (n=182) were excluded. Univariable and multivariable logistic regression analysis was performed, stratified by gender and sexual preference, to analyze patient characteristics associated with CHB.

**RESULTS**
In the 9 year study period 12,149 CHB cases were notified. 405,646 SHC consultations were included in the analysis and 1452 CHB cases (0.4%) were detected at SHCs .The proportion of CHB cases detected at SHCs ranged between 12.4% (200/1613) in 2008 and 10.8% (106/980) in 2016. 87% of CHB cases were among first generation migrants (FGM) originating from high-endemic countries for sexually transmitted infections or men who have sex with men (MSM). In multivariable analysis an older age category, migration background and being a commercial sex worker (CSW) were associated with CHB in all stratified analysis. 88% of CHB cases among CSW were FGM.

**CONCLUSIONS**
The contribution of SHCs is relevant to case finding of CHB in the Netherlands. SHCs should therefore be considered as an important health setting to screen for HBV in high-risk groups, especially among MSM and FGM, to achieve a reduction in the HBV related disease burden.

**Keywords:** Hepatitis B chronic, Public Health Surveillance Sexually transmitted Diseases, Preventive Health Services
**ABSTRACT ID:** 420
**PRESENTED BY:** Stijn Raven / stijn.raven@radboudumc.nl

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Effects of Improving Partner Notification on HIV and gonorrhea transmission among men who have sex with men in the Netherlands

**M. Reitsema [1]**

J. Wallinga [2], B. van Benthem [3], E. op de Coul [4], A. van Sighem [5], M. Schim van der Loeff [6]

[1, 2, 3, 4] RIVM

[1] LUM

[5] Stichting HIV Monitoring

[6] Public Health Service Amsterdam

### BACKGROUND
Men who have sex with men (MSM) are disproportionally affected by HIV infections in the Netherlands. Partner Notification (PN) is an important element of controlling the transmission of sexually transmitted infections (STIs). To study the effects of improving PN we constructed an agent-based model to simulate the transmission of HIV and *Neisseria gonorrhoeae* (NG) among Dutch MSM.

### METHODS
In baseline simulations: 14.3% and 29.8% of casual and steady partners of the index patient were tested for HIV/STIs after three weeks. We examined three improved PN scenarios: (1) 41% of the index' partners get tested; (2) the time between tests of index and partner decreased to one week; (3) 41% of the index' partners get tested, the time between tests decreased to one week. Effects are expressed as cumulative change from the baseline simulation after 15 years.

### RESULTS
Scenario 1 led to a change in new NG infections of -44% (95%CI, -21% to -62%), while there was hardly any change in HIV infections (-4.0%; 95%CI, -28.1% to 25.5%) or in HIV/STI tests performed (4.1%; 95%CI, -5.6% to 12.1%). Scenario 2 led to a change in NG infections of -14.1% (95%CI, -3.2% to -23.5%), hardly any change in HIV infections (6.0%; 95%CI, -11.6% to 31.0%) or in number of HIV/STI tests (-0.8%; 95%CI, -4.3% to 2.0%). Scenario 3 led to a very large change decrease in NG infections of -55.6% (95%CI, -26.4% to -73.9%), hardly any change in HIV infections (6.9%; 95%CI, -23.7% to 62.8%) or in number of HIV/STI tests (-0.5%; 95%CI, -13.9% – 12.1%).

### CONCLUSIONS
Improved PN led to a substantial decrease in NG with hardly a change in HIV infections or the number of HIV/STI tests performed.

**Keywords:** HIV, Partner notification, MSM, Modelling, STI
**ABSTRACT ID:** 126
**PRESENTED BY:** Maarten Reitsema / maarten.reitsema@rivm.nl

# FIRESIDE SESSION 2
DAY 1, 23 NOVEMBER 2022
11:00 – 12:30

## Sexually and community acquired infections, including HIV

**MODERATOR**
Aura Georgina Aguirre-Beltran

## Abstract

### Questionnaire data identifies monkeypox common exposure events at sex-on-premise venues and festivals, England

**A. Løchen** [1]

J. Yuan [2], C. Ryan [3], K. Cella [4], E. Gilham [5], N. Bray [6], A. Graham [7], C. Turner [8], C. Byers [9], K. Wrenn [10], R. Vivancos [11], O. Edeghere [12], S. Walker [13], H. Charles [14], M. Prochazka [15], L. Bishop [16], P. Blomquist [17], C. Anderson [18]

[1-18] UK Health Security Agency
[3] Lancaster University

### BACKGROUND
The large monkeypox outbreak in England since May 2022, is affecting mostly gay, bisexual, or men who have sex with men (GBMSM). Enhanced surveillance questionnaires aim to inform public health action, including targeting venues where transmission may have occurred. We describe the findings and use of this data in identifying these locations.

### METHODS
Questionnaire data asking about attendances in incubation and infectious periods was analysed to identify common exposure events, defined as two or more cases reported attending the same venue on the same date. Venues were categorised as sex-on-premise, festival, bar, nightclub, gym/swimming pool, event, private sex party, sauna, other, or unknown.

### RESULTS
Between 6 May 2022 and 8 September 2022, there were 3668 cases of monkeypox in England: 1019 (27.8%) responded to the questionnaire, and 40.3% provided information about event/venue attendances. 933 reported events (domestic and international) were attended by 411 cases (11.2% of cases), resulting in 40 common exposures attended by 142 unique individuals. Venues were visited an average of 1.23 times within the study period. Of the 40 common exposures, up to 36 people reported same-day attendance at the same event. Sex-on-premise venues were the most frequent common exposures (27%), followed by festivals (26%). Results were shared with local public health teams to enable direct support to affected venues, including: venue decontamination, awareness-raising among venue attendees about monkeypox symptoms, and testing and isolation, as well as prioritisation to vaccinate attendees of venues of interest.

### CONCLUSIONS
While questionnaire uptake was limited, venues featuring sexual or close contact are commonly reported and plausible monkeypox transmission settings. These data support public health interventions in specific venues to prevent further spread and raise awareness among groups at risk.

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

How COVID-19 fast-tracked the development of a national microbiology laboratory database for surveillance in Norway: Success factors

**N. Aasand** [1]

M. Storm [2], O. Håvelsrud [3], H. Løwer [4], M. Øgle [5], A. Kran [6], A. Løvlie [7], K. Johansen [8]

[1-8] Norwegian Institute of Public Health

**BACKGROUND**
The Norwegian Surveillance System for Communicable Diseases (MSIS) was, pre- pandemic, based on manual reporting of cases from laboratories and clinicians. There was a need for more timely and comprehensive surveillance data, enabling real time monitoring of both cases and test activity. A national microbiology laboratory database could facilitate the surveillance of all infectious diseases and reduce the burden and errors associated with manual reporting. A legal framework and project plans were already in place in January 2020. However, national authorities were not convinced that the benefit exceeded the costs. We describe the process of establishing a complementary surveillance system for infectious diseases in The MSIS Microbiology Laboratory Database (MMLD), focusing on key enabling success factors for rapid development.

**METHODS**
This is an experience-based, descriptive study of the process of developing MMLD during the COVID-19 pandemic.

**RESULTS**
In addition to existing plans and changes in legal framework, preconditions included national standards for clinical laboratory reporting and messaging, and technological infrastructure. Clear prioritizations from the authorities were essential and ensured availability of IT resources with in-depth domain knowledge. MMLD was established within two weeks in March 2020, and by April 1, all Norwegian laboratories reported their COVID-19 results. By September 2021, the microbiology laboratories started reporting results for all pathogens. As of May 2022, 75 % of Norwegian laboratories are reporting all microbiological results to MMLD.

**CONCLUSIONS**
The rapid development of MMLD was driven by the COVID-19 pandemic, which led to clear prioritization from the authorities. However, this had not been possible without multiple factors already in place. This rapid development served as a cornerstone to facilitate more timely and comprehensive surveillance of COVID-19, and subsequently other infections.

**Keywords:** Surveillance, COVID-19 pandemic, Laboratory services, Clinical, Microbiology, Database
**ABSTRACT ID:** 271
**PRESENTED BY:** Nina Aasand / NinaTherese.aasand@fhi.no

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

### Impact of universal Tuberculosis (TB) vaccination cessation on the epidemiology of paediatric TB cases in Ireland, 2011-2021

**S. Jackson** [1]

Z. Kabir [2], C. Comiskey [3]

[1] Health Service Executive Health Protection Surveillance Centre (HSE-HPSC)
[2] University College Cork (UCC)
[1,3] Trinity College Dublin (TCD)

**BACKGROUND**
Universal Bacillus Calmette-Guérin vaccine (BCG) vaccination was discontinued in Ireland in April 2015 due to lack of vaccine supply. We analysed notifications from the Irish National Tuberculosis (TB) Surveillance System from 2011-2021 to examine the direct impact of vaccination cessation on active TB cases among 0-4 year olds.

**METHODS**
We compared TB age specific incidence rates (ASIRs) among 0-4 year olds born during a period of BCG vaccination (January 2007- March 2015) with those born after BCG vaccination ceased (April 2015-December 2021) by person, place and time. We calculated ASIRs using census population denominators and performed temporal trend analysis of ASIRs using Negative-binomial regression.

**RESULTS**
No significant temporal trend was detected in overal ASIR by notification year during 2011-2021 (IRR:0.98; 0.85-1.1). However, the temporal trend for cases born during universal vaccination was significantly declining (0.72; CIR: 0.56-0.93) while cases born after vaccination ceased had a non-significant increase (1.4; CIR: 0.99-1.96). No meningitis cases were reported during universal vaccination compared to one case reported after vaccination ceased. The proportion of cases reported as vaccinated decreased from 58% during universal vaccination to 21% after vaccination ceased. Four cases born after vaccination ceased would have been eligible to receive BCG under a selective programme. No significant difference in the proportion of cases associated with outbreaks was detected across the two periods. Regional ASIRs increased in two eastern regions after vaccination ceased, while they declined in the remaining six regions.

**CONCLUSIONS**
Universal BCG cessation has not directly impacted on new TB cases among 0-4 year olds yet, but timely surveillance is needed to monitor the impact of vaccination cessation. A selective BCG programme may have prevented cases diagnosed in certain risk groups.

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

### A systematic review on the impact of COVID-19 on cervical cancer prevention, diagnosis and treatment

**P. Ferrara** [1]

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[1-6] Department of Public Health, Experimental and Forensic Medicine, University of Pavia, 27100 Pavia, Italy

**BACKGROUND**
The COVID-19 pandemic has disrupted healthcare services globally, delaying both prevention and management of several vaccine-preventable diseases including cervical cancer. The aim of this systematic review is to summarize the available epidemiological studies on the differences in service access and care delivery for human papillomavirus (HPV) before and during COVID-19 pandemic, with the aim of extensively describing the extent of the pandemic impact on prevention, diagnosis and treatment of cervical cancer.

**METHODS**
We searched three electronic databases (PubMed, Embase, and Scopus) in which we applied algorithms tracing keywords for the topics of human papillomavirus (HPV) prevention, and cervical cancer diagnosis and treatment, as well as COVID-19 pandemic. Efforts to include further relevant articles included cross-referencing of the citation lists of the retrieved articles.

**RESULTS**
A total of 715 titles were screened, 34 of which met inclusion criteria, corresponding to 42 reports covering HPV vaccination (7 reports), cancer screening (19), diagnosis (8), and treatment (8). Seven studies observed reductions in HPV vaccination uptake and coverage during COVID-19. Studies on cervical screening and cancer diagnosis showed a substantial impact of the pandemic on access to preventive services and diagnostic procedures. All but one report that investigated cervical cancer treatment reported changes in the number of women with cervical lesions who received treatments, as well as treatment delay and interruption.

**CONCLUSIONS**
This systematic review showed that COVID-19 and restriction measures resulted in a substantial disruption in HPV vaccination and cervical cancer screening and management, with a major effect during the first pandemic wave of 2020. Since the cervical cancer burden is expected to increase due to this disruption, urgent policy interventions are needed for recovering cervical cancer prevention and care.

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

### The impact of the COVID-19 pandemic and non-pharmaceutical interventions on infectious diseases under national surveillance in the Netherlands from 2020 to Q1 2022

**D. van Hout** [1]

G. Klous [2], A. Teirlinck [3], D. van Meijeren [4], A. Steens [5], E. Franz [6], R. van Gageldonk-Lafeber [7],

H. de Melker [8], M. van Rooijen [9], J. Wallinga [10], S. van den Hof [11], A. Meijer [12], A. van Hoek [13]

[1-13] National Institute for Public Health and the Environment (RIVM)

**BACKGROUND**
The COVID-19 pandemic let to implementation of a series of non-pharmaceutical interventions (NPIs) which also affected other infectious diseases. We aimed to describe the impact of the pandemic on other infectious diseases in the Netherlands.

**METHODS**
Notifications from 2015-2021 were included for 15 notifiable infectious diseases with a yearly average of >50 notifications in 2015-2019. We used negative binomial regression analysis to estimate the relative change in notifications during 2020 and 2021 compared to 2015-2019. In addition, circulation of non-notifiable respiratory syncytial virus (RSV) and influenza virus was assessed using virological laboratory surveillance data from week 01-2015 to week 12-2022 (week of data extraction).

**RESULTS**
Compared to the pre-pandemic period of 2015-2019, notifications decreased for 13 and 12 of the included notifiable diseases in 2020 and 2021, respectively. The relative decrease varied from -83% (pertussis) to -11% (legionellosis) in 2020, and from -99% (mumps) to -9% (Shiga toxin-producing *Escherichia coli* O157 infections) in 2021. Infections that remained largely stable or increased compared to 2015-2019 were listeriosis and psittacosis (+1% and +49% in 2020 and +0% and -13% in 2021, respectively). There were no regular epidemics of RSV and influenza virus in the respiratory season 2020/2021, but out-of-season epidemics started in June 2021 and March 2022, respectively.

**CONCLUSIONS**
During the COVID-19 pandemic there was a decline in notifications in the Netherlands of almost all infectious diseases analysed, possibly in part due to under detection, but likely also due to changes in transmission dynamics. Continuous monitoring is warranted as this might have implications for build-up of immunity and new seasonal patterns. These results highlight the importance of optimized national surveillance systems for early detection of unusual patterns.

**Keywords:** Surveillance, Public Health, Non-pharmaceutical Interventions (NPI), Pandemic preparedness, Infectious diseases
**ABSTRACT ID:** 222
**PRESENTED BY:** Gijs Klous / denise.van.hout@rivm.nl

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

### The impact of the COVID-19 pandemic on the transmission of hepatitis B virus among men who have sex with men: a mathematical modelling study

**M. Xiridou [1]**
P. Adam [2], A. Meiberg [3], M. Visser [4], A. Matser [5], J. de Wit [6], E. Op de Coul [7]

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[2] Centre for Social Research in Health, UNSW Sydney - Institute for Prevention and Social Research
[5] Public Health Service Amsterdam - Amsterdam Institute for Infection and Immunity, Amsterdam University Medical Centre
[6] Department for Interdisciplinary Social Science, Utrecht University - Centre for Social Research in Health, UNSW Sydney

**BACKGROUND**
Disruptions in healthcare services and restrictive measures during the COVID-19 pandemic resulted in considerable reductions in hepatitis B virus (HBV) vaccinations and HBV testing among men who have sex with men (MSM). Reduced sexual activity has also been reported. We assessed the impact of these COVID-19-related changes on HBV transmission among MSM in the Netherlands.

**METHODS**
We used a mathematical compartmental model that describes HBV transmission among MSM. We accounted for COVID-19-related changes in sexual activity, estimated from data from the "COVID-19, Sex, and Intimacy Survey". Changes in HBV testing and HBV vaccination were established from national surveillance data among MSM.

**RESULTS**
With an observed reduction of 20% in numbers of sex partners, 75% in HBV testing, and 70% in HBV vaccination during the first lockdown, we estimated a decline of 6.6% in HBV incidence in 2020, compared to the respective level without the COVID-19-related changes. With numbers of sex partners rebounding close to pre-pandemic level in 2021 and a reduction of 15% in testing and 30% in vaccination in 2021, we expect that HBV incidence my increase by 1.4% in 2021 and 3.7% in 2022, compared to the respective incidence without the COVID-19-related changes. The number of HBV vaccinations needs to increase by at least 60% in 2022, compared to its pre-pandemic level, to bring HBV incidence in 2023 to the level that it would have had without the COVID-19-related changes.

**CONCLUSIONS**
Despite reductions in sexual activity during the COVID-19 pandemic, the decrease in HBV vaccinations may result in a small increase in HBV incidence after 2021. HBV vaccination uptake must exceed its pre-pandemic level to prevent increase in HBV transmission among MSM.

# FIRESIDE SESSION 3
DAY 1, 23 NOVEMBER 2022
13:30 – 15:00

## Secondary public health impacts

**MODERATOR**
Julien Beaute

## Abstract

### Estimated averted COVID-19 hospitalisations by the COVID-19 vaccination campaign in the Netherlands, 2 August 2021 through 30 August 2022

**S. van Iersel** [1]

S. McDonald [2], B. de Gier [3], M. Knol [4], H. de Melker [5], H. van Werkhoven [6]

[1-6] National Institute for Public Health and the Environment (RIVM)

**BACKGROUND**
Vaccines against COVID-19 have proven effective in preventing COVID-19 hospitalisation. In this study, we aim to quantify the public health impact of COVID-19 vaccination by estimating the number of averted hospitalisations during a period (2nd August 2021 – 30th August 2022) in which all adults were eligible for COVID-19 vaccination in the Netherlands.

**METHODS**
Using calendar-time specific vaccine effectiveness (VE) estimates and vaccination uptake (VU) by vaccination campaign (primary series, first booster and second booster) and the observed number of hospitalisations, we estimated the number of averted hospitalisations per age group between 2nd of August 2021 and 30th August 2022. From 25th January 2022, when the reason of hospitalisation was registered, hospitalisations not due to COVID-19 were removed. Sensitivity analysis addressed the uncertainty in VE estimates.

**RESULTS**
In the study period, there were 44,728 observed and an estimated 87,745 (66.2%) averted hospitalisations. Estimated averted hospitalisations ranged from 7,569 for age-group 12-49 years (51.0%) to 29,256 for age-group 70-79 years (72.6%). The estimated averted hospitalisations ranged from 77,770-98,452 (63.5%-68.8%) when using the 95%CI bounds for VE estimates. In all age-groups except 80+ years relatively more estimated hospitalisations were averted in the Delta period than the Omicron period, with 13.5, 19.2, 9.2, 7.7 and -2.0 percentage point difference for age-groups 12-49, 50-59, 60-69, 70-79 and 80+ years respectively.

**CONCLUSIONS**
COVID-19 vaccination prevented a large number of hospitalisations. It is likely that we have underestimated the public health benefits since we did not take indirect vaccination effects nor the add-on effects of alleviating peak health care pressures into account. These findings underline the public health importance of the vaccination campaign to policy makers and the public.

**Keywords:** COVID-19, SARS-CoV-2, Vaccination, Vaccine effectiveness
**ABSTRACT ID:** 505
**PRESENTED BY:** Senna van Iersel / senna.van.iersel@rivm.nl

# FIRESIDE SESSION 4
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

## Abstract

### Vaccine effectiveness against COVID-19 and associated death in Alpha and Delta variant outbreaks in long-term care facilities in Germany

**M. Sandfort** [1]

E. Meyer [2], S. Boender [3], G. Bojara [4], J. Enkelmann [5], H. Fickenscher [6], C. Frank [7], J. Hecht [8], A. Hofmann [9], H. Schlosser [10], S. Schumacher [11], I. Sperle-Heupel [12], W. Hellenbrand [13], T. Harder [14], D. Matysiak-Klose [15], V. Schönfeld [16]

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[10, 11] Local Public Health Authority, Bergstraße, Germany

**BACKGROUND**
High age and co-morbidities render residents of long-term care facilities (LCTF) vulnerable for severe COVID-19. As aged and co-morbid individuals were underrepresented in clinical trials, vaccine efficacy estimates may be invalid for them.

**METHODS**
We investigated three SARS-CoV-2 Alpha and Delta variant outbreaks in LTCF in Germany from March-August 2021 in a pooled retrospective cohort study, defining PCR-positive residents or staff as cases. Using logistic regression, we evaluated effectiveness (VE) of 2-dose immunization against symptomatic infection and death due to COVID-19, adjusting for confounding variables identified by directed acyclic graph-modelling: sex, age, co-morbidities, and residents' level of care (from 0, no impairment, to 5, heaviest impairment). Individual co-morbidities were tested for association with COVID-19-related death and VE against death was adjusted for relevant co-morbidities.

**RESULTS**
Among 180 residents and 180 staff members, 54 (30%) and 23 (13%) symptomatic infections occurred, respectively; no staff but 20 residents died due to COVID-19 (11%). The adjusted VE against symptomatic infection was 46.4% [95%-confidence interval: -37.0-78.7%] for residents and 78.5% [17.3-94.3%] for staff. Of co-morbidities, diabetes was associated with COVID-19-related death among residents (odds ratio 4.6 [1.7-13.5]), adjusted for vaccination, sex, age, and care level. VE against death in residents was 61.8% [-123.1-92.7%] for care levels 0-3, 42% [-187.9-85.1%] for levels 0-4, and 22.5% [-266.9-78.3%] for all, adjusted for sex, age, and diabetes.

**CONCLUSIONS**
Two-dose VE for staff against symptomatic Alpha and Delta infection was high, consistent with population estimates, but lower for residents, as was VE against death. Two-dose immunization may be insufficient to protect residents from COVID-19 and death. Possible explanations include age, (immunocompromising) co-morbidities, or psychosocial conditions. Our results underline the importance of booster vaccinations and non-pharmaceutical interventions.

# FIRESIDE SESSION 4
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

## Abstract

### Primary course and booster vaccine effectiveness against Omicron: Results from a European multicentre study at primary care/ambulatory level

**E. Kissling [1]**

M. Hooiveld [2], V. Sandonis Martín [3], I. Martínez-Baz [4], J. Murray[5], M. Knol [6], A. VIlcu [7], L. Domegan [8], C. Mazagatos [9], S. de Lusignan [10], A. Rodrigues [11], M. Riess [12], A. Meijer[13], C. Pascu [14], J. Castilla [15], J. Evans [16], M. Kooijman [17], A. Falchi [18], J. O'Donnel l[19], A. Martínez [20], R. Tsang [21], A. Machado [22], Å. Wiman [23], T. Jansen [24], M. Mihai [25], I. Casado [26], N. William [27], S. Hahné [28], S. van der Werf [29], C. Bennett [30], V. Gallardo [31], H. Whitaker [32], R. Guiomar [33], A. Carnahan [34], F. Dijkstra [35], M. Lazar [36], M. Maurel [37], S. Bacci [38], L. Pastore Celentano [39], M. Valenciano [40]

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[6, 13, 17, 28, 35] National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
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## BACKGROUND

In early 2022 SARS-CoV-2 Omicron dominated in Europe. We conducted a multicentre test-negative study at primary care/ambulatory level in 10 European study sites (seven countries) to measure primary course and booster vaccine effectiveness (VE) overall and by vaccine product against Omicron in the target group for booster vaccination aged ≥20 years.

## METHODS

Practitioners swabbed patients presenting with acute respiratory infection/COVID-19 symptoms, collecting demographic, vaccination and clinical information. Cases were RT-PCR positive and controls negative for SARS-CoV-2. We designated the Omicron period from the week when ≥90% of sequenced viruses in each country (source: GISAID) were Omicron and included patients until 28 February 2022. We calculated VE using logistic regression, adjusting for study site, age group, sex and swab date. We estimated VE by days since booster vaccination in 30-day increments, sample size permitting.

## RESULTS

Between 27 December 2021 and 28 February 2022, we included 1453 cases and 1949 test-negative controls. Any brand primary course VE was 12% (95%CI:-14–33) and mRNA booster VE was 54% (95%CI:42–63). mRNA booster VE was 54% (95%CI:40–64), 47% (95%CI:26–62) and 48% (95%CI:15–69) for those receiving two dose primary course of Pfizer, AstraZeneca and Moderna vaccines, respectively.

mRNA booster VE ranged from 61% (95%CI:43–73) at <30 days to 45% (95%CI:7–68) at 90+ days since vaccination for Pfizer primary course and from 69% (95%CI:47–82) at <30 days to 27% (95%CI:-18–55) at 60+ days since vaccination for AstraZeneca primary course.

## CONCLUSIONS

Our results suggest mRNA booster vaccination provided extra protection against symptomatic COVID-19 in a primary care/ambulatory setting and support the recommendation of a booster. While there may be waning of booster VE, precision is low. Regular VE monitoring in this setting can help inform vaccination policies.

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

## Abstract

### COVID-19 vaccine effectiveness against SARS-CoV-2 infection during the Delta period in the Netherlands: A nationwide study adjusting for chance of exposure

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**BACKGROUND**

Differential SARS-CoV-2 exposure between vaccinated and unvaccinated individuals may confound vaccine effectiveness (VE) estimates. We conducted a test-negative case-control study to determine the VE of COVID-19 vaccination against SARS-CoV-2 infection among adults testing at community facilities, and to assess the presence of confounding by SARS-CoV-2 exposure and whether VE can instead be accurately estimated using routinely collected data without details on exposure.

**METHODS**

We included adults tested for SARS-CoV-2 between 4 July and 8 December 2021 (Delta period). VE against SARS-CoV-2 infection after primary vaccination with an mRNA vaccine (Comirnaty or Spikevax) or vector-based vaccine (Vaxzevria or Janssen) was calculated using logistic regression adjusting for age, sex and calendar week (model 1). We additionally adjusted for comorbidity and education level (model 2), and SARS-CoV-2 exposure (number of close contacts, visiting busy locations, household size, facemask wearing, contact with SARS-CoV-2 case (model 3). We stratified by age, vaccine type and time since vaccination.

**RESULTS**

VE against infection (model 3) was 64% (95% CI 50%;73%), only slightly lower than in model 1 (68%; 95% CI 58%;76%) and model 2 (67%; 95% CI 56%;75%). Estimates stratified by age group, vaccine and time since vaccination remained similar between models: e.g. mRNA VE (model 3) among those aged 50+ years decreased from 81% (95% CI 66%;91%) at ‹120 days to 61% (95% CI 22%;80%) at 120+ days after vaccination. It decreased from 83% to 59% in model 1 and 81% to 56% in model 2.

**CONCLUSIONS**

SARS-CoV-2 exposure only slightly influenced COVID-19 VE against infection, suggesting VE may be accurately estimated using routinely collected data without details on exposure.

Abstract presentations - Fireside sessions

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

## Abstract

### Covid-19 vaccination programme effectiveness against SARS-CoV-2 related infections, hospital admissions and deaths in the Apulia region of Italy: a one-year retrospective cohort study

**T. Homan** [1]

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**BACKGROUND**
COVID-19 vaccine effectiveness decline for some outcomes and populations during 2021 has been reported. We estimated the effectiveness of the whole COVID-19 vaccination programme in Apulia region, Italy, at preventing SARS-CoV-2 infections, COVID-19-related hospital admissions and deaths during alpha and delta variant dominant periods, including waning effects.

**METHODS**
Using electronic health records of persons 16 years and older, we conducted a retrospective cohort study assessing effectiveness of combined BNT162b2, mRNA-1273, ChAdOx1-S and Ad26.COV2.S vaccines against rtPCR-confirmed COVID-19 infection, hospitalisations and deaths, by time since vaccination and variant dominant period, calculating Hazard ratios from Cox-regression models.

**RESULTS**
Between 1-Jan/1-Dec 2021, we included 3,530,967 persons in the cohort. 2,770,299 were fully vaccinated and 158,313 were COVID-19 positive at the end of the study period. Programme vaccine effectiveness for fully vaccinated against COVID-19 infection, hospitalisation and death were 87.69% (87.73-88.18), 94.08% (93.58-94.54) and 95.95% (95.26-96.54) respectively. The effectiveness during alpha and delta periods was 88.20% (87.60-99.78) and 59.31% (57.91-60.67) against infection, 93.89% (92.67-94.90) and 88.32% (86.50-89.90) against hospitalisation and 93.83% (91.65-95.45) and 85.91 (79.98-90.09) against death.
Waning effects regarding COVID-19 infection during delta period were stronger than for alpha, with 75.85% (74.38-77.24) effectiveness after 1-2 months and 8.35% (3.45-13.01) after 5-6 months after full vaccination. Effectiveness against hospitalisation and death during the delta period waned rapidly since 1-2- and 7-8-months full vaccination with respectively 27.67% (7.48-43.45) and 48.47 (53.97-34.82).

**CONCLUSIONS**
Our study suggests that the vaccination program in Apulia was strongly protective against COVID-19 infections, hospitalisation, and death due to alpha as well as delta variants, although effectiveness decreased over time. We recommend booster doses, primarily to vulnerable groups and additional effectiveness studies of new variants to inform public health policy.

**Keywords:** COVID-19, COVID vaccine-programme, Effectiveness, SARS-CoV-2 variants, Waning immunity, Italy
**ABSTRACT ID:** 55
**PRESENTED BY:** Tobias Homan / homan.tobias@gmail.com

# FIRESIDE SESSION 4
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

## Abstract

### Estimation of COVID-19 vaccine effectiveness against hospitalisation in individuals aged 65+ years using electronic health registries; pilot study in four EU/EEA countries, January-February 2022

**A. Sentís Fuster** [1]

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**BACKGROUND**
Within the ECDC infrastructure to monitor COVID-19 vaccine effectiveness (CVE), this study aims to use data on exposure and outcome routinely collected in health registries in EU/EEA countries. Using a common pilot study protocol, we estimated CVE against COVID-19 hospitalisation in Denmark, Navarre (Spain), Norway, and Portugal in January-February 2022.

**METHODS**
Study population included community-dwelling country residents aged ≥65-years-olds without documented prior SARS-CoV-2 infection. The outcome was hospitalisation with laboratory-confirmed SARS-CoV-2 infection in Denmark and hospitalisation due to COVID-19 elsewhere. We estimated CVE as (1−hazard ratio)*100 for complete primary vaccination and first booster (vs. non-vaccinated) adjusted for age, sex, region, comorbidities, and sociodemographic status, using Cox-regression. We pooled site-specific CVE using fixed-effects meta-analysis, using random-effects as sensitivity analysis.

**RESULTS**
Total study population with primary and booster vaccination was, respectively, 0.38 and 2.86 million individuals aged 65-79-year-olds and 0.11 and 1.07 million aged ≥80-years-olds. Pooled CVE for complete primary and booster vaccination was 48.9% (95% Confidence Interval (CI95%=42.1%-54.9%) and 87.8% (CI95%=86.4%-89.0%) in 65-79-year-olds; 44.9% (CI95%=38.0%-51.0%) and 85.9% (CI95%=84.6%-87.2%) in ≥80-years-olds. CVE varied considerably across sites: from 6.1% to 76.2% and 76.5% to 95.0% for primary and booster vaccination in 65-79-year-olds, and from 16.4% to 53.0% and from 78.9% to 91.8% in ≥80-years-olds. Sensitivity analysis did not significantly change point estimates but gave wider confidence intervals.

## CONCLUSIONS

Results indicate higher CVE against hospitalization with booster compared to primary vaccination. These results support the administration of booster doses in 65+ and suggest sustained effectiveness up to February 2022 in populations that had recently (<12 weeks) received a booster. The successful piloting of a common protocol providing preliminary results will inform the wider use of health registries for CVE.

# FIRESIDE SESSION 4
DAY 2, 24 NOVEMBER 2022
11:00 − 12:30

## COVID-19: vaccine effectiveness

**MODERATOR**
Mirjam Knol

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## Abstract

A new challenge for control selection in influenza vaccine effectiveness test-negative design studies in the COVID-19 context: Results from the European I-MOVE multicentre study at primary care level

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## BACKGROUND

Influenza A(H3N2) dominated in the 2021–22 influenza season in Europe, concomitant with Omicron SARS-CoV-2 circulation. The test-negative design, commonly used to estimate influenza VE (IVE), relies on influenza vaccination not affecting other respiratory virus influenza-negative control distributions. A high correlation between COVID-19 vaccination and influenza vaccination may violate this assumption. The I-MOVE primary care network conducted a test-negative multicentre study to measure IVE in nine European countries. Using these data we explored the effect of SARS-CoV-2-positive controls on IVE.

## METHODS

Physicians swabbed patients with acute respiratory infection or influenza-like illness, testing for influenza and SARS-CoV-2 viruses. Cases were RT-PCR positive for influenza A(H3N2) and controls were negative for influenza virus. We calculated VE using logistic regression, adjusting for study site, age, sex, symptom onset time, and chronic condition presence. We estimated VE among those aged ≥18 years and among the influenza vaccine target group, including and excluding SARS-CoV-2-positive controls.

## RESULTS

We included 879 influenza A(H3N2) cases and 6183 controls, of which 1943 (31%) were also SARS-CoV-2 positive. Among controls, where COVID-19 vaccination status was known (3979;64%), 3664 (92%) were vaccinated (correlation coefficient with influenza vaccination: 0.159, p<0.001).
A(H3N2) VE among those aged ≥18 years was 33% (95%CI: 14–48) and 42% (95%CI: 24–56), including and excluding SARS-CoV-2-positive controls, respectively. A(H3N2) VE among the vaccine target group was 31% (95%CI: -1–53) and 34% (95%CI: 0–57), including and excluding SARS-CoV-2-positive controls, respectively.

## CONCLUSIONS

Although 31% of controls were positive for SARS-CoV-2, excluding them increased IVE estimates by <10% overall, and only 3% in the vaccination target group. Nonetheless, further research is needed to understand if excluding SARS-CoV-2-positive controls when COVID-19 incidence is high, impacts the representativity of the control group.

# FIRESIDE SESSION 5
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### Comparative risk of cerebral venous sinus thrombosis (CVST) following SARS-CoV-2 vaccination or infection: A national cohort study using linked electronic health records

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**BACKGROUND**
Vaccine safety surveillance is critical to vaccination programmes. Following post-vaccination cerebral venous sinus thrombosis (CVST) events, we investigated and compared risk of CVST after SARS-Cov-2 vaccination or infection, using a national cohort, to inform the public and policy makers.

**METHODS**
Cohort study including 2,643,699 individuals aged 17 years and above, alive and resident in Wales on 1$^{st}$ January 2020 followed up through multiple linked data sources until 28th March 2021. Exposures were first dose of Oxford-ChAdOx1 or Pfizer-BioNTech vaccine or polymerase chain reaction (PCR)-confirmed SARS-Cov-2 infection. Outcome measure was an incident record of CVST. Hazard ratios (HR) were calculated using a multivariable Cox regression model adjusting for confounders. HR from SARS-Cov-2 infection was compared with that for SARS-Cov-2 vaccination.

**RESULTS**
We identified 910,556 (34·4%) records of first SARS-Cov-2 vaccination and 165,862 (6·3%) records of SARS-Cov-2 infection. A total of 1,372 CVST events were recorded during the study period, of which 52 (3·8%) and 48 (3·5%) occurred in the 28 days after vaccination and infection, respectively. We observed a slight non-significant risk of CVST within 28 days of vaccination [aHR: 1·34, 95% CI: 0·95-1·90], which remained after stratifying by vaccine [BNT162b2, aHR: 1·18 (95% CI: 0·63-2·21); ChAdOx1, aHR: 1·40 (95% CI: 0·95-2·05)]. Three times the number of CVST events were observed within 28 days of a positive SARS-Cov-2 test [aHR: 3·02 (95% CI: 2·17-4·21)].

**CONCLUSIONS**
The risk of CVST following SARS-Cov-2 infection is 2.3 times that following SARS-Cov-2 vaccine. This is important information both for those designing COVID-19 vaccination programmes and for individuals making their own informed decisions on the risk-benefit of vaccination. This record-linkage approach will be useful in monitoring the safety of future vaccine programmes.

# FIRESIDE SESSION 5
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### Risk of SARS-CoV-2 infection among members of a fitness centre chain in Stockholm, Sweden 2020: Is going to the gym risky?

**A. Kongelf** [1]

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**BACKGROUND**
COVID-19 outbreaks have been reported in fitness centres. It is unknown if attending fitness centres carry higher risk of transmission on a population level than other indoor environments. Friskis and Svettis (F&S) is the largest fitness centre chain in Sweden and was all-year open in 2020 under Swedish regulations to prevent transmission. We estimated and compared the risk of SARS-CoV-2 infection among active and inactive F&S-members in Stockholm, 2020.

**METHODS**
In a retrospective, register-based, matched case-control study we measured the association between fitness centre exposure and SARS-CoV-2 infection. Cases were F&S-members with laboratory confirmed SARS-CoV-2 infection in the national COVID-19 registry during the study period. Controls were F&S-members susceptible to infection at cases' selection date, matched on age and sex, based on an incidence density design. Exposure to fitness centres was measured through member's attendance activity. 'Active members' were those attending F&S 7-days before infection of the case(exposure period). Attendance was grouped into type(Outdoor/Gym/Low-intensity/ High-intensity) and frequency(no.of sessions) of attendance during the exposure-period. We estimated incidence rate ratios(IRR) of infection among active and inactive F&S-members, using conditional logistic regression.

**RESULTS**
Among 81,276 members, 8,049 participated in the study, with 505 cases and 40,077 matched controls (median:86; range:6-163). We found no significant association between active members and the risk of infection compared to inactive members (IRR:0.91,95%CI:0.80-1.03).

**CONCLUSIONS**
The study is based on available register data without possibility to assess risk of behaviours and exposures outside the context of F&S. Despite study limitations, the results suggests that fitness centres may not constitute an increased risk for transmission, in an otherwise 'open' society where prevention measures are implemented. Keeping fitness centres open under authorities' regulations seems appropriate, considering the health benefits exercise provides.

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### Bus riding as amplification mechanism for an explosive COVID-19 outbreak after import of SARS-CoV-2 by air travellers, Germany, 2021

**M. Schöll** [1]

C. Höhn [2], J. Boucsein [3], F. Moek [4], J. Plath [5], M. an der Heiden [6], M. Huska [7], S. Kröger [8], S. Paraskevopoulou [9], C. Siffczyk [10], U. Buchholz [11], R. Lachmann [12]

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**BACKGROUND**
A local public health authority (PHA) in Germany noticed a sudden rise of COVID-19 cases among children of local schools possibly linked to short bus rides. We investigated the outbreak to understand factors that may aid in formulating preventive recommendations.

**METHODS**
To identify transmission chains, we utilized routine surveillance data, searched for cases and conducted laboratory and phylogenetic analyses. We interviewed cases with a symptom onset (or test date) between 2021-09-06 and 2021-10-15 focusing on bus transportation, conducted a cohort study and investigated potential links to SARS-CoV-2 infections among travellers returning from Georgia on 2021-09-08 and a local bus company.

**RESULTS**
We identified 191 cases (median age: 17.5 years, 50% female) across 4 case generations. Five cases received in-patient treatment (3%), 4 cases (> 70 years of age) died (2%). Sixty-four cases were elementary school children (34%). The attack rate among bus riding children – with individual rides lasting between 9 and 18 minutes – was about 4 times higher compared to children not taking a bus to school. We did not find any other common risk factor. Among bus riding children, not wearing a mask and proximity to a case were not associated with higher risks. We identified a phylogenetically unique strain linking cases among school children and other bus passengers with the travellers returning from Georgia, the staff of the bus company (transporting the travellers back from the airport), and/or their respective household members.

**CONCLUSIONS**
To identify super-spreading events, PHA should ask cases about the use of public transport (including schedules) and consider multiple short bus rides (< 20 minutes) as a potential amplification mechanism for COVID-19 outbreaks. Individuals with respiratory symptoms should stay at home.

**Keywords:** COVID-19, Outbreak, Bus, Schools, Travel, Whole genome sequencing
**ABSTRACT ID:** 264
**PRESENTED BY:** Meike Schöll / schoellm@rki.de

# FIRESIDE SESSION 5
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### Disease severity and outcomes of COVID-19 in cases infected with SARS-CoV-2 Delta and Omicron variants, Skåne region, Sweden, December 2021 - January 2022

**A. Kongelf** [1]
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[1, 2, 3, 4] Public Health Agency of Sweden (PHAS)

**BACKGROUND**
SARS-CoV-2 surveillance through NAAT-based typing has been applied in Sweden to quickly detect occurrence and expansion of newly introduced variants of concern (VOCs). On 26/11/2021, ECDC escalated the Omicron (B.1.1.529) as a VOC. Based on confirmed SARS-CoV-2 cases notified from Skåne region (population: 1,378,000) during 1/12/2021- 9/1/2022, we investigated the association between severe clinical outcomes by variant, to inform the risk assessment of Omicron transmission replacing Delta (B.1.617.2) since week 51, 2021 in Sweden.

**METHODS**
Data was extracted from national registries. We compared notified cases with severe clinical outcomes defined as hospitalisation, ICU-admission and death to cases without respective severe outcome. For each outcome we compared the odds of being infected with Omicron-variant or Delta-variant determined by NAAT-based typing. We used logistic regression to calculate adjusted odds ratios (aOR) controlling for age, sex, previous notified SARS-CoV-2 infection, and expected vaccine effect (no/one dose, and time since last dose for fully vaccinated cases).

**RESULTS**
43,214 cases were notified, of which 21,293 cases with available variant information were included in this case-case study. 10,007 (47%) were infected with Delta and 11,286 (53%) by Omicron. Cases with each severe outcome respectively were more likely to be infected with Delta-variant compared to non-severe cases, with aOR 1.6 (95%CI 1.3-2.1) for hospitalisation; aOR 3.1 (95%CI 1.3-7.5) for ICU-admission and; aOR 2.4, (95%CI 1.2-4.6) for death.

**CONCLUSIONS**
Risk of hospitalisation, ICU-admission or death are lower among cases infected with SARS-CoV-2 Omicron-variant compared to the Delta-variant. These findings correspond with other international studies. NAAT-based typing has the potential to enable in-depth comparison of disease characteristics and outcomes of different variants of SARS-CoV-2 in real-time to inform risk assessment at times of introduction of new VOCs.

Abstract presentations - Fireside sessions

# FIRESIDE SESSION 5
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### A comparison of COVID-19 critical care admission incidence in Wales by vaccine status

**M. Barry** [1]
V. McClure [2], S. Cottrell [3], C. Johnson [4]
[1-4] Public Health Wales

**BACKGROUND**
Data on critical-care admissions (CCA) due to COVID-19 provide a useful measure for impact of the COVID-19 vaccination programme over time. In this study, we developed a data linkage approach to monitor COVID-19 CCA in unvaccinated and vaccinated populations (1 dose only, primary course only and booster) in Wales from week 18 2021 to week 16 week 2022.

**METHODS**
The number of COVID-19 CCA for each vaccine status was calculated, for each week, by linking the Welsh CCA dataset at person level, using NHS number, with the Welsh Immunisation System (WIS). Patients were considered vaccinated for each dose if they received the vaccine at least 14 days before testing positive for their CCA admission episode.
In order to estimate weekly COVID-19 CCA incidence, rolling weekly population denominators were calculated for each vaccine status, relative to the start of each ISO week over the analysis period.

**RESULTS**
Overall, the weekly CCA admission rate ranged from 0 per 100,000 observed in week 20 and 23 of 2021 to 0.98 per 100,000 in 2021 week 43.
When considering CCA incidence in each vaccine status group, the highest rate was 1.98 per 100,000 observed in the unvaccinated group in week 51 of 2021. Weekly CCA admissions in vaccinated groups were consistently lower than the unvaccinated population (highest rates in each of the vaccinated groups were: 1.21 per 100,000 for one dose only, 0.91 per 100,000 for primary dose, and 0.63 per 100,000 for booster dose).

**CONCLUSIONS**
This method of calculating weekly incidence of CCA from routinely collected data takes into account the rapidly changing vaccine coverage denominators and can provide useful measurement of trends for surveillance.

# FIRESIDE SESSION 5
DAY 2, 24 NOVEMBER 2022
11:00 – 12:30

## COVID-19: surveillance action

**MODERATOR**
Nick Bundle

## Abstract

### Estimate of school-specific reproductive number during weekly screening in the Auvergne-Rhône-Alpes region, France, week 47 to 50, 2021

**E. Colosi** [1]

G. Bassignana [2], B. Lina [3], C. Elias [4], P. Vanhems [5], V. Colizza [6]

[1, 2, 6] Institut national de la santé et de la recherche médicale (INSERM)

[3, 4, 5] Hospices Civils de Lyon

**BACKGROUND**
Reactive screening strategies were applied nationwide in France in the Fall 2021 in response to the Delta wave. In the same period (week 47 to 50, 2021), 24 primary schools in the Auvergne-Rhône-Alpes region participated to an experimental weekly screening protocol aimed to early case isolation. Here, we estimate the impact of the experimental protocol in terms of school transmission and resulting reduction of cases, compared to expectations.

**METHODS**
We extended an agent-based model for SARS-CoV-2 transmission on empirical contact patterns in primary school (Colosi et al, The Lancet Infectious Diseases, 2022) and fitted it to the prevalence observed in the 17 schools included in the analysis, accounting for introductions. The model was parameterized to the Delta variant dominant in the study period.

**RESULTS**
We estimated a relative contribution of school transmission compared to introduction equal to 28.0% (95%CI 26.6-28.6) in the Rhône department and 28.6% (95%CI 27.2-29.4) in the Savoie department in the study period. The case reduction achieved by the experimental protocol was estimated to be 31% (95%CI 23-36) over the full period.

**CONCLUSIONS**
Through field estimates, these findings confirm previous model predictions anticipating the efficacy of systematically screening the school population to reduce the overall number of cases through early detection and isolation. They also provide key information to improve prevention and control strategies at school for possible SARS-CoV-2 case resurgence in the upcoming Fall.

**Keywords:** SARS-CoV-2, Children, School, Screening, Reproductive number, Detection
**ABSTRACT ID:** 410
**PRESENTED BY:** Elisabetta Colosi / elisabetta.colosi@inserm.fr

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

## Abstract

### Nosocomial acquisition not associated with increased mortality amongst hospitalised COVID-19 cases in Wales, Feb 2020-Mar 2022

**R. Polani** [1]
V. McClure[2], J. Beer[3], M. Morgan[4]

[1-4] Public Health Wales NHS Trust

**BACKGROUND**
Hospital populations are vulnerable to COVID-19, but the relative severity compared to community-acquired cases is not known. We described mortality in hospitalised COVID-19 patients and investigated differences between nosocomial and community-acquired cases.

