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EPIDEMIOLOGY
OF INFECTIOUS DISEASES

SCIENTIFIC SEMINAR ON INFECTIOUS DISEASES

Brussels, 19 May 2022

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Sciensano
Epidemiology and public health
Epidemiology of infectious diseases
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Scientific seminar on infectious diseases | 19 May 2022 |
Royal Museums of Fine Arts of Belgium, Brussels, Belgium

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PROGRAMME

08:30	Registration with walking breakfast / Visit of stands
	SESSION 1 **Boudewijn Catry (Sciensano) & Denis Pierard (VUB)**
09:15	Welcome address
09:30	A look at some useful antibiotics currently not available/recently approved for use in Belgium- Rakan Nasreddine (ULB) & Hugues Malonne (FAGG/AFMPS)
10:00	Bigger and better? Impact of clinical laboratory consolidation on infectious disease surveillance in the future - Olivier Vandenberg (LHUB-ULB)
10:25	Trends of influenza virus and other respiratory viruses during covid pandemic – Nathalie Bossuyt (Sciensano)
10:45	Update on Pre-Exposure Prophylaxis for HIV in Belgium – Jessika Deblonde (Sciensano)
11:10	Coffee break / Visit of stands
	SESSION 2 **Emmanuel André (UZLeuven) & Steven Van Gucht (Sciensano)**
11:40	COVID-19 vaccine surveillance in Belgium: the LINK-VACC project – Joris Van Loenhout (Sciensano)
12:05	Lesson's learned from covid comissariat – Pedro Facon (covid commissariat)
12:30	Waste water surveillance for covid and future application – Marie Lesenfants & Raphaël Janssens (Sciensano)
13:00	Lunch
	SESSION 3 **Pierette Melin (ULiège) & Naïma Hammami (Agentschap Zorg and Gezonheid)**
14:10	Investigation of an international Outbreak of Monophasic Salmonella Typhimurium associated with Chocolate Products, April 2022 – Dieter Van Cauteren (Sciensano)
14:25	Reporting of infectious pathologies in the province of Liège after the flood disaster of 15 July 2021– Tiffany Dierinck (AVIQ)
14:50	Past, present and future of anti-pneumococcal vaccines – Sophie Blumental (ULB)
15:15	The meaning of self-testing – Elizaveta Padalko (UZGent)
15:35	Drug resistant Shigella sonnei infections in MSM – Pieter-Jan Ceyssens (Sciensano)
15:45	Closing address and end of seminar

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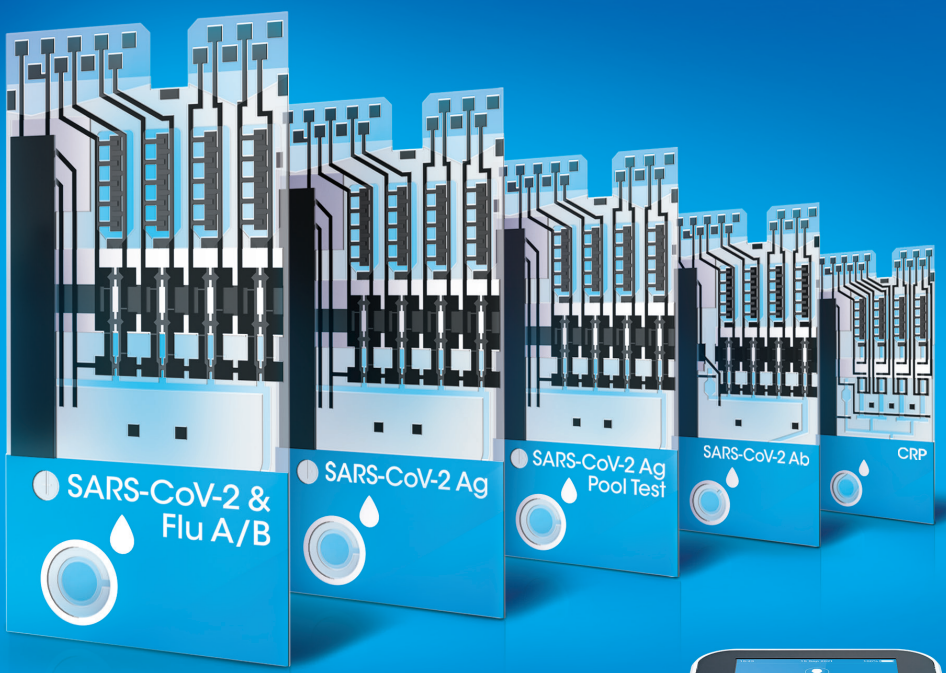

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ABSTRACTS OF PRESENTATIONS

RAKAN NASREDDINE

ULB

BIOGRAPHY

Infectious disease physician and researcher at Saint-Pierre University Hospital in Brussels.

A LOOK AT SOME USEFUL ANTIBIOTICS CURRENTLY NOT AVAILABLE/RECENTLY APPROVED FOR USE IN BELGIUM

This presentation will describe antibiotics for the treatment of gram-positive and gram-negative infections that are either newly approved for use in Belgium or that are not available in Belgium but would be useful to have.

HUGUES MALONNE

FAGG/AFMPS

BIOGRAPHY

Hugues Malonne got his Bachelor and Master degrees in Pharmaceutical Sciences as well as his Ph.D. in Pharmacology from the Faculty of Pharmacy of the University of Brussels (ULB). He also holds an Executive Master in Management (Hospital and Healthcare facilities) from the Solvay Brussels School of Economics and Management. He recently moved to the Director General "PRE-Authorization" position after a 5 years assignment as Director General "POST-Authorization" at the Federal Agency for Medicines and Health Products. Before joining the Public Service, he held various positions of increasing responsibilities related to Market Access and Public Policy in Europe and Asia for the pharmaceutical industry. After his studies Hugues held academic positions at the University of Brussels. He is currently visiting professor at the ULB and UNamur. From 2013 to 2019 he was a member of the Board of Directors of the Integrated Biobank of Luxembourg and the Luxembourg Institute of Health, two prominent public research institutions. His current position deals with Innovation and Regulatory Sciences in Medicines, Medical Devices and In-vitro Diagnostics.

A LOOK AT SOME USEFUL ANTIBIOTICS CURRENTLY NOT AVAILABLE/RECENTLY APPROVED FOR USE IN BELGIUM

This part of the presentation will develop the main elements that explain the sluggishness of the antibiotic pipeline. We will start with a short appraisal of the few marketing authorizations obtained between 2018 and 2021. After that, we will analyse together the main obstacles encountered by a new drug candidate during its development cycle and will propose some avenues for adjustments from the first stages of development until market launch. Next, a state of play is given for the specific antibiotics, mentioned by Dr. Nasreddine in the first part of the presentation. To conclude, we will briefly mention the operational objectives and concrete actions in the Belgian National Action Plan against AMR, aimed at ameliorating the disponibility of both new and innovative, as well as of 'old', narrow-spectrum antibiotics.

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OLIVIER VANDENBERG

LHUB-ULB

BIOGRAPHY

Olivier Vandenberg has been trained as Clinical Microbiologist (2001) and completed his PhD in Biomedical Sciences (2006) at Université Libre de Bruxelles (ULB). From 2008 to 2017, he was appointed Head of the Department of Microbiology of the Brussels university hospitals network.

In 2016, Dr Vandenberg joined the Division of Infection & Immunity, University College London (UCL) as Honorary Senior Lecturer. Since 2017, he took the lead of the Innovation and Business Development Unit of the University Laboratory of Brussels (LHUB-ULB). In addition, he is currently Professor of Microbiology in the School of Public Health and in the Faculty of Medicine of the ULB.

Most of his research focus on the clinical impact of new diagnostic tools in both industrialized and low-resource settings. Since 2000, he has also supervised the consolidation of several microbiology laboratories allowing the implementation of infectious disease surveillance programmes in industrialized but also in Low and Middle Incomes Countries (LMIC). Besides this, he collaborates with different manufacturers in the development of new approaches for the diagnosis and control of infectious diseases.

BIGGER AND BETTER? IMPACT OF CLINICAL LABORATORY CONSOLIDATION ON INFECTIOUS DISEASES SURVEILLANCE IN THE FUTURE

With over 6.2 million cumulative deaths, the outbreak of coronavirus disease (COVID-19) reminds us that infectious diseases remain a serious public health concern globally, while the need for reliable and representative surveillance systems remains as acute as ever. In most European countries, the public health surveillance of infectious diseases uses reported positive results from sentinel clinical laboratories or laboratory networks, to survey the presence of specific microbial agents known to constitute a threat to public health in a given population. This monitoring activity is commonly based on a representative fraction of the microbiology laboratories nationally reporting to a single central reference point. However, in recent years a number of clinical microbiology laboratories (CML) have undergone a process of consolidation involving a shift toward laboratory amalgamation and closer real-time informational linkage. The centralization of diagnostic services over a large geographical region gave rise to the concept of regional-scale "microbiology laboratories network" and has generated the mandatory infrastructure used in validation and implementation of newer high-throughput diagnostic approaches. In this lecture, we describe the range of opportunities that the changing landscape of CMLs in Europe can contribute towards improving the quality of patient care but also the early detection and

enhanced surveillance of public health threats caused by infectious diseases. We also illustrate that the real-time integration of high-throughput whole genome sequencing platforms available in consolidated CMLs into the public health surveillance system is not only credible but also advantageous to use for future surveillance and prediction purposes. Ultimately, we also highlight the role of large scale diagnostic platforms in the evaluation of new diagnostic tools; and the advancement in computational approaches for genomics and bioinformatics allowing better diseases surveillance.

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NATHALIE BOSSUYT

SCIENSANO

BIOGRAPHY

Nathalie Bossuyt (MD, MSc) is since 2013 responsible for the epidemiological surveillance of acute respiratory infections (including influenza) within Sciensano's Epidemiology of Infectious Diseases Service.

TRENDS OF INFLUENZA VIRUS AND OTHER RESPIRATORY VIRUSES DURING COVID PANDEMIC

At the start of the COVID-19 pandemic, subsequent unusual occurrences of influenza and other respiratory viruses were to a certain extent anticipated, as during previous pandemics similar observations were made and as the public health measures aiming to prevent and/or control SARS-CoV-2 transmission in the community were also expected to influence the transmission of the usual respiratory viruses. This expected loss of normal seasonality was indeed observed for most respiratory pathogens already from spring 2020 onwards. First, mainly sharp reductions in circulation were seen, followed in some cases by peaks at unusual times. During the presentation, a brief overview will be given of circulation and seasonality of influenza, RSV and a few other respiratory viruses, both at national and international level.

JESSIKA DEBLONDE

SCIENSANO

BIOGRAPHY

Jessika DEBLONDE has a master's degree in Law and a PhD in Social Health Sciences. In 2012, she joined Sciensano, as a scientific collaborator of the HIV/AIDS surveillance unit where she is responsible for the national PrEP, PEP and HIV testing surveillance and involved as investigator in research as regards HIV prevention and health-related quality of life.
She acts as scientific expert in the ECDC assignment to elaborate a "standardized monitoring tool of pre-exposure prophylaxis (PrEP) in EU countries". She is member of the Belgian PrEP Network and co-coordinator of the Belgian Monitoring Committee of the HIV Plan.

UPDATE ON PRE-EXPOSURE PROPHYLAXIS FOR HIV IN BELGIUM

Since 1 June 2017, Pre-Exposure Profylaxis (PrEP) has been available in Belgium and is reimbursed for persons at increased risk of sexually acquired HIV infection. PrEP can be obtained in the HIV Reference Centres (HRC). A 3-monthly follow-up consultation is foreseen, among others to perform an STI-screening.

Reimbursement data regarding the purchase of emtricitabine/tenofovir as PrEP for HIV in a Belgian pharmacy are obtained from Pharmanet. It concerns a dataset with anonymous individual data including gender, age, place of residence (province) and number of purchased pills during the last 3 years. Aggregated data are collected from the HRC regarding the profile of people who had a first PrEP consultation, the number of new STI diagnoses during follow-up consultations and reported chemsex.

In 2020, there were 3983 PrEP users: 99% were male; 64% were in the age group of 30-49 years. In 2020, 1354 people used PrEP for the first time which corresponds to 34% of PrEP users. Among those with a first PrEP consultation in an HRC, 96% were men having sex with men (MSM); 75% were Belgian. During the follow-up visits in 2020, at least one new STI was diagnosed in 21% of the users; gonorrhoea and Chlamydia diagnoses were the most common. There were 3 HIV seroconversions due to inconsistent PrEP adherence. Chemsex was reported by 21% of the users.

Since the national implementation of the PrEP programme in June 2017, there has been a steady increase in the number of PrEP pills purchased, slowed down in 2020 by the COVID-19 epidemic. In line with other countries, the uptake of PrEP in Belgium has been almost entirely limited to MSM, mainly Belgians. Some.

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JORIS VAN LOENHOUT

SCIENSANO

BIOGRAPHY

Joris obtained a MSc in Toxicology and Environmental Health at Utrecht University, the Netherlands. He started his career at the department of Environmental Health at the Public Health Services Gelderland-Midden. Within that position, he coordinated several EU-funded projects on environmental health topics, and he also carried out a study on indoor temperature in relation to health of elderly residents. In 2010, he started his PhD at the Radboud University in Nijmegen, in parallel with his position at the Public Health Services. He successfully defended his PhD thesis on the long-term health impact of Q fever in February 2015.

Joris has worked at the Centre for Research on the Epidemiology of Disasters (CRED) within UCLouvain from 2014 to 2021. He focussed his research in particular on the human impact of heatwaves. Since 2016, he has been co-responsible for maintaining the international disaster database EM-DAT. Joris was also responsible for applying for and undertaking a study on adherence to COVID-19 measures among the Belgian population, funded by Fondation Louvain.

Since 2021, Joris works for Sciensano, where he is currently leading the team responsible for assessing the impact of the Belgian COVID-19 vaccination campaign.

COVID-19 VACCINE SURVEILLANCE IN BELGIUM: THE LINK-VACC PROJECT

All vaccines, including COVID-19 vaccines, are only allowed onto the European market after being evaluated as qualitative, safe and effective by the European Medicines Agency (EMA) in an extensive authorization procedure. Nonetheless, when rolling-out a vaccination campaign with a newly registered vaccine, it remains important to monitor a number of indicators in what is called post-authorization surveillance.

This post-authorization surveillance includes, amongst others:

Measurement of uptake and coverage of the vaccination. This allows to estimate the percentage of the population (and of certain target groups) already vaccinated. This way suboptimal uptake in certain target groups can be identified.

Estimation of vaccine effectiveness. This indicator tells us the degree in which vaccination is capable of preventing illness (infection, severe illness, death). Moreover, mutations in the virus that emerge also affect the effectiveness of the vaccine.

Monitoring of the vaccine's safety. This allows to identify breakthrough cases (cases of COVID-19 in vaccinated individuals) and possible adverse events of vaccination.

To allow this post-authorization surveillance, Sciensano launched the LINK-VACC project. For the purpose of this project, no new data are collected, but existing databased are linked. The following data is being used from the, already existing, databases mentioned below:

Vaccinnet+: demographical data of all persons to whom a COVID-19 vaccine has been administered in Belgium, as well as data on the vaccine administered.

Laboratory Test Results database : demographical data of all persons who had a COVID-19 test done in Belgium, as well as data on the test results.

HealthData COVID-19 Clinic Database: demographical data and clinical data of persons hospitalized with a confirmed COVID-19 infection in Belgium.

STATBEL: demographical and socio- economic data of all Belgian citizens who have received at least one COVID-19 vaccine and/or had a COVID-19 test done in Belgium.

Database of the Intermutualistic Agency (IMA): data on comorbidities, based on reimbursement of relevant medication or treatment of all persons who have received at least one COVID-19 vaccine and/or had a COVID-19 test done in Belgium.

Common Base Registry for Healthcare Actors (CoBRHA): demographical data of all persons who are registered as a healthcar.

REFERENCES

1. Although the project runs until December 2023, several outputs have already been produced. This includes reports on the coverage among specific groups (nursing home residents, healthcare workers) and the coverage and impact of vaccination among the general adult population. Scientific articles that have been published so far include studies on vaccine effectiveness and on characteristics of persons with a breakthrough infection. An overview of the methodology and the outputs until now will be presented during the session.

PEDRO FACON

COVID COMMISSARIAT

BIOGRAPHY

Pedro Facon (°1981) is a public management professional in public health, social security and health crisis governance and management. He worked successively in research, teaching, advisory and management positions at the Public Management Institute (KULeuven), the National Institute for Health and Disability Insurance, the Cabinet Office of the Belgian federal minister of Social Security and Public Health and the Belgian Ministry of Health.

From October 2020 until April 2022 he was designated Government Commissioner COVID-19 by the Belgian federal government.

As from April 2022 he returned to public administration as Deputy General Administrator of the National Institute for Health and Disability Insurance.

He's Fellow at the Medical Campus of the Free University of Brussels and Guest Professor at the Department of Public Health & Primary Care of the University of Ghent.

LESSON'S LEARNED FROM COVID COMISSARIAT

The COVID-19 pandemics showed the importance of data and surveillance, as well as for detecting, analysing and managing a health crisis. During the crisis we were confronted with a constant quest for matching supply and demand of data. Moving into the pandemic end game changes the needs and expectations with regard to data and surveillance. My intervention wants to reflect on how we dealt with these challenges as well as the road ahead.

MARIE LESENFANTS & RAPHAËL JANSSENS

SCIENSANO

BIOGRAPHY

In 2009 Marie Lesenfants graduated from the Faculty of Bioengineering Sciences of UCLouvain with a specialization in chemistry and biotechnologies applied to environmental technologies. In 2011, Marie started her career for some years for the Belgian development agency, in Belgium and abroad, mainly in Sénégal, Morocco and Burundi, as an expert in Geographical Information Systems and Environment. Since 2019, she works at Sciensano in the Epidemiology of infectious diseases Service and has dedicated her work to environmental surveillance, starting with Polio surveillance, and then implementing and coordinating the National COVID-19 surveillance in wastewaters.

In 2019, Raphael Janssens completed a Ph.D. thesis assessing the toxicity of anti-cancer drugs in wastewater effluents. This research was conducted in the group devoted to eco-efficient processes for sustainable chemical and biochemical engineering at UCLouvain. In 2020, he started working for the national institute of public health in Belgium, Sciensano. Firstly performing exposure assessment of the Belgian population to the steviol glycosides food additive, and secondly joining the national wastewater-based epidemiology project dedicated to COVID-19.

WASTE WATER SURVEILLANCE FOR COVID AND FUTURE APPLICATION

Wastewater-based surveillance is used by Sciensano to monitor the SARS-CoV-2 circulation in the Belgian population. Over 5 million inhabitants representing 45% of the Belgian population are monitored at 42 wastewater treatment plants since September 2020. During the entire period, a high correlation was observed between the daily number of new cases and the wastewater concentration corrected for rain impact and covered population size. Three wastewater indicators were developed and included in weekly epidemiological assessments: High Circulation, Fast Increase, and Increasing Trend. The indicators were computed on normalized concentrations for each treatment plant to allow a comparison to a reference period as well as to avoid using absolute concentration values provided by different laboratories. Rainy events were assessed to cause an underestimation of the indicators computed on the viral concentrations. Despite this negative impact, the indicators permitted us to effectively monitor the evolution of several virus wave. Therefore, the aims of the wastewater surveillance program were successfully reached as weekly wastewater reports communicated to the Risk Assessment Group were considered complementary and valuable information to conventional epidemiological indicators.

Beyond Covid, Wastewater-based surveillance has also shown potential for other public health treats, such as Poliovirus, Antibioresistance or Illicit substances.

DIETER VAN CAUTEREN

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Dieter Van Cauteren joined the direction Epidemiology and public health of Sciensano in 2017, First at the Health services research unit as coordinator of a national sentinel GP network and since September 2019 as a epidemiologist at the service of Epidemiology of infectious diseases. His research mainly focuses on surveillance and the burden of bacterial foodborne infections. Before 2017 he worked for several years on vector-borne, foodborne and zoonotic infections at the department of infectious diseases of Santé publique France, the French Public Health Agency. He obtained a PhD in Public health-epidemiology at the university of Paris-Saclay in 2016.

INVESTIGATION OF AN INTERNATIONAL OUTBREAK OF MONOPHASIC *SALMONELLA TYPHIMURIUM* ASSOCIATED WITH CHOCOLATE PRODUCTS, APRIL 2022

Background:
17 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 assigned cases into two clusters (HC5:296366 and HC5:298160). We assessed the extent of the outbreak in Belgium and the need for 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. All isolates of probable cases and positive food isolates will be analysed by whole genome sequencing (WGS).

Results:
By 6 May 2022, 352 cases were reported in 12 European (EU) countries, the United Kingdom, Switzerland, Canada and the United States. In Belgium 62 probable cases were identified (39 cluster HC5:296366 and 23 cluster HC5:298160), with illness onset from mid-January until April and a peak in cases mid-February, 2022. Of these 62 cases, 87% were aged 1-9 years old and 48% had been hospitalized. Among the 44 interviewed cases, 41 (93%) reported consumption of products of the factory among whom 35 (85%) reported consumption of Kinder Surprise. Seven food products tested positive for *Salmonella*; WGS analysis indicated matches with both clusters. In December 2021, there was a positive auto-control 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.

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TIFFANY DIERINCK

AVIQ

BOGRAPHY

Nurse specialized in intensive care and urgent medical aid, I continued my learning by completing a Master's degree in Public Health Sciences with a critical patient focus, specializing in cardiac perfusion.

After working as an emergency nurse and cardiac perfusionist for several years, I reoriented myself towards pathologies with compulsory notification at the Infectious Diseases Surveillance Unit of the AViQ.

Passionate about germs of all kinds, I was able to improve my expertise while supporting Public Health. To do this, I contribute to the health alert system, to the surveillance and monitoring of infectious diseases, while offering scientific support to the various sectors of health prevention in collective environments, regardless of the target population.