**METHODS**
Using patient identifiers, we linked SARS-CoV-2 PCR tests from Feb 2020-Mar 2022 to their hospital admission dates, to identify nosocomial cases. Specimens taken on admission days 1-2 were community-acquired hospital admitted (COHA); specimens taken >7 days after admission were nosocomial (NO). We measured death from any cause at 28 days post positive specimen (Mortality), by nosocomial status. We used multivariable logistic regression to compare 28ACM in COHA and NO, adjusting for confounders (age, sex, pandemic wave (w1:27/02/2020-26/07/2020; w2:27/07/2020-16/05/2021; w3:17/05/2021-19/12/2021; w4: 20/12/21-31/03/2022) and vaccination status), computing adjusted odds ratio (aOR) with 95% confidence intervals (95%CI).

**RESULTS**
We identified 12,013 NO and 9,892 COHA. 28ACM was 23% for NO and 20% for COHA (crude OR= 1.2, 95%CI= 1.1-1.3). After adjustment for age, sex, vaccination status and wave, there was no association between nosocomial acquisition and increased 28ACM (aOR= 0.8, 95%CI= 0.8-0.9). Older age (85+vs <25 years: aOR= 94.8, 95%CI=48.3-222.6) and male sex (aOR= 1.5, 95%CI= 1.4-1.6) were associated with higher 28ACM, and vaccination (aOR= 0.6, 95%CI= 0.5-0.7) and later pandemic waves associated with lower ACM (w4 vs w1: aOR= 0.5, 95%CI= 0.4-0.6).

**CONCLUSIONS**
Amongst hospitalised COVID-19 patients, we found no significant association between nosocomial acquisition and increased 28ACM, after controlling for potential confounders. Vaccination reduced mortality by 40%. Patients with longer hospital stays are likely to have other serious co-morbidities and be older, increasing their likelihood of death irrespective of SARS-CoV-2 infection.

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

## Abstract

### Incidence rate and risk factors associated with SARS-CoV-2 infection in healthcare workers from three European hospitals, July 2021-April 2022

**C. Savulescu [1]**

A. Prats Uribe [2], A. Mougkou [3], D. Plachouras [4], A. Agodi [5], M. Barchita [6], K. De Gaetano Donati [7], S. Lamonica [8], M. Latorre Millán [9], L. Clusa Cuesta [10], V. Rapisarda [11], R. Murri [12], A. Milagro Beamonte [13], C. Suetens [14], A. Nardone [15], NOSO Study group

[1] Epiconcept, France
[2] Epiconcept - University of Oxford, UK
[3, 4, 14] ECDC
[5, 6, 11] Università degli Studi di Catania
[7, 8, 12] Università Cattolica del Sacro Cuore
[9, 10, 13] Instituto de Investigación Sanitaria de Aragón - Miguel Servet University Hospital
[15] Epiconcept

**BACKGROUND**
Healthcare workers (HCWs) are at high-risk for SARS-CoV-2 infection due to their occupational exposure. We measured incidence and identified risk factors of SARS-CoV-2 infection in HCWs from three hospitals.

**METHODS**
We conducted a prospective cohort study of HCWs from Catania and Rome (Italy) and Zaragoza (Spain), who were tested for SARS-CoV-2 by PCR at enrolment, and then weekly during July-November 2021 (Catania) and July 2021-April 2022 (Zaragoza and Rome). We collected demographic, clinical, community- and work-related data. We computed incidence rates (IRs) and hazard ratios (HRs) using Cox regression. We included exposures with p<0.2 in the multivariable analysis.

**RESULTS**
We followed-up 751 HCWs for 95,378 person-days; 111 (15%) had a SARS-CoV-2 infection: 16 before and 95 after 1/12/2021. Before 1/12/2021, the IRs were 4.0, 3.7, and 0.9/10,000 person-days in HCWs from Catania, Zaragoza and Rome hospitals, respectively, and 11.9 and 14.8/10,000 persons-days in HCWs from Zaragoza and Rome hospitals after 1/12/2021. Crude HRs were the highest in HCWs that were household contacts (HR=20.8, 95%CI=13.2-32.6), followed by HCWs working face-to-face with patients (HR=2.3, 95%CI=1.3-4.1), admission/reception staff (HR=2.1, 95%CI=1.1.-20.6), and the lowest in HCWs living in urban area (HR=0.4, 95%CI=0.2-0.8) or who had received ≥1 dose of COVID-19 vaccine (HR=0.2, 95%CI=0.05-0.91). In the multivariable analysis, being household contact (HR=16.3, 95%CI=9.6-27.7) and age <40 years (HR=1.9, 95%CI=1.1-3.5) remained risk factors after adjusting for other exposures.

**CONCLUSIONS**
Incidence of SARS-CoV-2 infection in HCWs was higher after 1/12/2021 (circulation of Omicron variant), than before 1/12/2022 (circulation of Delta variant). Contact with a household case and younger age were the main risk factors for infection in participating HCWs. Our results should be confirmed with longer follow-up, during various COVID-19 waves and in different hospitals

**Keywords:** SARS-CoV-2 infection, Healthcare workers, Risk Factors, COVID-19 virus infection, Active surveillance
**ABSTRACT ID:** 221
**PRESENTED BY:** Camelia Savulescu / c.savulescu@epiconcept.fr

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

## Abstract

### Determinants of healthcare workers' self-reported compliance to infection prevention and control during the COVID-19 pandemic: a cross-sectional study in Dutch residential care facilities

**F. Houben** [1]

C. den Heijer [2], N. Dukers-Muijrers [3], J. Nava [4], C. Hoebe [5]

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[4] Department of Epidemiology, Care and Public Health Research Institute (CAPHRI), Faculty of Health, Medicine and Life Sciences, Maastricht University, The Netherlands

**BACKGROUND**
Healthcare workers' (HCWs) compliance to infection prevention and control (IPC) is key to patient safety. Nevertheless, IPC compliance and determinants thereof have not previously been studied in the disability care setting. This study aimed to assess levels of self-reported IPC compliance and its determinants among HCWs in residential care facilities (RCFs) for people with intellectual and developmental disabilities (IDDs).

**METHODS**
An online survey was conducted between March 2021 and March 2022 (during the COVID-19 pandemic) among HCWs from 16 large Dutch RCFs for people with IDDs. Participants (n=287) reported their IPC compliance (assessed in 8 domains, based on national guidelines) and responded to statements examining guideline, individual professional, client, professional interaction, and organisational factors. Multivariable linear regression analyses were performed to examine their relationships.

**RESULTS**
51% of HCWs reported overall sufficient levels of IPC compliance (defined as mean score of 4 or higher on 5-point likert scale), with behavioural specialists having the lowest IPC compliance levels compared to other occupations (p<0.001). There was considerable variation between specific IPC procedures, with compliance to personal hygiene measures being the lowest (44%). The belief that IPC interferes with the professional-client relationship (B= -0.13, p= 0.01) and the perception that the professional is not trained for IPC (B=-0.15, p= 0.01) were significantly associated with lower levels of self-reported IPC compliance.

**CONCLUSIONS**
Efforts to improve IPC compliance in the disability care setting should focus on strategies to alter HCW's beliefs and other attitudinal factors. An initial recommendation is to engage behavioural-oriented professionals in IPC practices and future interventions to improve IPC. A further recommendation is to implement IPC courses at the undergraduate level to improve HCWs' abilities to comply to IPC practices.

**ABSTRACT ID:** 218
**PRESENTED BY:** Famke Houben / famke.houben@ggdzl.nl

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

## Abstract

### Assessing the robustness of SARS-CoV-2 vaccine trial results: systematic review and meta-analysis

**N. Hoang** [1]
L. Quach [2], F. Vogt [3]

[1, 2, 3] Australian National University
[3] University of New South Wales

**BACKGROUND**
Vaccines have become the single most important public health intervention against COVID-19, but no evidence exists to date about how robust the underlying vaccine trial results actually are. Our objective was to assess the robustness of SARS-CoV-2 vaccine efficacy (VE) trials.

**METHODS**
We conducted a COCHRANE and PRISMA-compliant systematic review and meta-analysis of all SARS-CoV-2 trials published worldwide until 26 April 2022. We calculated the fragility index (FI) and fragility quotient (FQ) incl. interquartile ranges (IQR) of included studies and investigated their associations with selected trial characteristics (risk of bias, blinding type, VE, trial phase, sample size, and loss to follow up [LTFU]) using Wilcoxon rank-sum tests and Kruskal-Wallis H tests. We used the Spearman correlation coefficient to quantify the strength of correlation of FI and FQ with sample size, LTFU, and VE.

**RESULTS**
We included 29 studies out of 4,191 screened records. The overall median FI and FQ were 53.5 (IQR 17-124) and 0.41% (IQR 0.18-0.8%), respectively. While FI was positively associated with trial sample size (p-value <0.001) and LTFU (p-value 0.004), FQ was positively associated with VE (p-value 0.01). The Spearman correlation coefficient for FI with sample size was moderately strong (0.618), and weakly positive for FI and FQ with VE (0.126 and 0.353, respectively). The FI exceeded the number LTFU in two studies.

**CONCLUSIONS**
SARS-CoV-2 VE trial results were robust overall but showed considerable variation, particularly for trials with small sample size and high LTFU, suggesting the need for careful contextualization of results. Trial robustness should become standard reporting practice for randomized controlled trials, in particular for interventions as pivotal for public health as SARS-CoV-2 vaccines in the midst of a global pandemic.

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

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## Abstract

### Socioeconomic patterns of COVID-19 vaccine uptake in children aged 5-11 in Italy (January - April 2022)

**A. Mateo Urdiales** [1]

C. Sacco [2], A. Oradini Alacreu [3], D. Petrone [4], M. Del Manso [5], F. Vescio [6], F. Riccardo [7], M. Rota [8], A. Bella [9], P. Pezzotti [10], P. Pezzotti [11]

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[3] Università Vita-Salute San Raffaele

**BACKGROUND**
In November 2021, vaccination against COVID-19 was approved in children aged 5-11 in the EU with a reduced dosage of Comirnaty vaccine. However, uptake across Europe has been relatively low. Evidence from previous studies suggest that living in deprived areas may be associated with low vaccination uptake. We aimed to measure the association between contextual deprivation and COVID-19 vaccination in Italian children.

**METHODS**
We obtained data on COVID-19 vaccinations in children aged 5-11 from the National Vaccination Registry. We measured monthly uptake from the beginning of the vaccination campaign (January 2022) until the end of April 2022. Children were assigned to quintiles based on the vulnerability index of the municipality where they reside. Multilevel negative binomial regression models, adjusting for age, sex, month of vaccination and region of residence (random effects) were conducted to evaluate the association between contextual deprivation and COVID-19 vaccination uptake.

**RESULTS**
We included 1,764,678 children living in 7,535 municipalities (98% of total municipalities). Overall, uptake of COVID-19 vaccination in Italian children aged 5-11 was 40.1%, with those living in municipalities in the least deprived quintile having the highest uptake (42.1%) and those living in the most deprived quintile the lowest (36.4%). Results from the multivariate models show that the likelihood of being vaccinated decreased as deprivation increased. Overall, those living in the most deprived quintile were 28% less likely to be vaccinated compared with those living in the least deprived quintile [IRR 0.72, 95% Confidence Interval: 0.70-0.73].

**CONCLUSIONS**
Children living in deprived areas are less likely to be vaccinated against COVID-19 in Italy. These results could inform public health authorities to investigate, and address, contextual barriers that prevent children to participate in vaccination campaigns.

**Keywords:** COVID-19, Vaccination, Children, Inequalities, Equity
**ABSTRACT ID:** 347
**PRESENTED BY:** Alberto Mateo Urdiales / amateo250@hotmail.com

# FIRESIDE SESSION 6
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## COVID-19: intervention and health promotion

**MODERATOR**
Harold Noël

## Abstract

### The association between SARS-CoV-2 seroprevalence and cross-border mobility for visiting family or friends among Dutch residents of a border province

**D. Pagen** [1]

C. den Heijer [2], N. Dukers-Muijrers [3], C. Hoebe [4]

[1, 2, 3] Department of Sexual Health, Infectious Diseases, and Environmental Health, South Limburg Public Health Service, Heerlen, The Netherlands - Department of Health Promotion, Maastricht University, Care and Public Health Research Institute (CAPHRI), Maastricht University, Maastricht, The Netherlands
[4] Department of Medical Microbiology, Maastricht University Medical Center (MUMC+), Care and Public Health Research Institute (CAPHRI), Maastricht, the Netherlands

### BACKGROUND
Closing borders was implemented by several countries as infection prevention measure to interrupt between-country COVID-19 transmission. Closing borders impacts border region residents, as their professional and social life is often intertwined across national borders. Hence, we studied whether crossing borders to visit family and friends in neighbouring countries (cross-border mobility) was associated with SARS-CoV-2 seroprevalence in Dutch adults, residing in a province neighbouring Belgium and Germany.

### METHODS
In November 2020, SARS-CoV-2 serostatus was measured (negative/positive) to determine previous infection in 10.001 adults. Travelling behaviour to Belgium and Germany in February-March 2020 was questioned. The association between cross-border mobility and seroprevalence was tested using multivariable logistic regression analyses. Stratification by living in a border municipality was needed due to interaction.

### RESULTS
Overall seroprevalence (SP) was 19.5%. Among the 10.001 adults 36.8% (n=3680) had cross-border family/friends. Of these, one third (n=1309) visited their cross-border family/friends in February-March 2020. Compared to residents not having cross-border family/friends (SP=20.6%), seroprevalence was significantly lower in participants visiting family/friends (SP=16.3%), and participants not visiting them (SP=18.2%). More frequent cross-border activity resulted in a even lower seroprevalence ($SP_{visited\ 1-4\ times}$=17.0% $SP_{visited\ \geq 5\ times}$=13.4%). After adjusting regression analyses for confounders (geographical region of residence), no significant association was established for cross-border mobility with seroprevalence, for both participants living in a border municipality ($OR_{family/friends\ not\ visited}$=0.90 [95% CI:0.78-1.04], $OR_{family/friends\ visited}$=0.87 [95% CI:0.73-1.04]) and participants not living in a border municipality ($OR_{family/friends\ not\ visited}$=0.93 [95% CI:0.73-1.18], $OR_{family/friends\ visited}$=0.67 [95% CI:0.45-1.00]).

### CONCLUSIONS
Based on our analyses, closing borders to neighbouring countries was not crucial for controlling COVID-19 transmission early in the pandemic for the Netherlands, as the seroprevalence was not higher in participants with cross-border mobility.

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

## Abstract

### Regional shift in Pogosta disease incidence during 2021 epidemic in Finland

**E. Otte im Kampe** [1]

M. Suvanto [2], E. Korhonen [3], R. Uusitalo [4], E. Huhtamo [5], T. Dub [6]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC)

[1,6] Finnish Institute for Health and Welfare (THL)

[2] Department of Veterinary Biosciences, University of Helsinki - Department of Virology, University of Helsinki

[3,4,5] Department of Virology, University of Helsinki - Department of Veterinary Biosciences, University of Helsinki

**BACKGROUND**
In 2021, an epidemic of Pogosta, a mosquito-borne disease caused by the Sindbis virus, occurred in Finland. Symptoms include joint manifestations for years implying considerable public health importance. We describe characteristics of the epidemic in 2021 and possible changes overtime since the last epidemic of similar size in 2002 to update regions and groups at risk and raise awareness among the population and clinicians.

**METHODS**
Reporting of laboratory confirmed Pogosta cases to the National Infectious Diseases Register (NIDR) is mandatory in Finland. We analysed NIDR case numbers for the period 2002-2021 and calculated annual incidence per 100.000 nationwide, by age, sex and residential hospital district. We calculated monthly cases for each year to describe seasonality.

**RESULTS**
In 2021, 565 cases were reported corresponding to an incidence of 10/100.000 nationwide. Regional incidences ranged from 41/100.000 in North Savo (central Finland) to 0,82/100.000 in Southwest Finland. Incidence peaked in age-group 50-59 (22/100.000) and was lowest in age-group <30 (2,5/100.000). For women, the incidence (13/100.000) was approximately twice as high as for men (6,6/100.000). Cases occurred from June to December peaking in September (55% of all cases). In 2002, incidence was similar (11/100.000) nationwide, but the epidemic was geographically less widespread peaking in North Karelia (eastern Finland) (80/100.000). We observed the same risk groups, regional variation, and seasonality in 2002-2020. Annual nationwide incidences ranged from 0,27-4,03/100.000 in 2003-2020.

**CONCLUSIONS**
Our results suggest a shift in risk from eastern to central Finland in 2021. No other considerable change in disease patterns occurred during 2002-2021. More awareness, particularly in new risk regions, could improve disease recognition in clinicians and the general population, and the adoption of preventive measures specifically targeting women and summer/autumn.

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

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## Abstract

### Risk of lymphoma increased after Puumala virus infection in Finland, 2009-2019: a retrospective register-based study

**S. Kääriäinen** [1]

T. Dub [2], J. Ollgren [3], O. Laine [4], M. Sinisalo [5], J. Sane [6], O. Lyytikäinen [7]

[1] EPIET

[1, 2, 3, 6, 7] Finnish Institute for Health and Welfare (THL)

[4, 5] Tampere University Hospital

**BACKGROUND**

*Vibrio vulnificus* is an opportunistic, climate-sensitive bacterial pathogen, which occurs in warm, low-salinity waters. Frequency of infections are low, but impacts are high; *V. vulnificus* is capable of causing rapid, necrotizing wound infections in humans with a fatality rate of ~18%. Despite increasing bacterial concentrations in seawater, systematic assessments of changing disease patterns or projections of climate change impacts are rare. Here we quantify the changing incidence and spatial extent of *V. vulnificus* wound infections along the East Coast of North America and explore the likely influence of climate change upon their future spatial distribution.

**METHODS**

*V. vulnificus* case data were obtained from the US Cholera and Other *Vibrio* Illness Surveillance (COVIS) database. A 'presence-absence' regression modelling approach and CMIP6 climate data are used to predict the future distribution of *V. vulnificus* wound infection risk under different Shared Socioeconomic Pathways (SSPs) of climate change.

**RESULTS**

In Eastern North America, the incidence of *V. vulnificus* wound infections has increased 8-fold between 1988 and 2018; the northern extent of cases has increased annually by 48km between the same 30-year period. By 2081-2100, we predict that *V. vulnificus* infections may expand from their current limit (~Pennsylvania, 39.98°N) to New York (40.71°N) under SSP126, a low-emissions scenario, and to every Eastern Coastal US State under SSP370, a medium-emissions scenario.

**CONCLUSIONS**

Cases of waterborne *V. vulnificus* infection along the US East Coast have risen dramatically. We provide strong evidence that climate change is likely to lead to a further northward shift in the distribution of *V. vulnificus* infections into regions with increasingly older, more susceptible, populations throughout the 21st Century. This highlights the importance of *V. vulnificus* as an indicator of climate change.

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

## Abstract

### An Easter Surprise: Salmonella Typhimurium outbreak linked to chocolate products in the United Kingdom, 2022; a case control study

**A. Vusirikala** [1]

Y. Chan [2], A. Hoban [3], A. Simbo [4], J. McCormick [5], C. Pulford [6], S. Gokool [7], L. Browning [8], J. Cowden [9],
N. Verlander [10], T. Potter [11], C. Gathumbi [12], C. Handford [13], S. Balasegaram [14], L. Larkin [15]

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[8, 9] Clinical and Protecting Health Directorate, Public Health Scotland, Glasgow, United Kingdom
[10] Statistics, Modelling and Economics Department, UK Health Security Agency, London, United Kingdom
[11, 12, 13] Food Standards Agency, London, United Kingdom
[14] Field Service, Health Protection Operations, UK Health Security Agency, London, United Kingdom

**BACKGROUND**
In February 2022, the United Kingdom (UK) reported a five-single nucleotide polymorphism (SNP) single linkage cluster of Salmonella Typhimurium cases, designated t5.7575. By early April, 150 cases, predominantly in children, were reported in the EU and UK with sample dates from 21 December to 28 March. Initial case interviews in the UK suggested Brand A chocolate eggs was the likely vehicle of infection. These products were recalled on 2 April. We conducted a case-control study to further establish Brand A eggs as the vehicle of the outbreak.

**METHODS**
We interviewed t5.7575 cases in the UK with targeted questionnaires. Controls were recruited via a market research panel and frequency matched by age and sex based on the distribution of UK cases. Multivariable logistic regression was conducted. Sensitivity analysis was restricted to those interviewed before the product recall.

**RESULTS**
The case-control study included 26 cases and 106 controls aged under 11. Multivariable analysis demonstrated that cases who had eaten Brand A chocolate eggs had an adjusted odds ratio (aOR) of 55.0 (95%CI 9.9-306.4). Other items which showed an association with illness were Brand A bars (aOR=6.4,95%CI 1.4-28.0), Brand B chocolate (aOR=10.9, 95%CI 1.6-72.5) and chicken (aOR=7.3, 95%CI 1.6-33.9). Sensitivity analysis showed similar results.

**CONCLUSIONS**
This study provides strong evidence that Brand A chocolate eggs were a vehicle for this S. Typhimurium outbreak and supports the rapid recall of Brand A products based on descriptive epidemiology and food chain investigations. Although other products showed a significant association in the model, this was not of the same magnitude as Brand A chocolate eggs and without further supporting evidence from other investigations, these products can't be considered as key vehicles for UK cases.

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

## Abstract

### International outbreak of Salmonella Typhimurium linked to a chocolate factory in 2022: Belgian findings

**V. Laisnez [1],**

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**BACKGROUND**
Mid-February 2022, the United Kingdom reported via EpiPulse a cluster of monophasic *Salmonella* Typhimurium infections. Epidemiological and traceback investigations revealed a multi-country outbreak linked to chocolate products from a Belgian factory of an international brand. Microbiological investigations indicated two clusters: HC5_296366 (cluster 1) and HC5_298160 (cluster 2). We assessed the extent of the outbreak in Belgium and took measures to limit further spread.

**METHODS**
Probable and confirmed cases were identified using ECDC case definitions. Case-interviews focused on exposure to chocolate products of the concerned brand. Raw materials and finished food products collected at the factory were analysed for *Salmonella* spp. using real-time PCR. Whole genome sequence (WGS) analysis of isolates of probable cases and positive food samples is still ongoing.

**RESULTS**
We identified 62 probable cases (39 cluster 1, 23 cluster 2), with illness onset from mid-January until April and a peak in cases mid-February 2022. Of these 62 cases, 54 were aged 1-9 years old. Among the 44 interviewed cases, 19 have been hospitalized and 41 reported consumption of products of the factory among whom 35 reported consumption of Kinder Surprise. Seven of 229 food products tested positive for *Salmonella*; WGS analysis indicated matches with both clusters. In December 2021, *Salmonella* was found in samples during a self-check in the factory, these isolates matched with the later identified clusters. Eleven types of products were recalled worldwide and food safety authorities shut down the factory 8 April 2022.

**CONCLUSIONS**
Epidemiological and microbiological investigations confirmed the link between *Salmonella* cases and products from a Belgian chocolate factory. A strong collaboration and information sharing between different stakeholders resulted in comprehensive measures to stop the spread of this international outbreak.

**Keywords:** *Salmonella* Typhimurium, International Foodborne outbreak, Whole genome sequencing
**ABSTRACT ID:** 47
**PRESENTED BY:** Valeska Laisnez / valeska.laisnez@sciensano.be

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

## Abstract

### Whole Genome Sequencing identified a prolonged Salmonella Poona nursery outbreak (2016-2021) in North West England, UK

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#### BACKGROUND
In October 2021, we investigated an intermittent outbreak of *Salmonella* enterica serotype Poona ST308 in North West England. The outbreak (12 cases between 2016 and 2021) was discovered through routine *Salmonella* surveillance whole genome sequencing (WGS) which enables detection of clusters of genetically similar isolates. Previous cases were investigated over the time period but links were not identified, and several cases appeared to be sporadic.

#### METHODS
In October 2021, data from available enhanced questionnaires was combined with trawling questionnaires from the six most recent cases to identify potential common exposures. We described the cases and investigated commonalities. Environmental and staff sampling was conducted at the implicated setting.

#### RESULTS
In total, the outbreak comprised 13 cases; 11 were aged under three years, and two were adults. The earliest case (2016) had attended nursery A; the remaining 10 child cases (Dec 2018-Sep 2021) had attended nursery B at the time of their infection. No other common exposures were identified.
Staff sampling in Nursery B led to the identification of an asymptomatic staff member (case 13) who had been employed there since 2018 and who tested positive for the outbreak strain. This staff member had also worked at Nursery A in 2016, at the time the first case was reported.

#### CONCLUSIONS
We demonstrate the utility and importance of combining epidemiological and WGS data to identify and investigate intermittent *Salmonella* outbreaks. This outbreak highlights the possibility of persistent carriage and shedding of S. Poona and the implications of this where individuals work with vulnerable groups, necessitating consideration of more enhanced risk management measures such as exclusion of the individual or changing their duties until clearance is achieved.

**Keywords:** Salmonella, Disease Outbreaks, Whole genome sequencing, United Kingdom, Salmonella Enterica, Risk Management
**ABSTRACT ID:** 317
**PRESENTED BY:** Joanna Garner / joanna.garner@phe.gov.uk

# FIRESIDE SESSION 7
DAY 3, 25 NOVEMBER 2022
11:00 – 12:30

## Food and water borne and vector diseases

**MODERATOR**
Moa Rehn

## Abstract

### Climate Warming and increasing *Vibrio vulnificus* infections in North America

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C. Baker-Austin [2], T. Osborn [3], N. Jones [4], J. Martínez-Urtaza [5], J. Trinanes [6], J. Oliver [7], F. Colón-González [8], I. Lake [9]

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**BACKGROUND**
*Vibrio vulnificus* is an opportunistic, climate-sensitive bacterial pathogen, which occurs in warm, low-salinity waters. Frequency of infections are low, but impacts are high; *V. vulnificus* is capable of causing rapid, necrotizing wound infections in humans with a fatality rate of ~18%. Despite increasing bacterial concentrations in seawater, systematic assessments of changing disease patterns or projections of climate change impacts are rare. Here we quantify the changing incidence and spatial extent of *V. vulnificus* wound infections along the East Coast of North America and explore the likely influence of climate change upon their future spatial distribution.

**METHODS**
*V. vulnificus* case data were obtained from the US Cholera and Other *Vibrio* Illness Surveillance (COVIS) database. A 'presence-absence' regression modelling approach and CMIP6 climate data are used to predict the future distribution of *V. vulnificus* wound infection risk under different Shared Socioeconomic Pathways (SSPs) of climate change.

**RESULTS**
In Eastern North America, the incidence of *V. vulnificus* wound infections has increased 8-fold between 1988 and 2018; the northern extent of cases has increased annually by 48km between the same 30-year period. By 2081-2100, we predict that *V. vulnificus* infections may expand from their current limit (~Pennsylvania, 39.98°N) to New York (40.71°N) under SSP126, a low-emissions scenario, and to every Eastern Coastal US State under SSP370, a medium-emissions scenario.

**CONCLUSIONS**
Cases of waterborne V. *vulnificus* infection along the US East Coast have risen dramatically. We provide strong evidence that climate change is likely to lead to a further northward shift in the distribution of *V. vulnificus* infections into regions with increasingly older, more susceptible, populations throughout the 21st Century. This highlights the importance of *V. vulnificus* as an indicator of climate change.

# FIRESIDE SESSION 8
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### Linkage of SARS-CoV-2 sequencing results to the Bavarian surveillance system from January 2021 through February 2022, Germany

**L. Coyer** [1]

D. Marosevic [2], L. Weise [3], C. Berger [4], A. Dangel [5], M. Böhmer [6], N. Ackermann [7], K. Katz [8], A. Sing [9]

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**BACKGROUND**
In Germany, laboratories are legally required to upload sequencing results to a centralised database (DESH), which assigns an identification number (IMS-ID) for linkage to surveillance data. We evaluated the implementation of the IMS-ID in Bavaria, Germany from January, 2021 through February, 2022 since linking genomic to epidemiological data would provide valuable insights into the introduction and spread of SARS-CoV-2 variants, and their relation to COVID-19 severity.

**METHODS**
Within the surveillance dataset of all notified Bavarian SARS-CoV-2 cases, we determined completeness (proportion of records with IMS-ID out of all with an indication of sequencing) and internal validity (proportion of IMS-IDs with correct format). Additionally, we assessed linkage of sequencing results through correctly formatted IMS-ID from (1) the Bavarian Health and Food Safety Authority (LGL) laboratory and (2) all Bavarian laboratories (including LGL) uploaded to DESH, to the surveillance dataset. We also assessed submission of IMS-IDs from the surveillance dataset to the Robert Koch Institute (RKI). We evaluated all outcomes overall, over time, and per district and notification software, where possible.

**RESULTS**
Of 2,469,612 surveillance records, 50,295 (2%) had an indication of sequencing; 29,586/50,295 (59%) had an IMS-ID (completeness), whilst 23,009 had an IMS-ID without indication of sequencing. Internal validity was 91% (47,839/52,595). Linkage to the surveillance dataset was 59% from the LGL laboratory and 44% from DESH, and >99% from the surveillance dataset to RKI. Completeness, internal validity and linkage improved over time. Completeness and internal validity varied between district and software.

**CONCLUSIONS**
Whilst IMS-ID implementation improved over time, it was suboptimal, with Bavarian surveillance data missing sequencing results. Action is needed to improve this. Analyses using linked data should be mindful of potential biases due to missing data.

**Keywords:** COVID-19, SARS-CoV-2 variants, Genomics, Population surveillance
**ABSTRACT ID:** 173
**PRESENTED BY:** Liza Coyer / liza.coyer@lgl.bayern.de

# FIRESIDE SESSION 8
DAY 3, 25 NOVEMBER 2022
13:50 – 15:00

## COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### Using a novel 'difference-in-differences' method and syndromic surveillance to estimate the impact of media reporting on local healthcare utilisation during an early stage of the COVID-19 pandemic

**A. Nikhab** [1]
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**BACKGROUND**

UKHSA national real-time syndromic surveillance (SS) supplements traditional laboratory reporting for infectious disease surveillance, using symptoms/diagnoses to indicate changes in the health and wellbeing of the population. SS is known to be affected by external factors, such as media reporting. Prior to widespread COVID-19 community surveillance, SS was one of several systems utilised to provide real-time information on changes in healthcare-seeking behaviour. However, early COVID-19-related events challenged interpretation of local SS data. Here we use a novel statistical method to identify the impact of local media reporting around these early pandemic events.

**METHODS**

A quasi-experimental retrospective difference-in-differences (DiD) study was conducted to estimate the impact of five events in January-February 2020 in England on five routinely monitored SS indicators (telehealth calls, GP consultations in-hours and out-of-hours, emergency department attendances).
We estimated time 'exposed' to a media event using internet search intensity inferred from Google Trends data as a proxy. We constructed a negative-binomial regression model for each indicator and event to estimate a direct effect.

**RESULTS**

We estimated a four-fold increase in NHS 111 'cough' calls and a 1.4-fold increase in hospital admissions for acute respiratory illness in Brighton and Hove, when a so-called 'superspreading event' in this location was reported in local and national media. No statistically-significant increases were found for the other media events.

**CONCLUSIONS**

We used a novel DiD approach to directly estimate the potential media effect on SS, providing contextual information on interpretation of changes in health indicators. With further validation, this method could be used for novel pathogens/situations where obtaining real-time direct estimates of impact on SS indicators would inform public health action, particularly where intense media reporting could influence people's healthcare-seeking behaviour.

# FIRESIDE SESSION 8
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### Wastewater surveillance for SARS-CoV-2 closely mirrors incidence data: results from national surveillance in Denmark, October 2021 – May 2022

**O. McManus** [1]

L. Krogsgaard [2], N. Bahrenscheer [3], L. Von Kappelgaard [4], T. Christiansen [5], L. Rasmussen [6],

S. Richter [7], K. Franck [8], L. Christiansen [9], S. Ethelberg [10]

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[1-10] Statens Serum Institut, Denmark

**BACKGROUND**
Denmark has an extensive wastewater surveillance system for SARS-CoV-2. As the level of human testing declines, it is still uncertain how well wastewater surveillance can serve as a substitute. Therefore, we investigated the association between wastewater data and positive human SARS-CoV-2 tests.

**METHODS**
We enrolled 198 wastewater treatment plants (WWTPs), covering 85% of the Danish population. We collected three weekly 24-hour composite samples per WWTP, from October 2021 to May 2022. SARS-CoV-2 RNA concentrations were measured by RT-PCR. We calculated daily SARS-CoV-2 copies per inhabitant for each WWTP as the measured SARS-CoV-2 RNA concentrations multiplied by the volume of wastewater flowing into each WWTP, divided by the population of the catchment area. We collapsed our wastewater data into national weekly numbers, taking the weighted median of all measurements, weighted by the log10 of the WWTP populations. We used linear regression to model national weekly SARS-CoV-2 incidence according to our wastewater data and the level of human testing, with all variables on the log scale.

**RESULTS**
SARS-CoV-2 incidence varied from 500 to 50,000 weekly cases per 100,000 in our study period. Our model predictions fit the incidence curve well, explaining 97% of the variation in incidence throughout the period. Each log increase in wastewater copies per inhabitant was associated with a 0.71 log increase in incidence (95% confidence interval 0.66 – 0.77).

**CONCLUSIONS**
Our simple model, incorporating only wastewater data and human testing frequency, mirrors the observed SARS-CoV-2 incidence very well. This suggests that wastewater data can provide a good estimate of the true level of SARS-CoV-2 in the community. Wastewater surveillance may play an important role in situations where human testing is limited.

Abstract presentations - Fireside sessions

# FIRESIDE SESSION 8
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### SARS-CoV-2 Genomic Surveillance: Lessons Learned from the EMERGEN Consortium, France, 2021-2022

**J. Schaeffer** [1]
J. Castro Alvarez [2], A. Feri [3], G. Destras [4], C. Rodriguez [5], V. Enouf [6], D. Descamps [7], P. Fournier [8], S. Kemeny [9], B. Roquebert [10], M. Jimenez-Pocquet [11], S. Ducreux [12], T. Denecker [13], J. Sudour [14], M. Pretet [15], A. Maisa [16], L. Fournier [17], S. Bernard-Stoecklin [18], G. Spaccaferi [19], A. Bozorgan [20], H. Raoul [21], B. Coignard [22], Santé publique France Regional Offices, the EMERGEN consortium

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[21] ANRS Maladies infectieuses émergentes, Paris, France

**BACKGROUND**
Variant emergence is a normal consequence of viral evolution but can have major public health consequences. The emergence of SARS-CoV-2 variants has completely redefined this pandemic, underlining the importance of genomic surveillance in order to detect emerging variants and evaluate their public health impact.

**METHODS**
The EMERGEN consortium was created in January 2021 to enhance and structure SARS-CoV-2 genomic surveillance in France. Coordinated by Santé publique France and ANRS|MIE, it includes more than 60 public health and research actors. Among these, 56 public and private sequencing laboratories cover both metropolitan France and overseas territories and the French Bioinformatic Institute (IFB) developed a centralized infrastructure hosting genomic data.

**RESULTS**
As of 04/01/2022, 317 521 SARS-CoV-2 sequences were produced by EMERGEN partners. SARS-CoV-2 genomic surveillance was organised around three pillars: random sampling, targeted sequencing (for example severe cases, immunocompromised or travel-related) and investigation (cluster or unusual signal). Weekly random "Flash" surveys provided a representative picture of circulating variants, and the two other pillars provided complementary data on cases and situations of public health importance. Results were disseminated through weekly COVID-19 epidemiological bulletins, an Internet dashboard and open data. Data also contributed to risk analyses evaluating the public heath impact of circulating variants. Consortium partners supported prompt investigations, e.g., when detecting early 2022 a novel Delta/Omicron recombinant, later named XD. This collective effort allowed to quickly describe this variant through epidemiological investigations, and in *vitro/in vivo* studies.

## CONCLUSIONS

The EMERGEN consortium greatly enhanced genomic surveillance capacities in France and helped producing timely and reliable data for orienting decision makers. Associating complementary skills (public health and research, epidemiology and microbiology) strengthened its ability to detect and investigate emerging SARS-CoV-2 variants.

Abstract presentations - Fireside sessions

# COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### How do we keep a cohort engaged? Lessons from one year of following up over 44,000 SIREN study participants, UK

**A. Howells** [1]

K. Munro [2], S. Foulkes [3], J. Khawam [4], J. Ye Aung Kyaw [5], N. Platt [6], D. Sparkes [7], E. Monk [8], C. Neill [9], N. Fowles-Gutierrez [10], M. Cole [11], A. Atti [12], C. Brown [13], J. Islam [14], S. Hopkins [15], V. Hall [16]

[1] Public Health Fellow
[1-16] UK Health Security Agency (UKHSA)

**BACKGROUND**
Cohort studies represent an important research-tool, yet participant retention is notoriously difficult. Conducted at scale over 135 sites during a global pandemic, the SIREN Study has faced particular challenges. We investigated participant retention and explored the multifactorial approach to cohort engagement.

**METHODS**
We designed an evolving cohort retention programme including newsletters, webinars, video-messages and celebration events, informed by our Participant Involvement panel. As a decentralised study we provided ongoing support to sites to assist their participant engagement, including quality improvement tools and withdrawal reports. We described cohort retention by time, demographics and site, comparing proportions with a chi-squared test. We described length of follow-up for withdrawals, and withdrawal reasons.

**RESULTS**
The proportion of participants completing their 12-month follow-up was 84.6% (n=37,686). Participant retention decreased gradually over time. The highest proportion of withdrawals occurred in April 2021 (10.4%), when 90% of active participants had received their second vaccine dose. The median length of follow-up at withdrawal was 198 days (IQR: 112-281). The most common withdrawal reasons were workload commitments (35.6%), moving sites/ leaving the NHS (18.5%) and medical reasons (10.7%). Retention increased with age (75.5% <25-years vs 88.6% 55-64-years; P<0.001). Participant retention was highest in the Black ethnic group (90.1% vs 84.9% white ethnic group; p<0.001). Retention varied over sites (range: 65.5% to 96.2%) and was higher among smaller sites (86.4% across sites <200 participants vs. 81.9% across sites >800 participants; p<0.001).

**CONCLUSIONS**
Despite inherent challenges in running a multicentre prospective cohort study in an evolving pandemic, cohort retention in SIREN was very high, supported by an innovative retention programme. Further work is ongoing to evaluate specific interventions and site factors, to help identify lessons for future studies.

# FIRESIDE SESSION 8
DAY 3, 25 NOVEMBER 2022
13:30 −15:00

## COVID-19: Surveillance approaches

**MODERATOR**
Carlos Carvalho

## Abstract

### Surveillance of vaccine effectiveness against mortality from different SARS-CoV-2 variants in southern Sweden between December 2020 and June 2022

**D. Dietler** [1],

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**BACKGROUND**
Recent studies showed that the emergence of the Omicron SARS-CoV-2 variants substantially reduced vaccine effectiveness (VE) against infection, although protection against severe disease outcomes remained high. However, there is limited evidence on the temporal variation of VE against death.

**METHODS**
Using data from the total population of the Skåne region, we estimated VE against all-cause and COVID-19-related mortality (deaths within 30 days after a positive SARS-CoV-2 test) between 27 December 2020 and 3 June 2022. Vaccination rate with at least two doses in the end of the study period was 82.3%. Two datasets were created using all deaths occurring during the study period (N=17 797) and a sub-sample of COVID-19-related deaths (N=1 567), respectively. Cases were matched based on age and sex with 10 controls that were alive at the selection date. VE was estimated using conditional logistic regression adjusting for comorbidities and prior infection.

**RESULTS**
Over the whole study period, VE among people receiving two doses was 30% (19–40%) against all-cause mortality and 63% (41–77%) against COVID-19-related mortality. A third and fourth dose increased VE significantly. There is evidence of waning VE although the third and fourth doses maintained the protective effect. The emergence of the Omicron variants did not substantially affect VE against all-cause and COVID-19-related mortality. Interestingly, prior infection only showed additional protective effects among the unvaccinated.

**CONCLUSIONS**
Our study indicates that VE against mortality is predominantly affected by the time since the last dose rather than the dominant virus variant. With more frequent infections also among the vaccinated, a better understanding of the protective effects of hybrid immunity patterns against severe outcomes of COVID-19 is needed to guide future vaccination efforts.

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## Late breakers

**MODERATOR**
Eleanor McNamara

## Abstract

### Exploring non-viral exposures causatively or contributorily associated with paediatric cases of acute hepatitis of unknown aetiology in the United Kingdom, 2022

**H. Taylor [1],**

A. Hoban [2], H. Crabbe [3], L. Larkin [4], N. Iqbal [5], K. Foxall [6], R. Close [7], G. Godbole [8], F. Tony [9], G. Leonardi [10]

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**BACKGROUND**
An increase in acute hepatitis cases of unknown aetiology in children continues to be detected in several countries including the United Kingdom. Clinical severity is high, with 6% (15/270) confirmed cases requiring liver transplantation. While adenovirus is the most frequently detected pathogen, lack of apparent direct toxic effect of adenovirus on liver tissue and other results suggests this may be part of a multiple-step process. We explored potential food-, drink- and water-related environmental exposures that could have an association with cases.

**METHODS**
A literature review was conducted to identify potential causative or contributory environmental exposures. Data on potential exposures was collected using questionnaires completed with cases' guardians and in-depth exploratory-interviews. Where the proportion of cases reporting exposure exceeded a >20% threshold in questionnaire data or >50% from interviews, these were compared to national dietary surveys for age-group based consumption.

**RESULTS**
The literature review identified 54 papers. These and an initial rapid review confirmed plausibility of hepatotoxicity via pesticide (initial review only) or mycotoxin contaminated food; alone or with a virus. From 77 trawling questionnaire responses, higher consumption of cucumbers (52%), strawberries (37%) and fish fingers (29%) were identified compared to national surveys (39%, 28% and 11% respectively). Additional food items, with consumption rates above the national surveys, were identified from the nine exploratory-interviews. These include potatoes (89%), peas (67%) broccoli (78%), sweetcorn (56%), rice (67%), porridge (56%) and tortilla wraps (67%).

**CONCLUSIONS**
Consumption of some food items, which have plausible associations with acute hepatitis, was higher than expected. When investigating disease of unknown aetiology, environmental and chemical exposures, and their potential role in multi-step processes, should be considered alongside viral pathogens in analytical studies and surveillance system design.

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## Late breakers

**MODERATOR**
Eleanor McNamara

## Abstract

### Monkeypox vaccination acceptance among male users of gay dating apps in Europe

**J. Reyes** [1]

A. D'Ambrosio [2], R. Croci [3], B. Bluemel [4], O. Cenciareli [5], A. Pharris [6], N. Dukers-Muijers [7], W. Nutland [8],
S. Niaupari [9], J. Badran [10], G. Spiteri [11], T. Noori [12]

[1, 2, 3, 4, 5, 6, 11, 12] ECDC

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[8] LSHTM

[9] Grindr

[10] Hornet

**BACKGROUND**
We assess MPX vaccination acceptance among male adults in the European region.

**METHODS**
We conducted an online survey through two smartphone-based dating apps targeting men who have sex with men (MSM), from 30 July to 12 August 2022. We developed Bayesian hierarchical logistic regression models to investigate MPX vaccination acceptance, its geographical heterogeneity and the association with the survey questions. We present results as estimated vaccination acceptance and association relative risks (RR), with [90% credible interval].

**RESULTS**
Overall, 32,902 MSM responded to the survey, 53% were aged ≤40 years and 16.3% were foreign-born. The overall crude vaccination acceptance was 82%. Modelled vaccination acceptance showed a clear geographical trend, varying from 87.8% (84.2% - 90.7%) in northern Europe to 65.9% (59.3% - 71.9%) in eastern Europe. Acceptance strongly increased with perception of MPX disease severity (RR: 2.75 [2.0-4.0]) and transmission risk (RR: 2.1 [1.6-2.7]). Being engaged with healthcare was also relevant: HIV-positive people on anti-retroviral therapy (RR: 1.1 [1.0-1.2]), individuals using pre-exposure prophylaxis (RR: 1.2 [1.1-1.3]), and those recently diagnosed with a sexually transmitted infection (RR: 1.1 [1.1-1.2]) were more favourable to vaccination. Respondents who were worried about being treated differently due to MPX (RR: 1.2, [1.1-1.4]) and those with general vaccine acceptance (RR: 1.3 [1.2-1.5]) were more likely to be willing to be vaccinated.

**CONCLUSIONS**
Overall, MPX vaccine acceptance was high among European MSM using dating apps. Operational research and health communication efforts are needed to ensure increased acceptance of MPX vaccination, particularly in groups and regions where there are indications that acceptance is lower.

**Keywords:** Monkeypox, Vaccination, Process, Acceptance, Men who have Sex with Men, Survey
**ABSTRACT ID:** 535
**PRESENTED BY:** Juliana Reyes / juliana.reyes@ecdc.europa.eu

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:30 −15:00

## Late breakers

**MODERATOR**
Eleanor McNamara

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## Abstract

### Monkeypox cases in women in England: Characterising transmission routes and monitoring spread outside of GBMSM

**K. Wrenn** [1]

C. Overton [2], K. Cooper [3], N. Love [4], P. Blomquist [5], L. Hounsome [6], F. Cumming [7], R. Vivancos [8]

[1-8] UKHSA

**BACKGROUND**
The UK Health Security Agency (UKHSA) has been managing a large monkeypox outbreak in England since May 2022, with over 95% of cases in gay, bisexual, and other men-who-have-sex-with-men (GBMSM). As data on sexual behaviour is not routinely available, we monitor spread and transmission routes in women to assess if the outbreak is moving away from the initial core group.

**METHODS**
We used laboratory, questionnaire data, and case-management notes from UKHSA's case management system to identify cis- and trans-gender women and likely transmission routes. To investigate temporal changes in the gender-distribution of cases, we used a binomial exact test to compare the weekly distribution of cases to a baseline, based on the gender-distribution across the start of the outbreak (1st May to 1st July 2022).