REPORTING OF INFECTIOUS PATHOLOGIES IN THE PROVINCE OF LIÈGE AFTER THE FLOOD DISASTER OF 15 JULY 2021

During the month of July 2021, the eastern provinces of Belgium have been struck by a massive flood. Mostly concerned by this calamity, the province of Liège has been severely touched by the floodwaves in the Vesdre valley.

Since July 2021, the Infectious Disease Surveillance Unit of the Wallonian Region (SURVMI) has received several alerts of notifiable disease that could be related to the aftermath of this event. In our presentation, we show an overview of some of those cases mostly in the province of Liège but also in the surrounding provinces (Namur, Brabant-Wallon, Luxembourg). Those cases show a possible or confirmed link with the flooding. Additionally, we report the numbers of notifiable infectious disease reported to SURVMI during the months following July 2021 up to now.

We mostly focused on food-borne diseases, leptospirosis and legionellosis. Our aim is to show those numbers placing in the spotlight some specific clinical cases that could be interesting form a public health point of view. Also, we discuss and present the pros and cons of our project.

SOPHIE BLUMENTAL

ULB

BIOGRAPHY

Sophie Blumental, MD, PhD, is a pediatrician specialized in pediatric infectious diseases, consultant at Hôpital Universitaire des Enfants Reine Fabiola, Brussels. Her main fields of expertise are fungal infections, tuberculosis, *S. aureus* and *S. pneumoniae* diseases, congenital immunodeficiencies and varicella. After being graduated Medical Doctor in ULB with several dean of faculty awards, she did her pediatric training and ID specialty in the Brussels ULB network and 1 year in Necker hospital, Paris, France where she was trained to the management of primary immunodeficiencies. She further performed scientific researches in the Institute of Child Health, UCL, London, UK and in Hôpital Robert Picqué, Bordeaux, France in the setting of her PhD obtained in 2022 about preventing *S. pneumoniae* burden of disease. In this context, she also recently collaborated with the Belgian National Reference Lab for *S. pneumonia*, KULeuven, in studying invasive pneumococcal diseases epidemiology and dynamics. In 2014, she was granted by the award of the Belgian Society of Pediatrics for her clinical research. She is involved in academic teaching activities at ULB and is an active expert of the National Superior Health Council section vaccination.

PAST, PRESENT AND FUTURE OF ANTI-PNEUMOCOCCAL VACCINES

Streptococcus pneumoniae is a major human pathogen causing a wide range of invasive diseases (IPD) as well as respiratory tract infections. Recent data estimate that this bacterium is responsible for 14.5 million annual infections worldwide and >800,000 deaths in children less than 5 years of age. Outside the COVID-19 pandemic, *S. pneumoniae* is the first etiologic agent of low respiratory tract infections, encompassing community acquired- (CAP) and nosocomial- pneumonia, which accounts for 15% of childhood mortality and endorses significant impact in elderly. Unfortunately, major imbalances remain all over the world in terms of burden of this pathogen despite huge efforts of GAVI and WHO to roll-out vaccination. In developing countries, *pneumococcus* remains the leading cause of meningitis related- morbidity and -mortality among young children.

In our era when expansion of antibiotics resistances represents a major threat for human beings, global vaccination has now become the key component of the strategy to fight against *S. pneumoniae* burden. Launched for more than 30 years, anti-pneumococcal vaccination mainly relies on 23-valent polysaccharidic vaccine and protein-conjugated polysaccharides vaccines (PCVs) of variable valences. While introduction of PCVs in childhood vaccination programs definitely demonstrated substantial benefits worldwide by reducing total and vaccine-serotypes related IPD incidence, the emergence of serotypes not included in the vaccines (“replacement”) partly hindered the

success of vaccination campaigns, in addition to the persisting circulation of more invasive or resistant lineages, variable effectiveness across countries and existence of vaccine failures. Because directly due to the serotype-specificity of the PCV model, the replacement phenomenon appears to be a recurrent source of troubles arising after some years with variable patterns in every country where PCV mass vaccination has been implemented.This ineluctable limitation of PCVs opens the door for reflection around new tools and strategies for prevention such as development of innovative vaccines platforms independent from capsular serotypes, thorough monitoring of mid- and long-term vaccine impacts, identification of pathogenic clones and follow up of *S. pneumoniae* epidemiology according to genotypes (not only serotypes) and deeper investigation.

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ELIZAVETA PADALKO

UZ GENT

BIOGRAPHY

Elizaveta Padalko, M.D., Ph.D., is a Head of Clinic in the Laboratory of Medical Microbiology at Ghent University Hospital as well as Associate Professor of Clinical Virology at the Faculty of Medicine and Biomedical Sciences at Ghent University. She is an active member of several national organizations including Belgian National Committee for Eradication of Poliomyelitis and Sciensano Committee of Excellence in Infectious Serology. Elizaveta Padalko is the President of the Belgian National Verification Committee of the National Committee for Elimination of Measles and Rubella as well as the President of the Belgian National Microbiology Working Group, a part of the Committee for the Reimbursement in Clinical Biology. She serves as a nominated expert of the Belgian Superior Health Council. Her areas of research include evaluation of methods for diagnostic laboratories with accent on the Women's Health including role of infections in assisted reproduction, sexually transmitted infections, viral-based screening methods for cervical cancer, congenital and neonatal infections. In the present time of SARS-CoV-2 pandemic, she serves as a member of Belgian National Task Force on Test Strategy.

THE MEANING OF AUTOTESTING

Traditionally self-testing in general and for infectious diseases in particular is positioned for the laboratory parameters with rather intimate connotation (eg. pregnancy, sexually transmitted infections (STI's)) and/or intended use in vulnerable populations (eg. sex workers). Self-testing for STI's, in particular human immunodeficiency virus (HIV) and syphilis, has been intensively studied in the first place in the developing countries as necessary additions to the healthcare services. Also in developed world the self-testing for especially HIV has been welcomed, also by regulatory authorities, and included in the national strategies to combat HIV. Another successful use of rather self-sampling with unsupervised specimen collection can be observed as strategy to improve uptake for non-attendees of physician-provided services within national screening programs for cervical cancer in several countries with already implemented primary human papillomavirus (HPV) screening approach.

Despite the obvious advantages of self-testing including rapidity and individual organisational ease, there are concerning pitfalls ranging from adherence to pre- and analytical procedures till psycho-social support and linkage to care in case of positive result.

Unnecessary to mention that in the event of overwhelmed healthcare, as was worldwide the case during the last 2 years of coronavirus disease (COVID-19) pandemic, inclusion of availability of self-testing within the national strategies was applied and promoted. Nevertheless the success of the implementation of the self-testing with obvious help as welcome addition to the diagnostic tests performed in clinical laboratories or pharmacies and clear patient empowerment as result as well, state-of-the-art use of the test in the

relevant populations and frequencies of testing poses also now challenges to the health professionals.

Current presentation will focus on the variety and performance of self-testing strategies in different populations and for different purposes with overview of the available knowledge and modern trends in STI self-testing in developing and developed world as well as during COVID-19 pandemic discovered potential of application of self-testing as sustainable health control measure.

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PIETER-JAN CEYSSENS

SCIENSANO

BIOGRAPHY

Since little more than five years, I head the Unit 'Antibiotics & Resistance' at Sciensano. This unit is embedded on the division of Bacterial Diseases, which groups National Reference Centers (NRCs) of *Salmonella, Shigella, Listeria, Yersinia, Neisseria* and *Mycobacteria*. On a routine basis, we monitor emerging drug resistance in these human pathogens on both phenotypic and genotypic level.

The last years, my personal research focus included (i) the implementation of a quality control system for therapeutic bacteriophages, to be used in magisterial preparations, (ii) the genetic analysis of increasing AMR in *Shigella* and *Salmonella spp.*, and (iii) the development of a novel diagnostic for phenotypic drug susceptibility testing in *Mycobacteria,* based on quantification of RNA biomarkers. I am One Health focal point for Antimicrobial Resistance at Sciensano (2018-2023), elected member of the board of directors of the Belgian Society of Microbiology (2021-2027), member of the National Antibiogram Committiee, Belgian Pharmacopeia submission Biology (2021-2026) and chair of the EU working group on the establishment of a General Chapter on phage therapeutics in the European Pharmacopeia.

DRUG RESISTANT *SHIGELLA SONNEI* INFECTIONS IN MSM

Shigella species are highly virulent Gram-negative bacteria belonging to Enterobacteriaceae family. Around 300-400 cases are annually reported in Belgium with *S. sonnei* (75%) and *S. flexneri* (21%) being the two most important subgroups. A decrease of *S. sonnei* cases reported occurred between February 2020 and August 2021 (possibly related to the COVID-19 pandemic and the measures taken to limit close contacts). Since September 2021 (lifting measures, travel) numbers are rising again.

On 27 January 2022, the United Kingdom reported an increase in extensively-drug resistant *Shigella sonnei* infections, mainly in adult men who have sex with men (MSM). Several European countries (including Belgium) then reported cases (sampling dates from 2020 to 2022) with isolates either closely genetically related by whole genome sequencing (WGS), or with the same or very similar resistance profile. WGS is not routinely performed on all *Shigella* samples in Belgium. Analysis made by the NRC of a random set of resistant S.sonnei samples (n=20) identified 4 strains belonging to the UK cluster, isolated from male patients between July and September 2021. Phenotypic AMR assessment of these isolates indicates resistance against azithromycin, ciprofloxacin and cephalosporins for 24% (31/128). Additionally, the NRC identified successive/parallel clusters of drug-resistant *S. sonnei* circulating among MSM (five with the new UK cluster included) in a retrospective analysis of a set of S. sonnei strains (2017-2019).
I will present the latest updates on this outbreak, and measure taken to curtail it.

For more than 170 years, we have worked to make a difference for all who rely on us. Every day, we apply our science and our global resources to bring therapies to people that extend and significantly improve their lives.

#ScienceWillWin

Breakthroughs that change patients' lives

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ABSTRACT OF POSTERS

EMERGENCE OF THE EPIDEMIC EUROPEAN FUSIDIC ACID-RESISTANT IMPETIGO CLONE (EEFIC) IN BELGIUM

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Introduction

The Belgian *Staphylococcus* National Reference Centre (NRC) collects and analyses prospectively *S. aureus* isolates sent on a voluntary basis by clinical laboratories for exotoxins detection. This allowed the detection in 2018 of clusters of community-acquired (CA) skin and soft tissues infections (SSTIs) caused by a particularly virulent and resistant epidemic clone: the Epidemic European Fusidic acid-resistant Impetigo Clone (EEFIC), a CC121 Methicillin-Sensitive *S. aureus* (MSSA) carrying exfoliatin A and/or B genes (*eta* and/or *etb*). A national surveillance was subsequently conducted aiming at assessing the epidemiology of *S. aureus* causing CA-SSTIs and the EEFIC prevalence.