**RESULTS**
As of September 13, there were 43 women among 3,385 monkeypox cases in England (1.3%); including 15 trans-gender women. Of these, 42% (n=18) reported likely transmission via sexual contact, due to sex with a known case or high-risk sexual behaviours, and 19% reported possible non-sexual routes e.g., household transmission. The remainder had unclear transmission routes. The proportion of cases in women increased from 0.3% during the baseline period to 3.5% in the week commencing 26/08/2022, with a significant deviation from the baseline occurring during July 2022. However, no significant deviation is seen when analysing only cis-gender women.

**CONCLUSIONS**
Women remain a minority of cases, with a small proportional increase only in trans-women, who may be more closely linked to GBMSM networks. Additionally, most known transmission in women is through sexual contact, consistent with GBMSM cases. This indicates current interventions targeting GBMSM are appropriate, though should be continuously monitored.

**Keywords:** Monkeypox, GBMSM, Women, Public Health Interventions, Surveillance, Atypical cases
**ABSTRACT ID:** 561
**PRESENTED BY:** Katie Wrenn / katie.wrenn@ukhsa.gov.uk

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## Late breakers

**MODERATOR**
Eleanor McNamara

## Abstract

### Decreasing mortality linked to SARS-CoV-2 infections in long-term care facilities in Luxembourg: results from national surveillance March 2020-September 2022

**C. Ernst** [1]

D. Bejko [2], A. Vergison [3], J. Mossong [4]

[1] Health Directorate Luxembourg
[2] Luxembourg Institute of Health
[3, 4] Health Directorate

**BACKGROUND**
A periodic PCR-based national screening programme was established in all 52 long-term care-facilities (LTCFs) during 2020 in Luxembourg targeting its 6,764 residents. During 2021, 95% of LTCF residents received three vaccine doses. We investigated the evolution of mortality in LTCF residents by comparing it over the three pandemic years, taking into account vaccination status and variants.

**METHODS**
All laboratory confirmed SARS-CoV-2 cases among LTCF residents were identified using electronic reporting and followed up via contact tracing including deaths. Whole-genome sequencing was performed for a subset of cases with representative samples analysed for infections in 2022. We estimated 28-day-case fatality rate (CFR) for 2020, 2021, and 2022 and assessed associations with vaccination status through calculating adjusted odds ratios (aORs) by binary logistic regression analysis.

**RESULTS**
Between March 2020 and September 2022, we registered 5,002 SARS-CoV-2 infections and 413 (8.3%) deaths affecting 4,501 (67%) residents. While the majority of cases occurred in 2022 (61%), the CFR was significantly lower (p<0.001) in 2022 (3.6%) compared to 2021 (17%) and 2020 (15%). Overall, the majority (66%) of deceased cases was unvaccinated. Compared to unvaccinated residents, the risk of dying in relation to a SARS-CoV-2 infection was 81% lower (aOR: 0.19, 95% CI: 0.153-0.249) in residents vaccinated with at least three vaccine doses. Of 636 successfully sequenced samples in 2022, Omicron subvariants BA.2 (367, 58%), BA.1 (236, 37%), and BA.5 (23, 3.6%) accounted for the vast majority of infections.

**CONCLUSIONS**
Our study illustrates a clear decoupling of SARS-CoV-2 cases from deaths in 2022 as a result of both vaccination and lower Omicron virulence. Nevertheless, LTCF residents remain a vulnerable group that needs close monitoring and prioritisation in vaccination campaigns.

**Keywords:** SARS-CoV-2, Nursing homes, Mortality, Vaccination
**ABSTRACT ID:** 519
**PRESENTED BY:** Corinna Ernst / corinna.ernst@ms.etat.lu

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:30 – 15:00

## Late breakers

**MODERATOR**
Eleanor McNamara

## Abstract

### Primary series and booster vaccine effectiveness against the SARS-CoV-2 Omicron variant in a cohort of healthcare workers in Albania, January – May 2022

**I. Finci** [1]

M. Rojas Castro [2], I. Preza [3], I. Hasibra [4], J. Sulo [5], A. Fico [6], R. Daja [7], A. Vasili [8], M. Kota [9], A. Guseinova [10], B. Mühlemann [11], C. Drosten [12], R. Pebody [13], K. Lafond [14], E. Kissling [15], M. Katz [16], S. Bino [17]

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[2, 15] Epiconcept, Paris, France

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[14] US Centers for Disease Control, Atlanta, Georgia, USA

**BACKGROUND**
Healthcare workers (HCWs) have experienced high rates of COVID-19 morbidity and mortality. We estimated two-dose primary series and booster COVID-19 vaccine effectiveness (VE) against symptomatic PCR-confirmed infection among HCWs in three Albanian hospitals during January-May 2022, an Omicron-predominant period. Primary series and booster dose uptake among Albanian HCWs, nationally, are currently 83% and 18%, respectively.

**METHODS**
All HCWs at the three hospitals were eligible to enroll. Participants completed weekly symptom questionnaires, underwent PCR testing when symptomatic, and provided quarterly blood samples. We estimated VE using Cox regression models (1-hazard ratio), with validated vaccination status as the time-varying covariate and unvaccinated HCWs as the reference group. Estimates were adjusted by potential confounders: age, sex, previous infection (SARS-CoV-2 confirmed by PCR, rapid antigen test recorded in national databases, or antibody seropositivity), and self-reported comorbidities.

**RESULTS**
At study start, 76% of 1,470 HCWs had received a primary series, 10% a booster dose, 5% one dose and 9% were unvaccinated; 1,200 (82%) HCWs had evidence of prior infection. Overall, 86% of primary series vaccines and 98% of booster doses received were Pfizer-BioNTech. The median time since receiving the second dose and the booster to study start was 289 days (IQR:210-292) and 30 days (IQR:22-45), respectively. Adjusted VE was 34% (95%CI: -31;67) for the primary series and 77% (95%CI: 18;94) for the booster.

**CONCLUSIONS**
Among Albanian HCWs, most of whom had been previously infected, COVID-19 booster dose offered improved VE. The modest non-significant primary series VE estimate may reflect high levels of prior infection among participants, and waning immunity among vaccinated participants, as most HCWs completed their primary series >7 months prior. Our findings support promoting booster dose uptake among Albanian HCWs.

**Keywords:** COVID-19, Omicron, Healthcare workers, Vaccine effectiveness
**ABSTRACT ID:** 531
**PRESENTED BY:** Iris Finci / fincii@who.int

# FIRESIDE SESSION 9
DAY 3, 25 NOVEMBER 2022
13:030 – 015:00

## Late breakers

**MODERATOR**
Eleanor McNamara

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## Abstract

### High vaccine effectiveness against severe COVID-19 outcomes during the Omicron era in Luxembourg, December 2021-August 2022

**D. Bejko** [1]

C. Ernst [2], A. Vergison [3], J. Mossong [4]

[1] Luxembourg Institute of Health
[2, 3, 4] Health Directorate Luxembourg

**BACKGROUND**

Luxembourg experienced three major SARS-CoV-2 infection waves due to Omicron variants during 2022 while having achieved a high vaccination coverage in 2021. We investigated severe outcomes (hospitalisation, death) among adults in relation to variants, vaccination status and prior infection.

**METHODS**

We linked reported adult cases aged 20 years or older of SARS-CoV-2 from contact tracing with SARS-CoV-2 related hospitalisation and SARS-CoV-2 related deaths. We defined three time periods where different Omicron variants predominated, i.e. represented more than 75% of sequenced cases: i)BA.1 period from 27/12/2021-13/02/2022, ii)BA.2 from 14/03/2022-15/05/2022, iii)BA.5 from 20/06/2022-15/08/2022. Logistic regression was performed adjusting for age, gender, period, vaccination status and reinfection.

**RESULTS**

Between December 27th 2021 and August 15th 2022, we recorded a total of 160,280 SARS-CoV-2 cases, 499 (0.31%) hospitalisations and 256 (0.16%) deaths. Compared to the earlier BA.1 period, both risks of hospitalisations and deaths were significantly lower during the BA.2 period (OR 0.40, 95%CI 0.31-0.51 and OR 0.60, 95%CI 0.44-0.82, respectively) and BA.5 period (OR 0.65, 95%CI 0.50-0.84 and OR 0.43, 95%CI 0.27-0.68, respectively). Compared to unvaccinated adults, the risk of hospitalisation was 55% lower (95%CI 41%-66%) with a complete vaccination and 75% lower (95%CI 69%-80%) with a booster dose. Compared to unvaccinated adults, the risk of death was 82% lower (95%CI 75%-87%) with a booster. Previous infection was not associated with lower hospitalisation or mortality.

**CONCLUSIONS**

Our findings suggest that the risk of severe outcome differed during the three waves of Omicron infections in 2022. Complete vaccination and booster but not previous infection were protective against hospitalisation and death. Further monitoring will be required to assess the effectiveness of Omicron adapted vaccines.

# Poster tours

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## POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

## Abstract

### The COVID-19 pandemic impacted syphilis testing at anonymous consultation clinics in North-Rhine Westphalia state, Germany, 2019-2021

**K. Siling** [1]
P. Grotegut [2], A. Jurke [3]

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[1, 2, 3] NRW Centre for Health (Landeszentrum Gesundheit NRW–LZG.NRW), Bochum, Germany

**BACKGROUND**
COVID-19 pandemic disrupted testing for sexually transmitted infections (STI) worldwide. We aimed to assess the impact of the pandemic on syphilis testing in North-Rhine Westphalia state (NRW).

**METHODS**
We analysed annual aggregated syphilis testing data from the NRW sentinel surveillance network covering 53 local health authorities. Overall and by subgroups, we described test volume, the number of positive tests, and test positivity, in 2019 and during the pandemic years 2020 and 2021.

**RESULTS**
During the pandemic, 6,274 (47%) and 5,333 (39.9%) fewer syphilis tests were conducted in 2020 and 2021, respectively. A similar drop in the number of tests conducted was observed in men, women, and men who have sex with men (MSM). For sex workers and people who inject drugs (PWID), the respective decrease in the number of tests was 63.7% (95% CI:61.5-66.6) and 66.3% (95% CI: 56.3-76.3) in 2020 and did not rebound in 2021.
The number of syphilis infections detected during the pandemic declined by 37.7% (2020) and 59.0% (2021), most notably among sex workers (-49.7%, 2020 and -62.1%, 2021), and PWID (-43.8%, 2020 and -18.8%, 2020).
Test positivity for first syphilis infection remained stable (3.7% in 2019, 95% CI: 3.3-4.1). Test positivity was higher in men than in women (9.0% vs 3.5% in 2019) and did not change substantially during the pandemic. In MSM and sex workers, test positivity increased marginally. In PWID, a 12-14.7% increase was observed.

**CONCLUSIONS**
During two years of the pandemic, syphilis test volume and the number of detected infections decreased, indicating that some infections may have been missed. Continued monitoring is needed to understand the impact of the pandemic on the epidemiology of syphilis and to inform interventions.

# POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

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## Abstract

### Translating the COVID-19 epidemiological situation into policies and measures: the Belgian experience

**G. De Muylder** [1]
V. Laisnez [2], G. Stefani [3], T. Lernout [4]

[1-4] Sciensano

**BACKGROUND**
In 2008, in line with the WHO International Health Regulation, Belgium put in place a Risk Assessment Group (RAG) and a Risk Management Group (RMG) to ensure optimal health crisis management. The RAG, involving permanent (public health) experts supported by specific experts, analyses events causing possible risk to health and proposes prevention and control measures to the RMG. The RMG, composed of health authorities, decides on measures to be taken and follows-up the implementation. During the COVID-19 pandemic, the RAG provided advises on a wide range of topics. Among those, a weekly assessment of the epidemiological situation was performed to guide policy makers. We present here the method used for this assessment, and the link with recommended measures.

**METHODS**
A comprehensive evaluation of the epidemiological situation was performed on a weekly basis using basic (cases, hospitalisations, testing, positivity rates, …) and supporting (waste water, nursing homes, schools, mobility, …) surveillance indicators.

**RESULTS**
The first epidemiological risk assessment on COVID-19 was performed by the RAG on January 20, 2020, followed by regular updates. From August 2020 onwards, a weekly update was provided, with as of early May 2022, 87 weekly assessments done. In addition, a dynamic tool was developed to link the epidemiological situation to a risk level, using colours and/or phases. The indicators and thresholds evolved over time, depending on advancing knowledge, immunity and vaccination of the population, changes in test strategy and new variants.

**CONCLUSIONS**
The assessment by experts from different disciplines in an autonomous scientific advisory body and the classification of the risk according to different levels supported policy makers to decide on non-pharmaceutical interventions and testing strategy, at national and regional level.

**Keywords:** COVID-19, Epidemiology, Surveillance, Public Health Measures
**ABSTRACT ID:** 418
**PRESENTED BY:** Geraldine De Muylder / geraldine.demuylder@sciensano.be

# POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 − 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

## Abstract

One Health in policy and practice: A UK case study of *Corynebacterium ulcerans* in a pet and challenges managing human health risk for zoonotic disease where guidance is focused on human cases

**P. Cresswell-Jones** [1]
Corynebacterium Ulcerans Incident Management Team

[1] Public Health Wales

### BACKGROUND
*Corynebacterium ulcerans* is a rare but increasingly prevalent zoonotic infection of public health importance due to potentially fatal diphtheria-like illness in humans. Domestic animal contact is a risk factor. We present a case study of the human public health management following detection of *Corynebacterium ulcerans* in a pet in the United Kingdom, to raise awareness of a One Health approach and discuss challenges in using human public health guidance for zoonotic disease.

### METHODS
*Corynebacterium ulcerans* isolated from a pet's wound swab was notified to the acute public health team by animal health. An 'One Health' Incident Management Team (IMT) was formed with human and animal health colleagues. Human close contacts of the animal were identified and managed according to national guidance for public health control and management of diphtheria (2015, England and Wales).

### RESULTS
Human close contacts were risk assessed, swabbed, offered chemoprophylaxis and prophylactic vaccination as appropriate. No human cases were identified. Further testing of the animal demonstrated clearance.
The case raised issues on funding responsibilities for testing and treatment of an animal where the benefit is for the public health of humans, and highlighted challenges in interpreting and using diphtheria guidance focused on human index cases. Since this case, updated guidance has been released.

### CONCLUSIONS
The case demonstrates collaboration and cross-sector working with animal and human health colleagues.
Our recommendations include:
- Raising awareness of *Corynebacterium ulcerans*
- Highlighting updated public health guidance on diphtheria (England) and prompting review in other regions
- Prompting consideration of where funding responsibilities lie regarding veterinary procedures for human public health benefit
- Promoting the One Health approach
The opportunity and scope for this learning extends to other zoonotic infections of public health interest.

**Keywords:** Corynebacterium, Bacterial Zoonoses, Pets, One Health
**ABSTRACT ID:** 72
**PRESENTED BY:** Penelope Cresswell-Jones / penelope.cresswell-jones@wales.nhs.uk

# POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

## Abstract

### Importance of regional networking in building national FETP: Experience of Lebanon

**Z. Farah** [1]

H. Abou El Naja [2], I. Abu Khader [3], K. Danis [4], P. Stefanoff [5], N. Ghosn [6]

[1, 2, 6] Ministry of Public Health (MOPH)
[3] Eastern Mediterranean Public Health Network (EMPHNET)
[4, 5] Mediterranean and Black Sea Programme Intervention Epidemiology Training (MediPIET)

**BACKGROUND**
In February 2022, the Epidemiological Surveillance Unit (ESU) at the Lebanese MOPH launched the national Field Epidemiology Training program (nFETP) to enhance public health professionals' capacities in communicable disease surveillance and outbreak investigation. The main objective of nFETP is to build a critical mass of field epidemiologists at central and peripheral levels. This work describes the steps in setting up the FETP, the resources needed and the lessons learned.

**METHODS**
Preparing for the nFETP required years of continuous work. It started with building capacity of the ESU team through the 2-year MediPIET fellowship; one of the 5 graduates was designated as nFETP coordinator. EMPHNET provided the regional expertise including the curriculum, the training platform (LMS) and logistic support. Following that, the three-month basic FETP level was adopted, competencies and curriculum adapted and nFETP guide developed. Finally, the nFETP team (director, coordinator, mentors and assistants) was formed.

**RESULTS**
On Feb 22nd 2022, the nFETP was launched. The first cohort, expected to graduate in June 2022, includes 15 fellows from ESU central and peripheral teams and the National Influenza Center. By May 9th, fellows had successfully completed the first workshop and fieldwork assignment with 75 weekly reports on COVID-19 surveillance, covering all provinces. Fellows also conducted 60 data quality audit visits to hospitals for improving disease reporting. Improvement in fellows' knowledge and skills was documented. Fellows reported being satisfied with the course activities.

**CONCLUSIONS**
Despite the faced challenges like the economic crisis and brain drain, Lebanon succeeded in launching its nFETP due to the support provided by regional FETPs like EMPHNET and MediPIET. Next steps will be to ensure sustainability, quality assurance, and expansion of the program.

# POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 − 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

## Abstract

### Assessment of infection prevention and control in hospitals providing medical care for coronavirus infection (COVID-19) in Bishkek, Osh cities and Chui region, Kyrgyzstan, 2020

**A. Dzhalimbekova** [1]

S. Temirbekov [2], D. Nabirova [3]

[1] State Sanitary Surveillance Department, Bishkek, Kyrgyzstan
[1,2] Resident of the Applied Epidemiology Program for CDC in Central Asia
[3] U.S. Centers for Disease Control and Prevention, Central Asia Region Field Epidemiology Training Program, Almaty, Kazakhstan

**BACKGROUND**
We evaluated infection prevention and control practices (IPC) implementation in health facilities providing for COVID-19 patients in the regions with the highest COVID-19 incidence among health care worker (HCW): Bishkek (31%), Osh Cities (14%), and Chui (18%) region, Kyrgyzstan.

**METHODS**
A cross-sectional study was conducted in 16 health facilities in Bishkek, Osh cities and Chui oblast in September 2020. We used a structured questionnaire developed using CDC and WHO IPC assessment guidelines. We interviewed staff on IPC program implementation, personal care protective equipment (PPE) measure, IPC trainings; screening of HCWs, conducted unannounced audit of triage and isolation of patients, existing environmental measures; and reviewed supporting documents for PPE and ventilation systems. We show percentages in a range across region.

**RESULTS**
Only 69% (region range 50-100%) of the sites observed had an approved written IPC program. The budget for compliance with IPC measures was allocated only in 50% of facilities (16-100%). All health facilities had 100% stock of required amount PPE, but only 81% (50-100%) were able to calculate the costs and needs of PPE, hand hygiene products and disinfectants. Screening of HCWs for COVID-19 is carried out only in 50% (0-87%) of health facilities. Only 69% (22-100%) of hospitals organized separation of clean and dirty areas, and isolation of patients was not possible in adapted outpatient facilities. Only one facility had mechanical ventilation systems in place. Recirculators were used in 35% (22-100%) of hospitals and only 43% (0-72%) had functional unshielded ultraviolet irradiators.

**CONCLUSIONS**
We observed poor IPC implementation in studied hospitals which may have contributed to the high registration of cases of COVID-19 among HCWs. We recommended implementation regularly screening of HCWs for COVID-19.

**Keywords:** IPC, COVID-19, Hospital, Medical Worker
**ABSTRACT ID:** 247
**PRESENTED BY:** Altynai Dzhalimbekova / a_djalymbekova@mail.ru

# POSTER TOUR 1
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Knowledge for policy and practice

**MODERATOR**
Gabrielle Schittecatte

## Abstract

### Activation of crisis management structures at the Robert Koch Institute during the COVID-19 pandemic

**U. Grote [1],**

M. an der Heiden [2], V. Bremer [3], A. Halm [4], T. Jung-Sendzik [5], N. Litzba [6], I. Markus [7], T. Schneider [8], M. Schöll [9], M. Schranz [10], P. von Berenberg-Gossler [11], N. Zeitlmann [12], O. Hamouda [13], L. Schaade [14], U. Rexroth [15]

[1-13, 15] Department of Infectious Disease Epidemiology, Robert Koch Institute
[14] Centre for Biological Threats and Special Pathogens, Robert Koch Institute

**BACKGROUND**
The COVID-19 pandemic has burdened the Public Health Service in Germany in an unprecedented way. The Robert Koch Institute (RKI), as the national public health institute, has prepared for epidemic events of different magnitudes. We aim to describe key facts and good practices regarding the crisis management structures activated during the COVID-19-pandemic.

**METHODS**
Based on the RKI crisis management plan we activated in January 2020 a crisis committee for strategic decision-making and an Emergency Operations Centre (EOC) for operational support. We collected data e.g. on the number of days the EOC was activated, positions established and people included in a COVID-19-specific-EOC-roster.

**RESULTS**
From January 2020 through April 2022, the crisis committee met 353 times; the EOC was staffed on 823/838 days (98%). Within the EOC, up to 8 different positions were assigned to tasks such as answering inquiries by the government, public or scientific community or distributing information. The COVID-19-specific-EOC-roster comprised around 270 employees. Overall, 13.826 shifts were carried out with up to 12 employees per shift. Over 5.300 registered tasks had been coordinated by the EOC; several RKI-units contributed processing these tasks. We established position leads within the EOC to adjust staff assignments and collect feedback. Already existing plans and SOPs were adapted in the course of the pandemic.

**CONCLUSIONS**
It was highly challenging to manage an EOC for such a long period, involving a large number of personnel and large variety of tasks. Good preparation (e.g. existing SOP and premises) and opportunities for regular feedback and improvement helped mitigating these challenges. We recommend EOCs to plan resources for upscaling, adjusting and downscaling processes for an exceptionally intensive and prolonged flood of tasks such as the COVID-19-pandemic.

**Keywords:** COVID-19, Crisis Resource Management, Emergency Preparedness, SARS-CoV-2
**ABSTRACT ID:** 355
**PRESENTED BY:** Ulrike Grote / groteu@rki.de

# POSTER TOUR 2
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstract

### Modelling the human force of infection of West Nile virus in Europe

**G. Marini** [1]
A. Pugliese [2], W. Wint [3], N. Alexander [4], A. Rizzoli [5], R. Rosà [6]

[1, 5, 6] Fondazione Edmund Mach (FEM)
[2, 6] University of Trento (UniTN)
[3, 4] Environmental Research Group Oxford (ERGO)

#### BACKGROUND
West Nile Virus (WNV) is one of the most recent emerging mosquito-borne pathogens in Europe where each year hundreds of human cases are recorded. Here we present a relatively simple technique to model WNV force of infection (FOI) for European human population using normal distributions. We also investigated potential drivers of estimated FOIs, as it is well known that WNV transmission is largely influenced by climatic and environmental conditions.

#### METHODS
We collated WNV human cases data from The European Surveillance System – TESSy, provided by 15 European Countries and released by ECDC (not involved in this study). We modeled WNV FOI for each considered region and year through normal curves whose free parameters, namely average, variance and a rescaling factor (magnitude), were calibrated to observed cases. Finally, we investigated *a posteriori*, through regression linear models, how such parameters are associated to a set of climatic, environmental and demographic covariates.

#### RESULTS
Our modelling approach fits observed epidemiological curves quite well. We found that FOI magnitude is positively associated with spring temperature and larger in more natural areas while FOI peak timing is negatively related to summer temperature. Unsurprisingly, FOI is estimated to be greater in areas with larger shares of elderly people, who are likely to experience more severe infections.

#### CONCLUSIONS
Our results confirm that temperature plays a key role in shaping WNV transmission in Europe and provide new hints on how human presence and demography affect WNV burden. Our modelling approach, simple yet reliable, could be easily adopted for further epidemiological investigations, also for similar vector-borne infections.

**Keywords:** West Nile virus, Europe, Humans, Culex, Public Health
**ABSTRACT ID:** 31
**PRESENTED BY:** Giovanni Marini / giovanni.marini@fmach.it

# POSTER TOUR 2
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstract

### Risk assessment and preparedness plan development for West Nile Virus (WNV) transmission in the State of Baden-Wuerttemberg, Germany, 2022

**S. Nothdurfter [1]**

C. Wagner-Wiening [2], S. Brockmann [3], M. Meincke [4]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden
[1, 2, 3, 4] Baden-Wuerttemberg State Health Office, Stuttgart, Germany

**BACKGROUND**
WNV is a zoonotic pathogen causing West Nile Fever (WNF) in humans. In 2018, WNV was first detected among wild birds in Germany and has been endemic in Eastern Germany since 2019 when the first autochthonous human case was detected. In Baden-Wuerttemberg, no WNV case has yet been notified. This study assessed the risk of WNV transmission in Baden-Wuerttemberg and interviewed stakeholders to inform recommendations for a state level preparedness plan.

**METHODS**
Based on ECDC guidelines and WHO's One Health Framework, we assessed the WNV risk and conducted 14 semi-structured interviews with purposively selected WNV experts from different disciplines and levels. Main themes included surveillance, preparedness and response experiences together with recommendations. We applied an inductive thematic approach to analyse data.

**RESULTS**
Baden-Wuerttemberg is considered a predisposed area (risk level one), hence WNV transmission is possible due to favourable climate and vector presence. At this stage, ECDC recommends multi-sectoral collaborations including developing a preparedness plan. No national plan nor integrated vector management strategy is in place in Germany. Passive surveillance is conducted nationwide, including blood donation deferral and examination of dead wild birds. Additionally, Baden-Wuerttemberg tests horses showing neurological symptoms. Respondents indicated that most affected states did not implement additional surveillance activities. While inter-sectoral collaborations are well-established at national level, state level respondents perceived the lack of integrated surveillance as barrier for WNV preparedness. They expressed interest to advance this work, but COVID-19 hindered efforts for improvement.

**CONCLUSIONS**
For successful WNV preparedness in Baden-Wuerttemberg it is advised to follow ECDC recommendations and consider lessons learned from affected states. Strengthening multi-sectoral and interdisciplinary collaborations in a One Health approach is essential to ensure early WNV detection and timely response.

**Keywords:** West Nile virus, West Nile Fever, Arboviruses, Risk Assessment, One Health
**ABSTRACT ID:** 330
**PRESENTED BY:** Sabrina Nothdurfter / sabrina.nothdurfter@sm.bwl.de

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstract

### Predictors of Lassa fever diagnosis in suspected cases reporting in health facilities: A secondary data analysis of Nigerian surveillance data, 2018-2021

**S. Mba** [1]

L. Ntoimo [2], I. Onoh [3], F. Okonofua [4], M. Meremikwu [5], C. Dan-Nwafor [6], A. Iniobong [7], O. Nwafor [8], M. Dalhat [9], C. Ohonsi [10], M. Balogun [11], E. Ilori [12], C. Ochu [13], I. Adetifa [14]

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[2, 4] Nigerian Academy of Science

[1, 3, 6, 7, 8, 10, 12, 13, 14] Nigeria Centre for Disease Control (Nigeria CDC)

[5] Cochrane Nigeria, University of Calabar Teaching Hospital

[9, 11] African Field Epidemiology Network (AFENET)

**BACKGROUND**

Lassa fever (LF) remains endemic in Nigeria with the country reporting the highest incidence and mortality globally. Recent national data suggests increasing incidence and expanding geographic spread. Predictors of LF case positivity in Nigeria have been sparsely studied. We thus determined the sociodemographic and clinical determinants of LF positivity amongst suspected cases presenting to health facilities from 2018 to 2021.

**METHODS**

A secondary analysis of the national LF surveillance data between January 2018 and December 2021. Socio-demographic and clinical data of 20,027 suspected LF cases were analyzed using frequencies and Chi-square statistics with significant p-value set at $p < 0.05$. The odds of predictors of LF case positivity were assessed using multiple logistic regression models with 95% confidence intervals (CI).

**RESULTS**

Case positivity rate (CPR) for the four years was 15.8% with higher odds of positivity among age group 40-49 years (aOR: 1.40; 95% CI: 1.21-1.62), males (aOR: 1.11; 95% CI: 1.03-1.20), artisans (aOR: 1.70; 95% CI: 1.28-2.27), farmers (aOR: 1.48; 95% CI: 1.21-1.81), symptomatic individuals (aOR: 2.36; 95% CI: 2.09-2.68) and being a health worker (aOR: 0.69; 95% CI: 0.53-0.91). Males accounted for more of the suspected cases (52.6%), while female farmers had higher odds of positivity (aOR: 2.43; 95% CI: 1.76-3.38) than male farmers (aOR: 1.52; 95% CI: 1.19-1.96). Fever (aOR: 2.39; 95% CI: 2.00-2.84) and gastrointestinal (GI) symptoms (aOR: 2.15; 95% CI: 1.94-2.37) had the highest odds among symptoms.

**CONCLUSIONS**

Cumulative LF CPR appears high with clearly identified predictors. Targeted interventions with heightened index of suspicion for sociodemographic categories predictive of LF in suspected cases are recommended. Ethnographic and further epidemiological studies could aid better understanding of these associations.

Abstract presentations - Poster tours

# POSTER TOUR 2
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstract

### Spatiotemporal spread of tick-borne encephalitis in the EU/EEA, 2012-2020

**J. Van Heuverswyn [1]**

L. Hallmaier-Wacker [2], J. Beauté [3], J. Gomes Dias [4], J. Haussig [5], K. Busch [6], J. Kerlik [7], M. Markowicz [8], H. Mäkelä [9], T. Nygren [10], H. Orlíková [11], M. Socan [12], J. Zbrzezniak [13], M. Žygutiene [14], C. Gossner [15]

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[6] Public Health Agency of Sweden (FHM)
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[8] Austrian Agency for Food and Health Safety (AGES)
[9] Finnish Institute for Health and Welfare (THL)
[10] Robert Koch Institute (RKI)
[11] National Institute of Public Health (SZU)
[12] National Institute of Public Health (NIJZ)
[13] National Institute of Public Health – National Research Institute (PZH)
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**BACKGROUND**
Tick-borne encephalitis (TBE) is a vaccine-preventable disease involving the central nervous system. The causal virus is usually transmitted to humans through bites of infected ticks. In recent years, several EU/EEA countries detected their first human TBE cases and in 2020 some countries reported an increase in TBE cases. Therefore, we aimed to provide an updated epidemiological assessment of TBE in the EU/EEA, focusing on spatiotemporal changes.

**METHODS**
Descriptive analysis of case characteristics, time and place was performed using human TBE cases with disease onset in 2012-2020, reported by EU/EEA countries to the European Centre for Disease Prevention and Control. Analysis was performed at EU/EEA, national and regional levels. Notification rates were calculated using Eurostat population data. Dynamic regression models combining Fourier terms and ARIMA errors were used for temporal analysis.

**RESULTS**
Nineteen EU/EEA countries reported 24,974 TBE cases, of which 24,629 (98.6%) were autochthonous. The highest notification rates were recorded in Lithuania, Latvia, and Estonia (16.2, 9.5 and 7.5 cases per 100,000 population, respectively). Fifty regions, from ten countries, had a notification rate ≥5/100,000. There was an increasing trend in number of cases along the study period, with an estimated 0.053 additional TBE cases per week (p-value <0.001). In 2020, 11.5% more TBE cases were reported than predicted. A geographical spread of cases was observed with 130 additional regions reporting human TBE cases in 2014-2020 compared to 2012-2013, particularly in regions situated north-west of known endemic regions.

**CONCLUSIONS**
The TBE epidemiological situation in the EU/EEA is changing and a close monitoring of such changes is required to timely adapt vaccination recommendations. Further analyses are needed to identify populations and geographical areas where vaccination programs can be of benefit.

**Keywords:** Tick-borne Encephalitis, Tick-borne diseases, Vector-borne diseases, Vaccine-preventable diseases, Public Health Surveillance, Epidemiology
**ABSTRACT ID:** 149
**PRESENTED BY:** Jasper Van Heuverswyn / jasper.vh@hotmail.com

# POSTER TOUR 2
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstracts

### Elevated tick borne encephalitis seroprevalence in blood donors in regions classified as moderately-affected or low -risk in Poland, 2022

**K. Pancer [1], D. Rabczenko [2], M. Czarkowski [3], P. Grabarczyk [4], M. Rosińska [5]**

[1, 2, 3, 5] National Institute of Public Health NIH-NRI (NIPH NIH-NRI), Warsaw, Poland

[4] Institute of Hematology and Transfusion Medicine (IHTM), Warsaw, Poland

**BACKGROUND**
Case-based tick-borne encephalitis (TBE) surveillance data indicate marked differences across regions, attributed both to testing patterns and the true level of endemicity. As general population vaccination is recommended only in highly endemic regions it is important to monitor accuracy of classification based on surveillance. We aimed to estimate TBEV seroprevalence in blood donors in regions classified as low or moderate risk (reported annual incidence <1/100,000), where the estimated vaccination coverage is below 1%. It will allow to update vaccine recommendations if necessary.

**METHODS**
Stratified by age (<40,40+) and sex sample of remaining sera of candidate donors in Dolno?l?skie (classified as moderate risk region) and regions classified as low-risk: Podkarpackie, Kujawsko-Pomorskie and Zachodniopomorskie. Blood samples were donated in Jan-Feb 2022 and tested for anti-TBEV IgG with Euroimmun test. Seroprevalence was determined as percent of positive and borderline results (IgG level >0.8). Logistic regression was used to estimate prevalence predictors.

**RESULTS**
Overall 2248 specimens were included (1379 men and 869 women) in the analysis. Seroprevalence was generally 4.93% (111/2248), varying from 2.00% - 8.3% across regions, significantly higher in Kujawsko-Pomorskie (8.3%) and in Zachodniopomorskie (6.5%), both regions classified as low risk. Age group, sex and urban/rural residents were not significantly differentiating prevalence.

**CONCLUSIONS**
We confirm substantial seroprevalence even in regions classified as low-risk reporting <5 cases per year where uptake of vaccine is really low also. Previously, similar seroprevalence in general population was noted in highly endemic regions. This supports re-evaluation of endemicity level in all regions in Poland to issue accurate vaccination recommendations.

# POSTER TOUR 2
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Emerging and vector-borne diseases

**MODERATOR**
Patrizio Pezzotti

## Abstract

### Once more unto the breach: The public health response of an Australian state to the global Monkeypox outbreak 2022

**J. Marshall** [1]

R. Gilmour [2], V. Delpech [3], M. Rahaman [4], J. McAnulty [5]

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**BACKGROUND**
Monkeypox is a zoonotic virus usually associated with exposure to infected animals, primarily in Central and West Africa. Since May 2022 cases have been reported across Europe and North America. On 23 July 2022 the WHO declared the escalating global monkeypox outbreak a Public Health Emergency of International Concern.
The first case of monkeypox in New South Wales (NSW) was detected on 18 May 2022 in a man aged in his 40s who had recently returned from Europe. On 20 May 2022 monkeypox became a notifiable disease. On 26 July 2022 Australia's Chief Medical Officer declared the outbreak a Communicable Disease Incident of National Significance. NSW procured its first delivery of third generation smallpox vaccine in August 2022.
This presentation describes the epidemiology of monkeypox in NSW and the steps of the public health response.

**METHODS**
In NSW outbreak response activities are coordinated by the Ministry of Health and include enhanced surveillance and guidelines, case isolation and contact management, communication with healthcare workers, communication with priority populations, vaccination, and collaboration with other levels of government and experts.

**RESULTS**
To 12 September 2022 NSW has detected 51 cases of monkeypox. All are male, median age 37 (range 26-55). Most cases report same-sex sexual activity prior to illness. 23 high-risk and 55 medium-risk contacts have been identified. There have been no secondary infections reported in NSW. 4,609 people have been vaccinated.

**CONCLUSIONS**
There has been no evidence of sustained local transmission to date in NSW. Working with priority communities to increase awareness of risk and prevention measures, and access to and uptake of vaccination is important, especially as we approach the WorldPride event in Sydney in February 2023.

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 − 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### Integrated surveillance of SARS-CoV-2 and other human respiratory viruses in a public testing facility in Utrecht, the Netherlands to monitor co-circulation in a susceptible population

**S. Raven** [1]

N. Plantinga [2], M. van Lanschot [3], B. van Deursen [4], A. Rirash [5], S. Thijsen [6], T. Siksma [7], E. Fries [8], M. Mostert [9], G. Boland [10], R. Schuurman [11], M. Hofstra [12]

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**BACKGROUND**
Public health measures aiming at restricting SARS-CoV-2 transmission impact the circulation of other respiratory viruses and affected routine surveillance of respiratory viruses in GP practices. This study aims to evaluate integrated surveillance of SARS-CoV-2 and other respiratory viruses in a public testing facility.

**METHODS**
Respiratory surveillance was set up within an existing SARS-CoV-2 public testing facility. Community-dwelling (a)symptomatic persons provided verbal informed consent for completion of a questionnaire and additional respiratory pathogens testing on residual material from swabs taken for SARS-CoV-2 RT-qPCR (Allplex Seegene). Daily, a random subset was tested for sixteen respiratory viruses in three multiplex realtime quantitative PCRs (Seegene). Data were analysed at weekly intervals.

**RESULTS**
Between October 6$^{th}$ 2021 and April 22$^{nd}$ 2022, 7,045 subjects consented and completed the questionnaire; 3,696 subjects were tested for viral pathogens. The weekly median age ranged from 23 to 39 years. The percentage of individuals with respiratory symptoms fluctuated between 27.5% and 98.5%, depending on testing policy. The weekly prevalence of *any* respiratory pathogen including SARS-CoV-2, ranged from 19.6% in week 49 (2021) to 75.3% in week 14 (2022). Overall, SARS-CoV-2 was detected most frequently (27.3%, range 2.2-63.3%), followed by Rhinoviruses (15.0%, range 3.5-47.8%) and seasonal coronaviruses (3.8%, range 0-10.3%). Influenzavirus was systematically detected from week 6 (2022) and onwards in 3.0% of participants.

**CONCLUSIONS**
Integrated respiratory viral surveillance within public testing facilities is feasible and informative. Prevalences may be affected in response to measures to prevent SARS-CoV-2 transmission, changes in testing policies and virus evolution. Population characteristics are pivotal to interpret trends over time. Together with pre-pandemic surveillance in GP practices, these instruments may inform policy makers and hospitals for adequate preparedness during the COVID-19 pandemic.

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### Feasibility to estimate real-time influenza vaccine effectiveness: a pilot study across five European study sites

**M. Maurel** [1]

S. Cohuet [2], I. Martínez-Baz [3], A. Vilcu [4], T. Vega [5], A. McKenna [6], M. Hooiveld [7], I. Casado [8], S. Van Der Werf [9], F. Pozo [10], L. Domegan [11], A. Meijer [12], J. Castilla [13], A. Falchi [14], C. Mazagatos Ateca [15], J. O'Donnell [16], M. de Lange [17], P. Penttinen [18], A. Omokanye [19], E. Kissling [20], M. Valenciano [21]

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

**BACKGROUND**
Real-time influenza vaccine effectiveness (IVE) estimates may help to timely understand vaccine performance early in the season and duration of protection. Starting in February 2022, we conducted a pilot study to assess feasibility of estimating real-time IVE fortnightly at primary care level in five ECDC I-MOVE (Influenza Monitoring Vaccine effectiveness in Europe) sites.

**METHODS**
We estimated real-time IVE using a multicentre test-negative case-control design. Cumulative pooled IVE across the season was estimated overall and for influenza (sub)types, sample size permitting. We also estimated IVE by age-group (0–14 and 15–64 years) and by influenza vaccine target group.

**RESULTS**
All sites sent timely data to the coordination hub using a secure data transfer system. Fortnightly, the coordination hub cleaned the data, sent a data checking report to study sites for validation, analysed the data and created a report using R/Rmarkdown. The report presenting cumulative pooled IVE (current period and historical), descriptive analyses and site-specific IVE was shared fortnightly with participating sites and ECDC.
From week 44 2021 up to week 9 2022, the overall IVE point estimate was 39% (95%CI: 15–57) and decreased over time to 32% (95%CI: 17–44) by week 17 2022. For the 15–64 age group, the IVE point estimate was 41% (95%CI: 14–61) and decreased over time to 39% (95%CI: 23–53).

**CONCLUSIONS**
Estimating and reporting fortnightly 2021–22 pooled cumulative IVE at primary care level was feasible among five European study sites. An evaluation of this pilot is ongoing to understand if the burden of work is acceptable and IVE results are useful and accurate enough to continue the study and expanding to more sites in subsequent influenza seasons.

**Keywords:** Influenza, Influenza vaccine, Vaccine effectiveness, Multicentre studies, Case-control studies
**ABSTRACT ID:** 225
**PRESENTED BY:** Marine Maurel / m.maurel@epiconcept.fr

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### The epidemiology of respiratory syncytial virus in children during the COVID-19 pandemic measured by laboratory, clinical and syndromic surveillance in England: a retrospective observational study

**M. Bardsley** [1]

R. Morbey [2], H. Hughes [3], C. Beck [4], C. Watson [5], H. Zhao [6], J. Ellis [7], G. Smith [8], A. Elliot [9]

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**BACKGROUND**
Seasonal epidemics of respiratory syncytial virus (RSV) commonly cause a clinically significant burden of disease among young children. Following declaration of the COVID-19 pandemic, non-pharmaceutical interventions (NPIs) targeted at SARS-CoV-2 have impacted the transmission of other respiratory pathogens. We describe the change in epidemiology of RSV among children under five years-old in England during winter 2020/21.

**METHODS**
RSV surveillance data were extracted from national laboratory, clinical and syndromic surveillance systems from January 2015 to March 2021 for children under five years-old. Time-series analyses using generalised linear modelling (negative binomial) estimated the impact of SARS-CoV-2 NPIs on RSV indicators during winter 2020/21.

**RESULTS**
RSV-associated activity was substantially reduced for all indicators studied during winter 2020/21. Within the scope of the surveillance systems included, we estimate that 99·7% (n=12,320) of laboratory cases, 81·0% (92,692) hospital admissions, 85·3% (27,486) emergency department attendances, 73·7% (96,672) NHS 111 calls, 88·8% (2,924) out-of-hours GP consultations and 89·9% (91,304) in-hours GP consultations were avoided among children under five years-old compared to that expected during a 'normal' RSV season.

## CONCLUSIONS

We observed a substantial reduction in RSV-associated activity across numerous surveillance systems following the implementation of NPIs to prevent SARS-CoV-2 transmission in England. We hypothesise that the unprecedented absence of RSV during the 2020/21 winter has likely resulted in a cohort of children lacking natural immunity to RSV, thereby raising the potential for future increased RSV incidence, out-of-season activity and increases in health service pressures. Additionally, we will present an update on the epidemiology of RSV from April 2021 through winter 2021/22 to describe the subsequent impact of the relaxation of NPIs on RSV circulating in England and resulting out-of-season RSV activity.

**Keywords:** COVID-19, SARS-CoV-2, Respiratory syncytial virus, RSV, Laboratory surveillance, Syndromic surveillance, Respiratory pathogens, Paediatric infections, Non-pharmaceutical interventions
**ABSTRACT ID:** 236
**PRESENTED BY:** Megan Bardsley / megan.bardsley@phe.gov.uk

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### Differences found in the epidemiology of Tuberculosis (TB) among migrants versus non-migrants in Ireland, 2011-2020

**S. Jackson** [1]
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[1,3] Trinity College Dublin (TCD)
[2] University College Cork (UCC)

**BACKGROUND**
Despite declining TB crude incidence rates (CIRs) in Ireland, the CIR among migrants remains five times higher than among non-migrants. We analysed notifications from the Irish TB surveillance system to compare the epidemiology of active TB among migrants and non-migrants in Ireland from 2011-2020 to inform future prevention and control strategies.

**METHODS**
We analysed cases by person, place and time, defining migrants as being diagnosed in Ireland and born outside Ireland. We calculated CIRs per 100,000 population using census denominators stratified by country of birth, defining high TB incidence as >40/100,000 population. We performed temporal trend analysis using Negative-binomial regression.

**RESULTS**
Migrants accounted for 47% of the 3,158 cases notified. Annual CIRs declined from 25.2-13.65 among migrants (IRR: 0.95; CI: 0.94-0.97) and from 5.6-1.8 among non-migrants (IRR: 0.91; CI: 0.89-0.93).
Median age was 34 years among migrants and 53 year among non-migrants. Male to female ratio was 1.3 among migrants and 1.7 among non-migrants. Migrants had significantly higher odds of any drug resistance (1.7; 1.2-2.6), multi-drug resistance (19.4; 5.0-166) and HIV co-infection (4.0; 2.5-6.9), but lower odds of being linked to an outbreak (0.28;0.21-0.37) or sputum positive (0.76; 0.61-0.93).
Migrants originated from 96 countries, 80% originated from high TB incidence countries compared to 23% of the Irish population. The top ten migrant source countries differed when ranked by case numbers versus CIR. Four migrant source countries had higher CIRs in Ireland than reported by WHO for their country of origin.

**CONCLUSIONS**
The pace of TB decline among migrants is slower than non-migrants, with elevated CIRs among migrant subpopulations suggesting health access inequity. A renewed focus on migrant health strategy is required to achieve the global TB elimination goal.

**Keywords:** Tuberculosis, Human migration, Emigrants and Immigrants, Transients and Migrants, Epidemiology, Epidemiological monitoring
**ABSTRACT ID:** 239
**PRESENTED BY:** Sarah Jackson / jacksos2@tcd.ie

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### A SARS-CoV-2 Omicron outbreak among crew members on a cruise ship in Germany in early 2022

**S. Bühler** [1]

M. Dirksen-Fischer [2], K. Alpers [3], A. Dörre [4], P. Busch [5], A. Plenge-Bönig [6], J. Fornacon [7], A. Reichstein [8], C. Schäfers [9], S. Kleine-Kampmann [10], P. Wittkamp [11]

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[2,10,11] Hamburg Port Health Center, Institute for Hygiene and Environment, Free and Hanseatic City of Hamburg
[5] Institute for Hygiene and Environment, Free and Hanseatic City of Hamburg
[6] Division of Hygiene and Infectious Diseases, Institute for Hygiene and Environment, Free and Hanseatic City of Hamburg
[7] ship physician
[8,9] New-generation sequencing (NGS) laboratory

**BACKGROUND**
SARS-CoV-2-outbreaks on cruise ships, have rarely been investigated. In early 2022, we were informed about a SARS-CoV-2 outbreak on a cruise ship calling Hamburg's harbour after 10 infections among crew members were detected. We conducted an outbreak investigation in collaboration between ship owners, ship physicians and Hamburg´s Institute for Hygiene and Environment, to identify risk factors and to achieve containment.