Materials/methods

From 2012, isolates voluntary sent to the NRC for exotoxins detection were explored for their antibiotic sensitivity and the presence of the genes coding for the Panton-Valentine Leucocidin (*lukSF*-PV), the Toxic Shock Syndrome Toxin-1 (*tst*), and *eta* and *etb*. Additionally, from March 2020 to March 2021, Belgian clinical laboratories were invited to prospectively collect three consecutive non-duplicate SSTI-causing *S. aureus* isolates per month. These additional isolates were screened for cefoxitin, fusidic acid and mupirocin resistance. Resistant isolates underwent exotoxins detection and *spa*-typing. Isolates were defined as "EEFIC" if MSSA, fusidic acid-resistant, carrying eta and/or *etb* genes and a *spa*-type related to CC121.

Results

From 2012 to 2021, 2032 superficial skin lesions-related isolates were sent to the NRC including 1147 (56.4%) MSSA. Among MSSA, 355 (31.0%) strains carried *lukSF*-PV, 242 (21.1%) *eta* and/or *etb*, 87 (7.6%) *tst*. The proportion of MSSA carrying *eta* and/or *etb* increased dramatically from 13/100 (13.0%) in 2012-2013 to 69/201 (34.3%) in 2018. Meanwhile, the proportion of fusidic acid-resistant MSSA increased from 9/99 (9.1%) in 2012-2013 to 61/201 (30.3%) in 2018, of which 49/61 (80.3%) carried *eta* and/or *etb* including 45 EEFIC. The prevalence study gathered 526 isolates including 495 (94%) MSSA of which 81 (15.4%) were fusidic acid-resistant. *eta* and/or *etb* were found in 40 (49.4%) and 39/40 belonged to the EEFIC. Four (10.3% of EEFIC) were co-resistant to mupirocin. Of note, the median age was 8 years old for the EEFIC sub-group of patients as compared to 52 years old for the entire MSSA group.

Conclusion

Since 2018, EEFIC spread successfully in the Belgian community. Its diffusion is worrisome as it combines well-known virulence factors associated with impetigo and resistance to fusidic acid, a commonly used first-line topical ambulatory treatment. The prevalence of fusidic acid resistance should, from now on, be closely monitored, and its use as first-line treatment should be reconsidered, especially in children SSTI, as it could exert a selection pressure favouring EEFIC.

REDUCTION IN SEROTYPE 19A INVASIVE PNEUMOCOCCAL DISEASE IN YOUNGEST CHILDREN IN THE SECOND YEAR POST RE-SWITCH FROM PCV10 TO PCV13 IN BELGIUMM

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Background

Several switches in the childhood pneumococcal conjugate vaccines (PCVs) programme have taken place in Belgium. After introduction of PCV7 in 2007, PCV13 was installed in 2011, which was switched to PCV10 in 2015-2016. After this change, a re-emergence of serotype 19A invasive pneumococcal disease (IPD) in children was observed. In 2019, PCV13 was reinstalled in the childhood vaccination programme. Compared to PCV10, PCV13 includes three additional *pneumococcal* serotypes: 3, 6A and 19A.

Materials/methods

Surveillance of IPD in Belgium is based on a stable laboratory-based system involving yearly a mean of 100 laboratories, evenly spread over the country, sending their IPD strains to the National Reference Centre for Invasive Pneumococci, for capsular typing by Quellung reaction. IPD cases in children (<2 years) diagnosed in the years 2014 to 2021 were analysed.

Results

Due to the restrictive measures to contain the COVID-19 pandemic, a significant and sustained reduction in IPD cases in children was observed in 2020 and 2021, respectively a reduction of 39% and 34% compared to 2018-2019. Therefore, data of the proportion of serotypes 3, 6A and 19A was evaluated for all IPD cases diagnosed in 2014-2015 (PCV13), 2018-2019 (PCV10) and 2021 (second year after re-switch PCV13). As previously published, a significant increase of 19A cases was observed in children following the PCV13 to PCV10 switch (Desmet et *al.* 2021), multiplying the proportion of this serotype 10-times (3.3% for PCV13 period versus 33.9% for PCV10 period). After the re-switch to PCV13 we observed a reduction by 59%, to 14.0% serotype 19A in 2021. While serotype 6A was not reported in Belgium, a steady but slow increase of serotype 3 was observed, from 2.2% (PCV13) to 5.4% (PCV10), remaining stable at 5.4% in 2021.

Conclusion

Belgium has a unique experience of switching PCV's in the childhood vaccination programme over time. While IPD epidemiology is disturbed by the COVID-19 pandemic, serotyping data from 2021 indicate again a decrease in the proportion of serotype 19A IPD, one to two years post PCV10 to PCV13 switch.

DETAILED MOLECULAR TYPING OF ENTEROVIRUS POSITIVE SAMPLES FOR THE YEARS 2020 AND 2021 CONFIRMS ENTEROVIRUS SPECIES B AS MOST PREVALENT SPECIES IN BELGIUM

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Background

*Enteroviruse*s (EV) compromise a large genus including fifteen species: *Enterovirus species* A-L and *Rhinovirus* A-C. Human enteroviruses infect millions of people worldwide every year. While most infections are asymptomatic, they have also been associated with a wide spectrum of both common and uncommon illnesses. Since 2014, EVD68 is emerging worldwide and is receiving high attention of public health authorities because of its magnitude and clinical presentation.

Materials/methods

In the context of epidemiological surveillance in Belgium, enterovirus positive samples received by the national reference centre (NRC) at UZ/KU Leuven, were genotyped. Molecular typing was done by RT-PCR using different primer sets. Enterovirus species A and B were typed by sequencing part of VP1, while for species C and D, the VP4/VP2, VP1 and the non-coding region were used.

Results

For the years 2020 and 2021, respectively 4885 and 4511 samples originating from 90 and 47 Belgian laboratories were analysed, of which the large majority (85.4% and 83.8%) were respiratory samples subjected to a broad panel of respiratory parameters including *Enterovirus/Rhinovirus* detection. Of those, 577 (11.8%) and 560 (12.4%) samples respectively, originating from 393 and 413 individuals, were found to be EV-positive. For 2020, the large majority of respiratory samples (95.2%) were not genotyped and hence only classified as *Entero/Rhinovirus*. For the 34 cases (out of 393) for which molecular typing information was available, almost half of them were identified as EV species B, followed by EVD68 (23.5%), EV species A (14.7%) and *Rhinoviruses* (14.7%). For the 413 EV-positive cases of the year 2021, almost 90% was typed in detail: 67.3% as *Rhinoviruses*, 7.7% as EV species A, 19.7% as EV species B and 5.3% as EVD68. When excluding respiratory samples which can largely be attributed to *Rhinovirus* infections, EV species B was by far the most dominant species detected (85.2%) in the 54 faecal and CSF samples (more in detail 61.1% *echoviruses* and 13.0% *coxsackie* B).

Conclusion

For the samples for which typing information was available, EVD68 was detected in respectively 23.5% and 5.3% of the cases for 2020 and 2021. However, note that the share of samples that was typed substantially differs for these two years (8.7% and 88.7%) since not every year all respiratory samples are subjected to molecular typing. Focusing on the sample types CSF and faeces, for both years, EV species B was the most prevalent species detected. In general, the number of enterovirus positive cases for the years 2020-2021 was impacted due to the SARS-CoV-2 pandemic.

NATIONWIDE HARMONIZATION EFFORT FOR SEMI-QUANTITATIVE REPORTING OF SARS-COV-2 PCR TEST RESULTS IN BELGIUM

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Background

The rapid scale-up of testing capacity in combination with a testing strategy linked to contact tracing, including intense screening of asymptomatic persons, resulted in the massive roll-out of PCR assays to combat the SARS-CoV-2 pandemic. Most PCR assays report in cycle threshold values that can highly vary across different methods, complemented with supply chain issues forcing many clinical laboratories to adopt multiple SARS-CoV-2 PCR methods, causing the need to report beyond a qualitative test result. As most PCR assays are not designed to report quantitatively, it was chosen to move towards a semi-quantitative approach to provide more details to clinicians with respect to the stage of infection, and indirectly the potential link with infectivity, although interpretation still requires a clinical and/or serological context.

Materials/methods

A proposal to harmonize the reporting of test results in Belgium was drafted by the National Reference Centre (NRC), distinguishing four categories of positivity based on RNA copies/ml: very strongly positive (≥10^7 copies/ml), strongly positive (≥10^5 - <10^7 copies/ml), moderate positive (≥10^3 - <10^5 copies/ml) and weak positive (<10^3 copies/ml). Pre-quantified SARS-CoV-2 control material was prepared and shipped in February 2021 to 124 recognized COVID-19 testing laboratories across Belgium to setup a standard curve to define thresholds for their specific assay(s) in use.

Results

The SARS-CoV-2 control material was determined with a viral load of 9.04 log copies/ml and classified as type 20A according to Nextclade and to Pangolin lineage B.1.160 following whole-genome sequencing. In total, 91 labs shared the results of the respective standard curve(s) with the NRC. When applying predefined inclusion criteria, the results for 17 PCR assays were considered for downstream analyses. The top five most commonly used kits were: TaqPath COVID-19 CE-IVD RT-PCR kit (n=21), Allplex™ SARS-CoV-2 Assay (n=20), Xpert® Xpress SARS-CoV-2 (n=12), GeneFinder™ COVID-19 Plus RealAmp Kit (n=11) and Xpert® Xpress SARS-CoV-2/Flu/RSV (n=11). For each of the 17 assays, the mean cycle threshold (Ct) value or equivalent metric, and the corresponding standard deviation, was calculated per target gene, for the three concentrations (10^7, 10^5

and 10^3 RNA copies/ml) that determine classification into the four proposed categories. If more than one SARS-CoV-2 target gene was included in the assay, an advice was provided on the gene recommended for semi-quantitative reporting, based on sensitivity, accuracy and reproducibility complemented with the current knowledge on circulating SARS-CoV-2 variants with respect to potential impact on PCR performance.

Conclusion

Thanks to this harmonization effort, many Belgian laboratories currently report in the same semi-quantitative manner to clinicians and to healthdata.be, supporting the national contact tracing system. Due to the massive roll-out of PCR assays, including in the context of intense screening of asymptomatic persons, and the high number of infections, recently contact tracing only focused on infections being categorized as very strongly positive and strongly positive SARS-CoV-2 test results.

EPIDEMIOLOGICAL SURVEILLANCE OF *HANTAVIRUSES* IN THE YEARS 2020 AND 2021

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Background

Hantaviruses are the only zoonotic viruses found worldwide and are associated with two severe human diseases, haemorrhagic fever with renal syndrome (HFRS) and hantavirus pulmonary syndrome. The European variant *Puumala orthohantavirus* (PUUV), carried by *Myodes glareolus* or bank vole, causes a specific form of HFRS, called nephropathia epidemica, of which over 3000 cases have been confirmed in Belgium. *Hantavirus* infections in humans are caused by inhalation of aerosolized virus particles from excreta of infected rodents.

Materials/methods

Diagnosis of hantavirus infections can be performed by demonstration of specific IgM antibodies (Abs) and a rising IgG titre, or by RT-PCR. At the National Reference Centre (NRC), IgM and IgG detection is performed by ELISA, detecting Abs to various hantavirus species (PUUV, DobravaBelgrade and Hantaan virus), while other species are only detected by an Immunoblot assay. In urgent cases, a rapid PUUV IgM assay is performed.

Results

Compared to the years 2018 and 2019, for which samples of respectively 600 and 713 suspected cases were analysed in the context of hantavirus diagnosis, the SARS-CoV-2 epidemic clearly influenced the number of cases that were sent to the NRC in 2020-2021. With 536 and 502 suspected cases respectively for these years, a decrease of almost 25% to 30% was observed compared to 2019. Typically, epidemic years of hantaviruses alternate, with the year 2018 accounting for a positivity rate (PR) of 7%, while 2019 was classified as an epidemic hantavirus year due to an increased PR of 15.7%. For 2020, again a lower PR of 8.8% was identified at the NRC, accounting for 47 hantavirus cases, while 2021 can be appointed as epidemic year with a PR of 16.1% and 81 cases. While the province where the case is living is not necessarily the same where the person was infected, this information was used to evaluate the difference in number of cases between Belgian provinces. In 2020, most infections were associated to the province of Hainaut (31.9%), followed by Antwerp (23.4%). Overall, for 2020, 53.2% of the cases were in Wallonia, in contrast to the year 2021 for which more cases were associated to Flanders (64.2%) since the largest number of hantavirus cases were detected in Limburg.

Conclusion

While for 2020-2021 a lower number of hantavirus samples was sent to the NRC, the year 2021 was classified as a hantavirus epidemic year with a positivity rate of 16.1%. Despite 2020 being characterized with a lower number of hantavirus cases, a clear difference in geographical dispersion of the hantavirus infections is noted between the years 2020 and 2021.

AN INCREASE IN G2-GENOTYPE *ROTAVIRUS* STRAINS AMONG POSITIVE CASES TYPED AT THE NATIONAL REFERENCE CENTRE UZ/KU LEUVEN FOR THE SEASONS 2019-2020 AND 2020-2021

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Background

Rotavirus incidence and genotype distribution in Belgium have been monitored since the 1999-2000 rotavirus season at UZ Leuven. While rotavirus incidence has strongly decreased since the introduction of the Rotarix® and RotaTeq® vaccines into the Belgian childhood vaccination program in 2006 and 2007, it remains key to evaluate the effects of vaccination on the rotavirus population and to monitor the possible appearance of animal-like genotypes into the human population.

Materials/methods

A large number of hospitals, private laboratories and paediatricians across Belgium participate to the *Rotavirus* Surveillance Network Belgium, for which data for the thirteenth (20192020) and fourteenth (2020-2021) seasons are presented. Rotavirus genotype was determined using reverse transcription polymerase chain reaction assays at the national reference centre (NRC).

Results

For both seasons, a substantial lower number of samples was received at the NRC, most likely due to the SARS-CoV-2 pandemic. For 2019-2020 and 2020-2021, respectively 82.4% (94/114) and 65.5% (72/110) of the samples was found positive and could be genotyped. This low number of cases is also reflected in a low positivity rate of rotavirus gastroenteritis at UZ Leuven, respectively 1.5% and 1.1%. Despite the low number of rotavirus positive samples, the genotype distribution was in line with that of the two previous seasons characterized by multiple co-circulating strains, without a clear dominant genotype for season 2019-2020. For 2019-2020, the genotypes most often detected, were G1P[8] (11.7%), G2P[4] (26.6%), G3P[8] (14.9%) and G9P[4] (27.7%). For season 2020-2021, again a dominant genotype was identified, with 55.6% of the cases classified as G2P[4]. Despite the use of live attenuated vaccines for more than a decade, very little evidence of their circulation in the human population exists.

Conclusion

For the last two years, a very low number of samples has been sent to the NRC. While it will be hard to predict the impact of the SARS-CoV-2 pandemic on future rotavirus seasons, it could be speculated that more severe seasons are to be expected due to a decreased viral circulation and an increasing number of susceptible infants. Following the lowest prevalence of G2 since the start of

surveillance in Belgium for 2018-2019, in 2019-2020 this genotype was again detected in a quarter of cases, and this increasing tendency was continued in 2020-2021 with more than half of the cases being caused by G2 rotavirus strains. To retain a strong surveillance in a country with a high rotavirus vaccination coverage, we stress the importance of sending rotavirus positive samples to the NRC.

VALIDATION OF ELITE INGENIUS ® AND *BORDETELLA* ELITE MGB® KIT FOR THE MOLECULAR DIAGNOSIS OF *BORDETELLA PERTUSSIS* AND RELATES SPECIES

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The clinical laboratory of microbiology of the UZ Brussel, which acts as the Belgian National Reference Centre (NRC) for *Bordetella pertussis* together with the Sciensano Service of Immunology, currently utilises an in-house developed qPCR assay for the detection and identification of *Bordetella pertussis*, *B. parapertussis* and *B. holmesii* in respiratory samples (Martini et al., 2017).

We evaluated the CE-IVD-labelled ELITe InGenius® device, together with the Bordetella ELITe MGB Kit® (ELITechGroup) as an IVD-approved alternative to the in-house assay. Both assays are based on two screening targets: IS481 and IS1001; as well as two confirmation targets: *recA* and IS1002 (in-house assay) or *ptxA-Pr* (ELITe assay).

The ELITe InGenius®, an automated benchtop instrument, enables sample-to-result processing, as it is capable of nucleic acid extraction, real-time PCR and result interpretation in a single run. This limits the hands-on work time.

In our validation efforts, accuracy was evaluated by performing the assay on a selection of 85 respiratory samples, previously tested with the in-house PCR. Both methods showed full concordance with regard to the sample result after interpretation.

A limited verification of the sensitivity confirmed or surpassed the limits of detection claimed by ELITechGroup. This verification was done for all three species, using negative nasopharyngeal aspirates spiked with a known concentration of a reference strain or recent clinical strain.

Both intra-run and inter-run precision sufficed, with coefficients of variation not surpassing 3% for any of the targets or species.

Two runs were performed with alternating high-concentration samples and negative controls in order to check for cross-contamination. None was detected.

Finally, a selection of *Bordetella* spp. different from the three target species was tested in order to assess specificity. Most showed no cross-reactivity, minor cross-reactions were observed for *B. bronchialis*, *B. bronchiseptica* and *B. flabilis*, these results were concordant with those of the in-house PCR.

Significant cross-reactivity was observed for *B. petrii*, this is currently being investigated further.

In conclusion, the ELITe InGenius® and Bordetella ELITe MGB Kit® showed satisfactory results in terms of accuracy, sensitivity, precision and specificity, for the detection of *B. pertussis, B. parapertussis* and *B. holmesii* in respiratory samples.

THE IMPACT OF THE COVID-19 PANDEMIC ON THE INFECTION PREVENTION AND CONTROL PROGRAMMES IN BELGIAN ACUTE CARE HOSPITALS

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Background

In Belgium, several core components of infection prevention and control (IPC) programmes were defined by an expert group. Since 2014, acute care hospitals (N=104) are legally required to report these annually. Based on this registration a score per hospital is calculated and made publically available. The objective is to define, prioritize and implement strategies and interventions to prevent health-care associated infections (HCAI), in order to improve the quality of care. Based on the 2020 data we assessed the impact of COVID-19 on these IPC core components.

Materials/methods

A total of 65 indicators divided in 4 subgroups (organisation; resources; activities and process) were registered annually by the hospitals in a dedicated online platform. Due to the COVID-19 pandemic registration of 2020 data no longer was mandatory (participation rate 70%, n=73). For each indicator the proportion of hospitals implementing the indicator was calculated.

Results

At large 2020 findings were similar to 2015-2019 results. At least 95% of the participating hospitals met 33 of the 65 indicators and six of these were met by all hospitals. A decrease of more than 10% was seen in the proportion of hospitals that complied with specific indicators (n=12), of which most were related to auditing (n=10 out of 13; figure 1).

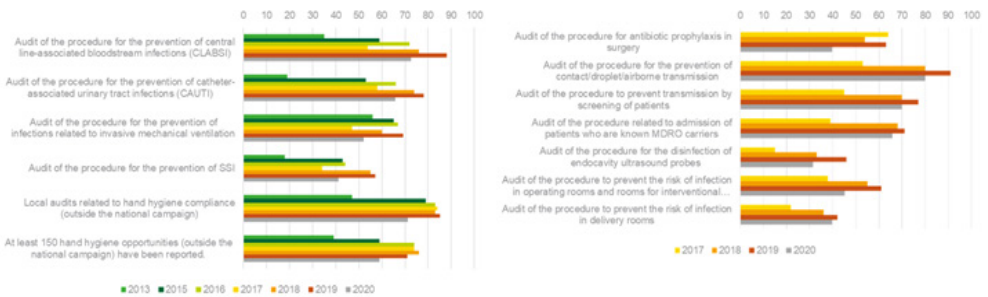

Figure 1: Proportion of Belgian acute care hospitals meeting indicators related to auditing, per year

Alcohol-based hand rub consumption can be seen as an indicator of hand hygiene compliance and is included as a process indicator within the project. Since 2013, this consumption increased, but a sharper increase has been observed between 2019 and 2020 (figure 2).

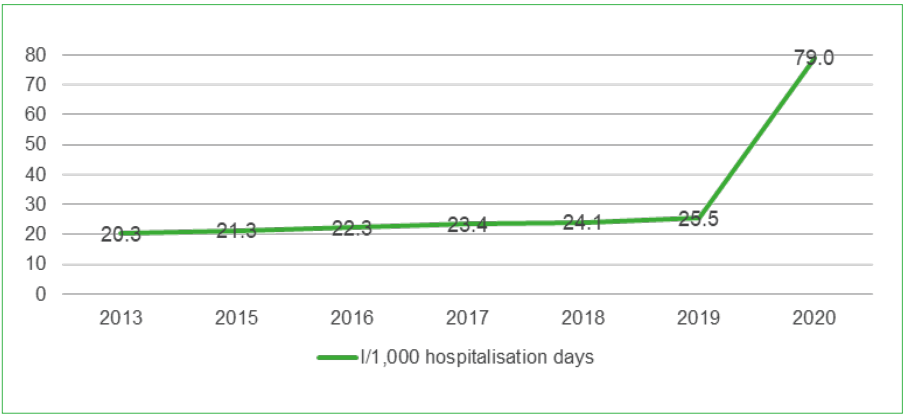

Figure 2: Alcohol-based hand rub consumption in litre per 1,000 hospitalisation days in Belgian acute care hospitals, per year

Conclusion

Despite the COVID-19 pandemic, at least 95% of the participating Belgian hospitals met half of the IPC core components in 2020. Less implemented IPC core components were often related to auditing. Possible hypotheses for this decrease are (1) time constraints due to additional tasks by the COVID-19 pandemic for the IPC team; (2) COVID-19 mitigation measures have hindered the implementation of these components hospital wide. Since the COVID-19 pandemic, a sharp increase in the consumption of alcohol-based hand rub has also been observed. Although, this registration could not verify if this was due to an improved hand hygiene compliance among the health care workers.