**METHODS**
In a cohort study among 165 crew members we collected data on age, sex, nationality, boarding-time, cabin use (single/shared), work place, and vaccination status. Cases tested SARS-CoV-2 positive at least once during daily screenings during the outbreak period (PCR or antigen-test). We investigated risk factors for infection by descriptive, univariable and multivariable analysis. We performed whole genome sequencing to identify SARS-CoV-2 variants.

**RESULTS**
We found 103 cases (attack rate (AR) 62.4%); 39/41 sequenced samples were BA.2 Omicron subtype, one BA.1 and one BA.1.1. Among boostered, AR was 38% versus 65% among those vaccinated once/twice. Among those <30 days on board AR was 31% versus 72% among those staying longer. Among Europeans AR was 53% versus 71% in non-Europeans. Adjusting for age and sex, cases were more likely to have received no booster vaccine (OR=2.66, 95% CI 0.99-7.13), to have spent more time on board (≥30 days OR=6.36 95%CI 2.81-14.40 versus <30 days) and to have a non-European nationality (OR=2.14 95%CI 1.08-4.27). The outbreak stopped shortly after isolation of cases off board.

**CONCLUSIONS**
This investigation confirms the importance of a booster vaccine against Covid-19. Longer stays on board could facilitate social mixing. Non-Europeans could have issues with health access or language barriers. Physical distancing together with screening and isolation can contain SARS-CoV-2 outbreaks on cruise ships

**Keywords:** SARS-CoV-2, Cruise Ship, Outbreak, Crew
**ABSTRACT ID:** 42
**PRESENTED BY:** Silja Bühler / silja.buehler@hu.hamburg.de

# POSTER TOUR 3
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Respiratory diseases

**MODERATOR**
Katie Palmer

## Abstract

### COVID-19 outbreak in an elderly care home: very low vaccine effectiveness and late impact of booster vaccination campaign

**K. Van Ewijk** [1]

E. Hazelhorst [2], S. Hahné [3], M. Knol [4]

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[1, 2, 3, 4] Centre for Infectious Disease Control, National Institute for Public Health and Environment (RIVM)

**BACKGROUND**
Elderly in long-term care facilities (LTCF) are at higher risk for (severe) COVID-19, yet evidence of vaccine effectiveness (VE) in this population is scarce. In November 2021 (Delta period), a COVID-19 outbreak occurred at a LTCF in the Netherlands, continuing despite measures and booster vaccination campaign. We investigated the outbreak to assess VE of primary COVID-19 vaccination against SARS-CoV-2 infection and mortality, and to describe the impact of the booster vaccination.

**METHODS**
We calculated attack rate (AR) and case fatality (CF) per vaccination status (unvaccinated, primarily vaccinated and boostered). We calculated VE – at on average 6 months after vaccination – as 1-risk ratio (RR), using the crude RR with 95% confidence intervals (CI) for the association between vaccination status (primary vaccination versus unvaccinated) and outcomes (SARS-CoV-2 infection and mortality <30 days after testing positive for SARS-CoV-2).

**RESULTS**
The overall AR was 67% (70/105). CF was 33% (2/6) among unvaccinated cases, 12% (7/58) among primarily vaccinated and 0% (0/5) among boostered. The VE of primary vaccination was 17% (95% CI -28%; 46%) against SARS-CoV-2 infection and 70% (95% CI -44%; 96%) against mortality. Among boostered residents (N=55), there were 25 cases in the first week after receiving the booster dose, declining to 5 in the second and none in the third week.

**CONCLUSIONS**
VE of primary vaccination in residents of LTCF was low against SARS-CoV-2 infection and moderate against mortality. There were few cases at 2 weeks after the booster dose and no deaths, despite the presence of susceptible residents. These data are consistent with the positive impact of the booster vaccination in curbing transmission. Timely booster vaccination in residents of LTCF is therefore important.

**Keywords:** COVID-19 outbreak, Vaccine effectiveness, Booster Vaccination, Long-term care Facility, Nursing home
**ABSTRACT ID:** 28
**PRESENTED BY:** Katja Van Ewijk / katja.van.ewijk@rivm.nl

# POSTER TOUR 4
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

Timely and reliable outbreak investigation using a non-probabilistic online panel as a source of controls - two parallel case-control studies investigating a Salmonella Braenderup outbreak in Germany

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**BACKGROUND**
We evaluated the use of controls recruited via an online panel in a case-control study (CCS) investigating a *Salmonella* Braenderup outbreak in Germany (March-May 2021) with melons presumed as vehicle of infection.

**METHODS**
We emailed questionnaires to the online panel controls, and interviewed by phone classical controls recruited via random digit dialling. Frequency matching (age, sex, federal state) was performed, before interviews for classical and after questionnaire completion for panel controls. Both control groups were queried about fruit consumption in two study periods: in April (when the outbreak occurred) and in July (when controls were interviewed). Logistic regression was applied for single and multi-variable analyses to determine adjusted odds ratios (aOR) and 95% confidence intervals (CI) for the association with disease.

**RESULTS**
The study included 32 cases, 110 classical and 81 panel controls. No substantial differences in frequency of consumption of melons and other explored fruit items, except cherries and mangos, were observed between the two control groups. Associations respectively for any melon and Galia melon with panel controls (aOR 19, CI: 6-71; aOR 12, CI: 3-66) as well as classical controls (aOR 32, CI: 11-121; aOR 55, CI: 8-1100) were two-three times stronger in April than in July. Recruitment of classical controls took 111h vs 8h for panel controls. Total recruitment costs were 5 times higher for classical controls.

**CONCLUSIONS**
The deployment of an online panel to recruit controls in a CCS proved successful in the identification of melons, particularly Galia melons, as the outbreak infection vehicle in substantially less time and at lower costs compared to using classical controls. We recommend to consider this timely and reliable control recruitment method when investigating diffuse foodborne outbreaks.

**Keywords:** Comparative Study Design, Outbreaks, Gastrointestinal Infection, Case-control studies, Online Panel
**ABSTRACT ID:** 328
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# POSTER TOUR 4
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

An outbreak of Escherichia coli-associated haemolytic uremic syndrome linked to consumption of an unexpected food vehicle, France 2022

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### BACKGROUND
In February 2022, Santé publique France identified an excess of paediatric haemolytic uremic syndrome cases. We conducted epidemiological, microbiological, and trace-back investigations to identify the outbreak source and implement control measures.

### METHODS
We defined cases as Shiga toxin-producing Escherichia coli (STEC) O26:H11 or O103:H2 infection with outbreak strains identified by whole genome sequencing (WGS) and symptom onset since Jan 1, 2022. We interviewed case caretakers about food exposures before symptom onset. Supermarket loyalty card information was requested to identify purchases and guide trace-back investigations. Stool and food isolates were characterized by multilocus variable-number tandem-repeat analysis and WGS at the National reference centre. We conducted a case-control study including O26:H11 cases and controls from parents registered on GrippeNet.fr (online population-based surveillance system).

### RESULTS
We identified 55 cases nationwide with onset between 18 January and 25 March (median age 7 years; sex ratio M/F: 1.3). Two children died. Eighty-eight percent (35/40) of cases with available information reported consumption of Brand X frozen pizza. Ninety-five percent (35/37) of cases with pizza purchases on loyalty cards purchased Brand X. The case-control study confirmed a strong association between consumption of Brand X pizza and disease (OR: 116 [95%CI 27-503]). Samples of Brand X pizza from case homes and from the manufacturer were positive for both outbreak strains.

### CONCLUSIONS
Outbreak investigations confirmed frozen pizzas as the source of the largest STEC-HUS outbreak ever documented in France. On 18 March, Brand X voluntarily recalled and withdrew the incriminated pizzas. This outbreak is highly unusual, as typical baking temperatures and times for frozen pizzas should eliminate infection risk. Investigations continue to understand the origin of contamination and the persistence of STEC in baked pizzas.

# POSTER TOUR 4
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

### Outbreak investigation of cholera in a peri-urban village of Panchkula district, Haryana, India, 2021

**S. Gupta** [1]

P. Padda [2], M. Kumar [3], S. Kumari [4], K. Dzeyie [5], I. Kaur [6], P. Bhatnagar [7], T. Nhu Nguyen [8]

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**BACKGROUND**
Untreated cholera causes severe diarrhoea with case fatality up to 50%. On 14 July 2021, 17 acute diarrhoeal disease (ADD) illnesses were reported from Abheypur village, Panchkula. We investigated to described the epidemiology and provide evidence-based control measures.

**METHODS**
We defined a suspect cholera case as ≥3 loose stools within 24 hours in a resident of Abheypur between 1–31 July 2021. We identified cases from passive surveillance and house-to-house survey and interviewed cases using semi-structured questionnaire for demographic, clinical and exposure history. We collected stool and water samples for bacteriological examination and residual chlorine level. We inspected water and sewage pipelines for potential contamination

**RESULTS**
We identified 520 cases (57% male) in 11,000 population (attack rate 4.7%) including one death (case fatality 0.02%). The median age was 21 years (range: 1-74), 228 (44%) were hospitalized; 112 (49%) had vomiting, 205 (90%) received fluid replacement and all were given antibiotics. Of 35 individual samples, 28 (80%) showed darting motility by microscopy and 10 (28%) showed Vibrio cholera by culture. Drinking water samples 35% (20/59) showed faecal contamination and 39% (70/178) had no residual chlorine. All 1270 households used pipe-water supply as the main source of drinking water, 125 (10%) used any water purification system. We identified four leakages points in the water pipeline within one metre close to sewer lines. The leakages were repaired, chlorine tablets supplied and water supply restored immediately

**CONCLUSIONS**
We confirmed a points source cholera outbreak in a village likely due to contamination of drinking water pipeline with sewage. We recommended daily testing and chlorination of water, maintenance of pipelines to prevent future cholera outbreaks. Prompt public health responses helped control the outbreak.

# POSTER TOUR 4
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

### Cholera Outbreak Investigation, Ballo Adda Mohalla, Lucknow District, Uttar Pradesh 2021

**S. Tripathi** [1]

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#### BACKGROUND
While cholera is endemic in many states of India, Lucknow has not reported cholera outbreak in a decade. On August 9, 2021, a suspected cholera outbreak including one death was reported from Ballo Adda. We investigated to describe the epidemiology and prevent spread.

#### METHODS
We defined a suspect cholera case as ≥3 loose stools within 24 hours in a resident of Ballo Adda from August 1-13, 2021. House-to-house active case search done and medical records at primary health centre reviewed. Cases were interviewed using a semi-structured questionnaire to understand the epidemiology. Stool samples were sent for bacteriological examination and water samples from tap water and water pumps (1-5) for bacteriological testing and residual chlorine level.

#### RESULTS
We identified 191 cases (attack rate=15%), with median age 45 years (range: ‹1-89 years). Seventy (37%) were hospitalized and one death (0.5%). Reported symptoms included abdominal pain 147 (77%), vomiting 113 (59%) and fever 62 (33%).84% (76) reported using water from water pump 1 and 7% (6) used municipality piped water. Five (55%) stool samples were positive for Vibrio cholerae 01 and 40% (5) water samples from water pump (1 and 4) showed coliform count ›10 MPN per 100 ml, with no residual chlorine. Samples from 26 taps that received municipal supply showed residual chlorine ~0.3 ppm and no coliform. During field visit, we observed a breached in a recently laid sewer pipeline near pump 1

#### CONCLUSIONS
This was a laboratory confirmed cholera outbreak likely due to contamination of underground water. We recommended the public health engineering department to chlorinate drinking water, community to boil water and ensure safety to the water lines while digging/laying sewer pipelines.

**Keywords:** Drinking water, India, Diarrhea, Disease outbreak, Acute diarrheal diseases
**ABSTRACT ID:** 337
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# Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

### Norovirus GII.3[P12] outbreak associated with the drinking-water supply in a rural area in Galicia, Spain, 2021

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**BACKGROUND**

On 30 September, the city council of Muxia reported an unusual increase of patients with acute gastroenteritis. Because geographically widespread villages belonging to the same water supply were affected, a waterborne outbreak was suspected.

**METHODS**

Probable cases were defined as a person with vomiting and/or diarrhoea between 28 September- 7 October who lived in the villages belonging to the water supply of Muxia. We conducted an unmatched case-control (1:1) study using a structured questionnaire to identify water and food exposures. We included only primary cases and controls with exposure to the water supply between 28- 30 September. Water and stool samples were genotyped by RT-PCR and Sanger/Metagenomic sequencing.

**RESULTS**

Overall, 115 probable cases were identified (attack rate: 5.7%), 54% female and age range of 0-92 years. Cases peaked on 29 September and subsided on 1 October. We obtained data for 62 cases and 46 controls. Univariate analysis showed that cases had a higher exposure to tap water through direct consumption (OR =86; 95% CI: 18-409) or vegetable-washing (OR =27; 95% CI: 7-98). Norovirus GII was detected in two terminal points of the water supply and in 14 stool samples. A unique genotype (GII.3[P12]) was identified in stool samples.

**CONCLUSIONS**

After 1 October, when a tap water ban was put in place and the water purged and chlorinated, the number of cases decline rapidly suggesting a waterborne point-source outbreak among the residents exposed to the water supply of Muxia. Metagenomics confirmed norovirus as the only pathogen present in stool ruling out massive faecal contamination of the water. Detection of faecal indicator bacteria and the absence of free chlorine suggests a breakdown in chlorination as the cause of the outbreak.

# POSTER TOUR 4
DAY 1, 23 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses

**MODERATOR**
Steen Ethelberg

## Abstract

### Impact of COVID-19 restrictions on the epidemiology of Cryptosporidium spp. in England and Wales

**J. Adamson** [1]

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[3] Public Health Wales - UK Field Epidemiology Training Programme
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**BACKGROUND**

In England and Wales, cryptosporidiosis cases peak in spring and autumn, usually associated with zoonotic/environmental exposures (*C. parvum*, spring/autumn) and with overseas-travel and water-based activities (*C. hominis*, autumn). COVID-19 restrictions reduced foreign-travel from the UK by 74% in 2020, but potentially increased environmental-exposures through more countryside activities locally. We investigated the impact of COVID-19 restrictions on the epidemiology of cryptosporidiosis.

**METHODS**

Confirmed cases were extracted from England and Wales's reference-laboratory database (01-January-2015 to 31-December-2021). We defined two periods for pre/post COVID-19 social-restrictions implementation: "pre-restrictions" between 2015-week 1 and 2020-week 12, and "post-restrictions" between 2020-week 13 and 2021-week 52. We conducted an interrupted time-series analysis, assessing differences in incidence, trends and periodicity between these periods using negative binomial regression with linear-splines and interactions.

**RESULTS**

There were 21,403 cases between 01-January-2015 to 31-December-2021 (*C. parvum*=12,315; *C. hominis*=9,088). Post-restrictions incidence of *C. parvum* dropped by 48.0% (95%CI: 36.7%-57.3%; p<0.001). There was no pre-restrictions incidence-trend (IRR=1.0003; 95%CI: 0.9997-1.0009; p=0.276) but an increasing incidence-trend existed post-restrictions (IRR=1.0067; 95%CI: 1.0033-1.0099; p=0.001). A periodicity change was observed post-restrictions, peaking one week earlier in spring and two weeks later in autumn.

Post-restrictions incidence of *C. hominis* dropped by 97.5% (95%CI: 95.5%-98.7%; p<0.001). A decreasing incidence-trend pre-restrictions (IRR=0.9976; 95%CI: 0.9969-0.9982; p<0.001) was not observed post-restrictions (IRR=1.0081; 95%CI: 0.9977-1.0186; p=0.128). No periodicity change was observed post-restrictions.

**CONCLUSIONS**

Introduction of COVID-19 restrictions reduced cryptosporidiosis infections; altering the burden, trends (*C. parvum* and *C. hominis*) and periodicity (*C. parvum*). The upward-trend in *C. parvum* post-restrictions may be consistent with changes to restrictions and people's compliance. The periodicity changes for *C. parvum* must be accounted for in future surveillance and exceedance reporting.

# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

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## Abstract

### Seroprevalence of SARS-CoV-2 IgG antibodies and factors associated with neutralizing activity among primary health care workers six months after vaccination rollout in France

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D. Decarreaux [2], C. Souty [3], A. Vilcu [4], P. Prévot-Monsacre [5], T. Fourié [6], P. Saba Villarroel [7], S. Priet [8], H. Blanché [9], J. Sebaoun [10], J. Deleuze [11], C. Turbelin [12], A. Werner [13], F. Kochert [14], B. Grosgogeat [15], P. Rabiega [16], J. Laupie [17], N. Abraham [18], C. Guerrisi [19], H. Noël [20], S. van der Werf [21], F. Carrat [22], T. Hanslik [23], R. Charrel [24], X. de Lamballerie [25], T. Blanchon [26], A. Falchi [27]

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**BACKGROUND**
Vaccination is crucial for the control of COVID-19. Real-world data on factors that affect neutralizing antibodies (NAbs) after vaccination are scarce but necessary to inform policy. We aimed to assess the immunoglobulin G (IgG) response and NAbs against SARS-CoV-2 among primary health care workers (PHCW) six months after vaccination rollout in metropolitan France, and to identify factors associated with the detection of NAbs.

**METHODS**
A cross-sectional study was carry-out in May-August 2021. A non-probabilistic sample of PHCW was recruited. Participants received a dried blood spot (DBS) home sampling kit and provided by mail a self-sampled DBS with a completed questionnaire. DBS samples were punched. IgG antibodies targeting SARS-CoV-2 nucleocapsid (N) and spike (S) proteins were detected with enzyme-linked immunosorbent assays and NAbs with plaque reduction neutralization assays. Determinants of NAbs detection were investigated using logistic regression analyses. Age, sex, comorbidities, previous SARS-CoV-2 infection (reported by participant and/or ELISA-N positive), vaccination (number of doses and time) were considered.

**RESULTS**
Data from 1,612 PHCW were included. Overall, 23.6% (95%CI: 21.6%–25.7%) had anti-N antibodies, 94.7% (93.6%–95.7%) anti-S, and 81.3% (79.4%–83.2%) NAbs. Detection of NAbs was significantly more likely in PHCW with a previous SARS-CoV-2 infection than in those with no such history among unvaccinated (adjusted odds ratio [aOR]=16.57; 95% confidence interval [CI], 5.96–59.36) and among vaccinated with one dose (aOR=41.66; 95% CI, 16.05–120.78). PHCW vaccinated with two doses within the last 3 months were more likely to have NAbs compared to those vaccinated earlier (OR, 5.28; 95% CI, 3.51–8.23).

**CONCLUSIONS**

In line with previous research, prior history of SARS-CoV-2 infection and time since vaccination should be considered when planning booster doses and the design of COVID-19 vaccine strategies.

**Keywords:** SARS-CoV-2, Vaccine immunogenicity, Seroepidemiologic studies, Neutralizing antibodies, Health Personnel

**ABSTRACT ID:** 259

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# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

## Abstract

**Direct and indirect vaccination effects on SARS-CoV-2 infection in day-care centers: evaluating the policy for early vaccination of day-care staff in Germany, 2021**

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### BACKGROUND

Due to initially limited supply of COVID-19 vaccines, certain groups, including day-care staff, were prioritized for early vaccination in Rhineland-Palatinate from 03/2021 onwards. The aim of this study was to assess the effect of early vaccination of adult day-care staff on SARS-CoV-2 transmission in day-care centers.

### METHODS

Data came from state-wide mandatory notification of SARS-CoV-2-cases in educational institutions, followed by contact tracing in a subgroup of notified cases. The mean number of secondary cases per index case (i) and the proportion of day-care staff among all notified cases from day-care (ii) were calculated in monthly intervals, from 10/2020 to 06/2021. Interrupted time series analyses were used to quantify the effect of the vaccination prioritization in day-care staff on these two outcomes.

### RESULTS

The mean number of secondary cases among the 566 index cases from day-care followed by contact tracing was 1.26. This number was highest in 03/2021 (2.12 cases per index) and dropped significantly afterwards (by -0.60 secondary cases per month (95% confidence interval (CI) -0.27;-0.92)). About 2200 day-care cases were notified in the study period, 57% (n=389) and 26% (n=388) of which affected staff in the pre- and post-intervention period, respectively. This proportion decreased by an absolute 27% immediately after intervention (95%CI -0.22;-0.32) and by further 6% each month (95%CI -0.04;-0.08). Between March and June 2021, exclusive vaccination of day-care staff, who constitute less than 30% of persons in day-care, prevented more than 47% of SARS-CoV-2 cases in this setting.

### CONCLUSIONS

Early vaccination of day-care staff reduced SARS-CoV-2 cases in the overall day-care setting and thus also protected unvaccinated children. This finding should inform future vaccination strategies.

# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

## Abstract

### Impaired immunity and high attack rates caused by SARS-CoV-2 variants among vaccinated long term care facility residents

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**BACKGROUND**
Long-term care facility (LTCF) residents are at high risk for severe coronavirus disease 2019 (COVID-19), and therefore COVID-19 vaccinations were prioritised for residents and personnel in early 2021. We investigated two LCTF outbreaks and compared the humoral and cell-mediated immunity of residents and healthcare workers (HCW).

**METHODS**
We calculated attack rates (AR), identified the responsible variant, and measured IgG antibodies to SARS-CoV-2 spike glycoprotein (receptor binding domain [RBD] and full-length spike glycoprotein [SFL]), neutralizing antibody (NAb) titers, and cell-mediated immunity markers from vaccinated and non-infected residents and HCWs. Sera was collected ≥14 days after the last dose of vaccine. We used the Wilcoxon - Mann-Whitney test to compare IgG and NAb distributions between residents and HCWs.

**RESULTS**
In LTFC-1 the outbreak was caused by an Alpha variant and the AR among once-vaccinated residents was 23%. In LTCF-2 the outbreak was caused by a Beta variant. Its AR was 47% although all residents had received their second dose one month before the outbreak. IgG levels were 5-fold higher in HCWs compared to residents (P=.0031 for RBD, P=.0024 for SFL) in once-vaccinated subjects. They were 6- (RBD) and 4-fold (SFL) higher (P<.001 and P=.0041 respectively) in twice-vaccinated ones. Most of the once-vaccinated subjects (>80%) had no NAb to the Alpha and Beta variants. Only 1/8 twice-vaccinated residents had NAb to the Beta variant in contrast with 10/12 HCWs. Cell-mediated immune response seemed better in HCWs compared to residents.

**CONCLUSIONS**
Vaccinated elderlies remain susceptible to Alpha or Beta variants breakthrough. The weaker vaccine response in the elderly needs to be addressed in vaccination protocols, while new variants capable of evading vaccine-induced immunity continue to emerge.

**Keywords:** COVID-19, Long-term Care, Antibodies, Neutralising, Cellular, Aged
**ABSTRACT ID:** 134
**PRESENTED BY:** Dorothée Obach / dorothee.obach@thl.fi

# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

## Abstract

### The effect of hybrid immunity during Omicron variant wave in a European healthcare worker cohort, December 2021 - April 2022

**C. Savulescu [1]**
ECDC VEBIS HCW VE study group

[1] Epiconcept

**BACKGROUND**
Previous SARS-CoV-2 infections may influence protection offered by COVID-19 vaccination against Omicron variant infections (hybrid immunity). We measured the relative vaccine effectiveness (rVE) of COVID-19 mRNA vaccine booster and previous infection in healthcare workers (HCWs) during the Omicron variant-dominated wave (December 2021-April 2022).

**METHODS**
We conducted a prospective cohort study among HCWs from nine EU/EEA hospitals. We defined previous infections as any reported SARS-CoV-2 episode before enrolment. Among HCW who had completed the primary vaccination course, we used four levels of exposure: booster vaccination and previous infection (booster/previous), primary schedule and previous infection (primary/previous), booster vaccination without previous infection (booster only) and primary schedule without previous infection (primary only). Using Cox regression, we calculated the rVE of booster vaccination with/without previous episodes compared to primary schedule and no booster (primary only reference) as (1-hazard ratio)*100, adjusted for age, sex, underlying condition, site and month of follow-up.

**RESULTS**
Of 1078 HCW followed-up during the study period, 226 (21%) had a previous SARS-CoV-2 infection, 141/226 (62%) of these vaccinated with a booster dose. We detected 197 SARS-CoV-2 infections, including 24 (12%) in HCW with previous infection. SARS-CoV-2 infection incidence rate was 3.4/1000 person-days (primary only) compared with 1.6/1000 (booster/previous), 2.1/1000 (primary/previous) and 3.0 (booster only). Compared to primary only, the adjusted rVE was 55% (95%CI: 16; 76), 30% (-32 to 63) and -5% (-61 to 32) for booster/previous, primary/previous, and booster only, respectively.

**CONCLUSIONS**
A low proportion of SARS-CoV-2 infections occurred in previously infected HCWs indicating that previous infection and booster vaccination may have offered additive protection. We will further investigate the hybrid immunity to determine the best timing for providing vaccination after a SARS-CoV-2 infection in HCWs.

**Keywords:** SARS-CoV-2 infection, Healthcare workers, Vaccine effectiveness, COVID 19 Vaccine, Active Surveillance
**ABSTRACT ID:** 331
**PRESENTED BY:** Camelia Savulescu / c.savulescu@epiconcept.fr

# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

## Abstract

### B cell mediated immunogenicity following boosting with the BNT162b2 SARS-CoV-2 vaccine in dialysis patients, Israel, 2021-22

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**BACKGROUND**
Chronic kidney disease patients (CKDP) are high risk for COVID19. CKDP sometimes require specific vaccination regimens to achieve optimal protection. We determined whether B-cell response following a third BNT162b2 vaccine dose (boosting) differed in CKDP and those with normal renal function, in order to inform vaccination policy in CKDP.

**METHODS**
At Ziv Medical Center, Israel, we recruited double-vaccinated, dialyzed CKDP and compared them to age-matched, double-vaccinated healthcare workers in terms of; (i) the proportion of peripheral B cells producing SARS-CoV-2 anti-spike IgG (SARS-CoV-2-B cells), measured using flow cytometry; (ii) geometric mean concentration (GMC) of SARS-CoV-2 anti-spike IgG antibodies in serum (IgG), measured by a quantitative serological assay at 3 time points: pre-boosting, 1-2 months and 4-6 months post-boosting. We compared the two groups using two-way ANOVA and Kruskal-Wallis tests.

**RESULTS**
Among the 45 CKDP and 47 controls, the proportion of SARS-CoV-2-B cells changed significantly ($p < 0.001$) over time, increasing from pre-boosting to 1-2 months post-boost (0.09% to 0.5% and 0.18% to 0.27% respectively) and decreasing 4-6 months post-boost (to 0.3% and 0.17% respectively). The proportion of SARS-CoV-2-B cells was similar between the two groups at all three time points ($p = 0.110$). Compared with controls, IgG GMC among CKDP was lower pre-boost (29 vs. 178 AU/ml, $p < 0.003$) and similar 1-2 months (2429 vs. 1139 AU/ml, $p < 0.06$) and 4-6 months later (257 vs. 447 AU/ml, $p < 0.14$).

**CONCLUSIONS**
BNT162b2 booster immunogenicity was comparable in healthy controls and CKDP for circulating peripheral SARS-CoV-2-B cells and IgG, suggesting that in CKDP, post-vaccination B cell response is preserved and normal vaccine formulation is suitable. Lower pre-boost IgG levels in CKDP require further investigation to determine the need for an earlier booster.

# POSTER TOUR 5
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccination and immunity

**MODERATOR**
Nathalie Nicolay

## Abstract

### Estimating COVID-19 and influenza vaccination coverage in homeless populations; Wales, UK

**G. Jones** [1]

M. Perry [2], J. Song [3], C. Johnson [4], S. Cottrell [5]

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**BACKGROUND**
Homeless populations experience extensive social and health inequalities. Despite being a priority group for COVID-19 vaccination in the UK, determining vaccination coverage is challenging. This study aimed to calculate uptake (%) of COVID-19 and 2021/22 influenza vaccine among those with lived experience of homelessness.

**METHODS**
Previously published methods were used to define an e-cohort with lived experience of homelessness, by linking routine health datasets available in Swansea University's Secure Anonymised Information Linkage (SAIL) Databank. The cohort was restricted to those aged ≥18years with lived experience of homelessness since 2014, alive and resident in Wales as at 28/02/2022. These data were then linked at person-level to COVID-19 vaccination status as at 10/03/2022, obtained from the Welsh Immunisation System. Influenza vaccination uptake was based on a sub-sample who were aged ≥50years and registered with one of the 80% of GP practices that submit data to SAIL databank. Vaccination uptake was compared to the general population.

**RESULTS**
In the e-cohort (13,545 individuals), COVID-19 vaccination uptake was 69.8% (95%CI 69.0%-70.6%), 59.3% (58.4%-60.1%) and 37.2% (36.4%-38.0%) for first, second and booster dose, respectively. This compared to 87.9% (87.9%-88.0%), 85.2% (85.2%-85.3%) and 71.4% (71.3%-71.4%) in the general population. In the sub-sample of 3,413 individuals aged ≥50 years, influenza vaccination uptake was 44.8% (43.1%-46.5%) compared to 60.3% (60.2%-60.4%) in the general population. Uptake of both vaccinations was highest in older age groups and females.

**CONCLUSIONS**
Calculated vaccination rates in those with a lived experience of homelessness were significantly lower compared to the general population. The true coverage of vaccination in this group may be even lower, as there is likely a lack of data for those on the more extreme end of homelessness.

**Keywords:** COVID-19, Vaccination, Healthcare disparities, Public Health Surveillance, Influenza, Homeless persons
**ABSTRACT ID:** 386
**PRESENTED BY:** Gethin Jones / gethin.jones6@wales.nhs.uk

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

### Deciding about maternal pertussis vaccination: associations between intention, and needs and values in a vaccine-hesitant religious group

**A. De Munter** [1]

J. Hautvast [2], H. Ruijs [3], H. Spaan [4], M. Hulscher [5], R. Ruiter [6]

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[6] Maastricht University, Department of Work & Social Psychology, Maastricht, The Netherlands

**BACKGROUND**
To investigate the decision-making process regarding maternal pertussis vaccination (MPV) among an under-vaccinated group, Dutch orthodox Protestant women, we used a previously developed decision-making framework. This framework describes three stages of decision-making: orientation stage, deliberation stage and final decision stage.

**METHODS**
A cross-sectional survey was conducted prior to the introduction of MPV in the Dutch Immunisation Programme. Data on women's decision-making regarding their intention to accept MPV were collected. Univariate multinomial logistic regression analysis was applied to determine associations between intention to accept MPV and women's decision-making needs in the orientation stage. Using factor analysis (eigenvalue<1 and screeplot), deliberation domains in the deliberation stage were identified from women's results on value-based deliberation statements. Using multivariate multinomial logistic regression analysis associations between intention and the deliberation domains were determined.

**RESULTS**
Among the 467 participants, the majority of the women (56%) was undecided about accepting MPV, 32% would certainly refuse, and 12% would certainly accept. Acceptors and undecided women showed the highest information needs and support needs from health-care providers (HCPs). Undecided women showed the highest needs to conversate with friends and family. Refusers showed the highest needs to read vaccine-critical and alternative health information. Three deliberation domains were identified: *Trust in the vaccine and vaccine-providing authorities, Individual deliberate decision-making and Contemplating religious arguments*. Acceptors showed the highest trust in the vaccine and vaccine-providing authorities (AOR=37.53, p<.001). Undecided women showed highest the need for *individual deliberate decision-making* (AOR=3.05, p<.001).

**CONCLUSIONS**
Differences and similarities found among acceptors, undecided women, and refusers in the MPV decision-making process of orthodox Protestant women provide relevant insights for HCPs and vaccine policy makers, which can be used in tailored vaccine decision-making support.

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

### Advocacy and community engagement in TB control: the Kano wellness on wheels (WoW) experience

**M. Tukur** [1]

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[2, 3, 4, 5, 6, 8] KNCV NIGERIA

[7] Ministry of Health Kano state

**BACKGROUND**
Knowledge about Tuberculosis and awareness about TB services remains low especially in rural and semi-urban communities, despite TB services been free in Nigeria, a lot of people don't have access to these services and continue to suffer and die needless deaths from this curable disease. We present findings from an enhanced stakeholder engagement for a community intervention in Nigeria.

**METHODS**
Prior to the deployment of WoW to any community, an advocacy visit is carried out to the community gatekeepers. Other stakeholders in the PHC department of the LGAs are also visited. Discussions during the advocacy center around sensitization and passing information about mode of transmission, management modalities, availability of free TB services, and where these services can be accessed. Mobilization of the communities is multipronged involving the use of town criers, voluntary community mobilizers, religious clerics, and motorized campaigns.

**RESULTS**
Over the past year, 24 advocacy visits were carried out across 24 LGAs to the district heads, village heads, Imams, and other community gatekeepers. The result of these advocacy visits is that notable dignitaries' including local government chairmen and senior district heads flagged off WoW campaigns. This has boosted the screening cascade such that in the past 1year a total of 38,351 Individuals have been screened for TB with 2810 presumptives identified, 751 TB cases diagnosed with 739 of them enrolled on treatment.

**CONCLUSIONS**
Patient advocacy and community engagement using WoW as a fulcrum has continued to ensure adequate mobilization of host communities as well as creating awareness about TB services to ensure a TB free Nigeria, this should be sustained and complemented by the government and other stakeholders towards the eradication of the disease in Nigeria.

**Keywords:** Tuberculosis, Advocacy, Mobilization, Community Gatekeepers
**ABSTRACT ID:** 393
**PRESENTED BY:** Mustapha Musa Tukur / ask4mmt@yahoo.com

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

### Hantavirus and Leptospira spp.: Seroprevalence, knowledge and preventive behaviour in seasonal harvesters in Lower Saxony, Germany, 2021

**S. Schmitz** [1]

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**BACKGROUND**

Seasonal harvesters are an at-risk group for rodent-borne infections, with outbreaks in Germany reported in the literature, but no seroprevalence data being available. We investigated the seroprevalence of hantavirus and *Leptospira* spp. antibodies, knowledge of and adherence to preventive measures among this group in Lower-Saxony.

**METHODS**

We collected blood samples from workers of an asparagus and strawberry farm in 2021 and tested them for IgG antibodies against hantavirus and *Leptospira* spp. strains via ELISA. The workers completed self-administered questionnaires. We calculated associations with Fisher´s exact test.

**RESULTS**

170 mostly male (n=97; 57%) workers, aged 19 to 69 (median 45), from Poland (n=96; 59%), Germany (n=34; 21%) and Romania (n=27; 16%) participated. One serum tested positive for anti-hantavirus-IgG (0.59%; 95%-Confidence Interval [CI]: 0.01-3.2) and three for anti-*Leptospira* IgG (1.8%; 95%-CI: 0.37-5.1). 67 (39%) participants stated to be informed, mostly by employers (n=48; 72%), about appropriate protection from both infections during work. Only 32 (48%) of those felt certain they could identify effective ways of protection. Certainty was significantly associated with the covering of abrasions during work (n=96; 56%; p=0.02) and wearing long-sleeved clothes during muddy conditions (n=92; 54%; p=0.001). It was not associated with wearing gloves (n=123; 72%, p=0.62), closed shoes during muddy conditions (n=113; 66%; p=0.54) and thoroughly washing hands after work (n=113; 66%, p=0.15).

**CONCLUSIONS**

Seroprevalences for both pathogens were low but might be unrepresentative as we included harvesters of only one farm. Disease awareness was low and self-perceived knowledge of preventive measures was connected to adherence to some but not all protective behaviours. We recommend to increase risk awareness to strengthen adherence. Therefore we developed multilingual information material for workers and a risk management plan.

Abstract presentations - Poster tours

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

### Considerable doubt about rubella screening and vaccination intention among unvaccinated orthodox Protestant women

**A. De Munter** [1]

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**BACKGROUND**
Unvaccinated women who are susceptible to rubella are at risk of infection during future pregnancies, and thus at risk of congenital rubella syndrome in their unborn child. Rubella outbreaks occur periodically in the under-vaccinated orthodox Protestant community in the Netherlands. The objective of this mixed-method study was to determine and understand personal experience with rubella, perceived rubella susceptibility, and intention to accept rubella screening and vaccination among unvaccinated orthodox Protestant women.

**METHODS**
A mixed-method study was conducted using an online survey and semi-structured interviews. Descriptive analysis was used for quantitative data. Qualitative data was analysed using codes and categories.

**RESULTS**
Results of the survey (167 participants) showed that most participants had personal experience with rubella (73.7%, 123/167), among which 101 women (60.5%) indicated they had had rubella themselves. More than half of the women were undecided whether to accept rubella susceptibility screening (56%; 87/156) or rubella vaccination if needed (55%; 80/146).
Qualitative findings (10 participants) showed that most women thought they were unsusceptible to rubella. Indecisiveness and negative attitudes to accept rubella vaccination were influenced by religious arguments to object vaccination and the absence of recent rubella outbreaks in the Netherlands; women did not consider rubella as an imminent threat. Furthermore, results showed presence of misconceptions among women in the interpretation of their susceptibility and high confidence in their parents' memory that they had experienced rubella as a child.

**CONCLUSIONS**
In light of possible future rubella outbreaks, health care providers should provide adequate information on rubella and support decision-making in order to stimulate women to make a deliberate, informed decision on rubella screening and, if necessary, subsequent rubella vaccination.

**Keywords:** Prenatal Care, Decision making, Vaccine hesitancy, Health Personnel, Religion
**ABSTRACT ID:** 384
**PRESENTED BY:** Anne De Munter / anne.demunter@radboudumc.nl

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

Lessons from a protracted iGAS outbreak with added complexity of concurrent scabies outbreak, in a UK residential nursing care facility 2020-2021

**P. Williams** [1]

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[4, 8] East Midlands Health Protection Team

[5, 6] Lincolnshire County Council

[7] Lincolnshire NHS Clinical Commissioning Group

### BACKGROUND
In June 2021, a residential care facility notified the PHE Health Protection Team of two resident invasive group A streptococcal (iGAS) infections, resulting in one death. Initial risk assessment identified an iGAS outbreak 11 months prior due to the same type (*emm* 1.0). Both outbreaks occurred despite enhanced Infection Prevention and Control (IPC) measures in the COVID-19 pandemic. A multi-agency outbreak control team was formed, involving care home management, to explore links between the outbreaks and identify control measures.

### METHODS
Outbreak control measures included an IPC review, staff prophylaxis, staff and resident screening for GAS isolates, reviewing the previous outbreak and whole-genome sequencing (WGS) of all clinical and screening GAS isolates (n=11) across both outbreaks alongside contemporary UK *emm* 1.0 sporadic strains (n=83). A concurrent scabies outbreak increased workload and complexity, requiring additional enhanced cleaning and anti-scabies treatment for all staff and residents.

### RESULTS
The IPC review indicated several areas requiring improvement. All staff received antibiotic prophylaxis. Screening identified 2/32 (6%) staff and 0/31 residents positive for *emm* 1.0 GAS isolates, the first outbreak screening identified 4/30 (13%) staff positive for the same. All staff subsequently screened negative after treatment. WGS data from all clinical cases and screening clustered within 0-5 SNP (average 1 SNP), whereas the variation observed amongst the sporadic isolates was 44 SNPs (0-127 SNP), indicating a single protracted outbreak spanning across 15 months.

### CONCLUSIONS
This outbreak highlighted challenges in controlling iGAS outbreaks in residential care facilities, with transmission occurring despite COVID-19 enhanced IPC measures. The use of staff and resident screening combined with whole-genome sequencing strengthened the understanding and supported control measures. Clear communication and multi-agency working contributed to containing the outbreak.

# POSTER TOUR 6
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Intervention and health promotion

**MODERATOR**
Frantiska Hruba

## Abstract

### Vaccine confidence among the adult population of Bishkek and Naryn, Kyrgyz Republic, 2021

**M. Malisheva** [1]

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**BACKGROUND**
Vaccines against COVID-19 are critical to controlling COVID-19. Knowledge of people's perceptions towards vaccines and their readiness to be vaccinated helps inform vaccine confidence messaging. Our study aimed to assess the level of vaccine confidence and identify associated factors in two cities in Kyrgyz Republic.

**METHODS**
In August 2021, we conducted a convenient sample study of adults (≥18 years old) at public service centers and malls in Bishkek and Naryn. A participant had high vaccine confidence if they (1) believed that the COVID-19 vaccine is important to protect oneself or to protect others in their community, and (2) had been vaccinated or planned to get vaccinated. We used logistic regression to assess associations with high vaccine confidence.

**RESULTS**
Of 1595 respondents, 29% had high COVID-19 vaccine confidence, 37% believed getting a vaccine was important to protect oneself, and 39% believed it was important to protect others in their community. But, 63% of respondents were not and did not plan on getting vaccinated, 61% reported concerns about safety, and 44% believed (incorrectly) that vaccines would not effectively COVID-19. Vaccine confidence increased with age (42% aged ≥50 years vs 21% aged 18-29 years) and education level (38% with higher education vs 22% lower education). Higher age (adjusted odds ratio: 1.8, 95% confidence interval: 1.4-2.3), higher education (1.5, 1.2-1.8), high COVID-19 knowledge (2.5, 1.6-4.1), prior COVID-19 testing (1.5, 1.3-1.8), and reporting healthcare workers as a primary source of COVID-19 information (1.3, 1.1-1.6) were associated with high vaccine confidence.

**CONCLUSIONS**
Results show that vaccine confidence building is needed, especially people that are younger or have lower education. Healthcare providers can work with populations to address safety concerns and promote effectiveness.

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

## Abstract

### International patient transfers causing healthcare associated outbreaks of carbapenem-resistant Acinetobacter baumannii in Germany, August – September 2021

**J. Baum** [1]

J. Hecht [2], J. Eisfeld [3], C. Wagner-Wiening [4], D. Leuze [5], Y. Zimnitskaya [6], D. Knautz [7], P. Heinmueller [8], S. Gatermann [9], T. Eckmanns [10], S. Haller [11]

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[8] Hesse State Health Office (HLPUG), Dillenburg, Germany

**BACKGROUND**
Public health departments in 3 federal German states notified concordant outbreaks of carbapenem-resistant *Acinetobacter baumannii* (CRAb) in four hospitals. We investigated at the federal level to identify a possible supra-regional link and prevent further spreading.

**METHODS**
We collected clinical, demographic and transfer data from responsible public health departments and affected hospitals. We typed isolates through pulse field gel electrophoresis and carbapenemase detection. A case was defined as hospitalized in Germany in 2021 with laboratory detection of one of three CRAb outbreak strains.

**RESULTS**
We identified 18 cases and distinguished 3 clusters with CRAb strains not previously documented in Germany. Cluster A (8 cases; OXA-72 acba_194) started with 6 cases in a hospital in RP, one of which was transferred to a hospital in HE, leading to 2 additional cases. Cluster B (3 cases; OXA-23 acba_192) occurred in RP on the same ward as Cluster A with 2 cases and a further case with identic pulsotype in another hospital in HE. Cluster C (7 cases, OXA-23 acba_191) comprised 6 cases in a hospital in BW plus one case with identical pulsotype at the second hospital in HE. Each cluster involved primary cases transferred from Romania, a country with high prevalence of CRAb (n=6). 3 cases tested positive in admission screening after transfer from Romania. Additionally, cluster A spread further through patient transfer within Germany.

**CONCLUSIONS**
Our investigation revealed 3 genetically distinct clusters. They share importation of CRAb strains from Romania through patient transfer as concordant cause, presumably facilitated by shortcomings in infection prevention and control (IPC) and admission screenings. Compliance with recommended screening for CRAb after patient transfer and IPC need to be improved to avoid future outbreaks.

**Keywords:** Outbreak, Acinetobacter baumannii, Patient transfer, Carbapenem-resistant, Acinetobacter Infections
**ABSTRACT ID:** 456
**PRESENTED BY:** Jonathan Baum / baumj@rki.de

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 − 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

## Abstract

### Emergence of carbapenemase-producing Enterobacterales causing infection in companion animals

**J. Moreira Da Silva** [1]

J. Menezes [2], L. Fernandes [3], A. Amaral [4], C. Pomba [5]

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**BACKGROUND**
Carbapenemase-producing Enterobacterales strains (CPEs) are increasingly being reported in Companion Animals (CAs), despite their use being prohibited in veterinary medicine. The aim of this retrospective study (January-December 2020) was to detect CPEs among Enterobacterales clinical strains from companion animals.

**METHODS**
Nine hundred and seventy-seven Enterobacterales clinical isolates were included in the study. Susceptibility data was obtained by the disc diffusion method and/or minimal inhibitory concentrations (MICs) determination. Phenotypic and genotypic confirmatory tests were also performed to detect beta-lactamase-producing Enterobacterales, including carbapenemases. Positive isolates were characterized by WGS. Assemblies were then used to screen for antimicrobial resistance genes (ResFinder 4.1) and mobile genetic elements (Mobile Element Finder v1.0.3). MLST was performed.

**RESULTS**
A high prevalence of ESBL-producing Enterobacterales was found (n=227; 23,2%), with *bla*CTX-M-15 being the most prevalent (n=104, 45.8%). Four ESBL- producing *Klebsiella pneumoniae* isolates were positive for carbapanemase genes: i) OXA-181-producing *K. pneumoniae* ST273, only resistant to ertapenem (MIC › 1 mg/L), ii) two KPC-3-producing *K. pneumoniae* ST147, and iii) one KPC-3-producing *K. pneumoniae* ST392. All isolates belonged to clonal group 147 and were resistant to carbapenems but susceptible to ceftazidime-avibactam. The *bla*KPC-3 gene was located on transposon Tn4401*d* on IncFIA type plasmid for *K. pneumoniae* ST147 isolates and on a IncN-type plasmid for *K. pneumoniae* ST392. Lastly, one *Escherichia coli* ST127 isolate (uropathogenic lineage) was found to only harbour *bla*OXA-48, being susceptible to 3rd generation cephalosporins and carbapenems.

**CONCLUSIONS**
Carbapenemase detection methods need to be implemented during routine microbiology in Veterinary medicine as to ascertain the impact carbapenem resistance has on Animal and Public Health. More data is urgently needed for the design of preventive measures.

**Keywords:** Veterinary Medicine, Whole genome sequencing, Pets, Carbapenems
**ABSTRACT ID:** 80
**PRESENTED BY:** Joana Moreira Da Silva / jmsilva@fmv.ulisboa.pt

Abstract presentations - Poster tours

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

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## Abstract

### Trends in antibiotic resistance in Portugal: analysis of surveillance data from 2015 to 2020

**V. Manageiro** [1]

E. Ferreira [2], M. Caniça [3], EARS-Net-Portugal participants

[1] ECDC fellowship Programme, Public Health Microbiology path (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden

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#### BACKGROUND
We are seeing across Europe, namely in Portugal, an increasing number of patients with multidrug-resistant bacteria infection. In this study, we aimed to analyse antibiotic-resistance (AR) surveillance data collected by Portuguese hospitals in order to describe the current situation and evaluate the need for improved public health strategies.

#### METHODS
The surveillance data was collected from Portuguese laboratories reporting AR data from invasive isolates from 2015 to 2020 (national population coverage:97%). Susceptibilities were determined with methods in use by the reporting laboratories and evaluated by an external quality control program. The statistical significance of trends was calculated based on data from the last six years (2015-2020) and assessed by a chi-square test for trend. A value of p<0.05 was considered significant.

#### RESULTS
The occurrence of methicillin-resistant Staphylococcus aureus (MRSA) in Portugal significantly decreased from 47%/2015 to 30%/2020 (p≤0.001). Regarding Streptococcus pneumoniae, Portugal showed an increasing penicillin-non-wild-type trend (11%/2015 to 14%/2020, p=0.349). Enterococcus spp., displayed a decreasing trend for vancomycin-resistant isolates (p≤0.001). Carbapenem- and colistin-resistant Escherichia coli remained sporadic in 2020 (0.3% and 0.6%, respectively). The occurrence of carbapenem-resistant Klebsiella pneumoniae indicated an increasing trend (4%/2015 to 14%/2020, p≤0.001). Indeed, for K. pneumoniae a statistically significant increase was observed for all antimicrobial groups under surveillance except for colistin (p=0.539). The trends for colistin-resistant Pseudomonas aeruginosa and Acinetobacter spp. increased significantly during the study period (p≤0.001 and p=0.002, respectively).

#### CONCLUSIONS
The AR situation in Portugal displays wide variations depending on the bacterial species and antibiotic group. The decreasing frequency of invasive-MRSA in the recent years it is an important achievement. However, strategies to minimize further spread of carbapenem- and colistin-resistant isolates are urgently needed.

**Keywords:** Antibiotic resistance, Colistin, Carbapenem, MRSA
**ABSTRACT ID:** 187
**PRESENTED BY:** Vera Manageiro / vera.manageiro@insa.min-saude.pt

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

## Abstract

### Increasing trends in extended-spectrum *β-lactamase* production in urine and blood Escherichia coli isolates in Finland in 2008–2019: a retrospective nationwide study

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Eastern Finland Laboratory Centre (ISLAB), Kuopio, Finland

**BACKGROUND**

*Escherichia coli* is the leading cause of urinary tract infections (UTI) and bacteraemias, and the emergence of resistance causes concern. We aimed to investigate extended-spectrum β-lactamase production (ESBL+) in urine and blood *E. coli* isolates in Finland during 2008-2019.

**METHODS**

Susceptibility test results of 1,568,488 urine (90% from females and 10% from males) and 47,927 blood *E. coli* isolates (61% from females and 39% from males) were obtained from all Finnish clinical microbiology laboratories during 2008-2019. Susceptibility tests were performed according to the guidelines of the Clinical and Laboratory Standard Institute during 2008-2010 and the European Committee on Antimicrobial Susceptibility Testing during 2011-2019. We applied a Poisson regression model to compare the observed trends over time and between different age groups and genders.

**RESULTS**

During 2008-2019, the annual proportion of ESBL+ *E. coli* in blood *E. coli* isolates increased from 2.4% to 8.6% among males (average annual increase, 7.7%; 95%CI, 4.4-11.0%; p<0.01) and from 1.6% to 6.4% among females (average annual increase, 9.3%; 95%CI, 4.8-14.0%; p<0.01). In urine *E. coli* isolates, this proportion increased from 2.2% to 7.2% among males (average annual increase, 8.8%; 95%CI, 6.5-11.3%; p<0.01) and from 1.0% to 3.1% among females (average annual increase 8.6%; 95%CI, 6.3-11.0%; p<0.01). The significant rise in these proportions was also observed in most of the age groups.

**CONCLUSIONS**

Considering the aging population and their risk of *E. coli* bacteraemia and UTI, the rise in the annual proportions of ESBL+ *E. coli* indicates a substantial burden related to antimicrobial resistance. The proportions were higher in blood than in urine isolates among both genders and overall higher in males than in females, limiting effective empiric therapeutic options, especially in severe infections.

**Keywords:** Escherichia coli, Drug Resistance Bacterial, Urinary Tract Infections, Bacteremia, Male, Female
**ABSTRACT ID:** 197
**PRESENTED BY:** Heikki Ilmavirta / heikki.ilmavirta@uef.fi

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

## Abstract

### Increase in extensively-drug resistant Shigella sonnei infections in Spain, 2021-2022

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### BACKGROUND
Between September 2021 and January 2022, United Kingdom reported an increase in multi-drug resistant (MDR) *Shigella sonnei* infections. Later, 9 European countries reported a total of 146 related cases. Hence, we conducted an active search for related cases in Spain to better assess the risk associated with the circulation of *S. sonnei* for the general population.

### METHODS
Probable cases were defined as a patient diagnosed with MDR-*Shigella sonnei* infection between 1 January 2021 and 30 April 2022. Confirmed cases were defined as probable cases with isolates showing ≤ 7 alleles distance with the UK outbreak reference sequences using cgMLST *E.coli* scheme. Antibiotic resistance was studied by disc-diffusion methods and by the analyses of assembled whole genome with ResFinder and PlasmidFinder.

### RESULTS
We identified 37 probable cases from which 33 were confirmed. In confirmed cases, 39% reported being men having sex with men. The MDR phenotype was explained by the presence of the IncFII plasmid, and the production of extended-spectrum β-lactamases conferred by $bla_{CTX-M-27}$. In addition, we detect an additional plasmid IncB/O/K/Z in 30 isolates. Finally, we report the circulation of two other clones in Spain which belong to sequence types ST3075 and ST5390 but with the same antimicrobial resistance profile.

### CONCLUSIONS
Although *S. sonnei* causes self-limiting diarrhea in most patients, it can lead to severe symptoms in immunocompromised patients. The circulation of multiple clones of MDR *Shigella sonnei* raises concerns about the spread of resistant *Shigella* infection in Spain and highlights the need to intensify surveillance of shigellosis. Moreover, antimicrobial treatment should be based on the results of susceptibility testing and to limited to moderate or severe cases to avoid further selection of antimicrobial resistance.

**Keywords:** IncFII Plasmid, MDR, MSM, Susceptibility testing WGS
**ABSTRACT ID:** 293
**PRESENTED BY:** Camille Jacqueline / camjacqueline.pro@gmail.com

# POSTER TOUR 7
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Antimicrobial resistance

**MODERATOR**
Annick Lenglet

## Abstract

### Failure of scabies treatment: a systematic review and meta-analysis

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**BACKGROUND**
Scabies incidence increased alarmingly in several European countries in the past years and so have reports on permethrin treatment failure. Treatment failure has never been assessed systematically.

**METHODS**
We conducted a systematic review on prevalence and predictors of treatment failure in scabies patients. We searched 5 databases from inception until August 2021 for randomized and non-randomized studies on scabies patients with clinical or confirmed diagnosis that reported treatment outcome or associated factors. Subgroup analyses were conducted for studies that implemented additional precautions to minimize mistakes in drug application, compliance or reinfestation, hence possibly hinting to drug resistance. We performed random-effects meta-analysis on prevalence of treatment failure and metaregression for trend over time.

**RESULTS**
The search yielded 3,536 unique records of which 147 studies were included. The overall prevalence of treatment failure was 15.2% (95% CI: 12.9 to 17.6). There is a trend for increase in overall and permethrin treatment failure over time (1983-2021). In subgroup analyses, prevalence of treatment failure was lower in patients treated with two doses of oral ivermectin (4.2% [95% CI: 0.7 to 9.5]) compared to those treated with one dose (13.1% [95% CI: 7.4 to 20.0]) or permethrin (9.9% [95% CI: 5.4 to 15.3]). Only 3 studies reported predictors of treatment failure.

**CONCLUSIONS**
Increasing failure of permethrin for scabies treatment over time and lower treatment failure with a second dose of ivermectin is possibly hinting towards decreased mite susceptibility. Evaluation of drug resistance needs to be implemented in future studies and updating of treatment guidelines should be considered.

**Keywords:** Scabies, Treatment Failure, Drug resistance, Ivermectin, Permethrin
**ABSTRACT ID:** 441
**PRESENTED BY:** Felix Reichert / reichertf@rki.de

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

*Candida auris* in Attica hospitals, Greece: yet another Hospital Acquired Infection

**L. Politi [1]**

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## BACKGROUND

*Candida auris* is a multidrug resistant yeast causing colonization and candidaemias among inpatients. In Greece, *C. auris* was first isolated in April 2019. Since November 2019, *C. auris* cases from tertiary and secondary Attica-based hospitals were reported to assess the need for a passive hospital-based surveillance system for *C. auris*.

## METHODS

We actively collected data on hospitalized cases with MALDI-TOF confirmed *C. auris* invasive infection and/or colonization from 11 hospitals in Attica from November 2019 to September 2021. Median number of days between date of first positive *C. auris* isolate and health outcome in terms of colonization versus infection, and proportions of resistance to antifungal drugs were calculated for descriptive analysis.

## RESULTS

Forty-nine isolates from 45 cases (median age was 72 years) were retrieved. All cases were admitted for reasons other than fungal infections. Twenty-two cases had an infection, 23 cases were colonized and time from hospitalization to first positive sample ranged between 2 and 133 days. Common factors among cases were presence of foreign bodies (catheters/ventilators, etc.) (91%), presence of underlying disease (73%), concurrent respiratory/bacterial infections (60%), and admission in an intensive-care unit (44%). Twenty-four cases died after a median of 7 days since first positive test (range 1-156 days). Resistance to fluconazole and amphotericin B was identified in 100% and 3% of tested clinical isolates, respectively.

## CONCLUSIONS

Since 2019, identification of *C. auris* cases within Attica-based hospitals highlights its presence as a hospital acquired pathogen. We need a hospital-based surveillance system for the rapid detection, testing, control of this pathogen and timely implementation of infection control measures to prevent its spread and to determine the extent of the occurrence of *C. auris* in Greek healthcare facilities.

**Keywords:** Candida auris, Hospital acquired Infections, Emerging pathogen, Antifungal susceptibility, Infection Prevention and Control Measures
**ABSTRACT ID:** 240
**PRESENTED BY:** Lida Politi / l.politi@eody.gov.gr

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

### Clostridioides difficile infection surveillance system in Norway: evaluation of the data completeness, 2019-2021

**L. Franconeri** [1]
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#### BACKGROUND
*Clostridioides difficile* infection (CDI) has been notifiable in Norway since 2012 in the Norwegian Surveillance System for Communicable Diseases (MSIS). In 2019, it switched from a laboratory-reported, non-identifiable data format to an identifiable format reported by clinicians or laboratories, for faster outbreak detection and response. Our aim was to evaluate data quality through completeness after the change was implemented.

#### METHODS
We analyzed CDI data reported in MSIS from 2019 to 2021. Variables were pre-selected to access useful information for CDI surveillance and their completeness (percentage of missing data / variable). ID, gender, age, reporting profession and place, birth city, reporting and sampling date, sample material, toxin, symptoms, genotype, and diagnostic method were retained. Number of notifications by primary and reference laboratories were, respectively, denominators for toxin and genotype completeness. Accepted minimum completeness was 80% but ID, gender, age, reporting place, birth city, reporting and sampling date needed to reach 100%.

#### RESULTS
2566, 2873 and 2985 CDI cases were notified in 2019, 2020 and 2021. ID, gender, age, reporting and sampling date, diagnostic method and material were complete. Completeness was above 98 % for laboratory profession reporting, reporting place, birth city and genotype. Completeness was 92 % for reporting place in 2019 but in subsequent years it improved to 98%. Completeness was low for clinician reporting (63% for each year), toxin (65% to 77%) and symptoms (49% to 55%).

#### CONCLUSIONS
Completeness remained high for most variables since the change of reporting in 2019. However, crucial data fields to detect changes in disease severity as clinician reporting, toxin or symptoms, showed gaps. Evaluate acceptability for clinicians and explore laboratories toxin notification could be needed to improve CDI surveillance data completeness.

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

### Wastewater-based surveillance of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae in Finland: Informed selection of sites for sampling

**D. Paspaliari** [1]

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**BACKGROUND**
Wastewater surveillance can complement clinical surveillance by providing information on circulating infectious agents and antimicrobial resistance at a community level. Sampling should be optimized, so that it remains representative, while costs from sample collection and transportation are minimized. We examined different sampling scenarios to optimize a pilot scheme for wastewater-based surveillance of extended-spectrum-beta-lactamase(ESBL)-producing *Escherichia coli* and *Klebsiella pneumoniae* in Finland.

**METHODS**
We retrieved all notifications of ESBL *E. coli* and *K. pneumoniae* between 01.2018-09.2021 from the National Infectious Disease Register. Based on the municipality of residence, we allocated cases to 28 wastewater-treatment plants (WWTPs), comprising the national wastewater surveillance network, and applied a correction factor to account for overlaps between municipalities and WWTPs. When calculating population-based incidence, we used as denominator the population serviced by the WWTPs.

**RESULTS**
We plotted monthly ESBL incidence, comparing nationwide incidence to that in: 1) the 28 WWTP network, 2) a smaller-scale representative network of ten WWTPs, 3) the WWTP serving the capital region. The mean monthly number and incidence of notified cases during the study period was 391 (7.1 per 100,000 population). For scenarios (1), (2) and (3) it was 250 (7.5 per 100,000), 151 (7.6 per 100,000) and 74 (8.6 per 100,000), respectively. The monthly trends in incidence of both the 28 and 10 WWTP networks fully followed and represented national trends. Conversely, the trends in incidence of only the capital region WWTP showed some deviation from the national trends.

**CONCLUSIONS**
Informed selection of WWTPs for wastewater surveillance can increase cost-efficiency. To pilot ESBL wastewater-based surveillance, we propose sampling from only ten WWTPs, which appear to sufficiently represent national trends, and confirming their representativeness by correlation with counts from wastewater samples.

**Keywords:** Drug resistance, Wastewater-based epidemiological monitoring, Waste Water, Escherichia coli, Finland, Beta-lactam resistance
**ABSTRACT ID:** 272
**PRESENTED BY:** Dafni Katerina Paspaliari / paspaliari.dafni@gmail.com

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

### Evaluation of random-digit-dialing (RDD) recruitment to invite participants for serological tests as a method to obtain a representative sample for general population seroepidemiological surveys

**M. Rosinska** [1]

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**BACKGROUND**
Seroepidemiological studies complement case-based surveillance and are especially useful if important fraction of cases remain undiagnosed, as in the case of SARS-CoV-2 infections. Obtaining a representative national sample is complicated by logistical issues and non-response. We aim to explore feasibility of two-step approach involving RDD recruitment followed by voluntary attendance to testing site, capitalizing on existence of commercial laboratory network with countrywide blood collection sites.

**METHODS**
We used data from the first round of the national COVID-19 serosurvey OBSERCO conducted in the general population of adults 20+ in Poland, between 29.03.-14.05.2021. Participants were recruited and interviewed through RDD using mobile and landline numbers. At the end of interview, they received a coupon for anti-SARS-CoV-2 antibody test, valid for 7 days at any of the 627 collection sites evenly distributed across country. We compared the demographic characteristics of the interviewed participants to those of the general population and conducted logistic regression to determine predictors of test attendance among interview respondents (adjusted odds ratios, AOR, are reported).

**RESULTS**
Of 271,827 phone numbers used, 25,812 (9.5%) participants were interviewed, and 6,242 (2.3%) were tested. When compared to general population, interview respondents were more likely to be older and reside in urban areas. AORs for getting tested were significant for age (40-59:1.4, 60+:1.5), female gender(1.3), urban residence(1.3), prior COVID-19 diagnosis(1.1), contact with COVID-19 case(1.3), prior COVID-19 symptoms(1.7), being vaccinated against COVID-19(1.1).

**CONCLUSIONS**
Although the proposed recruitment method is feasible, high non-response rate, associated with factors, which likely predict positive result, may introduce bias to seroprevalence estimates. Applying statistical techniques such as propensity weighting could reduce bias provided data on confouders is collected, which should be carefully considered in the pilot phase.

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

### Evaluation of 17 years of MERIN (Meningitis and Encephalitis register in Lower Saxony, Germany) surveillance program: acceptability survey and data quality assessment

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### BACKGROUND

Implemented in 2003, MERIN provides information on circulating enterovirus (EV) serotypes, supports management of patients with suspected aseptic meningitis, encephalitis or acute flaccid paralysis and contributes to the national surveillance in documenting polio free status. MERIN is based on voluntary contributions of participating hospitals. Therefore, our evaluation focusses on acceptability among participants and aims at identifying improvement and expansion possibilities.

### METHODS

An online-based survey (11/2021 to 01/2022) among 32 contributing hospitals investigated relevance of MERIN objectives, satisfaction with the diagnostic offer, timeliness, communication and distribution of results as well as the required workload. Ideas for improvement were collected in open fields. Aside from the survey, we also assessed data completeness, reporting rates of follow-up forms and timeliness from sample collection to different laboratory results.

### RESULTS

We received 30 questionnaires from 21 hospitals (66% response rate). Satisfaction with the scope of the diagnostic offer (93%), timeliness (84%), communication (99%) and distribution (86%) of the results was high, 97% of participants assessed the required workload as adequate. Providing digital medical reports as well as regular updates about circulating EV serotypes online were identified as areas for improvement.

Data completeness of selected variables ranged from 78.3 to 99.9%. Reporting rate of follow-up forms was 58%. Median time between sample collection and arrival at the laboratory was 2 days [IQR 1-3], and e.g.11 days [IQR 10-13] for EV diagnostics via cell culture.

### CONCLUSIONS

MERIN was evaluated as a highly acceptable surveillance system. Identified areas of improvement yielded to enhancing the program with regular reports on circulating EV serotypes and online access to the laboratory results. To increase the surveillance coverage, we currently identify and recruit additional hospitals in Lower Saxony.

**Keywords:** Surveillance, Polio-eradication, Evaluation, Enterovirus, Meningitis
**ABSTRACT ID:** 316
**PRESENTED BY:** Anna Luczynska / anna.luczynska@nlga.niedersachsen.de

# POSTER TOUR 8
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Surveillance: opportunities and evaluation

**MODERATOR**
Amelie Plymoth

## Abstract

### Evaluation and comparison of statistical algorithms for monitoring COVID-19 case and death trends in EU/EEA Member States

**C. Entradi** [1]

G. Marrone [2], S. Albert [3], N. Bundle [4], G. Spiteri [5], C. Carvalho [6], J. Gomes Dias [7]

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**BACKGROUND**
As part of its COVID-19 surveillance, the European Centre for Disease Prevention and Control (ECDC) monitors a variety of epidemiological indicators that can be used to monitor changes in disease incidence.
In order to detect significant changes in the trends of the indicators, different algorithms can be implemented. We describe here an evaluation of the performance of different algorithms, undertaken to identify the optimum one for detecting important changes in COVID-19 trends.

**METHODS**
A framework was developed with the aim of quantifying and comparing algorithm performance in a systematic way. The analysis focused on two epidemiological indicators: the weekly notification rate of new cases and the weekly notification rate of reported deaths. As a benchmark, we used the algorithm included in the ECDC weekly COVID-19 country overview reports. Seven different algorithms (cumulative sum (CUSUM) detector additive, CUSUM multiplicative, Farrington, Modified Farrington, Farrington without base count, Sliding linear model, Holt's linear trend model) were evaluated, by means of a set of performance indicators (sensitivity, specificity, positive and negative predictive value and power of detection of a trend change within two weeks).

**RESULTS**
The CUSUM multiplicative algorithm is the one that has the highest sensitivity and power of detection of a trend change within two weeks, capturing changes faster than the other algorithms.

**CONCLUSIONS**
The evaluation framework that we have developed is flexible as it allows us to extend the analysis to other algorithms and to include other performance indicators.
We found that the CUSUM multiplicative algorithm is the most sensitive of those tested, rapidly detecting changes in trend even with slow changes and small fluctuations. It is suitable for use at national as well as EU level.

**Keywords:** Epidemiologic methods, COVID-19 pandemic, Communicable diseases, Public Health Surveillance
**ABSTRACT ID:** 374
**PRESENTED BY:** Chiara Entradi / chiara.entradi@gmail.com

# POSTER TOUR 9
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Late breakers

**MODERATOR**
Iro Evlampidou

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## Abstract

### Association between Paediatric Hepatitis Cases of Unknown Aetiology and Adenovirus in Wales, July 2022

**F. Rowley** [1]

C. Harris [2], G. Jones [3], C. Hogg [4], C. McDermott [5], R. Polani Chandrasekar [6], C. Sawyer [7], M. Eveleigh [8], E. Jones [9], L. Gifford [10], S. Froude [11], C. Moore [12], C. Williams [13], A. Gjini [14]

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**BACKGROUND**
In March 2022, an increase in cases of paediatric hepatitis of unknown aetiology (PHUA) was reported by Public Health Scotland. By July 2022, 20 cases had been identified in Welsh residents. Many UK cases reported a recent adenovirus infection. We conducted a case-control study and examined routine surveillance data for adenovirus to investigate an association between whole blood adenovirus positivity and PHUA in Welsh cases.

**METHODS**
Cases were children <=5 years old, presenting with acute hepatitis (non A-E) with serum transaminase>500 IU/L (AST or ALT) between 01 January-02 May 2022. Controls were residual blood samples from children aged between 12 months and 5 years with an acute non-hepatitis illness, frequency-matched on sex and sample date. Cases and controls were tested for adenovirus presence. In addition, Adenovirus positivity in under-5's between January – May 2022 was calculated from routine surveillance data, and compared to the same period across 2017-2019 using two-proportion Z tests.

**RESULTS**
10 cases and 45 controls were included in the case-control. A crude odds ratio (cOR) of 48.9 was calculated (95%CI 4.9-2194.0, p<0.001), demonstrating evidence of an association between whole blood adenovirus positivity and PHUA. A sensitivity analysis, including 4 cases that were not tested for adenovirus, identified a smaller magnitude of association (cOR 9.8, 95%CI 2.1-47.6, p<0.001). There was a significant increase in adenovirus positivity between 2017 and 2019 (11.7%) and 2022 (18.9%, p<0.05).

**CONCLUSIONS**
In Welsh cases, PHUA was strongly associated with adenovirus detection in blood. The cases occurred at a time of increased adenovirus positivity in surveillance samples in a similar age group, strengthening evidence of association. Further research is required to explore causation, alongside surveillance for this rare syndrome.

**Keywords:** Case-control studies, Adenoviridae, Hepatitis, Child, Odds Ratio
**ABSTRACT ID:** 523
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# POSTER TOUR 9
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Late breakers

**MODERATOR**
Iro Evlampidou

## Abstract

### Largest reported outbreak of Crimean-Congo Hemorrhagic Fever (CCHF) in Georgia, 2022

**L. Liluashvili** [1]

T. Khargaladze [2], N. Mebonia [3], R. Revazishvili [4], N. Zhgenti [5], M. Mamardashvili [6], N. Buadze [7], O. Tsagareishvili [8], T. Napetvaridze [9], T. Chaligava [10], C. Ward [11], T. Kuchuloria [12], N. Mamuchishvili [13], G. Chakhunashvili [14], K. Zakhashvili [15], N. Malakmadze [16], T. Singh [17]

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[11, 12, 16, 17] U.S. Centers for Disease Control and Prevention (CDC)

**BACKGROUND**
Crimean-Congo Hemorrhagic Fever (CCHF) was first reported in Georgia in 2009. Since then, 172 cases have been reported in the country. On April 10, 2022, Georgia's National Center for Disease Control was notified of CCHF cases in Akhaltsikhe region. We initiated an investigation to identify extent of the outbreak and potential risk factors.

**METHODS**
We categorized cases as suspected (fever + 2 CCHF symptoms), probable (suspected + epidemiological link), and confirmed (IgM or RT-PCR positive). We interviewed CCHF patients in-person or by phone with a standardized questionnaire, including information on potential risk factors.
Disease data were obtained from the electronic integrated disease surveillance system.

**RESULTS**
Between April and September 13, 2022, 48 confirmed and 2 probable cases including 4 deaths were reported. Mean age of the patients was 53 years; 28 (56%) of them were men. We interviewed 41 of the 50 patients; 29 (71%) used common pastures for domestic animals, 23 (56%) participated in hay production, and 23 (56%) reported tick bites and removal or crushing of ticks using bare hands.
Of the 37 villages that reported cases, 27 had no history of CCHF cases in previous years.

**CONCLUSIONS**
This is the largest CCHF outbreak in Georgia since the first cases were reported in 2009. Identification of cases from villages that were previously unaffected might indicate increased spread of the disease.
We plan to conduct a case-control study to determine routes of transmission and risk factors. We developed and distributed information booklets on CCHF symptoms and prevention practices, including avoiding tick removal with hands and using repellents. Additionally, we are increasing CCHF awareness in health facilities in the affected regions.

**Keywords:** Crimean-Congo hemorrhagic Fever Virus, Risk Factors, Disease outbreak, Georgia
**ABSTRACT ID:** 540
**PRESENTED BY:** Levan Liluashvili / levanliluashvili29@gmail.com

## Late breakers

**MODERATOR**
Iro Evlampidou

## Abstract

Assessing the short- and long-term impact of behavioural changes and vaccination on the size of a future monkeypox outbreak: A modelling study among men who have sex with men in Belgium

**A. Tsoumanis [1]**

N. Hens [2], C. Kenyon [3], C. van Dijck [4]

[1, 4] Institute to Tropical Medicine - University of Antwerp

[2] University of Antwerp - Hasselt University

[3] Institute of Tropical Medicine - University of Cape Town

**BACKGROUND**
Since the beginning of the 2022 monkeypox epidemic, most infections have been diagnosed among men who have sex with men (MSM), suggesting transmission mainly through sexual contact. Public health recommendations include self-isolation, reduction of sexual activity and vaccination of high-risk individuals. This study aims to quantify the size of future epidemics if new monkeypox cases were introduced in the population.

**METHODS**
We built a network-based mathematical model to simulate a monkeypox outbreak that is transmitted during sexual contact in a network of 10,000 (3,000 high-risk and 7,000 low-risk) MSM in Belgium. We compared the impact of vaccination (assuming 85% efficacy) and of a temporary reduction in sexual activity among high-risk MSM, on the number of secondary cases during the initial outbreak (wave 1) and after introducing 10 new cases after one year (wave 2).

**RESULTS**
Although reducing sexual activity by 50% during 6 months in wave 1 resulted in 85% less secondary infections during that wave, there was a 262% increase of infections during wave 2. Assuming no reduction in sexual activity during wave 1, vaccinating 20% of high-risk MSM reduced the number of secondary cases in wave 2 by 52%, from 188.5 (IQR 120.8 – 332.5) to 91 (IQR 57.8 – 135.2). Varying vaccination between 40% and 80% of high-risk MSM resulted in a reduction of 78% and 84% respectively, over both waves.

**CONCLUSIONS**
While behavioural change could reduce the epidemic size of the initial monkeypox outbreak, it does not prevent future epidemics unless vaccination is considered. Even low levels of vaccination among high-risk MSM could substantially reduce the size of subsequent epidemics. Vaccination levels above 40% have little additional impact on the size of future epidemics.

# POSTER TOUR 9
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Late breakers

**MODERATOR**
Iro Evlampidou

## Abstract

### Use of network diagrams to support dynamic assessment of monkeypox transmission patterns in Wales, United Kingdom, 2022

**A. Yung** [1]
R. Merrick [2], C. Sawyer [3], L. Whelan [4], O. Orife [5], M. Hughes [6], C. Moore [7], K. Pheasant [8], D. Ishola [9], S. Mably [10], R. Firth [11]

[1-11] Public Health Wales

**BACKGROUND**
The ongoing international monkeypox (MPX) outbreak is associated with densely connected sexual networks. As of 2 September 2022, 44 MPX cases were reported in Wales. We describe how network diagrams were used to visualise relationships between MPX cases and contacts to assess novel transmission dynamics in Wales, 2022.

**METHODS**
Demographic, behavioural and contact information were collected for all laboratory-confirmed MPX cases in Wales. Microsoft PowerBI was used to demonstrate links between cases and contacts, by setting, risk category, potential exposure factors (e.g. travel, event attendance) and geography (national, regional). Network diagrams were reviewed weekly by the Incident Management Team (IMT).

**RESULTS**
Network diagrams highlighted that the majority of cases in Wales (82%, 36/44) were not knowingly linked to one another. Of those without known links, 42% (15/36) travelled outside Wales in the 21 days before symptom onset, including 28% (10/36) to England (of which, 6/10 to London) and 25% (9/36) to European and North-American countries also reporting a MPX outbreak.
Overall, 309 contacts were reported by cases (median=4, interquartile range=1-7). Half (51%, 157/309) of the contacts were assessed as category-2 (medium infection risk) and 59% (183/309) had a specific setting of contact reported (e.g. work, healthcare, household). Few (1%, 3/309) contacts became secondary cases, all of which reported household/sexual contact with a case.

**CONCLUSIONS**
Visualisation-based network analysis proved useful for outbreak investigation in Wales. Over 4/5 cases were not known to be linked to another case and secondary cases were few and limited to household contacts. These findings suggest a substantially import-based outbreak with low community transmission in this part of the UK. This is assisting IMT decision-making on public health actions for outbreak control.

# POSTER TOUR 9
DAY 2, 24 NOVEMBER 2022
15:15 – 16:00

## Late breakers

**MODERATOR**
Iro Evlampidou

## Abstract

### Should we use the 4CMenB (Bexsero®) meningitis vaccine to protect men who have sex with men (MSM) in England against gonorrhoea? A model-based analysis of impact and cost-effectiveness

**D. Nikitin** [1]

L. Whittles [2], P. White [3], J. Eaton [4]

[1, 2, 3, 4] Medical Research Council Centre for Global Infectious Disease Analysis (MRC GIDA)

[1, 2, 3] Imperial College London

**BACKGROUND**

In mid-April 2022 the first estimates of effectiveness against Neisseria gonorrhoea infection of the 4CMenB N.meningitidis serogroup-B vaccine were published, reporting 26%(95%CI:12-37%) and 40%(95%CI:22-53%) for 1- and 2-dose primary vaccination, respectively. We examined the impact and cost-effectiveness of approaches to vaccinating MSM in England.

**METHODS**

We built a new integrated health-economic transmission-dynamic compartmental model of gonorrhoea in MSM, with low- and high-risk activity groups (<5/≥5 partners/year), calibrated to surveillance data using a Bayesian framework. We calculated vaccination costs, reductions in gonorrhoea treatment costs, and QALY (quality-adjusted life-year) gains, over 10 years (discounting: 3.5%p.a), and assessed sensitivity to cost per dose. We considered two approaches to targeting higher-risk individuals (offering vaccination-on-diagnosis with gonorrhoea (VoD), or vaccination-according-to-risk (VaR): VoD plus vaccinating uninfected patients reporting ≥5 partners/year), with 1- and 2-dose primary-vaccination strategies. Initial protection lasts for 1.5 years; single booster doses protect those who received 2-dose primary vaccination for a further 3 years.

**RESULTS**

At the estimated UK cost of £18/dose administered (including £10/dose administration cost), vaccination is always cost-saving on average, irrespective of uptake. For moderate uptake (1st dose: 40%, 2nd dose (where offered): 75%), net savings for VoD(1-dose)/VoD(2-dose)/VaR(1-dose)/VaR(2-dose) are £2.29M(95%CrI:-0.01-5.72)/£4.71M(0.68-10.26)/£5.72M(0.08-15.60)/£12.76M(2.19-25.36), with corresponding QALY gains 30.3(12.0-60.3)/57.7(25.9-105.7)/70.6(21.0-153.5)/139.9(50.3-267.6). At the manufacturer's list price of £75/dose (i.e. £85/dose administered), the incremental cost-effectiveness ratio is always >£20k/QALY, therefore not cost-effective.

**CONCLUSIONS**

Reassuringly for decision-makers, at UK costs 4CMenB vaccination does not need a minimum uptake to gain QALYs and be on-average cost-saving, although promoting uptake will maximise benefits. The greater coverage of VaR, and greater protection of 2-dose strategies, produce greater savings and QALY gains. If other countries pay a higher price for 4CMenB then vaccination might not be cost-saving or even cost-effective.

# Late breakers

**MODERATOR**
Iro Evlampidou

## Abstract

### Feasibility of an ad-hoc participatory daily antigen rapid testing surveillance (DARTS) system for COVID-19 infection in Hong Kong

**N. Tsang** [1]

H. So [2], B. Cowling [3], G. Leung [4], D. Ip [5]

[1, 2, 3, 4, 5] WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong

**BACKGROUND**
The fifth wave of COVID-19 Omicron epidemic has caused unprecedented breakdown of PCR testing capacity for official case verification in Hong Kong. Aimed to provide a stable and reliable alternative data for surveillance of pandemic activity, a community-based participatory surveillance system was established using daily rapid antigen tests (RAT). However, the feasibility of building and maintaining a large cohort committing for regular RAT self-testing over an extended period of time for surveillance purpose remains poorly understood.

**METHODS**
We implemented an ad-hoc surveillance platform by enrolling 10000+ individuals over the territory. Participants were scheduled to regularly perform a RAT with a self-sampled throat-and-nasal swab, irrespective of symptom or exposure history, on an assigned day of the week. Daily point prevalence of COVID-19 infection was disseminated real-time on an online dashboard (https://covid19.sph.hku.hk/dashboard). We evaluated the feasibility of the surveillance system using the CDC guideline.

**RESULTS**
A representative cohort of 10,800 individuals was recruited and successfully followed up over 6 months (from 1st March-31st August), with a high retention rate of 99.99%. A cumulative number of 293,077 RAT results were captured, enabling the system to track the changing trajectory of the Omicron pandemic, with a rapidly subsiding phase from an initial high value of 12.7% (8.4-18.7) in March to a baseline activity (0.1-0.3%) over May, and stepwise increase in August to 2.1% (1.3-3.3). Most participants considered the system simple (98%) and stable (97%).

**CONCLUSIONS**
The successful establishment and maintenance of DARTS demonstrated that it is logistically and technically feasible for building an ad-hoc participatory large-scale surveillance system using RAT for situational awareness of the disease activity during an evolving community epidemic.

**Keywords:** COVID-19, SARS-CoV-2, Surveillance, Lateral flow rapid antigen Test, Evaluation
**ABSTRACT ID:** 543
**PRESENTED BY:** Nicole Ngai Yung Tsang / tsangny@connect.hku.hk

Abstract presentations - Poster tours

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

## Abstract

### SARS-CoV-2 in schoolchildren during the Delta variant wave August to December 2021– finding from the Danish comprehensive register-based surveillance system

**T. Funk** [1]

L. Espenhain [2], F. Trier Møller [3], S. Ethelberg [4]

[1] Statens Serum Institut, Copenhagen, Denmark - ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control, (ECDC), Solna, Sweden

[2, 3, 4] tatens Serum Institut, Copenhagen, Denmark

**BACKGROUND**
The role of schoolchildren as drivers of transmission in the COVID-19 pandemic continues to be debated. To get a national overview of SARS-CoV-2 transmission in schools, we aimed to describe SARS-CoV-2 cases and clusters in Danish schools.

**METHODS**
We linked SARS-CoV-2 testing data with school and class-level information of all schoolchildren in class-levels 0-10 (6-16years) in Denmark. A SARS-CoV-2 case was defined from first positive test. To identify cases leading to onward transmission, case introductions into a school/class-level were defined as the first case occurring after >14days without cases. A cluster was defined as ≥3 cases within 14 days in the same school/class-level as a proxy for transmission in schools. The study period was 9/08/2021-12/12/2021, when the SARS-CoV-2 delta variant was dominant, societal restrictions were limited and weekly testing of unvaccinated schoolchildren ≥9 years and testing as part of contact-tracing were recommended.

**RESULTS**
Ninety-three percent (n=587,224/631,846) of all schoolchildren got tested for SARS-CoV-2 at least once during the study period and 10% (n=62,530/631,846) had a positive test. Out of 17,717 case introductions, 36% were linked to clusters. In total, 6,426 clusters with 45,567 cases (i.e. 73% of all cases) were identified. Cases occurred in 95% and clusters in 70% of all 1,759 Danish schools.

**CONCLUSIONS**
One in three case introductions were linked to clusters, indicating that onward transmission from many introduced cases were prevented, even in the Danish setting where restrictions in schools were minimal. However, overall, the majority of cases were part of clusters, suggesting that once onward transmission occured, many schoolchildren can be affected and that school interactions likely contributed to transmission in these age-groups. Research into further characterising case introductions and clusters is ongoing.

**Keywords:** Surveillance, Schools, Transmission, SARS-CoV-2, School Children
**ABSTRACT ID:** 26
**PRESENTED BY:** Tjede Funk / tjfu@ssi.dk

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

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## Abstract

### Rapid establishment of a prospective surveillance system for child mortality and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection in England

**G. Smith** [1]

M. Gobin [2], R. Kwiatkowska [3], K. Jones [4], S. Stoianova [5], K. Luyt [6], I. Oliver [7], C. Beck [8]

[1] Field Epidemiology Training Programme (FETP), UK Health Security Agency, UK

[2, 3, 4, 8] Field Service South West, UK Health Security Agency, Bristol, UK

[3] Population Health Sciences, University of Bristol, Bristol, UK

[5, 6] National Child Mortality Database, University of Bristol, Bristol, UK

[7] Chief Scientific Officer Group, UK Health Security Agency, UK

**BACKGROUND**
Early reports from the COVID-19 pandemic indicated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection caused relatively mild disease among children, but evidence was sparse. We aimed to rapidly establish a prospective surveillance system linking child deaths to SARS-CoV-2 test results in England, to act as an early warning indicator of child mortality and inform policy and practice.

**METHODS**
All child deaths (<18 years) from all causes in England are reported to the National Child Mortality Database (NCMD) within 48 hours. A data sharing agreement was established enabling sharing of child death data and SARS-CoV-2 results between NCMD and Public Health England (PHE). A daily process linked child deaths to positive and negative SARS-CoV-2 results using multiple identifiers. Linked records were returned to NCMD for reporting to NHS England and a report produced for the PHE COVID-19 Incident Management Team.

**RESULTS**
First results were available three weeks after the project initiation in PHE. Of 1,481 child deaths reported from 01/03/2020 to 07/09/2020, 51% were linked to SARS-CoV-2 results between 01/01/2020 to 30/09/2020 and 2% (30/1,481) to positive results. Deaths linked to positive results peaked in epidemiological week 14 and were highest among males aged 13-17 years and females under 1 year. The majority (83.3%) of deaths linked to positive results were following a clinically compatible illness and another identified factor (e.g. pre-term birth).

**CONCLUSIONS**
A prospective surveillance system was rapidly implemented. Data from England supported indications from the literature that mortality potentially related to SARS-CoV-2 infection early in the pandemic was low among children. Essential to this process was effective inter-organisational working and support of data controllers in ensuring secure, rapid data sharing for public health action.

**Keywords:** Public Health Surveillance, SARS-CoV-2, COVID-19, Child, Mortality
**ABSTRACT ID:** 92
**PRESENTED BY:** Gemma Smith / gemma.smith10@gmail.com

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

## Abstract

Repeated nationwide serosurveillance of SARS-CoV-2 in the Netherlands during the second year of the pandemic: a prospective population-based cohort

**E. Vos** [1]

D. Wong [2], L. van den Hoogen [3], R. van Binnendijk [4], F. van der Klis [5], G. den Hartog [6], H. de Melker [7], C. van Hagen [8]

[1, 2, 3, 4, 5, 6, 7, 8] Centre for Infectious Disease Control, National Institute for Public Health and Environment (RIVM)

**BACKGROUND**
When collected at high temporal and spatial resolution, SARS-CoV-2 serosurveillance is key in complementing other surveillance tools. Here, we sero-monitored the Dutch population repeatedly to guide public health decisions throughout the second pandemic year.

**METHODS**
In this prospective population-based cohort (PIENTER Corona), participants (n=8,138) were randomly selected from the population registry in an age- and region-specific manner. In 2021, self-collected fingerstick blood samples were provided on three consecutive timepoints: February, June and November. Samples were tested for anti-S1 and anti-nucleocapsid IgG antibodies and combined with vaccination- and testing data to distinguish infection- and vaccination-induced humoral immunity. Estimates were weighted to match the population and adjusted for test-specifics.

**RESULTS**
Overall seroprevalence was 14% in February and rose steeply to 65% in June, reaching levels >90% in aged ≥50 years-olds, predominantly due to vaccination. Infection-induced seroprevalence increased from 12% to 20%, displaying a sustained age-pattern: highest rates in young adults (30%), followed by middle-aged adults (25%), and lowest in elderly (15%). Amidst the delta variant wave in November, overall seroprevalence rose to 93%. Of vaccinated persons, 99% was still seropositive up to 200 days after vaccination, 4% had serological proof of a breakthrough infection, of whom 70% induced anti-nucleocapsid antibodies. Meanwhile, infection-induced seroprevalence increased to 26%, and a relative steep rise was observed in ages 5-25 years, peaking at 45% in 20-year-olds.

**CONCLUSIONS**
A large part of Dutch adults had developed SARS-CoV-2 antibodies in 2021, contributing at least partially to protection against severe disease. Although being a main driver of the epidemic, the majority of younger age groups was still susceptible. This serological framework will be used to investigate different serological profiles in the context of emerging variants.

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

## Abstract

### Investigating opportunities for surveillance of long term chlamydia complications in the Netherlands: a qualitative study.

**E. den Boogert** [1]

F. van Aar [2], J. Heijne [3]

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[1, 2, 3] Centre for Infectious Diseases, Epidemiology and Surveillance, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands

**BACKGROUND**

*Chlamydia Trachomatis* (chlamydia) can result in complications such as Pelvic Inflammatory Disease (PID), ectopic pregnancy (EP) and Tubal Factor Infertility (TFI). Internationally, asymptomatic chlamydia testing is under debate. Changes in these strategies influence chlamydia infection surveillance, however it is unknown how changing strategies influence the occurrence of complications. We investigated the opportunity to introduce routine surveillance of complications.

**METHODS**

A qualitative study including 11 in-depth interviews with a purposive sample of gynaecologists, general practitioners (GP), sexual health and emergency doctors was conducted. Data saturation was reached for sexual health and emergency doctors but not for gynaecologists or GPs, requiring additional interviews. A semi-structured interview guide focused on experiences with diagnosis and registration of PID, EP and TFI and how a change in asymptomatic chlamydia testing strategy might influence this. Interviews were transcribed and analysed using a thematic approach.

**RESULTS**

Preliminary analysis showed that gynaecologists reported diagnosing PID, EP and TFI most frequently. Other professions rarely diagnose these complications, with emergency doctors only diagnosing EP. Respondents reported unique registration codes for PID and EP, but TFI is more ambiguous. They reflected that diagnosis and registration of PID, EP and TFI are handled differently within their profession. Most respondents acknowledged registration in diagnostic codes as a useful surveillance tool. They expressed concerns in representativeness (e.g. differences in interpretation of diagnosis criteria) and data completeness (e.g. missing diagnosis of asymptomatic complications and unknown causality between chlamydia and complication) for surveillance.

**CONCLUSIONS**

When establishing a chlamydia complication surveillance system, professionals should be engaged in further standardizing diagnosis and registration practices. This will improve complication surveillance and facilitate evaluating the impact of changing testing strategies on occurrence of complications.

**Keywords:** Chlamydia, Sexually transmitted Infections, Public Health Surveillance, Pelvic inflammatory disease, Ectopic Pregnancy, Infertility
**ABSTRACT ID:** 226
**PRESENTED BY:** Elke Den Boogert / e.den.boogert@ggdhvb.nl

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

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## Abstract

### Characterisation of measles transmission chains in three outbreaks in the post-elimination phase. Spain 2017-2019

**K. Bliek-Bueno** [1]

N. López-Perea [2], A. Fernández-García [3], J. Masa-Calles [4]

[1] Preventive Medicine Department. Miguel Servet University Hospital

[2, 3, 4] National Centre of Epidemiology,

**BACKGROUND**
Measles in Spain is in post-elimination phase since 2014, with fewer cases, smaller outbreaks, often in healthcare settings and in adults. With lower exposure to wild-type measles and a dependency on vaccine-induced immunity, there are doubts on whether elimination can be sustained. Our objective is to describe measles transmission in a high-vaccine-coverage context.

**METHODS**
We analysed three measles outbreaks reported to the National Epidemiological Surveillance Network in three Spanish regions between 2017-2019, considering the origin and vaccination status of each case. We identified and represented transmission chains within each outbreak based on information from the epidemiological investigation forms and considering the rash onset date as reference for establishing incubation and transmissibility periods.

**RESULTS**
All three outbreaks were moderate-sized, with 154, 97 and 98 cases. The index cases were imported and unvaccinated. Cases among the unvaccinated were most frequent with 234 (67.0%), followed by fully-vaccinated individuals (14.6%), cases with unknown status (9.8%), and those vaccinated with 1 dose (8.6%). We identified 4, 9 and 10 transmission chains, respectively. 73.4% of cases were linked to chains, with the remaining showing an association in time and place to the outbreak but no documented links to confirmed cases. Transmission occurred in healthcare settings in 11/23 chains (47.8%), involving 90% of fully-vaccinated cases within chains (27/30). One (4.4%) occurred at a kindergarten, with the remaining eleven (47.8%) taking place within family settings.

**CONCLUSIONS**
Measles transmission in the post-elimination phase is most relevant in family settings among the unvaccinated, and in healthcare settings among fully vaccinated individuals. Detection and control of imported cases and vaccination of healthcare professionals will be key to maintaining the elimination status in the future.