PERFORMANCE OF GRADIENT STRIP TESTS FOR DETECTION OF VANCOMYCIN RESISTANCE IN *ENTEROCOCCI*

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Background

Detection of vancomycin-resistant enterococci (VRE) can be challenging in case of low level resistance. EUCAST has recently issued a warning with regard to unreliable test results of gradient strip tests for VRE confirmation. Our study evaluates the performance of gradient strip tests in comparison with the reference broth microdilution (BMD) method for the detection of vancomycin resistance in enterococci.

Materials/methods

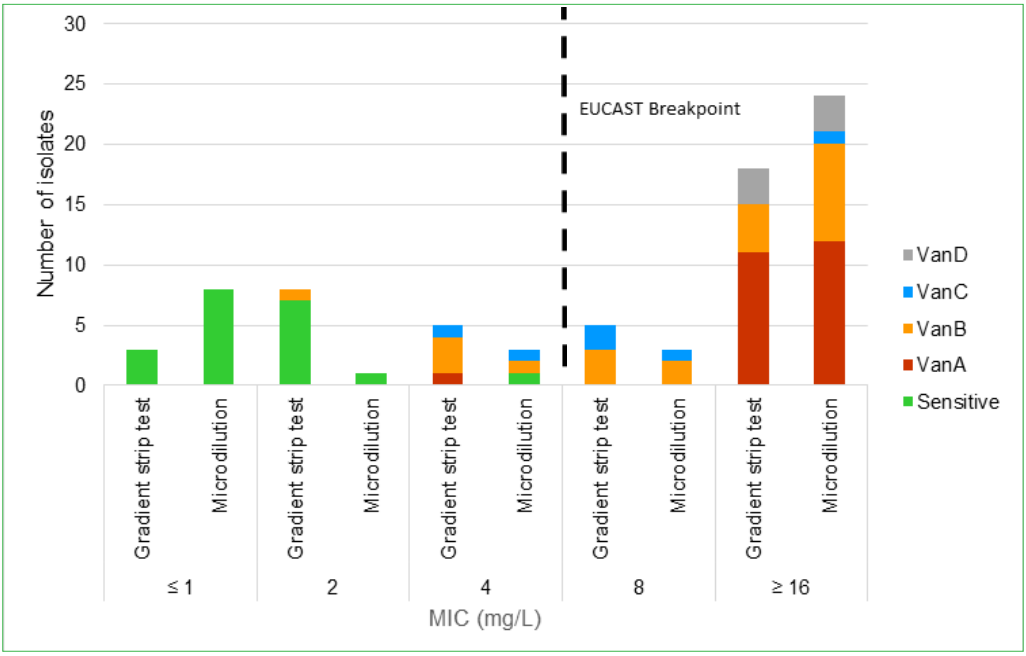
VRE resistant *Enterococcus spp*. strains (n=39), submitted to the Belgian National Reference Centre for Enterococci in 2017 to 2021, were selected based on different MIC values for vancomycin and different resistance mechanism. Glycopeptide resistance was confirmed by detection of a vancomycin resistance gene (van*A* - *D*) by in-house PCR. A 0.5 McFarland bacterial suspension was prepared to apply the vancomycin ETEST® (bioMérieux, France) or prepare the EUENCF microdilution plate (Sensititre™; Thermo Fisher Scientific, Cleveland, OH, USA). MIC values were interpreted after 24h of incubation by 35 ºC.

Results

The sensitivity of gradient strip tests for detection of vancomycin resistance was 79.3% compared to 89.7% for BMD. 1/12 *vanA* (8%), 4/11*vanB* (36%) and 1/3 *vanC* (33%) enterococci were interpreted as sensitive, with MIC values below the EUCAST breakpoint, using gradient strip tests. BMD resulted in higher MIC values and misclassification of 1/11 *vanB* (9%) and 1/3 *vanC* (33%) positive strain as vancomycin sensitive.

Conclusion

Mainly, *vanB* positive enterococci are difficult to detect with gradient strip tests compared to BMD. It should therefore be recommended to use an additional technique (like van gene PCR) to confirm/exclude vancomyin resistance when MIC values of 2 and 4 µg/ml are obtained by gradient strip tests.


30
25
20
15
10
5
0
Number of isolates
EUCAST Breakpoint
VanD
VanC
VanB
VanA
Sensitive
Gradient strip test
Microdilution
≤ 1
2
4
8
≥ 16
MIC (mg/L)

EFFECT OF COVID-19 VACCINATION CAMPAIGN IN BELGIAN NURSING HOMES ON COVID-19 CASES, HOSPITAL ADMISSIONS AND DEATHS AMONG RESIDENTS

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In view of the grave situation during the first two waves, nursing homes (NH) were prioritised for vaccination once available in Belgium. The aim of this study is to assess the effect of COVID-19 vaccination campaign on COVID-19 cases, hospital admissions and deaths among residents living in Belgian NH. All 1,545 Belgian nursing homes (NH) were invited to participate in a COVID-19 surveillance. In Belgium, before vaccination, COVID-19 morbidity and mortality rates were driven by the situation in the NH. Shortly after the COVID-19 vaccination and later the booster campaign the number of hospital admissions and deaths among NH residents dropped, while clear peaks could be observed among the general population (Figure 1). Although the impact of (booster) vaccination on virus circulation was less effective than expected and hoped, due to the high vaccination coverage, NH residents remain well protected against hospital admission and death due to COVID-19 more than one year after being vaccinated.

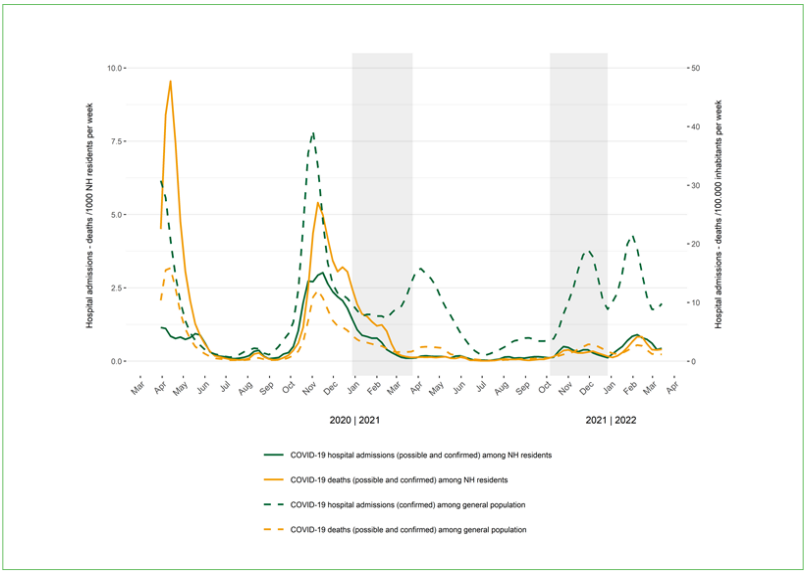

Figure 1: Hospital admissions and deaths per 1,000 nursing home (NH) residents and hospital admissions and deaths per 100,000 inhabitants (including NH residents), per week (two-week moving average), 6 March 2020 – 20 March 2022 - grey boxes indicate the COVID-19 vaccination campaign and the booster administration in NH

TOWARDS A NEW (H)ERA: PREPAREDNESS FOR OUTBREAK DETECTION AND RESPONSE

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In response to the COVID-19 pandemic, the European Commission established the European Health Emergency Preparedness and Response Authority (HERA) to strengthen its Member States' crisis preparedness and response to major national and cross-border health threats. The subsequent emerging novel *SARS-CoV-2* variants led to the launch of the HERA-Incubator, including an initiative aiming to improve the national capacities and infrastructures for Whole Genome Sequencing (WGS) for pathogen-typing. More specifically, the Belgian HERA-Incubator-WGS project focuses on sustaining the monitoring and reporting of *SARS-CoV-2* variants as well as building a preparedness infrastructure: a secured, national e-health infrastructure to strengthen preparedness to detect and respond to infectious disease outbreaks.

Laboratory capacities for pathogen WGS-analyses have increased tremendously during the COVID-crisis, however, no centralized and standardized national genomic data is available, and therefore, it is of importance to design that infrastructure. This project aims to design and implement a centralized Bio-Informatics (BioIT) platform linked to the e-health infrastructure to allow standardized and automated analysis and re-analysis of genomic data. Secondly, this project aims to facilitate the digitalisation of the national reference centres' (NRCs) data collections, in order to allow combined genomic-epidemiologic analysis and to strengthen the public health response.

To do so Sciensano, including healthdata.be, is describing the functional requirements of the to-be infrastructure, and collecting the needs of public health actors such as National Reference Centres (NRCs), Laboratory Information Management System experts, bioinformaticians, epidemiologists, and the regional health authorities. In the first phase, five study case pathogens (*Listeria, Salmonella, Tuberculosis, SARS-CoV-2*, and *Influenza*) are selected for the design, development, and validation of the system, due to their outbreak-prone nature and the added value of pathogen-typing for public health. The project envisages data input through standardized data collection definitions (DCDs) covering the "classic" NRC data collection, as well as WGS data, in other words: genomic data collected by national reference centers and clinical labs, as well as epidemiologic, and clinical information collected by the NRCs will be consolidated into the secure national e-health system. The data collections will include the host-identifier, which will be processed in line with data privacy and protection regulations. After processing, data outputs can be generated, in order to allow data exchange to the relevant public health actors, in line with data governance guidance, yet to be defined together with these actors. Moreover, the project aims for the infrastructure to allow for real-time data for mandated actors and the continuation and extension of the current automatic reporting, such as the early

warnings and the automatic dashboards. Finally, the infrastructure aims to allow a quick scale-up to process larger data volumes during an epidemic crisis situation.

In conclusion, this HERA project will strengthen the outbreak detection and investigation, by centralizing genomic, clinical, and epidemiologic surveillance. All these features of the database will lead to a significant increase in overall preparedness. Further perspectives, after the first-year design and implementation for the first study cases, are the roll-out to additional pathogens of all NRCs and National Reference Laboratories, including a one health perspective. The centralized and standardized approach opens additional opportunities to swiftly react to infectious disease outbreaks and hence, will start a new era of health emergency preparedness in Belgium.

POLYCLONAL BURKHOLDERIA CEPACIA OUTBREAK ORIGINATING FROM CONTAMINATED WASH GLOVES

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Introduction

Burkholderia cepacia complex (Bcc) bacteria are opportunistic pathogens that cause infections in cystic fibrosis and immunocompromised patients. Bcc bacteria can spread among hospitalised patients through person-to-person transmission, contaminated liquids and surfaces and are notorious for their persistence in aqueous solutions. We describe two episodes of a polyclonal *B. cepacia* outbreak at a Belgian intensive care unit due to contaminated wash gloves.

Materials/methods

Bcc was isolated from routine clinical samples from nine ICU patients of the Belgian intensive care unit (ICU) in April-May 2019 and January 2020. Cultures for Bcc were taken from several hygienic products and the suspected wash gloves. In the framework of the NRC Bcc, all resulting Bcc isolates were investigated by MALDI-TOF MS (Bruker) for identification and Randomly amplified polymorphic DNA (RAPD) for typing. Identification and genotyping were confirmed by *recA* gene sequence analysis and whole-genome sequence based multilocus sequence typing (MLST), respectively. More detailed genomic analyses were performed using single-nucleotide polymorphism (SNP) analyses.