# POSTER TOUR 10
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Surveillance approaches

**MODERATOR**
Raquel Medialdea Carrera

## Abstract

### Evaluating severity parameters for scaling up and down public health and social measures during the COVID-19 pandemic in select WHO Member States

**H. Sadler** [1]

A. Hammond [2], K. Vandemaele [3]

[1, 2, 3] World Health Organization (WHO) Global Influenza Programme

**BACKGROUND**
Pandemic Influenza Severity Assessments (PISA) enable WHO Member States to qualitatively assess current influenza activity relative to in-country historical levels to inform public health and social measures (PHSM).
We aimed to review the performance of PISA during the COVID-19 pandemic and identify parameters used for COVID-19 surveillance which could improve influenza severity assessments.

**METHODS**
We surveyed Member States on how the parameters they used for monitoring COVID-19 activity differed from those used for monitoring influenza, how thresholds were set to categorize levels of activity, the utility of parameters in adjusting PHSM, and the challenges encountered.

**RESULTS**
12 Member States across 4 WHO regions reported on a total of 211 parameters. 100 were used for both COVID-19 and influenza surveillance, 75 only for COVID-19 and 36 only for influenza. Of these 211 parameters, 61 were unique. The most common parameters for adjusting COVID-19 PHSM were the reproduction number, number of laboratory-confirmed COVID-19 cases, hospitalizations and deaths and the test positivity rate for SARS-CoV-2 from universal surveillance. Contrastingly, parameters used for influenza monitoring were mostly from sentinel sources and did not include the reproduction number.
Challenges included changes to surveillance systems and healthcare seeking during the pandemic, as well as ongoing concerns on data quality, timeliness, and representativeness.

**CONCLUSIONS**
Member States reported several differences in how they conducted surveillance for COVID-19 and influenza in terms of parameter choice and the use of sentinel data. The parameters used to adjust PHSM aligned well with two indicators in the PISA guidance which assess community transmission and impact on healthcare and other services. Future PISA guidance may emphasise improving the quality of data on the impact on healthcare systems to inform PHSM.

**Keywords:** Influenza, COVID-19, Surveillance, Severity Assessment
**ABSTRACT ID:** 209
**PRESENTED BY:** Holly Sadler / sadlerh@who.int

# POSTER TOUR 11
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

## Abstract

### Monophasic *Salmonella Typhimurium* outbreak linked to chocolate products, Ireland, 2022

**C. Nielsen** [1]

P. McKeown [2], P. Garvey [3], M. Cormican [4], N. DeLappe [5], M. Lenahan [6], O. Moore [7], K. Casey [8], S. Cotter [9], S. Gee [10], B. Aniugbo [11], E. Brabazon [12], A. Breslin [13], E. Burke [14], M. Casey [15], C. Conlon [16], A. Dillon [17], L. Evans [18], R. Kiernan [19], D. Kilmartin [20], C. Lawlor [21], R. McBride [22], R. McDermott [23], G. Meagher [24], K. Quintyne [25], M. White [26]

[1] ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Solna, Sweden|Health Service Executive (HSE) - Health Protection Surveillance Centre (HPSC), Dublin

[2, 3, 9, 10] Health Protection Surveillance Centre, Dublin

[4, 5] National Salmonella, Shigella & Listeria Reference Laboratory, Galway

[6, 7] Food Safety Authority of Ireland, Dublin

[8] Environmental Health Services, Health Service Executive, Dublin

[11, 24] Department of Public Health, Health Service Executive-Midlands

[12, 25] Department of Public Health, Health Service Executive-North-East

[13, 22] Department of Public Health, Health Service Executive-North-West

[14, 26] Department of Public Health, Health Service Executive-South-East

[15, 18] Department of Public Health, Health Service Executive-Mid-West

[16, 17] Department of Public Health, Health Service Executive-South

[19, 20] Department of Public Health, Health Service Executive-West

[21, 23] Department of Public Health, Health Service Executive-East

### BACKGROUND
An EpiPulse alert was issued by the UK on a monophasic *Salmonella* Typhimurium outbreak on 17/02/2022. Responses to this alert indicated an extensive outbreak. On 23/03/2022, an outbreak investigation was initiated in Ireland after identifying seven cases with a sequence identical to the strain responsible for the wider international outbreak. International descriptive epidemiological investigations indicated a link to chocolate products, which triggered a recall of products from a single producer.

### METHODS
We conducted a matched case control study to confirm the source of infection. Confirmed cases of monophasic S. Typhimurium indistinguishable from the outbreak strain notified after 07/03/2022 were matched by age and sex to other gastrointestinal disease cases (ratio 1:3) notified within the same two-week period. Conditional logistic regression was used to estimate matched odds ratios (mOR) and 95% confidence intervals (CI).

### RESULTS
We identified 15 outbreak cases (median age 4 years [range 1-56]; 80% females). Among those, 47% had bloody diarrhoea and 27% were hospitalised. There were no deaths. Nine cases and 24 matched controls were included in the study. The odds of having consumed product A was seven times higher in cases notified as monophasic *S.* Typhimurium versus cases of other gastrointestinal disease (mOR=7.8 [0.9-67.2]). Product A was consumed by seven of nine cases (78%). The odds of having consumed any of the recalled products was 10 times higher in cases notified as monophasic *S.* Typhimurium versus cases of other gastrointestinal disease (mOR=10.5 [1.2-88.6]).

## CONCLUSIONS

Epidemiological and microbiological investigations pointed towards Product A as a likely outbreak vehicle. Five weeks after recall of the implicated product, no additional cases had been identified, indicating that control measures were effective.

## POSTER TOUR 11
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

## Abstract

### Successful containment of a Listeria monocytogenes outbreak caused by shredded vegetables, Hesse/Germany, 2021-2022

**L. Becker** [1],

P. Heinmüller [2], B. Ladewig [3], U. Steinhof [4], A. Schiffmann [5], S. Halbedel [6], A. Flieger [7], M. Adler [8], S. Lüth [9],
S. Kleta [10], A. Holzer [11], R. Lachmann [12], K. Stark [13], I. Foppa [14]

[1] EPIET

[1, 2, 14] Hessisches Landesprüfungs- und Untersuchungsamt im Gesundheitswesen (HLPUG)

[3] Dezernat V 54 - Veterinärwesen und Verbraucherschutz - Task-Force Lebensmittelsicherheit,
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[4] Landesbetrieb Hessisches Landeslabor (LHL), Fachgebiet Tierische Lebensmittel, Kassel, Germany

[5] Landesbetrieb Hessisches Landeslabor (LHL), Fachgebiet Tierische Lebensmittel, Gießen, Germany

[6, 7] Unit for Enteropathogenic Bacteria and Legionella, Department of Infectious Diseases, Berlin, Germany

[6, 7, 11, 12, 13] Robert Koch Institute (RKI)

[8, 9, 10] Federal Institute for Risk Assessment (BfR), National Reference Laboratory for Listeria monocytogenes,
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[11, 12, 13] Unit for Gastrointestinal Infections, Zoonoses and Tropical Infections, Department of Infectious Disease
Epidemiology, Berlin, Germany

**BACKGROUND**
In November 2021, two cases of listeriosis were reported with hospital stays during their suspected exposure periods within the Hessian notification system. An outbreak investigation was conducted to identify the source of these potential nosocomial infections.

**METHODS**
Confirmed cases were defined as listeriosis patients with detection of the outbreak strain from October 2021 onwards. Data on consumption were collected by interviewing patients and extracted from hospital menus. Food and environmental samples were taken from hospitals´ kitchens and the premises of a food manufacturer who supplied the hospitals. Bacterial isolates were compared using core genome multi locus sequence typing (cgMLST) analysis.

**RESULTS**
Four patients belonged to the cluster (symptom onset: 10/2021 – 01/2022). The median age was 76.5 years. The outbreak strain was isolated from a retained salad sample in one hospital. Back tracing identified a manufacturer who processed vegetables for raw consumption and supplied several hospitals in Hesse. The infections in three patients could be epidemiologically linked to their preceding stay in two of the hospitals supplied by that manufacturer. The manufacturing site exhibited substantial hygiene deficiencies and the outbreak strain was detected in food (*e.g.* cucumber) and environmental samples. The manufacturer was banned from preparing food.

**CONCLUSIONS**
Our results provide strong epidemiological and microbiological evidence that *Listeria* contaminated vegetables of a certain manufacturer were the outbreak source. Our findings are consistent with previous studies that identified pre-cut salad as vehicle for *Listeria monocytogenes* infections. However, solved outbreaks in Germany were mainly driven by meat and fish products. We recommend excluding industrially pre-cut vegetables for raw consumption from the menu of vulnerable populations such as hospitalized patients. We also recommend more inspections within the food supply chain.

**Keywords:** Outbreak Investigation, Listeria monocytogenes, Vegetables, Nosocomial, Germany, Whole genome sequencing
**ABSTRACT ID:** 297
**PRESENTED BY:** Laura Becker / laura.becker@hlpug.hessen.de

## Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

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## Abstract

### Outbreak of monophasic *Salmonella* Typhimurium linked to fresh small tomatoes, Sweden, 2021

**K. Fischerström** [1]

R. Dryselius [2], N. Karamehmedovic [3], M. Lindblad [4], E. Löf [5]

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[1,2,3,5] Public Health Agency of Sweden (PHAS), Solna, Sweden

[4] Swedish Food Agency (SFA), Uppsala, Sweden

**BACKGROUND**
In October 2021, the Public Health Agency of Sweden detected a nation-wide outbreak of cases infected with identical monophasic *Salmonella* Typhimurium strains. National and regional authorities investigated the outbreak to identify a common source.

**METHODS**
Cases were identified through the national notification system and confirmed by whole genome sequencing. We collected exposure data, using a standardised trawling questionnaire, and supermarket receipts from cases. In a case-case study, we compared exposures of outbreak cases (cases) to other salmonellosis cases (control cases), notified during mid-September-November 2019-2021, excluding clusters ›5 cases. After univariable analysis, we calculated age and sex adjusted odds ratios (aOR) with 95% confidence intervals (95%CI) for exposures reported by ›50% of cases, using Firth logistic regression. Findings were shared with the Swedish Food Agency for further investigation

**RESULTS**
Forty cases with illness onset during 1-29 October 2021 were reported from eight regions; median age; 44 years (interquartile range 5-70); 65% females. Compared to control cases, cases were more likely to report grocery shopping at Supermarket A (aOR 8.7; 95%CI 1.4–52), consumption of tomatoes (aOR 4.2; 95%CI 1.2–15) and minced beef (aOR 3.1; 95%CI 1.1–9.1). Tomato consumption was reported by 87% of cases and 58% of control cases. Supermarket A receipts from five cases all contained small tomatoes (no common brand). Trace-back identified suppliers in Italy and Spain. No food samples were obtained for analysis.

**CONCLUSIONS**
We describe the second Swedish outbreak of monophasic *S.* Typhimurium, epidemiologically linked to small tomatoes from Supermarket A during autumn. The outbreak stopped before measures were taken, supporting the finding of a fresh vegetable with short shelf-life. Fresh small tomatoes should be considered a potential source in future *Salmonella* outbreaks.

**Keywords:** Salmonella, Salmonella Typhimurium, Outbreaks, Zoonoses
**ABSTRACT ID:** 139
**PRESENTED BY:** Karolina Fischerström / karolina.fischerstrom@folkhalsomyndigheten.se

# Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

## Abstract

### Cluster of dog bite injuries and rabies exposures - Tajikistan, 2022

**R. Sharifov** [1]

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**BACKGROUND**
People with craniofacial injuries from dog bites are at high risk for rabies. Rabies elimination efforts in Tajikistan have reduced human rabies deaths from 14 in 2017 to four in 2020. But annually 13,000 dog bites occur, and only 48% of dogs have been vaccinated against rabies in Tajikistan.

**METHODS**
We describe a rapid response to a cluster of dog bite injuries in three villages in Yavan district with population 228,400. We conducted patient and provider interviews, abstracted medical record data, and reviewed surveillance data.

**RESULTS**
On March 6, 2022, 18 people were injured by the same unknown always-free-roaming dog with suspected rabies. They sought treatment at a local hospital. Of these, 61% (11/18) were <5 years old, and 18% (5/18) were 5-17 years old. Half (9/18) had craniofacial injuries, 25% (5/18) had hand bites, 72% (13/18) had superficial bites with bleeding, 6% (1/18) had scratches, and 22% (4/18) had contact with the dog's saliva. Within two hours of hospitalization, 13 (72%) people with bites had received rabies vaccines and immunoglobulin, and five (28%) people with only saliva exposure had received rabies vaccines. No patients have developed signs or symptoms of rabies. In Tajikistan, there is no compulsory vaccination of free-roaming dogs. There were 63 cases of animal bites in the Yavan in 2022. Animal bites were 57% higher first quarter of 2022 than in the same quarter of 2021.

**CONCLUSIONS**
Rapid response with immediate measures reduced morbidity and mortality from dog bite injuries. Education on prevention of dog bites can reduce burden of injuries and exposure to rabies. There is a need to increase rabies vaccination and expand programs that control free-roaming dog populations.

**Keywords:** Rabies, Tajikistan, Dogs, Vaccination, Immunoglobulin, Animal bites
**ABSTRACT ID:** 158
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# Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

## Abstract

### High fatality rate from probable botulism linked to home canning - Tajikistan, 2021

**S. Shoeva** [1]

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**BACKGROUND**
Botulism is a rare but fatal illness often caused by consumption of foods containing *Clostridium botulinum* neuro-toxins. We investigated an outbreak among people having attended a family dinner in Kushkiya village, Tajikistan in December 2021.

**METHODS**
We interviewed dinner participants using a structured questionnaire to collect clinical, demographic, and prior 48-hour food histories. We abstracted data from medical records. A case was defined as a person who attended the event with symptoms clinically compatible with botulism.

**RESULTS**
Thirteen people attended the dinner event. Of these, 10 (77%) were classified as a case; five were children ‹ 12 years old. Symptoms included muscle weakness, dizziness, dry mouth, nausea, vomiting, abdominal pain, symmetric paresis, shortness of breath, and double vision. Median time from dinner to onset was 22 hours (range 17-30). Four patients died (40%). Deaths occurred on average 48 hours after the dinner (range 41-55). All cases had eaten home canned salad. Two additional dinner participants ate the salad, but did not get sick. The salad was made of tomatoes, onions, garlic, and oil. It had been prepared in September 2021. Due to limited capacity for botulism testing in Tajikistan diagnostics were not performed. The infectious disease hospital did not have botulism antitoxin in stock upon patient admission. Deceased patients had not received antitoxin. On the third day after exposure, botulism antitoxin (A, B, C and E) was given to 9 dinner participants; all of whom survived.

**CONCLUSIONS**
The high case fatality rate highlights the need to increase clinician awareness of botulism, educate and improve their ability to provide emergency and respiratory care, and ensure stocks of anti-botulinum serum in health facilities.

**Keywords:** Canned foods, Tajikistan, Botulism, Outbreak, Field epidemiology, Mortality
**ABSTRACT ID:** 267
**PRESENTED BY:** Sakina Shoeva / sakina1680@mail.ru

# POSTER TOUR 11
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## Food and water borne diseases and zoonoses: outbreaks

**MODERATOR**
Aine Collins

## Abstract

### Lassa fever in the East of England: the multiagency response

**E. Turner-Moss** [1]
D. Edwards [2], C. Brown [3], T. Rampling [4], J. MairJenkins [5], R. Mulla [6], N. Brown [7], D. Collier [8], L. Rivett [9], J. Preller [10], M. Ferris [11], G. Martell [12], J. Varley [13], A. Shaw [14], C. Chetcuti Ganado [15], J. Birch [16], P. Tisi [17], M. Edoo [18], A. Starling [19], K. Dowle [20], S. Salimee [21], S. Kapadia [22], A. Popay [23], A. Trindall [24], R. Puleston [25], C. Houlihan [26], C. Gordon [27], H. Callaby [28], S. Hopkins [29], UK Health Security Agency UKHSA, Cambridge University Hospitals CUH, Luton & Dunstable Hospital L&D

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**BACKGROUND**
Lassa fever is a High Consequence Infectious Disease causing Viral Haemorrhagic Fever (VHF). It is endemic in West Africa; transmitted from excreta of infected multimammate rats but can also be spread person to person via infected bodily fluids. Only eight imported cases have been reported in the UK since 1980.

**METHODS**
Three cases of Lassa fever within the same family, linked to foreign travel, were confirmed within the East of England in February 2022. UK Health Security Agency and National Health Service enhanced incidents were declared. Contacts were identified and managed by local Health Protection and hospital Occupational Health teams. A bespoke data collection template completed to inform daily situation reports was collated by the Field Service for the National Incident Command Cell.

**RESULTS**
A total of 872 contacts of Lassa fever cases were identified; 436 Category 1 (no risk), 191 Category 2 (low risk) and 245 Category 3 (high risk). Fewer than five were household community contacts, all low risk. Category 2 contacts completed passive surveillance and Category 3 contacts active surveillance (healthcare workers avoided patient contact) for 21 days. Staff absence resulted in a major incident for hospitals, with temporary closure of specialist care beds and suspension of services. A total of 75 contacts tested for Lassa fever (using real time PCR) were negative. No further cases were identified.

**CONCLUSIONS**
The response to this rare VHF ensured no onward transmission but several hundred healthcare staff were asked to self-isolate with substantial impact on health service capacity and continuity. Review of risk categorisation is underway by the Advisory Committee on Dangerous Pathogens. Regular exercising may benefit system incident response.

**Keywords:** Lassa fever, Lassa virus, Zoonoses, Public Health, Hospitals, Occupational Health
**ABSTRACT ID:** 442
**PRESENTED BY:** Eleanor Turner-Moss / eleanor.turner-moss@nhs.net

## POSTER TOUR 12
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

# COVID-19: burden of disease

**MODERATOR**
Lynn Meurs

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## Abstract

### Occupational risk factors for SARS-CoV-2 infection amongst healthcare workers in England during the second wave: the SIREN prospective cohort study, September 2020 - April 2021

**E. Monk [1]**

D. Pople [2], S. Evans [3], S. Foulkes [4], J. Islam [5], E. Wellington [6], A. Atti [7], R. Hope [8], J. Robotham [9],

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**BACKGROUND**
Healthcare workers (HCW) have been at disproportionate infection risk throughout the SARS-CoV-2 pandemic. This study explores the factors associated with primary infection during the second wave in susceptible HCW participating in the SIREN cohort study.

**METHODS**
SIREN participants underwent two-weekly polymerase chain reaction (PCR) and monthly antibody testing. Demographic, household, occupational, laboratory and vaccination data were collected from enrolment question-naires, national laboratory surveillance systems and the SARS-CoV-2 immunisation registry. We included active participants with no prior infection upon second wave entry and follow-up was between September 2020 and April 2021. Outcome was PCR-confirmed primary SARS-CoV-2 infection. We calculated overall attack rates and univari-able and multivariable (mixed-effects logistic regression) associations to investigate the impact of demographic, household and occupational risk factors.

**RESULTS**
We included 18,284 participants (female: 84.9%, 45-54 years-old: 30.4%). During follow-up, 12.9% were infected (2,353/18,284). Infections peaked late December and rapidly decreased in early 2021, coinciding with vaccination roll-out and social-distancing measures. Infection rates were highest amongst <25 year-olds and participants of black or Asian ethnicity. After adjustment (demographics, household factors and time-to-vaccination), occupational factors remaining associated were: frequent exposure to patients with COVID-19 (every shift: adjusted odds ratio [aOR] 1.79, 95% confidence interval [CI] 1.56-2.06), working in an emergency department/inpatient ward (aOR 1.76, CI 1.45-2.14), and being a healthcare assistant (aOR 1.43, CI 1.16-1.77) or bedside therapist (aOR 1.32, CI 0.99-1.76).

**CONCLUSIONS**
Second wave infection rates amongst HCW in England were high, despite their prioritised early vaccine roll-out. Occupational factors associated with infection included early admission settings and roles with close patient proximity/interaction. These areas/groups could benefit from infection prevention and control optimisation: future work is targeted at unpicking these associations, focusing on winter pressures.

# POSTER TOUR 12
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: burden of disease

**MODERATOR**
Lynn Meurs

## Abstract

### Milder disease trajectory among COVID-19 patients hospitalised with the SARS-CoV-2 Omicron variant compared with the Delta variant in Norway

**J. Stålcrantz** [1]

A. Kristoffersen [2], H. Bøås [3], L. Veneti [4], E. Seppälä [5], N. Aasand [6], O. Hungnes [7], R. Kvåle [8], K. Bragstad [9], E. Buanes [10], R. Whittaker [11]

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**BACKGROUND**
Surveillance of disease severity of new variants of SARS-CoV-2 has been crucial for the monitoring the development of the COVID-19 pandemic. We estimated the length of hospital stay (LoS), and risk of admission to an intensive care unit (ICU) and in-hospital death among hospitalised patients infected with Omicron compared to patients infected with Delta in Norway.

**METHODS**
We conducted a cohort study using individual-level national registry data including 1075 patients hospitalised with COVID-19 as the main cause between 06/12/2021 and 06/02/2022 (409 (38%) with Omicron and 666 (62%) with Delta). We used Kaplan Meyer curve to calculate crude LoS and Cox proportional hazards models to estimate differences in LoS, and risk of ICU admission and in-hospital death, adjusting for age, vaccination status and presence of underlying risk factors for severe illness.

**RESULTS**
The crude median LoS for patients with Omicron was 2.8 days (LQ-UQ: 1.5-6.2 days), compared to 5.9 days for those with Delta (LQ-UQ: 3.0-12.0 days). In a subgroup analysis of 860 patients aged 18-79 years where the proportional hazards assumption was fulfilled, Omicron patients had 48% lower risk of ICU admission (adjusted hazard ratio (aHR): 0.52, 95%CI: 0.34–0.80) and 56% lower risk of in-hospital death (aHR: 0.44, 95%CI: 0.24–0.79) compared to Delta patients.

**CONCLUSIONS**
Our findings add to the evidence of reduced disease severity among hospitalised Omicron patients compared with Delta patients, providing important information to assist in capacity planning in hospitals as a new variant appeared.

**Keywords:** COVID-19, Omicron, Hospitalisation, Length of stay, Intensive care, Severe disease, Norway
**ABSTRACT ID:** 138
**PRESENTED BY:** Jeanette Stålcrantz / jeanette.stalcrantz@fhi.no

# POSTER TOUR 12
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: burden of disease

**MODERATOR**
Lynn Meurs

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## Abstract

### The impact of the COVID-19 pandemic on health-related quality of life in the Dutch population: a preliminary analysis

**C. van Hagen** [1]

A. Huiberts [2], E. Mutubuki [3], E. Vos [4], H. de Melker [5], M. Knol [6], A. van Hoek [7]

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**BACKGROUND**
The COVID-19 pandemic had an unprecedented impact on people's daily life. We aimed to describe health-related quality of life (HRQoL) in the general Dutch population during the second year of the COVID-19 pandemic.

**METHODS**
Data were obtained between February 2021 and April 2022 from two prospective population-based cohort studies: PIENTER Corona (n=8,168) and VASCO (n=45,271). HRQoL was assessed using SF-6D utility scores from the SF-12 (1 indicating full health). All 18-85 year-old participants who completed the SF-12 at least once were included in this analysis (N=53,439). Per cohort, HRQoL was stratified by age and sex. Mean biweekly HRQoL was calculated and trends were compared with the Dutch Oxford COVID-19 Stringency Index.

**RESULTS**
Preliminary analyses in both cohorts showed the same mean baseline HRQoL (0.82 (SD 0.11)) and similar age-patterns in HRQoL. 18-30 year olds had poorest HRQoL (0.76-0.78). HRQoL increased with age up until 70-75 years (to 0.85) and declined at older age (to 0.82). At any age, men had better HRQoL than women (PICO: 0.83 vs 0.80; VASCO: 0.85 vs 0.82). Biweekly HRQoL showed small fluctuations over time (range 0.80-0.84), not consistently following Stringency Index fluctuations.

**CONCLUSIONS**
Preliminary results from two Dutch cohort studies indicate that HRQoL was more affected among young adults compared to older adults during the second year of the COVID-19 pandemic. This age-pattern contrasts with pre-pandemic HRQoL data, which shows a reversed trend by age. With better HRQoL among men, the observed sex-related difference was comparable to pre-pandemic estimates. Further exploration regarding physical and mental health components of these differences and comparison with pre- and post-pandemic data will elucidate if differences can be explained by vaccination- or infection status, or by non-pharmaceutical interventions.

**Keywords:** COVID-19, SARS-CoV-2, Pandemics, Quality of Life, Netherlands
**ABSTRACT ID:** 202
**PRESENTED BY:** Cheyenne C.E. van Hagen / cheyenne.van.hagen@rivm.nl

# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

### Effectiveness of BNT162b2 vaccine against SARS-CoV-2 infection and severe COVID-19 in children 5-11 years old in Italy (January-April 2022)

**A. Mateo Urdiales** [1]

C. Sacco [2], M. Del Manso [3], M. Rota [4], D. Petrone [5], F. Riccardo [6], A. Bella [7], A. Siddu [8], S. Battilomo [9], V. Proietti [10], P. Popoli [11], F. Menniti Ippolito [12], A. Palamara [13], S. Brusaferro [14], G. Rezza [15], P. Pezzotti [16], M. Fabiani [17]

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[8, 9, 10, 15] Ministry of Health

**BACKGROUND**
By 13th April 2022, in Italy, less than 40% of children aged 5-11 had been vaccinated against COVID-19 more than four months after the approval of vaccination with BNT162b2 vaccine (BioNTech-Pfizer) in this age group. It is important to estimate how effective vaccination is in children of this age in the current epidemiological context dominated by B.1.1.529.

**METHODS**
We retrospectively assessed vaccine effectiveness (VE) against SARS-CoV-2 infection and against severe COVID-19, defined as an infection leading to hospitalisation or death. By linking the national COVID-19 surveillance system and the national vaccination registry, all Italian children aged 5-11 years without a prior diagnosis of infection were followed from January 17th to April 13th, 2022. Using unvaccinated children as the reference group, we estimated VE in those partially vaccinated and in those fully vaccinated.

**RESULTS**
By April 13th, 2022, 1,063,035 of the 2,965,918 children aged 5-11 included in the study had received two doses of the vaccine, 134,386 only one dose and 1,768,497 were unvaccinated. During the study period, 766,756 cases of SARS-CoV-2 infection and 644 cases of severe COVID-19 (627 hospitalisations, 15 admissions to intensive care unit and two deaths) were notified. Overall, VE in fully vaccinated children was 29.4% (95% CI, 28.5-30.2%) and 41.1 % (95% CI, 22.1-55.4%) against SARS-CoV-2 infection and severe COVID-19, respectively. VE against infection peaked at 38.4% (95% CI 37.4-39.4%) 0-14 days after full vaccination and decreased to 20.8% (95% CI, 19.3-22.3%) 43-84 days after full vaccination.

**CONCLUSIONS**
Vaccination against COVID-19 in children aged 5-11 years in Italy was moderately effective in preventing SARS-CoV-2 infection and severe COVID-19. Effectiveness against infection appears to decline fast after completion of the primary vaccination cycle.

**Keywords:** COVID-19, Vaccination, Children, Evaluation
**ABSTRACT ID:** 343
**PRESENTED BY:** Chiara Sacco / chiara.sacco@iss.it

# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

### Monitoring vaccine effectiveness against SARS-CoV-2 infection in a Dutch cohort – The VAccine Study COVID-19 (VASCO)

**A. Huiberts** [1]
C. Hoeve [2], M. Kooijman [3], H. de Melker [4], S. Hahne [5], D. Grobbee [6], J. van de Wijgert [7], S. van den Hof [8], M. Knol [9]

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**BACKGROUND**
COVID-19 vaccine effectiveness (VE) should be monitored to inform vaccine policies. We aimed to estimate VE of primary and booster vaccination against symptomatic SARS-CoV-2 infection overall, and in four subgroups defined by age and medical risk group, in the Delta and Omicron dominant period.

**METHODS**
The VAccine Study COvid-19 is a prospective cohort study following vaccinated and unvaccinated Dutch adults. The primary endpoint was self-reported positive SARS-CoV-2 test. Participants who reported previous SARS-CoV-2 infection were excluded in the current analysis. Cox proportional hazard models with vaccination status as time-varying exposure and calendar time as underlying timescale were used to calculate VE, corrected for age, gender, educational level, and medical risk group. Models were stratified by Delta/Omicron period, age and medical risk group, and time since vaccination.

**RESULTS**
34,610 participants (mean age 58.5 years) with median follow-up time of 24.9 weeks, were included. In the Delta period, VE decreased from 82% (95%CI 74-87) within 3 months to 67% (54-77) 6-9 months after primary vaccination, and increased to 85% (60-95) within 1 month after booster vaccination. In the Omicron period, these estimates were 36% (6-56), 35% (2-45), and 61% (55-66), respectively; VE decreased to 51% (42-58) 3-4 months after booster vaccination. In the Omicron period, VE within 1 month after booster vaccination differed significantly by subgroup: 51% (18-71) and 63% (55-69) in participants 18-59 years with and without medical risk condition, respectively, and 47% (1-72) and 66% (53-76) in participants 60-85 years with and without medical risk condition, respectively.

**CONCLUSIONS**
Although effectiveness of vaccination was lower against Omicron infection than Delta infection, booster vaccination increased effectiveness substantially, underlining the need for booster vaccination, especially in medical risk groups.

**Keywords:** COVID-19, Vaccine effectiveness, SARS-CoV-2, Cohort Studies
**ABSTRACT ID:** 24
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# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

Vaccine effectiveness of mRNA vaccines against COVID-19 hospitalisation
uring Omicron circulation in Europe in adults ≥20 years: I-MOVE-COVID-19
and ECDC hospital networks, 27 Dec 2021–31 Mar 2022

**A. Rose [1]**
N. Nicolay [2], V. Martín [3], C. Mazagatos [4], G. Petrovic [5], S. Denayer [6], L. Seyler [7], J. Cauchi [8], A. Machado [9],
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G. Panagiotakopoulos [18], J. Howard [19], F. Pozo [20], C. Delgado-Sanz [21], D. Nonkovic [22], N. Bossuyt [23], T. Demuyser [24],
A. Dziugyte [25], I. Kislaya [26], L. Luong Nguyen [27], R. Duffy [28], M. Knol [29], G. Gefenaite [30], M. Simon [31], I. Martínez-Baz [32],
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E. Van Nedervelde [39], M. Borg [40], V. Gomez [41], Z. Lesieur [42], J. O'Donell [43], P. Bruijning-Verhagen [44], A. Mickiene [45],
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## BACKGROUND

Severe acute respiratory illness (SARI) surveillance systems in Europe provide a platform to measure vaccine effectiveness (VE) against COVID-19 hospitalisation. We pooled data from two large European SARI VE hospital networks (27 December 2021–31 March 2022) to measure VE of mRNA vaccines among hospitalised SARI patients aged ≥20 years during the Omicron-dominant period, in order to inform vaccination policy in Europe.

## METHODS

Fifty-one hospitals across both networks follow similar protocols using a test-negative design. Hospitalised SARI patients (fever, cough, shortness of breath or sudden onset anosmia/ageusia/dysgeusia) are PCR-tested: cases are SARS-CoV-2 positive, controls are negative. We defined patients in the booster dose target group as having complete primary series after two doses of mRNA vaccine (Comirnaty, Spikevax). We defined booster as an additional dose ≥150 days after the last primary series dose. We excluded those vaccinated <14 days before symptom onset. We used logistic regression to estimate adjusted VE (aVE) as 1-odds ratio of vaccination (%), adjusting by country, sex, age-group, swab date and chronic conditions.

## RESULTS

We included 973 SARI patients (673 cases, 300 controls). mRNA aVE was 78% (95%CI: 61–87) for primary series (all ages), 81% (66–89) for booster dose. Primary series aVE was 85% (64–94) in those aged 60–79 years and 84% (48–95) for those aged ≥80 years. For booster dose, aVE was 86% (67–94) and 83% (43–95), respectively.

## CONCLUSIONS

During predominant Omicron circulation, VE against hospitalisation with confirmed SARS-CoV-2 remained high for primary series and for booster doses, in all ages and in older adults. Further work will investigate VE by time since vaccination and for subsequent variant periods.

Abstract presentations - Poster tours

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# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

### Vaccine effectiveness of BNT162b2 COVID-19 in adolescents: results of a Portuguese population-based cohort study based on electronic health records linkage

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### BACKGROUND
Monitoring COVID-19 vaccine effectiveness (VE) in the 12 to 17 year population in the context of SARS-CoV-2 epidemiology evolution, using real-world data is essential to inform public health policies.
We aimed to estimate BNT162b2 complete schedule VE against laboratory-confirmed symptomatic SARS-COV-2 infection, considering time since vaccination, for Portuguese population aged 12-17 years old, in July 2021-January 2022.

### METHODS
We developed a cohort study based on deterministic data linkage of electronic health records. The target population included residents in mainland Portugal, aged 12-17 and eligible for vaccination followed from July 2021 to January 2022. Completely vaccinated persons were those with at least 14 days following the second dose. We stratified time since vaccination in 28 days intervals up to 124 days. VE was estimated as 100%*(1-HR) where HR is the confounding-adjusted hazard ratio obtained from time-dependent Cox regression, adjusted for age, sex, municipality deprivation, chronic diseases, number of SARS-CoV-2 tests during 2021 and previous influenza or pneumococcal vaccination.

### RESULTS
We included 542,565 individuals in the cohort study. VE against symptomatic infection in the 12-15 years-old cohort peaked at 71% (95%CI 65 to 76%) 14-41 days following complete schedule, declining to 3% (-4 to 9%) at 98-124 days. In the 16-17 years old cohort, VE was 76% (68 to 81%) 14-41 days following complete scheme, declining towards null effect at 98-124 days (VE= -3, 95%CI -12 to 5%).

### CONCLUSIONS
Our results suggest moderate-high VE of BNT162b2 primary schedule in the 12-17 years old population, peaking in the first month after vaccination (71-76%), declining after to low or null effect. Vaccines with more durable effectiveness are required if vaccination strategy in this populations aims to control SARS-CoV-2 transmission.

**Keywords:** COVID-19, Vaccine effectiveness, Electronic Health Records, Adolescent
**ABSTRACT ID:** 304
**PRESENTED BY:** Baltazar Nunes / baltazar.nunes@insa.min-saude.pt

# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

### Relative effectiveness of COVID-19 vaccine booster dose against Delta and Omicron SARS-CoV-2 infection in a European healthcare worker cohort, June 2021- April 2022

**C. Savulescu** [1]
on behalf of ECDC VEBIS HCW VE study group

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**BACKGROUND**
Healthcare workers (HCW) were one of the first priority groups for COVID-19 vaccination. We measured the relative vaccine effectiveness (rVE) of COVID-19 booster dose in HCW during two different SARS-CoV-2 waves.

**METHODS**
In this prospective cohort study, 2276 HCWs from 12 EU/EEA hospitals were tested for SARS-CoV-2 in respiratory or saliva samples at enrolment and during weekly/biweekly follow-up. We estimated the rVE of booster compared to primary vaccination schedules during Delta (01/06/2021-14/12/2021) and Omicron (15/12/2021–20/04/2022) – dominated waves. Using Cox regression, we calculated the rVE as (1-harzard ratio)*100 and adjusted for sex, age, underlying conditions, hospital and month of follow-up.

**RESULTS**
During the Delta wave, of 1602 HCWs with completed primary vaccination schedule, 232 (15%) reported a previous SARS-CoV-2 infection and 551 (34%) received a booster dose. Of the 47 SARS-CoV-2 infections detected, one reported a booster dose and none a reinfection. The adjusted rVE of the booster dose was 86% (95%CI: 39-97). During the Omicron period, of 1078 HCW with completed primary vaccination schedule, 226 (21%) reported a previous SARS-CoV-2 infection and 571 (53%) received a booster dose. Of 197 SARS-CoV-2 infections, 91 (46%) reported a booster dose and 24 (12%) a reinfection. The adjusted rVE was 15% (95%CI: -25-42): 43% (95%CI: -36-76) in HCW with a previous SARS-CoV-2 infection and 0% (95%CI: -57-37) in those without previous infection.

**CONCLUSIONS**
The COVID-19 vaccine booster dose offered additional protection during the Delta wave. During the Omicron wave, the follow-up period was insufficient to precisely estimate the relative vaccine effectiveness. The continuation of the study with more hospitals and including time since vaccination in the analysis will enable a better understanding of hybrid protection and inform COVID-19 vaccination policy.

**Keywords:** SARS-CoV-2 infection, Healthcare workers, Vaccine effectiveness, COVID 19 Vaccine, Active surveillance
**ABSTRACT ID:** 349
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# POSTER TOUR 13
DAY 3, 25 NOVEMBER 2022
15:15 – 16:00

## COVID-19: vaccine effectiveness

**MODERATOR**
Alexis Sentis

## Abstract

### Effectiveness of BNT162b2 mRNA booster doses and hybrid-immunity against SARS-CoV-2 infections during the Delta and Omicron variant waves; the UK SIREN study September 2021 to February 2022

**V. Hall** [1]

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SIREN Study Group

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**BACKGROUND**
COVID-19 vaccine boosters were widely deployed following vaccine waning and emergence of the Omicron-variant. We investigated the effectiveness of boosters and hybrid-immunity against SARS-CoV-2 infection in our frequently PCR-tested cohort of healthcare-workers.

**METHODS**
Effectiveness of BNT162b2 boosters and infection-acquired immunity was assessed by comparing the time to PCR-confirmed infection in boosted participants with those with waned dose-2 protection (≥254 days after dose-2), with follow-up time divided by dominant variant (Delta 07/09/2021 to 31/11/2021; Omicron 13/12/2021 to 28/02/2022). We used a Cox regression model with adjustment/stratification for demographic characteristics and staff-type. We explored interactions between vaccine-acquired and infection-acquired protection.

**RESULTS**
We included 18,429 participants, 29% previously infected. A total of 2,745 primary infections and 873 reinfections were observed during follow-up, with higher cumulative incidence rates against Omicron (primary: 43/10,000-days, reinfections: 33/10,000-days) than Delta (primary: 4/10,000-days, reinfections: 0.8/10,000-days). Boosters increased protection against both variants, but were less effective against Omicron (Vaccine Effectiveness (VE) 0-2 months post-booster, infection naïve, 3-doses BNT162b2: 35% (95% Confidence Interval (CI) 21%-47%) vs. 63% (CI 40%-77%) than Delta. Heterologous boosters (BNT162b2, 2-dose ChAdOX1) were especially effective; with VE 0-2 months post-boost over ≥68% for both variants. Booster protection waned rapidly against Omicron, with no additional benefit >4-months. When included as a marginal predictor, previous infection continued to provide additional protection against Omicron (71% (CI 53%-82%) 3-6 months post-infection), but this was markedly lower than against Delta, and waned after 9-months. We found no evidence of interaction between vaccine-acquired and infection-acquired protection.

**CONCLUSIONS**
Infection rates surged with Omicron emergence. Boosters provided short-term protection, with rapid waning. Our findings demonstrate the complexity of an evolving pandemic with potential emergence of immune-escape variants and the importance of continued monitoring.

# Online-only posters

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## ANTIMICROBIAL RESISTANCE

### Microbiology (incl. novel methods in microbiology, such as e.g. new diagnostic tools)

## Abstract

### Service evaluation of laboratory reporting practices of antimicrobial susceptibilities for urine samples in the East of England

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**BACKGROUND**

Clinical laboratories play a significant role in antimicrobial stewardship (AMS), including the functions of testing and reporting antimicrobial susceptibilities to clinical submitters, reporting of patient-specific information to facilitate appropriate prescribing, and adhering to guidance for specimen processing and reporting. Studies have shown differing laboratory practice for reporting antimicrobial susceptibility results can impact on prescribing behaviour. Selective reporting of susceptibility results has been suggested as an important mechanism for laboratories to encourage appropriate prescribing.

We sought to understand how laboratory reporting practices may influence antimicrobial prescribing, focusing on antimicrobial susceptibility reporting for urine samples.

**METHODS**

We conducted structured interviews with microbiologists from each East of England NHS laboratory, capturing characteristics of laboratory reporting systems, validation and audit processes, and barriers and enablers to promoting AMS. Thematic analysis identified differences and common themes.

**RESULTS**

Microbiologists described limitations with reporting systems including inability to modify sensitivity reporting order, or to suppress antibiotics for certain sample types. They often saw minimal clinical details from requestors. While some systems enabled laboratories to add contextual comments to reports, these were often restricted. There were often uncertainties and variation in whether these comments were visible to GPs.  Microbiologists acknowledged the challenge of creating information flows that both allowed for standardisation and addressed individual patient needs.

**CONCLUSIONS**

There was recognition of the need for clinical validation processes and selective reporting, and a desire for data on what GPs were prescribing to support understanding of how laboratory reporting influences prescribing. Results highlight the need for reporting system fields enabling recording of clinical characteristics including allergies and pregnancy status, with free text fields for contextual comments, in addition to standardised fields, aiding validation and audit.

Abstract presentations - Online-only posters

# ANTIMICROBIAL RESISTANCE

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

### Abstract

(Cost-)effectiveness of C-reactive protein point-of-care testing versus usual care to reduce antibiotic prescribing for suspected lower respiratory tract infections in elderly nursing home residents

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### BACKGROUND

Point-of-care testing (POCT) for inflammatory biomarker C-reactive protein (CRP) might help to reduce diagnostic uncertainty and unnecessary antibiotic prescribing for nursing home (NH) residents with suspected lower respiratory tract infections (LRTI). This study aimed to evaluate the effectiveness and cost-effectiveness of CRP POCT versus usual care to reduce antibiotic prescribing for NH residents with suspected LRTI.

### METHODS

A pragmatic, cluster-randomized controlled trial took place in Dutch NHs with access to CRP POCT (intervention group, N=6) or providing usual care (control group, N=5) for residents with suspected LRTI. Physicians collected data regarding clinical status, diagnostic work-up and management decisions. Cost-effectiveness analyses included total healthcare costs, and effect measures antibiotic prescribing (at initial consultation) and full recovery (at 3 weeks). Return-on-investment analyses included intervention costs and benefits related to antibiotic prescribing.

### RESULTS

Intervention group patients had 4.93 higher odds (95%CI: 1.91-12.73) of not being prescribed antibiotics compared with control group patients, irrespective of treating physician and baseline characteristics. In the intervention group (N=162), total healthcare costs were on average €32 higher per patient, the proportion of avoided antibiotic prescribing was higher (0.47 vs. 0.18; 0.30; 95%CI 0.17-0.42) and the proportion of fully recovered patients statistically non-significantly lower (0.86 vs. 0.91; -0.05; 95%CI -0.14-0.05) compared with the control group (N=79). The ICER was €137 per avoided antibiotic prescription. The probability of CRP POCT being cost-effective at willingness-to-pay of €650/antibiotic prescription avoided was 0.80. The probability of financial return of the intervention compared to control was 0.65.

### CONCLUSIONS

CRP POCT for suspected LRTI effectively reduced antibiotic prescribing compared with usual care. The implementation of CRP POCT in NHs requires an investment, but may contribute to the global fight against antimicrobial resistance.

**Keywords:** Point-of-care testing, Respiratory tract infections, Homes for the aged, Antimicrobial Stewardship
**ABSTRACT ID:** 74
**PRESENTED BY:** Tjarda M. Boere / tjarda.boere@rivm.nl

Abstract presentations - Online-only posters

## Surveillance

## Abstract

### Moving towards One Health surveillance of AMR in France: an evaluation of the level of collaboration within the AMR surveillance system

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**BACKGROUND**

The 2017 European Antimicrobial Resistance Action Plan has set an impulsion for a One Health approach against antimicrobial resistance (AMR). However, a recent mapping of the French surveillance system (SS) of AMR in humans, animals, food and the environment highlighted a highly complex and fragmented system, questioning the integration between surveillance programmes (SP). This study aimed to evaluate the degree and quality of multisectoral collaboration within the 48 SP and to formulate practical recommendations for improvement.

**METHODS**

To assess collaboration between SP, the semi-quantitative evaluation tool ECoSur (Bordier et al. 2019) was used. The 75 criteria were scored based on information from the literature and 52 semi-directed interviews with SP coordinators and key informants. The results were visualized via 22 scoring attributes and three output figures displaying aspects related to governance and functionality of collaboration.

**RESULTS**

Overall, the national collaborative strategy was well formalized and relevant with the objectives. Collaboration was operational for internal communication and dissemination of the results, including to decision makers. However, we identified a lack of a structured SP in the environment and of a cross-sectoral coordination body to help with the practical implementation of the national collaborative strategy. Data sharing and joint data analyses between SP were insufficient, mainly due to limited resources and data interoperability issues. Finally, 11 recommendations were proposed to decision makers to improve the One Health-ness of the French AMR SS and feed future strategies against AMR.

**CONCLUSIONS**

This first application of EcoSur to the French AMR SS demonstrated its adaptability to large and complex systems, producing concrete recommendations to foster integration. This can be of interest to other countries willing to move towards One Health integrated surveillance.

# COVID-19

## Burden of disease

## Abstract

### Post-covid fatigue after SARS-CoV-2 omicron infection and 3 vs 2 doses mRNA vaccines

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**BACKGROUND**

Fatigue is a common symptom in persons infected with the SARS-CoV-2 omicron variant and is also the most common persistent complaint after COVID-19. Persons vaccinated with 1 or 2 doses are reported to be less likely to develop such symptoms, however it is unknown whether third dose vaccination would lower the risk even further.

**METHODS**

We included all Norwegian residents aged 18-70 years with a positive test for SARS-CoV-2 identified as the omicron variant who had 2 doses (n=20 004, 49.1% women, mean (SD) age 35.4 (12.1) years) or 3 doses (n=2405, 57.0% women, mean (SD) age 49.1 (13.8) years) from December 1st, 2021, to January 14th, 2022, and who had a mild disease course not resulting in hospitalization. We used Cox regressions adjusted for age, sex, birth country, education level, comorbidities, prior primary care visits, and the number of prior negative tests, and calculated hazard ratios (HR) for having a medical record with fatigue in outpatient, primary care from 7 to up to 90 days after test date. Analyses were stratified on the test week to handle seasonal variation in test patterns.

**RESULTS**

Three doses of mRNA vaccine were associated with a reduced rate of fatigue for up to 90 days after infection with the omicron variant, compared to two doses only (HR=0.55, 95% CI=0.40-0.75).

**CONCLUSIONS**

Having three doses of mRNA vaccination against SARS-CoV-2 reduces the prevalence of post-covid fatigue and subsequent burden on healthcare systems in periods dominated by the omicron variant.

**Keywords:** COVID-19, Vaccines, Fatigue, Post-covid, SARS-CoV-2
**ABSTRACT ID:** 262
**PRESENTED BY:** Fredrik Methi / fredrik.methi@fhi.no

# COVID-19

## Burden of disease

### Abstract

**Physiotherapy use is increased for up to nine months after receiving respiratory support for COVID-19**

**K. Skyrud** [1]

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**BACKGROUND**

To explore whether physiotherapy use is increased after hospitalization with COVID-19 with or without respiratory support vs. other respiratory tract infections (RTI).

**METHODS**

In all Norwegian residents aged 18-80 years who were hospitalized with COVID-19 (N=5,344) or other RTI (N=82,235) between July 1st 2017 and August 1st 2021, we used a pre-post study design to explore the weekly individual average physiotherapy use in community care from 12 weeks prior to hospital admission, to 36 weeks after hospital discharge for men and women who received and who did not receive respiratory support.

**RESULTS**

Prior to the hospital stay, COVID-19 patients on respiratory support had 41-56 physiotherapist consultations per 1000 inpatients per week, whereas persons with other RTI on respiratory support had 45-60 consultations per 1000. COVID-19 patients on respiratory support had a higher increase in physiotherapy use after discharge than persons with other RTI on respiratory support (an additional 27.3 (95%CI= 10.2 to 44.4) per 1000 for men, and 41.8 (95%CI= 13.7 to 69.9) per 1000 for women)). The increase in physiotherapy use lasted for 6 months for men, and 9 months for women. COVID-19 inpatients without respiratory support had a similar change post-discharge physiotherapy use as inpatients with other RTI without respiratory support.

**CONCLUSIONS**

There was an up to 9 months lasting increased need for physiotherapy services following respiratory support for COVID-19 which was not seen following respiratory support for other RTI. These findings have implications for the etiologic understanding of severe COVID-19 relative to other severe RTI. They also demonstrate the need for the healthcare and physiotherapy services to improve their knowledge and capacity of COVID-19 rehabilitation.

# COVID-19

# Burden of disease

## Abstract

### Nursing assistants and nurses had the highest risk of Coronavirus Disease 2019 (COVID-19) among healthcare professionals during 1 February 2020 and 30 June 2021 in Finland

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### BACKGROUND

During Coronavirus Disease 2019 (COVID-19) pandemic, healthcare workers (HCWs) have been a risk group for contracting COVID-19. In this retrospective register-based study we assessed incidence, risk factors and outcomes of COVID-19 in HCWs during February 2020 and June 2021 in Finland in order to inform preventive measures in healthcare.

### METHODS

We linked two national registers, National Infectious Diseases Register (NIDR) and Register of Social Welfare and Healthcare Professionals (Terhikki), using national identity codes. COVID-19 cases were identified from NIDR notifications made by laboratories and physicians, and their healthcare professions from Terhikki. We categorized healthcare professions into seven groups and calculated cumulative incidences using Kaplan-Meier estimate during three periods (1.2.-30.6.2020; 1.7.-31.12.2020 and 1.1.-30.6.2021). We identified risk factors in a multivariable model using Cox's regression.

### RESULTS

We identified 8009 COVID-19-cases among HCWs, with cumulative incidence of 1.79%; 83% were female, median age was 40.9 years (interquartile range, 31.2-51.6). Physician notification data was available for 6113/8009 cases (76.3%); 244/6113 (4.0%) were hospitalized, 37/6113 (0.6%) in intensive care, 4/6113 (<0.1%) died. The incidence was higher (0.95%, 95% CI: 0.92-0.98%) during the latest period compared with the two former periods, 0.32% (95% CI: 0.31-0.34%) and 0.63% (95%CI 0.60-0.65%). Most COVID-19-cases occurred in nursing assistants (53%) and nurses (17%), who had the highest cumulative incidences at 2.07% (95%CI, 2.01-2.13%) and 1.82% (95%CI, 1.73-1.91%), respectively. Risk factors were male gender (hazard ratio (HR) 1.2; 95%CI, 1.1-1.3), foreign native language (HR 2.5; 95%CI, 2.2-2.9) and foreign country of birth (HR 1.2; 95%CI, 1.1-1.4).

### CONCLUSIONS

Nurses and nursing assistant, especially men and professionals with foreign background, were at higher risk of COVID-19 among HCWs. This should be specifically addressed during training and implementing infection control measures.

# COVID-19

## Communication and health promotion

### Abstract

Personal risk or societal benefit? Investigating adults' support for COVID-19 childhood vaccination

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**BACKGROUND**

Parental hesitancy has undermined the success of childhood vaccination programs in recent years, and COVID-19 vaccines represent no exception. We analyse parents' and non-parents' self-reported probability of supporting COVID-19 childhood vaccination, and test whether their opinion can be influenced via two survey experiments in Italy (n=3,524 participants) and the UK (n=3,066 participants). Respondents were randomly assigned to: a "risk treatment" that highlighted the potential risks of COVID-19 to a child, a "herd immunity treatment" that emphasized the community benefits of paediatric vaccination, or a control message. Similar appeals have proven effective in increasing intentions to vaccinate among adults, but little is known for paediatric vaccination.

**METHODS**

Participants' probability of supporting COVID-19 childhood vaccination was assessed on a 0-100 scale. We use the relative distribution method to analyse differences in the outcome distributions across treatments, stratified by parental status. This non-parametric tool enables the detection of significant differences between two groups across the entire distribution of a variable.

**RESULTS**

The outcome variable had a mass-polarized distribution on the extremes, both among parents and non-parents, and across treatment groups. We find the "risk treatment" to reduce the proportion of Italian parents strongly against vaccinating (0) by up to 29.6%, while increasing the proportion of neutral parents (50) by up to 45.0%. The "herd immunity treatment", instead, was only effective among non-parents, resulting in a lower proportion of individuals against pediatric vaccination and a higher proportion of individuals in favour (100) (both shifted by around 20%).

**CONCLUSIONS**

These results demonstrate the potential of information treatments in addressing parental vaccine hesitancy, but also document the need to carefully consider the treatment formulation depending on the targeted group.

Abstract presentations - Online-only posters

# Field epidemiology (e.g. outbreak investigations)

## Abstract

Prevalence of anti-SARS-CoV-2 antibodies among school children and staff in Belgium between December 2020 and 2021

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**BACKGROUND**

In Belgium, on April 5th 2022 only 16 of 31,494 COVID-19 related deaths have been reported within the age category 0 – 24, suggesting that children may be less effected by the virus. To assess virus circulation among children, we determined the prevalence of anti-SARS-CoV-2 IgG antibodies among children and staff in Belgian primary and secondary schools between December 2020 and 2021.

**METHODS**

We conducted a prospective cohort seroprevalence study including a representative sample of pupils and staff in Belgian primary and secondary schools. The three first testing periods contained all participants, two additional testing periods contained the at that time only non-vaccinated group, being primary school pupils. Prevalence of anti-SARS-CoV-2 antibodies was determined with a semi-quantitative IgG ELISA. Information on school (infection control and prevention measures) and individual (past infections, symptomatology and hospitalisations) characteristics was collected using an online questionnaire.

**RESULTS**

44 primary (710 pupils; 432 staff) and 40 secondary (575 pupils; 386 staff) schools participated. Between December 2020 and June 2020, seroprevalence increased from 13.6% (95%CI: 9.9 – 18.5) to 17.2% (95%CI: 13.1 – 22.7) among secondary school pupils and from 14.8 (95%CI: 12.2 – 18.0) to 21.1 (95%CI: 16.9 – 26.3) among unvaccinated staff. Between December 2020 and 2021, seroprevalence increased from 11.0% (95%CI: 7.6 – 15.9) to 50.9% (95%CI: 43.7 – 59.2) among primary school pupils. Since the start of the pandemic, 26.9% participating pupils reported a confirmed SARS-CoV-2 infections and no one was hospitalisations.

**CONCLUSIONS**

Differences in seroprevalence between testing periods and regions reflect the dynamics of the COVID-19 epidemic in the general Belgian population. Different than among the older population groups, children who experienced a SARS-CoV-2 infection rarely became seriously ill.

# COVID-19

## Field epidemiology (e.g. outbreak investigations)

### Abstract

Facility- and ward- level factors associated with SARS-CoV-2 outbreaks among residents in long-term care facilities

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**BACKGROUND**

Long-term care facilities (LTCFs) have been disproportionately impacted by coronavirus disease 2019 (COVID-19). Yet, the reasons why certain LTCFs are more affected by outbreaks are poorly understood. This study aimed to identify facility- and ward-level factors associated with SARS-CoV-2 outbreaks among LTCF residents.

**METHODS**

We conducted a retrospective cohort study of multiple LTCFs (n=60) in South-Limburg, the Netherlands, from November 2020 till June 2021. A dataset was constructed in which confirmed COVID-19 cases among LTCF residents at wards were linked to facility- and ward-level characteristics. The dataset was divided in two time periods (T), based on changes in testing policy, virus variant dominance and the introduction of vaccinations in LTCFs. Multilevel logistic regression analyses were performed to examine the associations between facility- and ward-level characteristics and the likelihood of a SARS-CoV-2 outbreak among residents.

**RESULTS**

From November to December 2020 (T2), 33/298 wards (11.1%) experienced a SARS-CoV-2 outbreak, whereas this applied to 52 wards (17.4%) from January to June 2021 (T3). On T2 (classic variant), recirculation of air was associated with an increased odds of a SARS-CoV-2 outbreak (aOR:5.9, 95% CI:1.6-22.1). On T3 (alpha variant), factors associated with increased odds of a SARS-CoV-2 outbreak included large ward size (>21 beds) (aOR:10.9, 95% CI:3.3-36.3), the ward type psychogeriatric care (aOR:3.0, 95% CI:1.1-8.7), and fewer restrictions on staff movement (aOR:5.9, 95% CI:1.4-24.0).

**CONCLUSIONS**

Policy and protocols on reducing recirculation of air in buildings, resident density and staff movement are recommended to mitigate facility and local spread and may enhance preparedness for future outbreaks in LTCFs. Furthermore, a special focus is needed on the implementation of low-threshold preventive measures among psychogeriatric residents, who appear to be a particular vulnerable group.

# COVID-19

## Field epidemiology (e.g. outbreak investigations)

## Abstract

Enhanced contact tracing and timely whole genome sequencing detailed transmission of the SARS-CoV-2 variant B.1.1.519 from introduction via a superspreading event to extinction in Denmark, spring 2021

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### BACKGROUND

Superspreading events have been thought to drive the COVID-19 pandemic. Following five weeks of no such cases, a surge of SARS-CoV-2 variant B.1.1.519 was observed in late spring 2021. We here describe the introduction, spread and containment of the variant during a period with low community transmission of SARS-CoV-2 B.1.1.7, high test and whole genome sequencing (WGS) activity, and restrictions in place to limit SARS-CoV-2 transmission in public places.

### METHODS

We identified cases with SARS-CoV-2 B.1.1.519 via WGS from the Danish COVID-19 surveillance and identified SARS-CoV-2 positive close contacts to cases through contact tracing. We obtained travel history, case information and contact details through contact tracing and a local restaurant outbreak investigation.

### RESULTS

We identified 234 cases during a 4-week period in April and May 2021; 204 (87%) occurred within 15 days of the first case. At least 26 chains of transmission were identified with up to five generations of transmission. A total of 195 (83%) cases could be epidemiologically linked to a restaurant where 40 people among 90 guests and staff were infected. Further transmission primarily occurred in households, schools and workplaces. No link to the restaurant could be established for 39 cases, including one early concomitant case with travel history to Mexico. In all, 67% infected restaurant guests reported having symptoms with onset of a median of 4 days (minimum 2 days) after exposure.

### CONCLUSIONS

Timely WGS surveillance and contact tracing allowed us to identify, follow – and possibly contain – the introduction and spread of B.1.1.519 in Denmark. A superspreading event caused multiple independent chains of transmission in motion, despite ongoing restrictions. However, after five generations of transmission the variant disappeared.

# COVID-19

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Clinical, biological and radiological characteristics of hospitalized COVID-19 patients in a regional hospital in the center east of Tunisia

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**BACKGROUND**

COVID-19 is a highly contagious and fatal disease that emerged in late 2019 and caused a pandemic, which to date threatens both human health and public safety. The purpose of this study was to describe the epidemiological, clinical, biological and radiological characteristics of patients hospitalized for COVID-19.

**METHODS**

This was a prospective descriptive study conducted in a general medicine ward of a regional hospital on COVID-19 patients confirmed by a rapid test or a reverse transcription real-time polymerase chain reaction (RT-PCR) tests hospitalized from October 2020 to August 2021.

**RESULTS**

A total of 247 patients were hospitalized. Mean age was 63.78±15.72 years with a sex ratio (M/F) at 1.12. The 2/3 had at least one comorbidity (61.53%): hypertension (40.1%), diabetes (33.8 %), heart disease (atrial fibrillation, heart failure, ischemic heart disease) (17.4 %) and chronic respiratory pathologies (asthma and obstructive pulmonary disease (COPD)) (10.9 %). The most frequent clinical signs were fever (71.7 %) followed by dyspnea (67.2%), cough (61.9%), asthenia (57.9%), and digestive symptoms (17.56). The most common blood test abnormalities were elevated C-reactive protein (CRP) in 85 %, decreased lymphocyte count in 60.7%, and Hyperleukocytosis in 30.8%. As regards radiological examinations, 55 patients underwent chest CT scans among them 34.54 % presented a damage above 50%. Two third (71.7%) had severe cases on admission. Majority (72.1%) was discharged, 17.4 % were transferred to other institutions for advanced care and 9.3% died.

**CONCLUSIONS**

Hospitalized patients were mainly male, with at least one comorbidity. Symptoms were dominated by fever and dyspnea. Knowledge of these factors can help in the management of COVID-19, especially in regional hospitals where human and material resources are limited.

# COVID-19

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

## Abstract

### Determinants of COVID-19 vaccination uptake in the Netherlands: an ecological analysis

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**BACKGROUND**

The COVID-19 vaccination uptake for at least one dose for individuals aged 12 years or over in the Netherlands was 88% by mid-April 2022. While overall uptake was high, it lagged behind in the four largest cities, in younger age groups and in municipalities with a large proportion of orthodox reformed individuals (60-74%). With this study we aimed to identify determinants that are (independently) associated with COVID-19 vaccine uptake at neighbourhood level in order to inform the strategy to directly improve uptake and guide research into barriers for vaccination.

**METHODS**

To investigate the determinants of COVID-19 vaccine uptake, we performed an ecological study using national vaccination register and socio-demographic data from Netherlands Demographic available at the neighbourhood level. Using multivariable generalized additive models with binomial outcome and logit-link function we examined the (potentially non-linear) effect of each determinant on COVID-19 vaccine uptake while correcting for effects of other determinants.

**RESULTS**

Results showed that the proportion of individuals with a non-Western migration background, and higher voting proportions for right-wing Christian and Conservative parties were associated with a lower COVID-19 vaccine uptake. A higher socioeconomic status and urbanization score and higher voting proportion for liberal and progressive parties were associated with a higher COVID-19 vaccine uptake. The final model explained 41.7% of the variance.

**CONCLUSIONS**

In this study, we identified determinants that are associated with COVID-19 vaccine uptake at neighbourhood level. Even though overall vaccine uptake in the Netherlands is high, we observed heterogeneity between different subpopulations. Since the goal of the vaccination campaign is not only to improve average uptake but also to limit health differences among groups, it is important to focus on these harder to reach populations.

# COVID-19

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

## Abstract

### A Shiny App to predict subnational COVID-19 outbreak risk in EU countries

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**BACKGROUND**

Recent COVID-19 waves caused by BA.4/BA.5 variants highlight the ongoing need for tools able to identify areas most at risk of outbreaks. Local COVID-19 outbreak risk depends on complex immunity patterns (from previous infections, vaccination, waning, immune escape). In collaboration with ECDC, we implemented a framework to forecast local COVID-19 incidence in various countries, and developed a RShiny App for public health professionals to visualise the forecasts, and alternative intervention and behaviour scenarios.

**METHODS**

We used a spatiotemporal regression model to forecast subnational case counts in France, Czechia, and Italy. Cases in local regions stem from importations or local transmissions. Our model is flexible, and links reported case counts to various covariates ( e.g. number of tests, vaccine coverage). Using simulations, we explored the impact of variations in transmission (due to interventions, or new variants) on forecasted cases.

**RESULTS**

Retrospective analysis of the case forecasts at a local level showed that the model was well-calibrated, and had similar accuracy to the gold-standard European COVID-19 Forecast Hub ensemble model at a national level. The Shiny App enables stakeholders to view local forecasts, identify areas most at risk, and analyse the impact of changes in contact patterns or transmissibility to inform local control policies.

**CONCLUSIONS**

Our model captured changes in local COVID-19 outbreak dynamics (caused by new variants and changes in behaviour), and highlights the value of making subnational surveillance data publicly available to improve outbreak control. Given emergence of variants and changes in contact patterns, the flexibility of the framework makes it particularly well-suited for short-term forecasts, and the visualisation tools developed in this project make it accessible and valuable to a wide range of public health professionals.

**Keywords:** COVID-19, Statistical models, Public Health, Forecasting
**ABSTRACT ID:** 496
**PRESENTED BY:** Alexis Robert / alexis.robert@lshtm.ac.uk

## Microbiology (incl. novel methods in microbiology, such as e.g. new diagnostic tools)

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## Abstract

### Test performance of lateral flow rapid antigen tests for SARS-CoV-2 infection in Welsh adult care home staff

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**BACKGROUND**

Lateral flow tests (LFTs) have been used to screen for SARS-CoV2 in Wales since January 2021, but real-world performance data are limited. Between May and August 2021, adult care home staff policy was for biweekly Innova LFT and weekly Polymerase Chain Reaction (PCR) testing while asymptomatic, with further PCR testing recommended for positive LFT cases. We estimated test performance of LFTs conducted in adult care home staff using PCR tests as a gold standard.

**METHODS**

Test results from surveillance data were matched by individual where both LFT and PCR were taken on the same day. We calculated LFT sensitivity, specificity, positive and negative predictive values (PPV and NPV). Agreement was calculated using Matthew's correlation coefficient (MCC) and tested using Fisher's exact test. Analysis was conducted using R v4.1.3.

**RESULTS**

We analysed 115,593 test pairs, 499 (0.43%) of which were PCR positive. Median age was 48 (IQR: 22) and 85.00% of the study population were female. Test result agreement was 99.59% (95%CI 99.55-99.63; MCC: 0.38, p<0.001). Sensitivity and specificity were 25.65% (95%CI 22.02-29.67) and 99.91% (95%CI 99.89-99.93), respectively. PPV was 55.90% (95%CI 49.42-62.17) and NPV was 99.68% (95%CI 99.64-99.71).

**CONCLUSIONS**

Specificity and NPV were high in an asymptomatic population of care home staff indicating this test is an effective tool to rule in SARS-CoV-2 infection. PPV results are lower than existing literature, yet should be considered in light of the asymptomatic study population and low prevalence (under 1%) at the time most of these tests were conducted. These results suggest LFTs are a reliable diagnostic tool but should not be used to 'rule out' infection due to the very low sensitivity of the test.

# COVID-19

## Modelling, biostatistics, and health informatics

## Abstract

### Determinants of social contacts in the post-acute phase of the COVID-19 pandemic in Europe in 2022

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**BACKGROUND**

The COVID-19 pandemic caused an unprecedented level of physical distancing. Now that most non-pharmaceutical interventions have been lifted by late-summer 2022, it is unclear how these have affected population contact patterns and how these relate to pre-pandemic ones. Quantifying this change is crucial for modelling infectious diseases with close-contact transmission risk.

**METHODS**

We performed a longitudinal survey in 9 European countries between April and August 2022. In each country, the sample was representative in terms of age, gender and region of residence. Participants recorded their social contacts and also filled-in a questionnaire on risk perception.

We used generalised linear mixed-effects modelling to explore the influence of risk perception and COVID-19 vaccination status on the number of contacts, accounting for participant heterogeneity, country differences, age of the participant, self-reported high risk status and household size. We used the results of this model to derive the expected number of contacts in different scenarios.

**RESULTS**

In total 26,500 unique participants provided 46,752 responses. The average number of daily contacts varied between 4 and 9.5, depending on the country; much lower than pre-pandemic values (ranging between 14 and 20). Perceived severity and COVID-19 vaccination played a significant role in modulating the number of contacts. Individuals with low levels of perceived severity had 1.28 (95% CI: 1.13 – 1.43) times more contacts than individuals with high levels of perceived severity. Additionally, vaccinated individuals had 1.15 (95% CI: 1.05 – 1.24) times more contacts than non-vaccinated individuals.

**CONCLUSIONS**

This study provides unique insights in close-contacts with transmission potential for the pandemic transition period in Europe in 2022. Scenario analysis shows that perceived severity has the highest potential in reducing the number of contacts.

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

## Abstract

**Post mortem community COVID-19 surveillance: implementing and evaluating a pilot surveillance system in the funeral sector in England**

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### BACKGROUND
Concerns were raised early in the COVID-19 pandemic that community deaths with SARS-CoV-2 infection were inadequately captured due to limited community testing. Post-mortem testing for respiratory viruses had never been implemented in the UK. We explored the feasibility and acceptability of post-mortem SARS-CoV-2 testing in community deaths using funeral directors (FDs) to capture 'missed' COVID-19 deaths at a time of limited testing.

### METHODS
We recruited four FDs to take upper respiratory tract samples from eligible adults who died outside hospital. The pilot ran from January 2021 to February 2022. We tested for SARS-CoV-2 and other respiratory viruses using PCR and matched results to the national COVID-19 mortality linelist. We evaluated the pilot for acceptability, quality of data provided (completeness, timeliness), and simplicity, using semi-structured interviews, a questionnaire, and data audit.

### RESULTS
Of 2865 deaths handled by FDs, 998 were assessed for eligibility, 383 were eligible, and 83 were tested. Eight were SARS-CoV-2 positive, of which four were not already identified by clinical testing. The programme was acceptable in principle to FDs and families, but FDs' participation was limited by the administrative burden of legal requirements (Human Tissue Act licences) and existing workloads. Families' willingness to consent fluctuated over time (monthly consent rate 4-83%, overall 30%); fewer consented when overall cases were low. Data quality was good in terms of completeness and timeliness. FDs judged the programme simple.

### CONCLUSIONS
The pilot established that post-mortem surveillance is feasible and acceptable and demonstrated, even with small numbers, the ability to detect 'missed' deaths. Fewer specimens were received than anticipated because of significant administrative obstacles to implementation. Alternative settings are being explored instead to address this gap in national surveillance.

# COVID-19

## Surveillance

### Abstract

Comparison of early symptoms and Ct-values in COVID-19 infections
with the alpha, delta and omicron variant among healthcare workers
in a Dutch academic medical centre

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C. Meijer [2], L. Nicoletti [3], M. McCall [4], C. van Daal [5], E. Bowles [6], C. Bleeker-Rovers [7], N. van der Geest-Blankert [8], A. Tostmann [9]

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#### BACKGROUND
A SARS-CoV-2 PCR testing facility for healthcare workers (HCW) was implemented early March 2020 in our academic medical centre, and is still operating to date. COVID-19 surveillance among HCW can serve as early detection of resurgences of virus circulation, and can provide useful information on symptom patterns and potential transmissibility of an emerging new SARS-CoV-2 Variant of Concern.

#### METHODS
SARS-CoV-2 testing of HCW is performed upon COVID-19 symptoms, after COVID-19 exposure and/or after a positive rapid antigen test. When tested positive, the Occupational Health Department contacts them for infection prevention advice, and to collect information for disease notification and contact tracing, and data on early symptoms. We described the symptom profile for the three most recent variants of concern (alfa, delta, omicron) and determined the association between Ct-values and symptomatology.

#### RESULTS
The most prevalent reported early symptoms among HCW with the alpha variant (N=265) were runny nose (42.0%), headache (32.2%) and sore throat (31.8%); among HCW with the delta variant (N=634) runny nose (58.4%), cough (36.0%) and headache (34.3%); and among HCW with the omicron variant (N=1037) sore throat (54.5%), runny nose (39.0%) and headache (32.9%). During all waves, Ct-values were lower in symptomatic HCW compared to HCWs with asymptomatic infection (e.g. during omicron: median Ct was 22.3 vs. 29.2 respectively; P<0.001).

#### CONCLUSIONS
Early symptoms of COVID-19 among HCW were different for the alpha, delta and omicron variants. Symptomatic HCW had lower Ct-values suggesting higher infectiousness. COVID-19 surveillance among HCW can provide a reliable indication of early symptoms, as data on all symptoms instead of only those triggering testing, are collected. This is important when new variants of concern emerge and can give input for COVID-19 testing guidelines.

# COVID-19

## Surveillance

### Abstract

Monitoring of COVID-19 vaccination and disease among staff and residents
of long-term care facilities in Germany from October 2021 until February 2022

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**BACKGROUND**

Coronavirus disease 2019 (COVID-19) caused high morbidity and mortality in long-term care facilities (LTCF). Thus,
staff and residents were prioritized for COVID-19 vaccination in Germany, beginning in December 2020. Mid-
October 2021 and mid-February 2022, 3rd and 4th doses were recommended for staff and residents. Mid-December
2021, vaccination became mandatory for staff until March 2022.

**METHODS**

To estimate vaccination coverage (VC) and proportions of PCR-confirmed COVID-19 in LTCF, we invited all LTCF in
Germany to monthly surveys since October 2021. We asked for total counts of residents and staff and COVID-19
case numbers, stratified into unvaccinated, (fully) vaccinated, or boostered individuals. We calculated odds ratios
(OR) of vaccinated versus unvaccinated COVID-19 cases by logistic regression.

**RESULTS**

Per month, 1,003-1,665 LTCF participated with 77,779-120,892 residents and 75,829-123,427 staff in total. VC in
staff increased from 81.1% [95%-confidence interval: 80.6-81.7%] to 91.7% [91.3-92.1%] and in residents from
87.8% [87.3-88.3%] to 93.7% [93.3-94.0%] from October-February 2022. Booster VC in staff increased from 23.4%
[22.8-24.3%] to 59.8% [59.1-60.5%], increasing most in December, and in residents from 48.7% [48.0-49.4%]
to 76.5% [75.9-77.1%], increasing most in November. COVID-19 cases occurred less among vaccinated versus
unvaccinated individuals (OR ranging from 0.14 [0.10-0.21] in November to 0.54 [0.39-0.78] in January for staff and
from 0.19 [0.11-0.34] in December to 0.51 [0.31-0.88] in January for residents).

**CONCLUSIONS**

Gaps in VC in LTCF residents and staff remain, particularly regarding booster immunization. Major increases in
booster VC coincide with official recommendations and vaccine mandates, reflecting the impact of these decisions.
The decrease in protection from COVID-19 by vaccination over time possibly reflects the more transmissible Omicron
variant and waning immunity. Vaccination efforts need to continue, particularly regarding booster vaccinations.

# COVID-19

## Surveillance

### Abstract

Sero-surveillance of SARS-CoV-2 in Welsh Blood Donors: a Collaborative Study

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**BACKGROUND**

Wales has experienced some of the highest rates of COVID-19 in Europe. However, surveillance of confirmed cases is biased by testing policy and practice. We established a sero-surveillance scheme, using residual samples from blood donation, to inform the pandemic response in Wales by identifying changes in sero-prevalence of SARS-CoV-2 antibodies in Wales by time, person and place.

**METHODS**

Residual samples from blood donations made in Wales between 29/06/2020 and 13/02/2022 were tested for antibody to the nucleocapsid antigen (anti-N) of SARS-CoV-2. Donations made between 12/04/2021 and 13/02/2022 were also tested for antibody to the spike antigen (anti-S). Results were presented at four-week intervals.

**RESULTS**

37,595 donors provided 53,161 samples over the 21 four-week periods. Age-standardised seroprevalence of anti-N antibody increased steadily from 4.4% to 7.4%, before increasing sharply to 16.7% (February 2021). Positivity fluctuated for the following nine intervals (13.2%-17.6%) before increasing to 29.9% in February 2022. For anti-S, seroprevalence increased from 67.1% to 98.9% between May 2021 and February 2022, reflecting vaccine uptake. Seroprevalence of anti-N antibody was highest in younger donors and in donors of Black, Asian and other minority ethnicities. In contrast, seroprevalence of anti-S was highest in older donors of White ethnicity. Both anti-N and anti-S were highest in urban South Wales. . 11,645 donors were repeatedly tested for N and the majority were negative at all donations (76%). For anti-N, there is evidence of seroconversion and seroreversion (9% and 1% respectively), whereas anti-S only showed seroconversion (7%).

**CONCLUSIONS**

We successfully set up serological surveillance of SARS-CoV-2 using residual samples from blood donations. Data from this surveillance scheme have complemented data on case rates and vaccination uptake to inform the ongoing response.

Abstract presentations - Online-only posters

# COVID-19

## Surveillance

### Abstract

#### Booster vaccine willingness differs between countries in the Meuse-Rhine Euroregion (the Netherlands, Belgium, and Germany)

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#### BACKGROUND

Booster vaccination has shown to protect against infection with SARS-CoV2 and subsequent severe disease. Evidence that immunity decreases over time underscores the necessity of booster vaccination. Differences in booster vaccine intention and uptake between countries may exist as a result of different policies, attitude towards institutions, and cultural aspects. This longitudinal cross-border study aims to identify factors associated with COVID-19 booster vaccine intentions in the fully and partially vaccinated adult population living in the Euroregion Meuse-Rhine (EMR; including the Netherlands, Belgium, and Germany) and differences between countries.

#### METHODS

Data collection took place in the spring and autumn of 2021 and consisted of questionnaires and self-finger-prick blood samples. Data from 3180 fully and partially vaccinated adults were used for multivariable logistic regression analyses, weighted by age group, sex, and country.

#### RESULTS

In September-October 2021, 75.5% of fully and partially vaccinated adults had the intention to take the booster vaccine once available (N=2401), whereas 24.5% was uncertain (N=581) or unwilling (N=198). Compared to German residents, Dutch residents (OR=2.72;95%CI=2.15-3.43) and Belgian residents (OR=1.40;95%CI=1.05-1.88) were more likely to be uncertain or unwilling to receive a booster vaccine. Age below 60 (OR=1.60;95%CI=1.22-2.08), female sex (OR=2.07;95%CI=1.69-2.54), absence of comorbidities (OR=1.29; 95%CI=1.07-1.55), negative opinion about communication of COVID-19 measures (OR=2.38;95%CI=1.85-3.05), and regarding measures as ineffective (OR=1.09;95%CI=1.07-1.11) were independently associated with uncertainty or unwillingness.

#### CONCLUSIONS

These results indicate that booster vaccine intentions differ between countries in the EMR and identify potential targets for future booster campaigns. Booster vaccine unwillingness is prevalent in all European countries, but to a different extent, as shown in this study. We can learn from each other- especially in Euregions where most inhabitants do not feel borders exist in daily life.

# COVID-19

# Surveillance

## Abstract

**Rapid implementation of real-time SARS-CoV-2 sequencing supports outbreak understanding in acute tertiary hospitals, Wales, October – December 2020**

**N. Pacchiarini [1],**

A. Plimmer [2], C. McKerr [3], H. Asad [4], M. Morgan [5], C. Williams [6], T. Connor [7]

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### BACKGROUND

Nosocomial COVID-19 presents a considerable burden of illness and mortality in vulnerable hospital populations, even in times of lower community prevalence. Viral whole genome sequencing (WGS) combined with epidemiological data provides a powerful way of monitoring outbreak dynamics. We investigated three large hospital outbreaks from autumn 2020, to determine if cases were seeded by the local community and if they represented multiple smaller outbreaks.

### METHODS

Outbreak cases were identified using local systems and WGS undertaken by the Pathogen Genomics Unit using the ARTIC SARS-CoV-2 sequencing protocol. Patient clinical and demographic data were merged with microbiological information and descriptive analysis undertaken in R. Cases were grouped based on genomic similarity (UK phylotypes) and contextualised in time and space with sequenced community cases to delineate possible transmission routes and understand provenance.

### RESULTS

Of 1188 outbreak cases, 43% were successfully sequenced (67% patient, 33% staff); >90% were lineage B.1.177 and 7 distinct genomic clusters identified. Hospital cases were driven by the same phylotypes circulating in the community in 6/7 clusters. There was evidence of multiple introductions (>30 distinct phylotypes identified per hospital), including implicating staff with phylotypes consistent with community circulation. This supported local reviews of infection prevention and testing approaches (e.g. admission screening, routine asymptomatic screening), and reiteration of assurances around interventions such as isolation and mask wearing.

### CONCLUSIONS

We implemented a rapid SARS-CoV-2 surveillance system which enabled detection of transmission events in hospital settings, supporting real-time interventions, as well as indicating potential links between cases not identified from traditional epidemiology. This work highlights the complementary role of real-time genomic surveillance to traditional epidemiological methods and provides key insights into how SARS-CoV-2 enters enclosed settings.

# Surveillance

## Abstract

### Enhanced process error detection using dataset linkage through retrospective analysis of COVID-19 testing data

**C. Hogg** [1]

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[1, 2, 3, 4] Public Health Wales

#### BACKGROUND

In 2021 in the UK, an estimated 43,000 incorrect negative COVID-19 Polymerase Chain Reaction (PCR) result notifications were sent to patients, including 6,600 in Welsh residents. This incident began w/c 06/09/2021, six weeks before detection and investigation (w/c 11/10/2021). In Wales, lateral flow tests (LFTs) are reported separately to PCR, enabling identification of discordant results in routine reports. We explored analytic approaches that might have detected this earlier in order to inform future reporting methods.

#### METHODS

LFT and PCR data was linked by individual where PCR was conducted on the same day or +/- 1 day. We identified discordant LFT+/PCR- pairs and looked at alternative aggregation periods, lag period adjustment, and outlier assessment, evaluating the timeliness of each for detecting this anomaly. Upper bound for outlier classification was defined as above $Q3+1.5*IQR$. Analysis was conducted using R v4.1.3.

#### RESULTS

Using an initial 4 week rolling aggregation, there was no clear signal in routine reporting data prior to 11/10/2021. However, weekly or daily aggregation of the data would have shown an outlier defined increase in discordant LFT+/PCR- pairs at least two weeks prior to this. Furthermore, removal of the additional week lag built into reporting would have yielded another week, but introduced risk of incomplete data. Weekly aggregate reporting yielded more timely and accurate reporting following re-analysis of the incident data.

#### CONCLUSIONS

Weekly comparison of PCR and LFT data could have detected this error at least two weeks sooner. In implementing this change to practice, we intend to support more timely detection and investigation of incidents. We recommend applying similar linkage methods across other multi-platform disease surveillance systems, adding downstream robustness to existing laboratory quality assurance.

# Surveillance

## Abstract

### Evaluating the validity of a national surveillance system for COVID-19 hospital admissions, Wales, July to December 2021

**R. Merrick** [1]

V. McClure [2], S. Cottrell [3], M. Perry [4], C. Williams [5], M. Morgan [6]

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[1, 6] UK Field Epidemiology Training Programme (UK-FETP)

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[6] UK Health Security Agency, UK

**BACKGROUND**

Accurately monitoring COVID-19 hospitalisations is crucial to ascertaining the burden of severe disease attributable to SARS-CoV-2. Hospital admission within 28-days of a positive SARS-CoV-2 test is the metric published by Public Health Wales to report COVID-19 hospitalisations in the previous week. We evaluated the national COVID-19 hospitalisation surveillance system to determine its validity for estimating hospitalisation due to, rather than with, COVID-19.

**METHODS**

In this cross-sectional study, we matched the national COVID-19 hospitalisations dataset on National Health Service (NHS) number to the Patient Episode Database for Wales (PEDW) for 01/07/2021 – 30/12/2021 (data extracted: 20/04/2022). PEDW is a standardised but untimely dataset (37 days mean clinical coding lag) for inpatient activity in NHS Wales hospitals. Validity was defined as episodes in the COVID-19 hospitalisation dataset confirmed to have a primary COVID-19 diagnosis (ICD-10 codes in PEDW: U00-U49), described cumulatively and weekly.

**RESULTS**

Among 7,568 cases in the COVID-19 hospitalisations dataset, 6,554 (87%) matched to PEDW episodes. Among matched episodes, 61% (3,964/6,554, 95% CI: 59-62%) had COVID-19 as primary diagnoses and 19% (497/2,590) were missing data. Validity ranged from 59% to 71% for most weeks (20/27, 74%) and decreased with time, declining to 37% (124/332, 95% CI: 31-45%) in week 52. Where COVID-19 was not the primary diagnosis, circulatory / respiratory symptoms (83/2,590, 3%) and digestive / abdominal symptoms (76/2,590, 3%) were the primary reasons for admission.

**CONCLUSIONS**

At least three in five cases in the COVID-19 hospitalisations dataset were confirmed as hospitalised due to COVID-19; existing metrics may overestimate the healthcare burden caused by SARS-CoV-2 but still provide a timely indication of severe disease trends. Repeat evaluation is advisable following changes to the national SARS-CoV-2 testing strategy.

# COVID-19

## Surveillance

### Abstract

Monitoring SARS-CoV-2 variant emergence in the SIREN prospective cohort study: March 2020 to April 2022, United Kingdom

**S. Foulkes** [1]

E. Monk [2], A. Atti [3], D. Sparkes [4], E. Gallagher [5], P. Barbero [6], A. Lackenby [7], M. Chand [8], S. Hopkins [9], V. Hall [10], M. Cole [11], The SIREN Study Group

[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11] UK Health Security Agency

**BACKGROUND**

Running since June 2020, the SIREN Study is a large, multi-centre prospective cohort of healthcare workers in the United Kingdom (UK). As the UK adapts to 'Living with COVID-19' and reduced testing, SIREN remains an important national surveillance tool for monitoring emerging variants and establishing rates of primary infection, reinfection and vaccine breakthrough. In this study, we describe SIREN's genomic surveillance results to date.

**METHODS**

Participants underwent fortnightly polymerase chain reaction (PCR) testing, with results reported through the UK's national laboratory system. Positive PCRs were prioritised for sequencing and triggered delivery of self-swabs for additional PCR and sequencing centrally. Quality-controlled genomes were uploaded to the Cloud Infrastructure for Microbial Bioinformatics and variant calls established.

PCR-confirmed infections were classified as primary infections (no laboratory evidence of previous infection) or reinfections (evidence of a positive PCR >90 days previously or antibody positivity >28 days previously whilst unvaccinated). Infection rates for both were calculated according to variant call.

**RESULTS**

Between March 2020 and April 2022, 16,473 positive PCR results were recorded, of which 5,151 (31.3%) were successfully sequenced (4,242 primary infections and 909 reinfections). The BA.1 Omicron variant was first detected on 21 November 2021 and BA.2 on 17 December 2021.

The rate of reinfection in the SIREN cohort increased substantially during the Omicron wave, peaking at 82/1,000 participants tested. Reinfections represented 29.3% of BA.1 and 25.6% of BA.2 cases, compared to 6.0% of cases associated with other variants.

**CONCLUSIONS**

SIREN detected BA.1/BA.2 at a similar time to the first UK cases and found higher rates of reinfection in Omicron-associated cases compared to preceding variants. SIREN is well positioned to monitor for new variants and changes in reinfection rates nationally.

# COVID-19

## Surveillance

## Abstract

### Impact of COVID-19 on individuals living in residential care homes restricted to learning disabilities and autism care in England

**E. Tessier** [1]

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**BACKGROUND**

In England, an estimated 22,135 individuals with learning disabilities and/or autism lived in residential care facilities in 2018. We evaluated the impact of the SARS-CoV-2 pandemic infection on residents of facilities specifically for individuals with learning disabilities and/or autism by characterising risk of infection, outbreaks and mortality up to 31 January 2022.

**METHODS**

We used surveillance data in England for all COVID-19 test-positive (LFT or PCR) cases and deaths. We linked residential addresses to care homes that cared for only people with learning disabilities and/or autism, as identified by the national regulator using unique property refence numbers. We calculated cumulative incidence and defined outbreaks as two or more cases at the same residence within a rolling 14-day window. We used multivariable logistic regression to assess the excess risk for death among these individuals compared with individuals in private residences restricted to flats or detached, semi-detached or terraced houses.

**RESULTS**

A total of 1,672 individuals with learning disabilities and/or autism residing in care homes tested positive for SARS-CoV-2, of which 61% were male with the greatest number of cases (29%) being between 50-58 years old and 5.9% died. Most cases (77%) were part of an outbreak, but only 36.9% of care home residences had one or more cases. With adjustment for age, ethnicity, and sex, care home residents had twice the risk of death (aOR=2.27, 95% CI 1.81 – 2.85) compared with those living in private residences.

**CONCLUSIONS**

Our findings show an increased risk of COVID-19 among individuals in care facilities that care for der7 people with learning disabilities and/or autism.

## Surveillance

## Abstract

### COVID-19 vaccine coverage in pregnant women and socioeconomic inequities, 2021-2022; Wales UK

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**BACKGROUND**

Pregnancy is associated with elevated risk from COVID-19 infection. From 16/04/2021 onwards, all pregnant women in the UK should have routinely been offered COVID-19 vaccination in line with the clinical at risk priority group. Maximising timely protection in this vulnerable group requires monitoring of the timing of vaccine uptake in relation to pregnancy and consideration of factors leading to inequitable uptake.

**METHODS**

Data from the all Wales COVID-19 vaccination register were joined to maternity datasets. Socioeconomic deprivation quintile was assigned by ranking Lower Super Output Area small level geography of residence by the Welsh Index of Multiple Deprivation 2019 scores.

**RESULTS**

From 01/05/2021 to 01/04/2022, there were 21,757 women recorded as giving birth in Wales, 21,175 of whom could be matched to a vaccination registry record. At the point of giving birth, 36.3% (n=7,680) had received at least one dose of vaccine and 27.0% (n=5,713) had received two doses. In total 6,988 (33.0%) received any dose of vaccine during their pregnancy.

Of the 13,495 women in this cohort who were not vaccinated at the point of delivery, 7,929 (58.8%) subsequently received their first dose after giving birth. The odds of being unimmunised at the point of delivery were significantly higher in the most deprived compared to the least deprived areas, 2.18 (CI 95% 1.99–2.39). Patterns of coverage with different doses were similar.

**CONCLUSIONS**

Wales has been successful in achieving high levels of COVID-19 vaccination coverage in the general population, however coverage in pregnant women remains suboptimal. Coverage increases after delivery suggesting some women are waiting to receive their vaccination. Non-vaccination appears linked to deprivation and further work to address uptake in this group may require targeted interventions.

# COVID-19

# Surveillance

## Abstract

### Coverage of a national sequence-based SARS-CoV-2 surveillance system, Wales, April 2020 to January 2022

**R. Merrick** [1]

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[4] Cardiff University, School of Biosciences, Cardiff, UK

**BACKGROUND**

As of April 2022, 12% of SARS-CoV-2 samples in the United Kingdom (UK) have been sequenced, similar to Europe's largest sequencer, Denmark (15%). We assessed the coverage, over time and by geography, of the COVID-19 genomic surveillance system in Wales to evaluate representativeness.

**METHODS**

In this cross-sectional study, data from the COVID-19 testing and sequencing surveillance system in the UK from 01/04/2020-01/01/2022 were used to calculate sequencing coverage by residence in Wales (nation, 7 regions, 22 local authorities). SARS-CoV-2 samples of sufficient quality were randomly selected from hospital and community testing and sequenced by the Public Health Wales Pathogen Genomics Unit and Wellcome Sanger Institute. Coverage was defined as the proportion of confirmed COVID-19 episodes with an available genome sequence for each defined geographic area, described cumulatively and weekly. Chi-square test was used to detect differences in coverage (regional vs. national, local authority vs. regional).

**RESULTS**

Among 675,532 episodes, 168,487 (25%) were sequenced; >99% (168,012/168,487) had sufficient address data. Weekly coverage increased across all geographic units from week 1 2021, peaking at 73% (797/1,091) in week 24 2021. Cumulative coverage by region ranged from 22% (27,576/125,408) to 30% (39,810/130,956), with divergence being significantly different compared to the national estimate (p<0.001) and to local authorities (p<0.001), where coverage ranged from 18% (2,958/16,041) to 33% (6,897/20,961).

**CONCLUSIONS**

One in 4 SARS-CoV-2 samples in Wales being sequenced represents the highest proportion of any European country. Each geographical unit achieved coverage above the UK average despite variation across lower geographies, which nonetheless decreased with time to accomplish representativeness. Repeat evaluation is advisable to maintain and improve the representativeness of national SARS-CoV-2 sequencing surveillance.

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

## Abstract

### Be prepared: Risk management plan and early warning system as toolkit for rapid response and risk communication upon zoonotic alerts

**C. Klier** [1]

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**BACKGROUND**

Zoonotic diseases are on the rise worldwide. Preparedness of public health authorities is important to provide rapid risk communication and response. An early warning system (EWS) and structured risk management plan (RMP) for primary and secondary prevention fosters taking rapid and targeted actions. This study developed toolkits focused on *Leptospira spp.* and *hantavirus*.

**METHODS**

The needs and requirements of local public health authorities (LPHA) for timely and targeted risk communication and response were assessed in workshops. Materials for primary and secondary prevention were developed. The RMP is triggered by an EWS for hantavirus-infections or by increased case notifications to LPHAs. The EWS is based on a CART-analysis trained with hantavirus case counts from 26 districts in 2006–2021.

**RESULTS**

CART analysis identified temperature and beech flowering intensity from the two previous years, and deciduous forest proportion as predictors, reaching R2>0.6 and risk class accuracy >75%. Needs and requirements of LPHA comprised information that can be readily tailored to the target audiences (at-risk groups, minorities). Use of social media is suitable to access hard-to-reach communities. The toolkit comprises templates e.g. for press releases, multilingual information on preventive measures targeting different audiences (public, at-risk groups) and basic tools for outbreak response.

**CONCLUSIONS**

EWS allows early forecast in fall and timely initiation of risk communication for the following year. The RMP was applied successfully in Lower Saxony. Templates were used to formulate press releases prompted by the EWS. Tools were successfully employed both in a hantavirus outbreak investigation in an unusual setting and in conducting investigations on the first autochthonous Seoulvirus case in Germany. Involving LPHA early in RMP development ascertains that their needs e.g. targeted material are taken into account.