Results

Five out of seven patient isolates from April-May 2019 were identified as *B. cepacia* (n=5). One of two tested wash glove packages was culture positive and the investigated wash glove isolate was identified as B. cepacia. RAPD typing showed an identical pattern for four *B. cepacia* patient isolates and the wash glove isolate, and a different pattern for the remaining *B. cepacia* patient isolate. MLST analysis confirmed the RAPD typing results and identified the two *B. cepacia* RAPD patterns as ST-1649 (n=5) and ST-767 (n=1). The manufacturer confirmed the contamination of one lot by *Burkholderia* (but provided no cultures) and reported to have taken measures to avoid further contamination.

The three patient isolates from January 2020 were all *B. cepacia* ST-767 (n=3, two isolates from same patient). One out of four tested wash glove lots was culture positive and yielded both *B. cepacia* ST-767 and ST-1649. After abandoning the use of wash gloves from this manufacturer no new cases were recorded SNP analysis showed a maximum of 12 and 6 SNPs among B. cepacia patient and wash glove genomes of ST-767 and ST-1649, respectively

Conclusion

Recovery of *B. cepacia* from several ICU patients led to a small-scale outbreak investigation and identified contaminated wash gloves as the outbreak common source. Remarkably, in the course of the present study, *B. cepacia* ST-767 and ST-1649 contaminated wash gloves from the same manufacturer were reported as the cause of an outbreak in a heart clinic in Switzerland.

References

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USEFULNESS OF SYSTEMATIC MOLECULAR INFLUENZA SCREENING IN PATIENTS ADMITTED TO THE HOSPITAL DURING AN EPIDEMIC WAVE: POSITIVITY RATIOS AND VIRAL LOADS ACCORDING TO SYMPTOMATOLOGY

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Introduction

Systematic molecular screening for SARS-CoV-2 was implemented for hospitalized patients in the "Ziekenhuis Netwerk Antwerp" in order to prevent nosocomial transmission. The screening was performed irrespective of symptoms or reason for admission. Nasopharyngeal swabs were analyzed on the Roche Liat platform (Roche Diagnostics®), producing results for both SARS-CoV-2 and Influenza A/B. The purpose of the study was to evaluate Influenza positivity ratios according to symptomatology at presentation. Viral loads were calculated in perspective of symptoms and Influenza vaccination status. The study was conducted during the Belgian epidemic 2022 Influenza wave, beginning in February.

Materials/methods

Only screenings performed for patients that were hospitalized following a visit at the emergency department were included. Results of the Roche Liat PCRs that were executed between 1st February 2022 and 23 March 2022, were extracted from the Laboratory Information System. The extraction included patient characteristics (age, gender, date of admission, date of discharge) and test characteristics (date of analysis, Ct-value for positive samples). The symptomatology and the reason for hospitalization were obtained from the medical reports. The vaccination status was found in the online national registry (Vaccinet). Classification of the symptomatology included: asymptomatic carriership for patients without viral symptoms, mild illness for patients with viral symptoms who did not have clinical evidence for lower respiratory disease, moderate illness for patients with evidence for lower respiratory disease (shortness of breath, abnormal chest imaging) but without the need for oxygen supply, severe illness for patients who needed oxygen supply (SpO2 <94%, respiratory rate >30 breaths/min), critical illness for patients with respiratory failure or evolution to shock, and deceased patients. Statistical analysis included the positivity ratio for each week, symptomatology distribution in positive subjects, Ct-value distribution for each category of symptomatology and comparison of symptomatology for vaccinated versus non-vaccinated patients.

Results

A total of 2523 patients were tested at hospital admission of whom 107 tested positive for Influenza A. The positivity ratio was 1.7%, 1.4%, 2.4%, 3.0%, 3.6%, 6.6%, 10.6% during week 5 to 11 of 2022. Of the 107 positive patients, 9.3% (n=10) were asymptomatic, 53.3% (n=57) had mild, 24.3% (n=26) had moderate, 10.3% (n=11) had severe and 1.9% (n=2) had critical symptoms. The symptomatology was unknown in one patient. The mean Ct-value was 26.4 in the asymptomatic, 20.3 in the mild, 22.4 in the moderate, 21.3 in the severe and 19.9 in the

critical category (p=0.03). 3 out of 10 asymptomatic patients carried high viral loads (Ct<24). 4 patients with a positive test had a registered Influenza vaccine of whom 1 had severe, 2 had moderate and 1 had mild symptoms. 3 of 4 vaccinated patients carried high viral loads.

Conclusion

During the first weeks of the Influenza 2021-2022 season, 4.2 % of admitted patients tested positive for Influenza A. Most of them presented with only mild symptoms. A smaller proportion presented as asymptomatic carrier. The Ct-value differed significantly between the groups with the highest Ct-value in the asymptomatic patients and the lowest Ct-value in patients with critical symptomatology. Some asymptomatic patients also presented with high viral loads. Our results show that, by only testing moderate/severe symptomatic patients during an epidemic Influenza wave, a substantial proportion of viral carriers will remain undetected, thereby potentially leading to nosocomial transmission.

LEGIONNAIRE'S DISEASE CASES BY THE NATIONAL REFERENCE CENTRE: A TEN-YEAR RETROSPECTIVE

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Number of cases

The National Reference Centre (NRC) for *Legionella* species gathered data for 454 infections in Belgium within the last decade 2011-2020.The number of cases of Legionnaires' disease (LD) increased over the years, in accordance with the data from the European centre for disease prevention and control (ECDC). Nevertheless, a decrease of cases was observed in 2020 (minus 43.3%), probably related to the COVID-19 pandemic and the related containment measures.

Involved *Legionella* species

L. pneumophila (Lp) was responsible of 439 (96.7%) infections, among them, 360 (82.0%) were *Lp* serogroup 1 (SG-1). The other Legionella species represented 15 (3.3%) cases, including 9 unidentified, 4 *Legionella bozemanii*, 1 *Legionella wadsworthii* and 1 *Legionella longbeachae*.

Reported methods for LD diagnosis

The cases were defined as "confirmed" when the urinary antigen test for *Lp* SG-1 (UAT) and/or the culture were positive whereas a PCR positive result alone were classified as "probable". 278 cases (61.3%) were diagnosed by UAT. 160 (57.7%) of these cases were also confirmed by culture. 84 (18.6%) cases were culture-positive only. 120 (26.4%) were UAT-positive only. 86 (19%) were PCR-positive only.

Settings of infections

186 (41.0%) infections were acquired in the community, 45 (9.9%) were nosocomial, 45 (9.9%) were travel related. Only 5 (1.1%) were healthcare-related and 5 (1.1%) domestic travel-related. The source was undocumented in 168 (37.0%) cases because the information was lacking on the NRC forms. The mortality rate cannot be evaluated by the NRC, as the information is often not known when the samples reach the laboratory.

Geographical distribution

East Flanders, Brussels Capital Region and Hainaut gathered the majority of the reported cases. Limburg, Namur, West Flanders, Walloon Brabant and Antwerp seemed to have less cases. The observed difference between the provinces is probably due to differences in the habits of the laboratories, some might not systematically send samples to the NRC.

Epidemics

Three epidemics were investigated during the observed period. In 2016 in Dendermonde with 17 cases (ST48). In 2017 in a potato factory in Nieuwkerke, 127 cases were associated but no ST was documented. In 2019, in a paper factory near Ghent, 32 cases were observed, associated with a cooling tower (ST921).

Environmental investigations

Only 53.8% of the nosocomial and healthcare-associated cases were followed by an environmental investigation. A matching isolate was found in 71.4% of these investigations. In 38.5% of the total infections, there was no information about the possible source of infection, again linked to an insufficient fill-up of the NRC forms.

HUMAN BOTULISM, BELGIUM NRC DATA : 10 YEARS OBSERVATION.

Botulism is a life threatening paralyzing and potentially fatal disease caused by botulinum neurotoxins (BoNTs) produced by the *Clostridium botulinum bacterium* and more rarely by *C. argentinense, C. baratii* and *C. butyricum*. Since 1988 Sciensano (former WIV-ISP) performs the role of National Reference Center (NRC) for *C. botulinum* and *C. perfringens* and since 2020 also *C. tetani* with key assignments such as the diagnosis, confirmation and surveillance of human botulism.

One of NRC tasks related to botulism consists of detecting botulinum neurotoxins (BoNTs) and/or the BoNT-producing germs in clinical samples of suspected cases. There are seven types of BoNTs classified from A to G based on their immunological properties. Human botulism is mainly associated with the toxin types A, B and E, and more exceptionally F, which can be detected in our laboratory.

The NRC has various validated and accredited methods (ISO 15189) for the laboratory diagnosis of botulism (in vivo reference method and molecular qPCR method).

For detection of BoNT, the in vivo reference method is used during which mice are injected intraperitoneally with extract of human faeces, serum or supernatant of culture. Serotyping is possible by adding the relevant antitoxin. In addition, the BoNT-producing germ can be detected by setting up multiple cultures from the sample. After an incubation period, the presence of BoNT-genes and BoNT can be detected (by PCR and in vivo method, respectively).

According to data collected by the NRC, over the period 2011-2020, samples of 126 suspected (based on clinical signs and symptoms) cases have been analyzed of which 8 cases could be confirmed. It consists of 4 cases of infant botulism and 4 cases of foodborne botulism, of which the source of 1 case could also be identified. All these cases were linked to serotype B. Based on this data, type B seems to be the most prevalent serotype in Belgium.

The last confirmed case of botulism (June 2020) involved a case of infant botulism. The 2-month-old baby had consumed honey from Morocco and subsequently showed typical symptoms of infant botulism. Both BoNT and BoNT-producing germ were detected in a faeces sample using the in vivo method but no BoNT was detected in serum. Serum assays for botulinum toxin are often negative in cases of infant botulism. Based on our data in 4 cases of confirmed infant botulism, 3 serum samples were analysed but all were negative. Analysing a faeces sample should be preferred for the laboratory diagnosis of Infant botulism.

MOLECULAR CHARACTERIZATION OF HUMAN PATHOGENIC *NOROVIRUS* CIRCULATING IN BELGIUM: 10 YEARS OF SYSTEMATIC MOLECULAR SURVEILLANCE DATA

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Norovirus is one of the leading causes of acute gastroenteritis outbreaks. Norovirus is a non-culturable single stranded RNA virus originally found during an outbreak of gastroenteritis in a school in Norwalk, Ohio in 1968. The virus was aptly named Norwalk virus and later renamed as norovirus. Sciensano houses the National Reference Center (NRC) of norovirus since 2011 and has provided 10 years of systematic molecular surveillance data of norovirus in Belgium. Since the mode of transmission is mainly person-to-person and foodborne the NRC works in close collaboration with the regional health inspection services and the Federal Agency for the Safety of the Food Chain and its National Reference Laboratory for foodborne outbreaks. The NRC performs besides diagnostic and confirmation analyses, molecular characterization of samples provided by clinical laboratories on voluntary basis. Norovirus is divided into several distinct genogroups, from which GI, GII and GIV are generally recognized as human pathogenic. Further characterization of the most common genogroups GI and GII is done using sequencing of the ORF1 (polymerase region) and ORF2 (capside region). Information is internationally exchanged via Noronet.