# EMERGING AND VECTOR-BORNE DISEASES

## Microbiology (incl. novel methods in microbiology, such as e.g. new diagnostic tools)

### Abstract

Species identification of travel-associated Leishmania positive cases in the Danish population between 2018 and 2020 using heat-shock protein 70 sequencing

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**BACKGROUND**

*Leishmania* is a parasite that is transmitted by the bite of a female sandfly and can cause leishmaniasis. In Denmark all cases of leishmaniasis are thought to be associated with travel to endemic areas. The disease can either be visceral, cutaneous or mucocutaneous; each with different clinical signs and treatments. Accurate species differentiation can be a challenge depending on the molecular targets used for diagnosis and detection and is critical for disease prognosis and treatment choice. The aim of this study was to implement a *Heat-shock protein (hsp) 70* gene-sequencing assay for improved identification of *Leishmania* species.

**METHODS**

The applicability of the *hsp70* assay was compared with an assay using the internal transcribed spacer (ITS) region of the ribosomal gene of *Leishmania*. Both are PCR-based methods but differ in the target region of the parasite.

**RESULTS**

We analysed 39 travel-associated real-time PCR-positive samples collected between January 2018 and December 2020 in Denmark. The *hsp70* assay was able to discriminate between *Leishmania* species based on single nucleotide polymorphisms at specific locations within the *hsp70* gene. Most of the samples were positive for *L. infantum* and *L. tropica*, which cause cutaneous/visceral and cutaneous leishmaniasis, respectively. No cases of *L. donovani* were detected in the sample set. We also detected several cases of New World *leishmaniasis*, including cases of L. *braziliensis* and *L. panamensis*.

**CONCLUSIONS**

In summary, the *hps70* assay offers a high resolution for species molecular typing. *L. infantum* was the most commonly observed parasite in our sample set. The validation of this assay has important public health implications for clinicians as case management and treatment options vary with species.

**Abstract presentations** - Online-only posters

# FOOD- AND WATERBORNE DISEASES AND ZOONOSES

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Cholera Outbreak Investigation, Kamarhati-Municipality, North-24-Parganas District, West Bengal, India 2021

**J. Mehta** [1]

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[1, 2] Appied Epiemology Programme, World Health Organization, India

[3, 4] World Health Organization, India

**BACKGROUND**

India reported 565 cholera outbreaks between 2011- 2020. Kamarhati Municipality in North-24-Parganas district, West Bengal, reported a suspected cholera outbreak on September 7, 2021. We investigated to describe the outbreak epidemiology, identify the source and provide recommendations for control and prevention.

**METHODS**

We defined a suspect case as ≥3 loose stools within 24 hours in a resident of Kamarhati Municipality, August 20- October 17, 2021. We conducted a house-to-house case search in affected wards 1-7, reviewed case registers at health facilities and interviewed cases for clinical presentation, treatment and drinking water source. Rectal swabs were collected for culture and water samples for bacteriology and residual chlorine.

**RESULTS**

We identified 703 cases (53% female), attack rate (AR)1.92/1000 population, including one death (case fatality rate=0.14%); 688 (98%) cases were from wards 1-7. The median age was 36 years (range: ‹1-85 years). The first case had symptoms onset on August 29 and the last on October 8. The household AR in wards 1-7 was 23% (254/1113); among the interviewed 254 cases, other reported symptoms were fever (22%) and abdominal pain (10%); 251 (99%) reported receiving medical treatment, 47 (19%) hospitalized. The government supplied pipe water was the main drinking water source. Of 9, 6 (67%) individual rectal swabs tested positive for *Vibrio Cholerae* type O1 OGAWA in culture; 5/10 (50%) water samples from wards 1 and 3 had *Vibrio cholerae* and 20/24 (83%) had residual chlorine level below 0.1 ppm.

**CONCLUSIONS**

This was a laboratory-confirmed cholera outbreak likely due to contamination of supplied drinking water. Prompt public health response in managing the affected individuals, recommended chlorination of drinking water and community awareness of boiling water before drinking helped control the outbreak.

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Botulism outbreak and response in Dangara District Tajikistan, October 2020

**D. Akhmedov** [1]

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[2] Epidemiological Department of the Dangara District, Tajikistan

**BACKGROUND**

At 17:35 on October 31, 2020 a suspected botulism case was reported to the infectious diseases department of the Central Hospital of the Dangara region of Tajikistan. By 19:00 on the next, 9 people had been hospitalized with suspect botulism. Botulism is a life-threatening intoxication caused by a powerful neurotoxin from *Clostridium botulinum*. In 2019, there were 19 cases of botulism and 3 deaths in Tajikistan; ingestion of improperly prepared food is frequently the cause of botulism outbreaks in the country.

**METHODS**

We conducted an outbreak investigation to confirm the etiology, source, and risk factors to prevent further cases. Prior <24 hour food histories were collected from patients. A botulism case was defined as having clinically compatible symptoms including blurred vision, diplopia, dysphonia, muscle weakness, fatigue, shortness of breath, or dry mouth. Laboratory confirmation is not available in the region.

**RESULTS**

Nine people were hospitalized with probable botulism. Patients had their stomach's flushed and were administered antitoxic polyvalent serum of types A, B, C and E. Mean age was 27 (range 6-44); 6 (67%) were male. Interviews revealed that patients were from the same village in the Dangara region and all reported having eaten home-made canned salad at a dinner. Investigators retrieved the salad and destroyed it. Three persons who were at the dinner, but that did not eat canned salad were observed by local doctors. There were no further cases and no fatalities resulted from this outbreak.

**CONCLUSIONS**

Consumption of improperly preserved foods were the source of the outbreak. Rapid identification of the source and quick intervention by local epidemiologists were critical in preventing d mortality. Campaigns informing people about safe canning methods can reduce outbreaks.

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Outbreak of suspected Clostridium perfringens associated with consumption of roast beef in a restaurant, January 2022 South West England

**K. Wilson** [1]

K. Jones [2], D. Hallett [3], N. O'Grady [4], D. Rajendram [5], C. Amar [6], C. Willis [7], B. Nozad [8], N. Young [9], S. Packer [10], The outbreak incident management team

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[8] South West Health Protection Team, UK Health Security Agency (UKHSA)

[9, 10] Field Service South West, UK Health Security Agency (UKHSA)

### BACKGROUND

*Clostridium perfringens* is a leading cause of infectious gastroenteritis worldwide, frequently resulting from unsafe food preparation. We describe an analytical study, used in conjunction with microbiological findings, to determine the potential cause of an outbreak of gastrointestinal illness in persons attending a restaurant.

### METHODS

A retrospective cohort study was undertaken following notification of an outbreak among diners who attended a restaurant in South-West England on a single day. Cases were defined as persons with diarrhoea or vomiting within 48-hours of attending the restaurant. Data was collected using an online questionnaire and telephone interviews. Descriptive and univariable analysis was followed by multivariable logistic regression adjusting for demographics and food items. Food, and human stool samples, were collected for bacterial and viral testing.

### RESULTS

Contact details were available for 40 of approximately 85 attendees; thirty-one (78%) provided information on food consumption and symptoms, of which 15 were cases (attack rate:48%). An epidemic curve suggested a point source outbreak with a median incubation time of 18-hours. Univariable analysis identified an association between illness and beef consumption (risk ratio (RR):2.8, 95% confidence intervals (CI):1.2-6.2), and brownie (RR:2.4, 95%CI:1.2-4.7). In multivariable models including other food items, only beef consumption was associated with illness (odds ratio (OR):6.0, 95%CI:1.0-34.5). Clinical stool (n=4/5) and beef (n=2/2) samples contained *Clostridium perfringens*, however only 1/4 stool and 0/2 beef samples were found to contain enterotoxigenic *Clostridium perfringen*s capable of causing illness.

### CONCLUSIONS

This study provided evidence linking beef consumption with illness, with *Clostridium perfringens* the most likely pathogen. The findings were used to focus food safety recommendations at the restaurant, primarily regarding temperature control. We recommend that premises ensure proper temperature control when cooking and storing beef.

# FOOD- AND WATERBORNE DISEASES AND ZOONOSES

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Outbreak of acute enteric disease associated with drinking water in a rural area f Kazakhstan: A matched case-control study

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**BACKGROUND**
Surveillance showed an uptick in enteric disease of unknown etiology in the village of Beskol (12,000 inhabitants) in North Kazakhstan. We conducted an outbreak investigation to identify risks and sources.

**METHODS**
Suspected cases were acutely ill residents presenting for medical treatment for diarrhea, fever, vomiting, or weakness from May 14 to June 15, 2021. Controls were residents matched by age ±2 years at a ratio of two controls for every case. Cases and controls were interviewed June 3-13th and their medical records abstracted. We mapped cases and conducted conditional multivariable logistic regression.

**RESULTS**
We identified 154 suspected cases of acute enteric disease; 46% were <7 years old. Most commonly reported symptoms were diarrhea, fever, vomiting, weakness, and decreased appetite. 107 (70%) cases and 219 controls agreed to participate. Among cases, 74% drank unboiled tap water compared to 18% of controls. This was the only risk factor significantly associated with disease (OR: 19, 95% CI=10-36). Drinking water from a dispenser or carbonated drinks was significantly protective than persons who did not drink from these sources. The city has two water supply networks; cases were clustered (107 cases in 70 foci) in one. The investigation found that monitoring of quality and safety of water according to national regulations had not been conducted since 2018. No fatalities occurred; no associated cases were reported after our investigation.

**CONCLUSIONS**
Results suggest that untreated tap water was the probable source of the outbreak. The water supply had been cleaned and disinfected twice by the facility 2 days before our investigation began. Regular monitoring of water supply facilities with rapid public notification when issues are detected can reduce likelihood of future drinking water associated outbreaks.

# FOOD- AND WATERBORNE DISEASES AND ZOONOSES

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Doughnuts for weight loss? A norovirus outbreak in the Australian Capital Territory, November 2021

**K. Allen** [1]

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[1] Australian National University, MAE
[1, 2, 3, 4] ACT Health Communicable Disease Control

**BACKGROUND**
An outbreak of gastroenteritis was investigated following complaints of illness after eating doughnuts from a food business in the Australian Capital Territory (ACT).

**METHODS**
Food poisoning complainants and contacts were surveyed using a standard gastroenteritis questionnaire including menu items from the food business. An outbreak case was defined as a person who reported vomiting and/or diarrhoea following consumption of food from the food premises. Descriptive analyses were performed for all responses. A case-control study was conducted for a group of 140 people at a catered function. Active case finding was not able to be pursued in this investigation. A food safety inspection was also conducted.

**RESULTS**
301 were surveyed, and 215 individuals met the case definition. Doughnuts were purchased over a five-day period. 100% of ill respondents reported eating a doughnut. The median incubation period was 33 hours (IQR: 28.6-42.4 hours) and the median illness duration of 48 hours (IQR: 29.3-72 hours), with diarrhoea, vomiting and abdominal pain most commonly reported. Eight specimens collected from ill individuals were positive for norovirus. 59 attendees of the catered function were surveyed, with an attack rate of 46% (27/59) among respondents. No single flavour was identified as the likely source of infection. Eating any kind of filled doughnut was statistically associated with a person becoming ill (OR:7.56, 95% CI: 1.22-200.61).
The suspected source of infection was an ill food handler.

**CONCLUSIONS**
Doughnuts are a novel vehicle for norovirus infection. While this was one of the largest foodborne outbreaks investigated in the ACT, the true extent of the illness remains unknown.  Active case finding should be pursued to determine the magnitude of outbreaks and build community trust in public health.

Abstract presentations - Online-only posters

# FOOD- AND WATERBORNE DISEASES AND ZOONOSES

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Assessment of water, sanitation, waste management and hygiene services among the populations of 19 Rohingya camps, Cox's Bazar, Bangladesh, 2022

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**BACKGROUND**

The high population densities and environmental conditions of the 33 Rohingya refugee camps in Cox's Bazar produce a crisis with acute water, sanitation and hygiene needs. A WASH infrastructure was implemented across the camps to address the demands of population; however, the monitoring and maintenance of these infrastructures have proven challenging over the last five years.

**METHODS**

From January to March 2022, a cross-sectional Lot Quality Assurance Sampling (LQAS) survey was conducted to identify priority camps for WASH intervention. Nineteen households in each camp were randomly selected by GPS. Data were collected using the Kobo Collect application and questions related to water, sanitation, hygiene, waste management and water-related diseases. Crude, weighted averages and 95% confidence intervals were calculated for each indicator and compared with pre-defined target values.

**RESULTS**

57% (16/28) of indicators didn't meet the pre-determined threshold and seven of those were particularly low. 99.4% (98.5-100% CI) of households used an improved water source for drinking. However, 56% (95% CI 51-61%) reported, water wasn't continuously available in past week and only 11% of people used an improved sanitation facility while 76% of latrines were overflowing. Females using acceptable menstrual hygiene kits dropped by 36% from 2018 LQAS study. Improper waste management system increase the risk of vector borne disease like dengue. Among targeted indicators, hygiene practice 83%, sanitation status 100% and solid waste management 60% performed unsatisfactory.

**CONCLUSIONS**

The WASH conditions in the camps are hazardous; require adequate and timely intervention from actors involved in WASH activities to control the likelihood of WASH-related potential outbreaks. Service mapping is crucial to identify the functionality of WASH infrastructure and advocate doing adequate maintenance by close monitoring of the implementing agencies.

Abstract presentations - Online-only posters

# HEALTHCARE-ASSOCIATED INFECTIONS

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Characterization and control of a VanA-mediated vancomycin-resistant Enterococcus faecium outbreak

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**BACKGROUND**

VanA-mediated vancomycin-resistant *Enterococcus faecium* (VREF) challenges the prevention and treatment of hospital-acquired infections, with ample clinical presentations, widespread asymptomatic carriage, and limited therapeutic options. Our objective is to describe the characteristics and control measures of a VREF outbreak in a third-level hospital

**METHODS**

Retrospective-observational study including all VREF isolates identified between May 2021-May 2022 at the Miguel Servet University Hospital, a 1200-bed tertiary acute-care centre in Zaragoza, Spain. Clinical histories were reviewed and cases defined by VREF identification in clinical or screening samples, and were classified as infections/colonisations, and as hospital/community-acquired. Isolates underwent antibiotic susceptibility and van-gene testing, and whole genome sequencing at the National Microbiology Centre. VREF analyses were included in routine surveillance of high-risk units, readmissions, and hospital transfers.

**RESULTS**

We identified 38 VREF cases (47.4% women, mean age 71.1years), of which 20 were infections and 18 were colonisations. 14 cases (36.8%) were community-acquired and 24 (63.2%) were hospital-acquired. All isolates were vanA-positive, only susceptible to tigecyclin and linezolid. All patients had previously received antibiotics, and had their treatments optimized upon VREF isolation. Two main clones were identified and shared in both community- and hospital-acquired cases. Active surveillance was established in all seven high-risk units and in three additional units upon VREF detections, using rectal swabs at admission and weekly thereafter, with 2,149 samples collected during the study period. Individual rooms and contact precautions were required for all patients, with the implementation of reinforced hygiene and disinfection protocols.

**CONCLUSIONS**

The increasing nosocomial detection of VREF denotes a growing issue at a community level. Early detection, the implementation of cross-transmission prevention measures, and the microbiological characterization of each isolate is key for effective surveillance and outbreak control.

**Keywords:** Antimicrobial resistance, Vancomycin-Resistant Enterococci, Enterococcus faecium, Vana, Healthcare associated infection, Epidemic outbreaks

**ABSTRACT ID:** 423

**PRESENTED BY:** Kevin Bliek-Bueno / kevinbliek@gmail.com

# HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

## Burden of disease

## Abstract

### High prevalence of sexually transmitted Chlamydia trachomatis infections in Slovenia among women less than 25 years old, 2016-17

**P. Klepac** [1]

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#### BACKGROUND

With aim to inform prevention and control, objectives of the second Slovenian National Survey of Sexual Lifestyles, Attitudes, and Health in 2016–17 were to estimate the prevalence of and identify risk factors for *Chlamydia trachomatis* (CT) infection among sexually experienced 18-49-year-olds in Slovenia.

#### METHODS

Data were collected from a stratified probability sample of the general population. Respondents were invited to provide urine for testing for CT infection with polymerase chain reaction. Data were weighted to adjust for the distribution of sex, age, region, and type of community of the general population. We estimated prevalence of CT infection and used logistic regression to calculate adjusted odds ratios (OR) with accounting for the sample stratification and clustering.

#### RESULTS

Of 3473 eligible individuals, 1046 sexually experienced respondents with a test result were included. The prevalence of CT infection was 0.5%(95% confidence interval [CI]:0.1–1.9) in men and 1.7%(95%CI:0.9–3.3) in women. The highest prevalence was among women 18-24 years old (5.6%;95%CI:2.0–14.4). New sex partner in the last year was associated with CT infection among women 18-49 years old (OR:8.9,95%CI:2.5–31.9).

#### CONCLUSIONS

CT infection prevalence was the highest among the youngest sexually experienced women. New sex partner last year was a risk factor for CT infection in women of all ages. By known evidence, impact of widespread young population screening on the reduction of the prevalence of infection is not clear. Targeted testing has been recommended: introduction of annual opportunistic testing for CT for sexually active women ‹25 years old in and offering testing to older women reporting a new sex partner during last year in primary healthcare gynaecology clinics should be considered in Slovenia.

# HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

## Surveillance

## Abstract

### Monitoring chronic hepatitis B prevalence through combination of seroprevalence and routine surveillance data: experience from Poland

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#### BACKGROUND

Reduction of chronic hepatitis B (CHB) incidence is feasible thanks to i.a. effective vaccines, in Poland mandatory to newborns since 1996. Due to previously high incidence, high CHB prevalence is expected. We aimed at estimating CHB prevalence and undiagnosed fraction in general population in Poland in 2015–2020 and at evaluating progress towards WHO target of diagnosing 90% of CHB cases by 2030.

#### METHODS

We randomly selected serum samples of adults from a representative biobank collected in 2015. HBsAg ECLIA was performed confirming positive results with neutralization test. We calculated prevalence in yearly birth cohorts not covered by newborns vaccination program. Literature estimates were used for the remaining birth cohorts. We applied direct standardization of prevalence to birth cohort distribution for each of the studied years. These estimates were adjusted using additional data for: incidence (case-based surveillance data), excess CHB mortality (vital statistics), spontaneous and treatment induced loss of HBsAg (treatment monitoring data). Diagnosis rate was calculated for 2015, defined as the annual number of CHB cases registered in surveillance divided by estimated number of undiagnosed infections.

#### RESULTS

5001 samples were tested and 39 (0.78%, 95%CI 0.55%-1.0%) were positive, of whom 18 (46%) were previously diagnosed. Neither of sex, age, urban/rural residence or medical exposures predicted significantly higher prevalence. We forecast stable decrease of general population prevalence from 0.66% in 2015 to 0.57% in 2020. Diagnosis rate in 2015 was 25.9 per 1000 undiagnosed cases, significantly higher in urban than rural areas (32.0 vs. 18.9).

#### CONCLUSIONS

Substantial prevalence and high proportion of undiagnosed infections with insufficient diagnosis rate warrants increasing testing efforts, focusing on rural areas. A validation seroprevalence study could be designed to assess accuracy of the forecasts.

# HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

## Surveillance

## Abstract

### A lesser-known Delta: Hepatitis D testing in England, 2010 – 2020

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**BACKGROUND**

Hepatitis delta virus (HDV) causes severe liver disease. It requires Hepatitis B virus (HBV) for replication. Although the European Association for the Study of the Liver recommends HDV testing on initial evaluation of patients with chronic HBV, little is known about testing patterns in England. New effective therapeutics for HDV are becoming available. We describe HDV testing to support their roll out.

**METHODS**

We obtained data on HDV testing from the sentinel surveillance blood-borne virus (SSBBV) system, which captures front-line testing by laboratories covering 80% of the population tested for HDV in England. HDV infection was defined as any laboratory evidence of HDV (antibody, RNA or antigen).

**RESULTS**

Between 2010 and 2020, 52,097 HDV tests were conducted on 39,907 individuals. Requesting service was known for 21% of tests; 64% (6,652/10,396) occurred within secondary care, 21% general practice, 11% sexual health, ‹ 1% in prisons and drug dependency services. Testing was highest among males (55%) and those aged 30 – 44 (46.4%). 1,727 (4.3%) individuals had evidence of HDV infection, of which 30.1% had an RNA result (71.5% positive). HDV positivity was highest among males (4.5%), those aged 30 – 44 (4.7%) and those of Pakistani ethnicity (7.5%). Further linkage to HBV testing data will be undertaken to better understand the population in which HDV testing is occurring.

**CONCLUSIONS**

HDV testing appears lower in settings where high risk groups present, however, the requesting service was mostly unknown. The failure to confirm HDV RNA positivity further reduces opportunities to identify patients most likely to benefit from emerging therapeutics. We recommend a more detailed audit of testing practices to target services for improved testing and introduction of routine molecular reflex testing.

# HIV, SEXUALLY TRANSMITTED INFECTIONS AND VIRAL HEPATITIS

## Surveillance

## Abstract

### Distribution of drug paraphernalia in Germany in 2021 – a cross-sectional study to assess the current status towards achieving international targets

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[3] Institute for Therapy Research, Centre for Mental Health and Addiction Research, Munich, Germany
[5] German AIDS Service Organization, Berlin, Germany

**BACKGROUND**
The World Health Organization (WHO) recommends the distribution of 300 sterile needles/syringes per person who inject drugs (PWID) annually by 2030 to prevent the transmission of blood-borne infections. We aimed to measure this indicator as well as the type and quantity of other distributed drug paraphernalia in Germany to inform harm reduction programs accordingly.

**METHODS**
We conducted a cross-sectional survey among low-threshold drug services in Germany between March-August 2022. We asked about the type and quantity of distributed drug paraphernalia, number of supplied PWID and the allocated budget in 2021 using an online and paper-based questionnaire. We conducted descriptive statistical analysis.

**RESULTS**
The estimated response rate was 30% (534 out of 1760 distributed questionnaires plus snowballing). Of all respondents, 204 drug services from 15/16 federal states confirmed drug paraphernalia distribution, covering 21% of Germany's rural and 48% of urban counties. Syringes (97%), needles (96%) and vitamin C (90%) were the most commonly distributed paraphernalia for injecting drug use. Pre-cut aluminum foil (79%) and pipes (28%) for inhalant use and sniff-tubes (43%) for nasal use were distributed less frequently. On average, 127 needles and 84 syringes per PWID were distributed, with pronounced regional differences. Nearly one-third of the services stated that their budget was insufficient. Overall, a median budget of 2000€ [range: 0-195,000€] was allocated for drug paraphernalia distribution per service.

**CONCLUSIONS**
The current national estimates of drug paraphernalia distribution seem far from meeting the WHO target. To reach this target, Germany needs to rapidly expand their drug paraphernalia distribution programs, and must sufficiently invest in harm reduction strategies. Further investigating determinants of adequate distribution is essential to reduce blood-borne infections in this key population.

**Abstract presentations** - Online-only posters

# INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

## Surveillance

### Abstract

**Symptoms reported by patients attending sentinel emergency departments in Wales due to acute respiratory infections, including influenza, RSV and SARS-CoV-2**

**J. Zitha [1]**

S. Cottrell [2], C. Moore [3], H. Hallum [4], P. Harris [5], C. McDermott [6], A. Lench [7], D. Howorth [8], R. Cox [9],
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**BACKGROUND**

Public Health Wales is piloting an active surveillance of severe acute respiratory infections (SARI) in five sentinel hospitals across Wales. Here we describe common clinical manifestations from different respiratory pathogens detected through this surveillance.

**METHODS**

Emergency Department (ED) clinicians completed surveillance forms for each patient with suspected respiratory infections, and collected throat swabs which were tested against a standard multiplex PCR panel including SARS-CoV-2, influenza, Respiratory Syncytial Virus (RSV) and other common seasonal respiratory pathogens (this test was unable to distinguish between enterovirus and rhinovirus and combined results are presented). This study includes symptomatic patients accessing urgent hospital care between week 9 2021 to week 18 2022.

**RESULTS**

1,771 respiratory pathogens were detected from a total of 5,668 samples from patients who reported symptoms. The most commonly detected respiratory pathogen was Rhinovirus/Enterovirus detected in 577 (10.2%) samples, then SARS-CoV-2 in 515 (9.1%) and RSV in 181 (3.2%) samples.
The frequency of reported symptoms varied between the organisms: in Rhinovirus/Enterovirus positive patients 69.5% of patients reported having a cough, 54.4% reported shortness of breath (SOB), 29.1% reported a fever and 20.6% had a runny nose. RSV positive patients followed the same pattern of symptoms with 79.0%, 59.7%, 35.4% and 29.3% reporting the same symptoms respectively. The primary symptom for SARS-CoV2 infection however was SOB (62.7%), followed by cough (49.9%), fever (32.2%) and fatigue (21.0%).

**CONCLUSIONS**

Although 9.1% of patients in this sample were symptomatic and positive for SARS-CoV2, it was not the most frequently detected pathogen. Additionally, varying presentation of symptoms among viruses is an important factor to be taken into consideration when establishing case definition for use in SARI surveillance.

# INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

## Surveillance

## Abstract

Molecular characterization of respiratory syncytial virus epidemic in Northern Italy during the 2021/2022 winter season

**C. Galli** [1]

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### BACKGROUND

Respiratory syncytial virus (RSV) has a relevant impact on influenza-like illnesses (ILIs). RSV is classified into subtypes A and B, further classified into genotypes. We aimed at molecularly characterising the RSV epidemic in ILIs during the 2021/2022 season in the framework of the Italian Influenza Surveillance Network (InfluNet).

### METHODS

Nasal-pharyngeal swabs (NPS) from ILI outpatients were collected in Lombardy (Northern Italy) within InfluNet during 2021/2022 season. RSV-positive samples were detected by real-time RT-PCR (matrix gene) and subtyped by RT-multiplex-nested-PCR (fusion gene). Nearly 10% of RSV-positive NPS was sequenced (glycoprotein gene, 988 nt) and phylogenetically analysed.

### RESULTS

From week 2021-40 to week 2022-02, 673 NPSs were collected from as many ILIs and 30% (202/673) were RSV-positive. 75% (152/202) of RSV-positive NPSs were collected from children ≤4 years old, and 78% (118/152) from children ≤2 years old.
RSV epidemic lasted from week 2021-43 to week 2022-48, reaching a peak in week 2021-46 (RSV-positivity rate: 23%).
187/202 (93%) RSV strains were subtyped: 78/187 (42%) were RSV-A, 108/187 (57%) RSV-B and 1/183 (1%) RSV-A and RSV-B. All RSV-A sequences (n=15) belonged to genotype ON1, sharing a mean nucleotide identity of 97.5% (range: 95.6-99.7%). All RSV-B (n=13) clustered within the BA genotype (mean nucleotide identity: 97.6%, range: 95.6-100%).

### CONCLUSIONS

During the 2021/2022 season, RSV epidemic lasted 6 weeks (from end October to beginning of December, earlier than usually observed) reaching a positivity rate of 23% in mid-November. RSV was detected mainly among children ≤2 years. RSV-A and RSV-B co-circulated and only the most recent genotypes (ON1 and BA) were detected. Investigating the epidemiological and molecular characteristics of RSV can provide baseline information before the introduction of vaccination.

Abstract presentations - Online-only posters

# INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

## Surveillance

## Abstract

### Knowledge, attitudes, and practices (KAP) towards seasonal influenza and influenza vaccine among adults with chronic diseases - Kyrgyzstan, 2019

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**BACKGROUND**

Influenza is an infectious disease in which the majority of the burden of mortality occurs in individuals with pre-existing comorbidities and chronic diseases. This present study is aimed to understand key motivators and barriers to vaccine uptake among patients with underlying diseases in Kyrgyzstan.

**METHODS**

We conducted a cross-sectional study among the patients with chronic diseases in Kyrgyzstan from December 2018 to March 2019. Participants were selected using systematic random sampling. A total of 1200 participants aged from 18 to 92 years having at least one underlying disease were recruited. Interviews were held in participant's homes or workplaces. Multivariate regression analysis was used to determine the association between variables and outcomes of the research.

**RESULTS**

Among 1118 participants enrolled in this study, more than half (63%) had an intention to be vaccinated with Influenza vaccine and 42% were vaccinated last year. Among participants at the age of above 50 years old, 75% had intentions to get the flu vaccine. In the multivariate analysis, respondents with university degrees (?OR=0.31, 95% CI=0.11–0.84, p=0.02) and divorced marital status had a significantly greater intention for vaccination (?OR=0.52, 95% CI=0.31–0.88, p=0.03). Residences in the South (42%, p<0.03) and Osh city (6%, p<0.001) were associated with higher intention of vaccination. Nearly half of respondents (45%) reported they did not receive any advice to get the influenza vaccine by healthcare providers. More than half (54%) of participants were ready to buy vaccines against Influenza, in case if people with chronic diseases are recommended for the vaccination and they can pay average US $3.3 per vaccine.

**CONCLUSIONS**

These findings underline the value of understanding sociodemographic context when developing targeted messaging to encourage influenza vaccine uptake.

**Keywords:** Influenza, Vaccination, Knowledge, Attitudes, Practices, KAP
**ABSTRACT ID:** 245
**PRESENTED BY:** Altynai Dzhalimbekova / a_djalymbekova@mail.ru

# INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

## Surveillance

## Abstract

### Influenza surveillance systems using traditional and alternative sources of data: a scoping review

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**BACKGROUND**

While the World Health Organization's recommendation of syndromic sentinel surveillance for influenza is perhaps the most efficient method to collect high-quality data, several limitations are undoubtedly present. Aligned with the Research Recommendation 1.1.2 of WHO Public Health Research Agenda for Influenza to identify complementary influenza surveillance systems which provide timely estimates of influenza activity, we performed a scoping review to map the extent, range and nature of published literature on the use of non-traditional sources of surveillance data for influenza.

**METHODS**

We searched three electronic databases (PubMed, Web of Science, and Scopus) for articles in English, French, and Spanish, published between January 1, 2007 and 28th January 2022. Studies were included if they directly compared at least one non-traditional surveillance system with a traditional influenza surveillance system in terms of correlation in activity or timeliness.

**RESULTS**

We retrieved 823 articles of which 57 were included for analysis. 15 articles considered Electronic Health Records (EHR), 11 participatory surveillance, 10 online searches and webpage traffic, 7 Twitter, 5 absenteeism, 4 telephone health-lines, 3 medication sales, 2 media reporting and 5 looked at other miscellaneous sources of data. Several articles considered more than one non-traditional surveillance method.

**CONCLUSIONS**

We identified eight categories and a miscellaneous group of non-traditional influenza surveillance systems with varying levels of evidence on timeliness and correlation to traditional surveillance systems. Data from electronic health records and participatory surveillance systems appeared to have the most agreement on timeliness and correlation to traditional systems. No studies suggested a non-traditional surveillance system as a replacement of the current system, but rather, the non-traditional systems were proposed as complements to traditional systems.

# INFLUENZA AND OTHER RESPIRATORY VIRUSES (EXCEPT SARS-COV-2)

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Influenza A and SARS-CoV-2 co-infection in Portugal, 2022: effects of relief in control measures and vaccination programs

**C. Rodrigues** [1]

D. Veiga [2], A. Barroca [3], M. Reis [4], A. Antunes [5], D. Passos [6], I. Soares [7], R. Aguas [8], J. Oliveira [9], P. Madaleno [10], A. Matos [11]

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[11] Chemical Process Engineering and Forest Products Research Centre (CIEPQF)

**BACKGROUND**

Relief on restriction and control measures of COVID-19 pandemic favored the circulation of other respiratory viruses, which have been residual in the last two years. From March 2022, Influenza A virus infections emerged in Portugal, and co-infection with SARS-CoV-2 started to be detected. We described the profile of outpatients with such co-infection in the Centre region of Portugal, during March and April 2022.

**METHODS**

Nasopharyngeal samples collected at Laboratory of Clinical Analysis from University of Coimbra for COVID-19 diagnosis were concomitantly evaluated for Influenza virus. Data on gender and age from patients with influenza or SARS-CoV-2 infection was collected and analyzed by chi-square and one-way ANOVA tests.

**RESULTS**

Our study included 1917 individuals, from which 5% were infected with Influenza A virus, 27% with SARS-CoV-2 and 1% with both virus (co-infection). No differences between gender were observed ($p=0.28$). Co-infected individuals were younger (median 21 years-old) than influenza-infected individuals (median 24 years-old, $p=0.36$) or SARS-CoV-2 infected patients (median 34 years-old, $p=0.002$). The majority of co-infected patients (88%) were under 30 years-old, and only one patient older than 45 revealed co-infection. None co-infection was detected in individuals older than 65, despite 7% of SARS-CoV-2 and 2% of influenza-infected patients belonged to this age group.

**CONCLUSIONS**

The relief on COVID-19 control measures in Portugal enabled the re-emergence of influenza in the community. Nevertheless, implemented flu vaccination programs effectively prevented infection in older individuals, and co-infection with SARS-CoV-2 was rarely observed among that risk group. Despite the relief in restrictions is ongoing, in order to assure a safe return to normal activities, it is crucial to emphasize the importance of adhesion to vaccination programs.

# PUBLIC HEALTH SCIENCES (GENERAL)

## International health and migration

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## Abstract

### Strengthening health care professionals' competencies on International Health Regulations (2005) during the COVID-19 pandemic

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**BACKGROUND**
The International Health Regulations (IHR) (2005) form the foundation of international law for managing public health emergencies of international concern. The Joint Action SHARP aims to strengthen IHR (2005) core capacities and competencies. While challenged with the COVID-19 pandemic we aimed to develop interactive online trainings that would engage public health experts from different sectors and levels all across Europe.

**METHODS**
We developed 5 modules covering central aspects of the IHR (2005) such as event detection and assessment, risk communication and the IHR (2005) Monitoring and Evaluation Framework. A combination of expert input, good-practice exchange, break-out sessions and interactive online tools was used to create a stimulating learning environment and facilitate professional exchange. The training was evaluated through an anonymous online survey.

**RESULTS**
Between 2020 and 2022 a total of 4 trainings with each 5 modules were held. In total, 88 health professionals from more than 20 European countries participated. Evaluation results indicated a high satisfaction with the trainings with on average 94/100 possible points. In particular, content and organization of the trainings were rated positively. Participants rated their knowledge of the IHR as 1.90 before the training and 2.95 after the training (with 5 being the best across all ratings).

**CONCLUSIONS**
There is a continued need to strengthen IHR (2005) core capacities and competencies. To meet this demand, high-quality, interactive training formats are needed, which contribute to capacity building and exchange of good practices. The online-trainings developed have proved effective. We recommend to continue developing and conducting such trainings.

# PUBLIC HEALTH SCIENCES (GENERAL)

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Twenty-five years of time, place, person: composition of the EPIET Alumni Network and its contribution to the European and global field epidemiology and public health microbiology workforce

**C. Hammer** [1]

J. Scheaffer [2], I. Evlampidou [3], S. Nielson [4], L. Bubba [5], Z. Igloi [6], T. Dub [7], A. Wendland [8], A. Torstmann [9], A. Baidjoe [10]

[1, 2, 3, 4, 5, 6, 7, 8, 9, 10] EPIET Alumni Network

**BACKGROUND**

The EPIET Alumni Network (EAN) is an association of professionals who have completed one of the advanced European field epidemiology or public health microbiology training programmes (EPIET, EUPHEM, associated programmes). We conducted a survey amongst EAN members to investigate the composition of the network and the impact of the fellowship on members' careers.

**METHODS**

Between September-December 2021, we distributed an online questionnaire to all EAN members to collect data on demographics, professional background and current position. We analysed data descriptively.

**RESULTS**

Of 732 members, 281 participated (response rate: 38%), 146(52%) attended EPIET, 38(13%) EUPHEM and 67(24%) one of the associated programmes, the remaining 30 (11%) were external members. The median age was 42 years (range: 25-66), 194(69%) were female.
The training was perceived to have had a positive impact on the professional trajectory for 191(88%) of graduated respondents, particularly by expanding technical skills (123, 56%) and professional network (39, 18%). Generalists with no specific diseases specialisation were the largest group (56, 20%). Currently, the majority of graduates work in national (101, 41%), sub-national public health entities (24, 10%) or at the WHO (21, 8.5%).

**CONCLUSIONS**

EAN is a unique network for continued engagement beyond the fellowship. It brings together highly-skilled professionals that speak a common language through their fellowship and the peer-to-peer professional development afterwards. This leads to a skilled field epidemiology and public health microbiology workforce that has generalist and unified skills as well as tight connections. Infectious disease control in Europe benefits from the resulting high adaptability in response to health threats. Maintaining well-resourced field epidemiology and public health microbiology programmes is key to strengthen European public health and the ability to counter cross-border health threats.

# TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

## Field epidemiology (e.g. outbreak investigations)

### Abstract

**Outbreak of Legionnaires' disease linked to unregistered cooling towers, West Midlands, England, July-September 2020**

**A. Nikhab** [1]

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**BACKGROUND**

An outbreak of Legionnaires' disease (LD) with a rare sequence-type (ST) profile was notified in a local authority of the West Midlands, England on 10/09/2020. An investigation was initiated to determine the source and extent of the outbreak and inform appropriate control measures.

**METHODS**

Potentially associated cases were residents in the area of interest, with symptom onset on/after 01/07/2020. Confirmed cases were defined as any national reference laboratory-confirmed case with *Legionella pneumophila* serogroup 1 and a ST profile consistent with ST2454.

Bespoke enhanced surveillance questionnaires were administered by telephone to cases, focussing on exposures within 14 days before symptom onset.

The geographical centre of case residences was calculated using ArcGIS. Ground-level investigations on foot in the area surrounding the geographical centre and publicly available satellite imagery were used to supplement locally-held registers of cooling towers. Environmental water samples taken from possible sources were analysed using sequence-based typing (SBT).

**RESULTS**

Nine cases were identified (symptom onset dates: 19/07/2020-10/09/2020), seven of which met the confirmed case definition.

A premises with two unregistered cooling towers within a 1km radius of the geographical centre of case residences was identified as a possible source. SBT of samples taken from the cooling towers showed mixed populations of STs which included ST2454, providing a further link between this location and cases with the same ST.

**CONCLUSIONS**

Environmental and epidemiological investigations provided good evidence that the identified premises was the source of infection. HSE prohibited operation of the towers (14/09/2020). After closure, no further cases were reported. These findings highlight the potential risks of unregistered cooling towers as a source of *Legionella* outbreaks and the value of physical, ground-level checks when cases reside near each other.

# TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

## Surveillance

## Abstract

**Evaluating the utility of the historic tuberculosis cohort review surveillance reports from the four tuberculosis networks in Southeast England**

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**BACKGROUND**

In England, tuberculosis multidisciplinary cohort reviews systematically examine cases and trends and evaluate service performance against targets. The associated surveillance outputs, historically produced by each local health protection team independently, are variably distributed to local TB service stakeholders (commissioners, local authority and health protection public health, TB teams and clinicians) and inform clinical and public health actions. Launch of the National TB Surveillance System, in September 2021, prompted evaluation of the utility of historic outputs, in the form of cohort review surveillance reports to inform their future development.

**METHODS**

An electronic survey was distributed in March 2022 to 70 tuberculosis stakeholders across the four southeast TB networks. We collected data on job role, cohort review attendance, report utility (focussing on recent case data, trends and tuberculosis service performance) and suggestions for future reports.

**RESULTS**

Twenty-two responses were received (15 clinical stakeholders, five health protection team-members, one local authority and one tuberculosis service commissioner). For the 14 respondents who historically received a report, utility was rated good for 93%, 64% and 86%, for recent cases, trends and service performance respectively. Provision, or improvement of, trend data and analysis was requested by five respondents. Suggestions for improvement included adding data, especially on risk factors and ethnicity, to better identify and prioritise actions, report standardisation, providing regional comparisons and highlighting case, trend or target indicator outliers.

**CONCLUSIONS**

All stakeholders found cohort reviews and surveillance reports useful in informing public health action, but areas for improvement were identified. Suggestions for improvements in reporting trends, report standardisation and highlighting outliers will be incorporated into a 2022 Southeast reproducible analytical pipeline pilot cohort review surveillance report.

**Keywords:** Tuberculosis, Surveillance, Epidemiology, Cohort review, Multidisciplinary, Evaluation
**ABSTRACT ID:** 90
**PRESENTED BY:** Hannah Taylor / hannah.taylor@phe.gov.uk

**Abstract presentations** - Online-only posters

# TUBERCULOSIS AND OTHER RESPIRATORY DISEASES (EXCLUDING VIRUSES)

## Surveillance

## Abstract

### Increase in invasive Streptococcus pyogenes disease among young children and adults, the Netherlands, March - July 2022

**B. De Gier** [1]

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**BACKGROUND**

After lifting of most COVID-19 prevention measures, higher numbers of invasive infections by *Streptococcus pyogenes* (group A *Streptococcus*, GAS) were observed from March to July 2022, compared to pre-COVID-19 years. We aimed to describe the characteristics of this iGAS upsurge and assess time trends in general practitioner (GP) consultations possibly related to iGAS incidence.

**METHODS**

National notifications of streptococcal toxic shock syndrome, necrotizing fasciitis and puerperal fever were analyzed and linked to bacteriological reference laboratory data. Time trends in GP-diagnosed impetigo, scarlet fever, pharyngitis and varicella zoster were assessed.

**RESULTS**

In March-July 2022, 156 notifications of non-puerperal iGAS were received, compared to 58-90 in the same period in 2016-2019. Of these, 21 cases (13.5%) were young children (0-5 years old), compared to 1-7 notifications among young children in March-July 2016-2019 (1-9% of all notifications) . Three young children were notified to have died, for four others a varicella zoster co-infection was mentioned. Especially GAS necrotizing fasciitis notifications were increased, both in young children and adults.

*Emm* typing data showed a diverse pattern. *Emm*1, *emm*4 and *emm*12 dominated in 2022, representing 67% of isolates. Also iGAS secondary to varicella zoster was caused by several *emm* types. GP consultations for varicella zoster were increased compared to pre-covid years, mainly in ages 5-14.

**CONCLUSIONS**

After two years of low incidence during COVID-19 prevention measures, more iGAS cases were notified than expected. Specifically the high incidence among young children and of necrotizing fasciitis caused worry among clinicians and the general public. The increase in iGAS among children age 0-5 years may be related to a post-COVID immunity debt, either for GAS itself and/or via varicella zoster.

# VACCINE PREVENTABLE DISEASES

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

## Abstract

The role of healthcare professionals in acceptance of maternal pertussis vaccination (MPV) in the Netherlands.

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### BACKGROUND

Maternal pertussis vaccination (MPV) is an effective strategy to prevent severe disease, in pregnant women and their infants during the first months of life, leading to a reduction of 91% in pertussis infections among young infants. Notwithstanding the public and individual health benefits of the MPV, coverage among pregnant women remains low (70%). Information regarding the MPV sometimes does not reach the pregnant women. We aim to clarify the role of healthcare professionals (HCP) in the decision-making process of pregnant women.

### METHODS

To assess the extent to which and in what way HCP influence the acceptance of the MPV, we conducted a cross-sectional survey among MPV refusers and acceptors in the Netherlands. The women responded with their main reason for acceptance or refusal of the MPV, if and in what way the MPV was discussed with their midwife or obstetrician, and if and how this played a role in their decision on acceptance or refusal;

### RESULTS

Preliminary results among 1334 respondents (1279 MPV acceptors) showed that 57% of the acceptors received a recommendation from their HCP, versus 39% of the refusers. 52% of the acceptors who discussed the MPV with their HCP, indicated that the discussion influenced their decision to accept the vaccination. Frequently stated reasons for accepting MPV were: protection of the infant in the first weeks (86%) and the fact that the infants needs one vaccination less (78%). Main reasons for refusing MPV: being against vaccinations during pregnancy (40%) and fear of side effects for the infant (27%).

### CONCLUSIONS

This study will clarify the perceived role of healthcare professionals regarding MPV decision-making. It will emphasize the importance of interdisciplinary cooperation in raising vaccination coverage.

**Abstract presentations** - Online-only posters

# VACCINE PREVENTABLE DISEASES

## Field epidemiology (e.g. outbreak investigations)

## Abstract

### Low-levels of knowledge, attitudes, and practices towards vaccination and COVID-19 vaccines among healthcare providers—Kazakhstan, 2021

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### BACKGROUND

Annually in Kazakhstan ~5,000 newborns are not vaccinated because of parental hesitancy. Hesitancy has resulted in resurgence of diseases with 16,967 measles cases registered nationally in 2019. Poor knowledge, attitudes, and practices (KAP) among healthcare providers contributes to vaccine hesitancy, and additional data was needed for developing interventions.

### METHODS

We conducted a cross-sectional study which included all healthcare providers directly involved in vaccine administration at 54 facilities in Shymkent, Turkestan, and Aktobe from March–May 2021. We used logistic regression to test association with good KAP; cut-off for good KAP was 70%.

### RESULTS

We interviewed 1,461 providers, 951 (65%) nurses, 360 (25%) general practitioner (GP), and 150 (10%) pediatricians. Among providers, 93% were females, mean age was 36 years old, 622 (43%) had good knowledge, 237 (16%) had good attitudes, and 473 (32%) had good practices. Additionally, 75% thought measles vaccines were effective, ‹49% thought COVID-19 vaccines were effective, and 59% would not get the COVID-19 vaccine. Good knowledge was associated with being female (OR: 3.1, 95% CI: 1.7–6.1), being a GP (1.7, 1.1–2.5), 11–20 years' work experience (1.5, 1.1–2.4), and ›21 years' work experience (2.5, 1.5–2.0). Good attitude was associated with ›21 years' work experience (2.7, 1.5–4.9). Good practice was associated with not living with people ›65 years old (1.5, 1.1–2.0), ›21 years' work experience (1.5, 1.1–2.0). Good knowledge and good attitudes was associated with good practice (4.2 [3.2–5.6] and 2.3 [1.8–3.0], respectively).

### CONCLUSIONS

Our study revealed low levels of KAP among healthcare providers. Results can be used to improve knowledge and attitudes towards vaccination, with focused effort on providers with less work experience, nurses and pediatricians.

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