Since 2011 the NRC has received and detected more than 1500 norovirus strains from both sporadic cases and outbreak clusters mainly in schools, camps, kindergartens, hospitals and nursing homes. Genogroup GI was detected in only a small number of the cases. This genogroup is currently divided in nine genotypes from which eight have been detected (GI.1 – GI.8) with the most common genotype GI.3. The majority of all detected norovirus strains belonged to genogroup GII. The NRC detected 16 out of the 27 described GII genotypes and GII.4 was by far the most prevalent genotype. Remarkably the genotypes GII.11, GII.18, GII.19 associated with swine were not detected. Further subtyping for the GII.4 strains into variants was based on phylogenetic clustering and a new GII.4 variant was recognized after it became epidemic in at least two geographically distinct locations. GII.4 variants Hunter 2004, Den Haag 2006, Osaka 2007, New Orleans 2009 and Sydney 2012 have been detected by the NRC. The latter variant has been the dominant strain in Belgium since the start of the surveillance with about 80% of the norovirus GII.4 strains belonging to this variant. The NRC observed a seasonal variation in the norovirus infections with a peak during the winter months and early spring and a lower detection in summer months.

MONITORING OF *HAEMOPHILUS INFLUENZAE* STRAINS ISOLATED FROM BOTH CARRIAGE AND LOWER RESPIRATORY TRACT INFECTIONS: PRELIMINARY RESULTS

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Introduction

The resistance patterns for *Haemophilus influenzae* (HI) is changing and HI strains with reduced susceptibilities to beta-lactams are emerging in Belgium. Given that non-invasive isolates are referred to our National Reference Centre on a voluntary basis, the epidemiologic features of such isolates in Belgium are currently unknown.

In this context, a national survey is currently running that aims to assess and characterize resistance mechanisms to antimicrobials among Belgian HI isolates collected from both carriage and lower respiratory tract infections.

Methods

Ninety-three Belgian clinical laboratories were invited to take part to the survey, 42 of which registered. Monthly, from November 2021 to April 2022, each participating lab is asked to send one HI "infection" isolate (isolated in pure culture from a deep respiratory sample and showing a high white blood cells /epithelial cells ratio) and one HI "carriage" isolate (isolated from a mixed salivary flora from a upper respiratory tract sample).

Identification by MALDI-TOF Mass Spectrometry, biotype and serotype are determined for all isolates as well as the susceptibility to penicillin 1U (screen), ciprofloxacin, cotrimoxazole, tetracycline and the presence of a beta-lactamase. For all penicillin 1U resistant isolates, the susceptibility to ampicillin, amoxicillin-clavulanic acid, cefuroxime, cefotaxime and meropenem are also determined using e-test.

Results

To date, 128 isolates from 33 clinical laboratories have been collected and analyzed, 15 of which were excluded (1 being no HI, 2 because of no growth, 12 because of missing data). Among the 113 remaining isolates, 65 were classified as "infection" isolates and 48 as "carriage" isolates. All but two isolates (f, carriage) were non-typeable HI. Only 2 "infection" isolate were resistant to ciprofloxacin and 1 carriage isolate was resistant to tetracyclin. A statistical difference was observed between "infection" and "carriage" isolates in terms of cotrimoxazol resistance (26,2% vs 8,3%). The same proportion of strains producing beta-lactamase was observed in both groups (infection 13,8%; carriage 10,8%). Because of decreased susceptibility to ampicillin and/or amoxicillin-clavulanic acid, mutations of the ftsI gene are suspected in 27,7% and 25,0% of "infection" and "carriage" isolates, respectively. One cefotaxime-resistant isolate was observed in each group and all isolates were susceptible to meropenem.

Conclusion

HI is a major pathogen causing community-acquired respiratory tract infections worldwide. Apart from beta-lactamase production, other resistance mechanisms occur that affect the susceptibility of HI strains to beta-lactams and C3-resistant isolates are now circulating in Belgium. Additional studies and a continued epidemiological monitoring of circulating strains is thus mandatory for a better understanding of these mechanisms and their clinical impact.

SEXUALLY TRANSMITTED INFECTIONS MAY BECOME UNTREATABLE IN THE NEAR FUTURE! STATUS OF ANTIMICROBIAL RESISTANCE OF *NEISSERIA GONORRHOEAE* AND *MYCOPLASMA GENITALIUM* IN BELGIUM.

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Introduction

The emergence of antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* and *Mycoplasma genitalium*, two sexually transmitted pathogens, is a major concern. *N.gonorrhoeae* has developed resistance to all antimicrobials used as treatment. In addition, multidrug resistant *M. genitalium* to the first- (azithromycin) and second line (moxifloxacin) treatment is also beginning to emerge. Our aim was to provide an overview of antimicrobial resistance of *M. genitalium* and *N. gonorrhoeae* to the current treatment options in Belgium since 2013 to 2021.

Methods

The National Reference Centre for Sexually transmitted Infections (NRC-STI) receives presumable *N. gonorrhoeae* isolated from every district of Belgium. In addition, the NRC-STI molecularly detects *M. genitalium* in the case of urethritis/cervicitis and when *N. gonorrhoeae* and *C. trachomatis* are excluded. Antimicrobial susceptibility testing of *N. gonorrhoeae* is performed via Etest (Biomerieux, France) for ceftriaxone, azithromycin and ciprofloxacin. Detection of resistance associated mutations (RAMs) to macrolides (23S rRNA gene) and fluoroquinolones (parC gene) in *M. genitalium* samples is performed via Sanger Sequencing.

Results

Ciprofloxacin resistance of *N. gonorrhoeae* fluctuated between 42.4 to 55.9% over the years 2013-2021. An increase in resistance is however noted for azithromycin from 0.2 in 2013 to 18.6% in 2021. Ceftriaxone resistance remains rare, only 13 cases were detected since 2013. Until now, no dual resistance to ceftriaxone and azithromycin has been found. Resistance to macrolides in *M. genitalium* is increasing. Almost all *M. genitalium* samples collected from men who have sex with men (MSM) harboured RAMs to macrolides in 2015. More alarming is that in 2021, more than 50% of the samples harboured RAMs to both antimicrobials in MSM but this number was even 61.5% among heterosexuals.

Conclusion

An increase in azithromycin resistance is noticeable for both STIs. Increase is higher among MSM and is probably fuelled by the overuse of azithromycin to treat other STIs such as *C. trachomatis*. *N. gonorrhoeae* is already resistant to many antimicrobials, but to date no dual resistance to ceftriaxone and azithromycin has been detected in Belgium. However, *M. genitalium* shows a very worrying increase in the presence of RAMs the first- and second line treatment. There is a need to reinforce surveillance of antimicrobial resistance of *M. genitalium* and *N. gonorrhoeae*.

MONITORING OF EXOTIC MOSQUITOES IN BELGIUM: THE CITIZEN SURVEILLANCE COMPONENT

J Rebolledo • MRG Hermy • MD Kont • V Laisnez • W. Van Bortel • I. Deblauwe • R. Müller • T Lernout

Introduction of the exotic mosquito specie *Aedes albopictus* has been recognized as a **potential threat for human health and biodiversity** in Belgium and across Europe. This mosquito is a known vector of viruses causing chikungunya, dengue or Zika. Therefore the surveillance of mosquitoes is of paramount importance to prevent or delay their introduction and establishment in Belgium. Neighboring countries like France have already established populations of *Aedes albopictus* (the tiger mosquito) where autochthonous outbreaks of dengue and chikungunya already occurred.

In order to **prevent autochthonous transmission of mosquito-borne diseases** in Belgium, a number of elements need to be in place including: a surveillance of exotic *Aedes* mosquitoes, a surveillance of mosquito-borne diseases (with detection of imported cases) and an integrated analysis to timely cross and interpret these information.

In this context, the Belgian federal authorities and federated entities for health and for environment (through NEHAP) funded in September 2021, the MEMO+ project. This project aims to ensure the monitoring of *Aedes albopictus* in Belgium, in order to early detect its introduction, delay its establishment and prevent local transmission of *Aedes*-borne diseases. This monitoring will be based on two complementary parts: 1) a **passive surveillance** (coordinated by Sciensano) through citizen science which will rely on citizen's notifications; and 2) an **active surveillance** (coordinated by the Institute of Tropical Medicine) on the collection of mosquitoes through mosquito traps and larval collections at specific points of entry like parking lots.

Sciensano coordinates the overall MEMO+ project and is also responsible for the passive surveillance. A **citizen science website** for the notification of tiger mosquitoes (Ae. *albopictus*) was developed. Citizens can upload pictures of potential tiger mosquitoes on this website which also serves as an education platform. Pictures will be analysed and validated to determine, by morphological identification, whether or not it is a tiger mosquito. When a tiger mosquito has been identified, further investigations including mosquito collections will be done and control measures will be taken if needed. The website is aimed to be launched at the beginning of May 2022 i.e., the start of the mosquito season.

ECONOMIE EVALUATION OF THE PEDIATRIC IMMUNIZATION PROGRAM IN BELGIUM

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OBJECTIVES

To evaluate the economic impact of the pediatric immunization program (PIP) in Belgium from both healthcare payer and societal perspectives.

METHODS

An economic mode! was developed focusing on the 6 vaccines included in Belgium's PIP, recommended in children aged 0-10 years. Separate decision trees were used to model each disease (i.e., diphtheria, tetanus, pertussis, poliomyelitis, Haemophilus influenzae B, hepatitis B, measles, mumps, rubella, pneumococcal, rotavirus, and meningococcal C). The 2018 birth cohort was followed over their lifetime, with the mode! projecting and comparing direct medical costs with and without immunization (based on current and pre-vaccine era disease incidence estimates, respectively). For the societal perspective, the model also included productivity loss costs associated with immunization and disease. The model estimated discounted incremental cases, disease-related deaths, life-years lost, quality-adjusted life-years lost, costs (2020 Euros), and an overall benefit-cost ratio (BCR). Scenarios considering hypothetical inclusion of va ri cella and meningococcal B immunizations were conducted.

RESULTS

Across ail 12 diseases, the PIP prevented more than 220,000 cases of infections, 200 deaths, 7,000 life-years lost, and 7,000 quality-adjusted life-years lost. The PIP was associated with vaccination costs of over €90 million from the healthcare payer perspective and over €120 million from the societal perspective. Vaccination costs were fully offset by disease-related costs averted. Pediatric immunization was associated with over €30 million in averted direct medical costs (BCR = 1.4) and over €240 million averted societal costs (BCR = 3.0). Estimates of the societal value of the PIP were similar when hypothetical introductions of varicella (BCR = 2.9) or meningococcal B (BCR = 2.5) immunizations were considered.

CONCLUSIONS

The PIP brings large-scale prevention of disease-related morbidity, premature mortality, and associated costs, which has not been systematically assessed before in Belgium. This highlights the value of continued investment in the PIP.

Abstract
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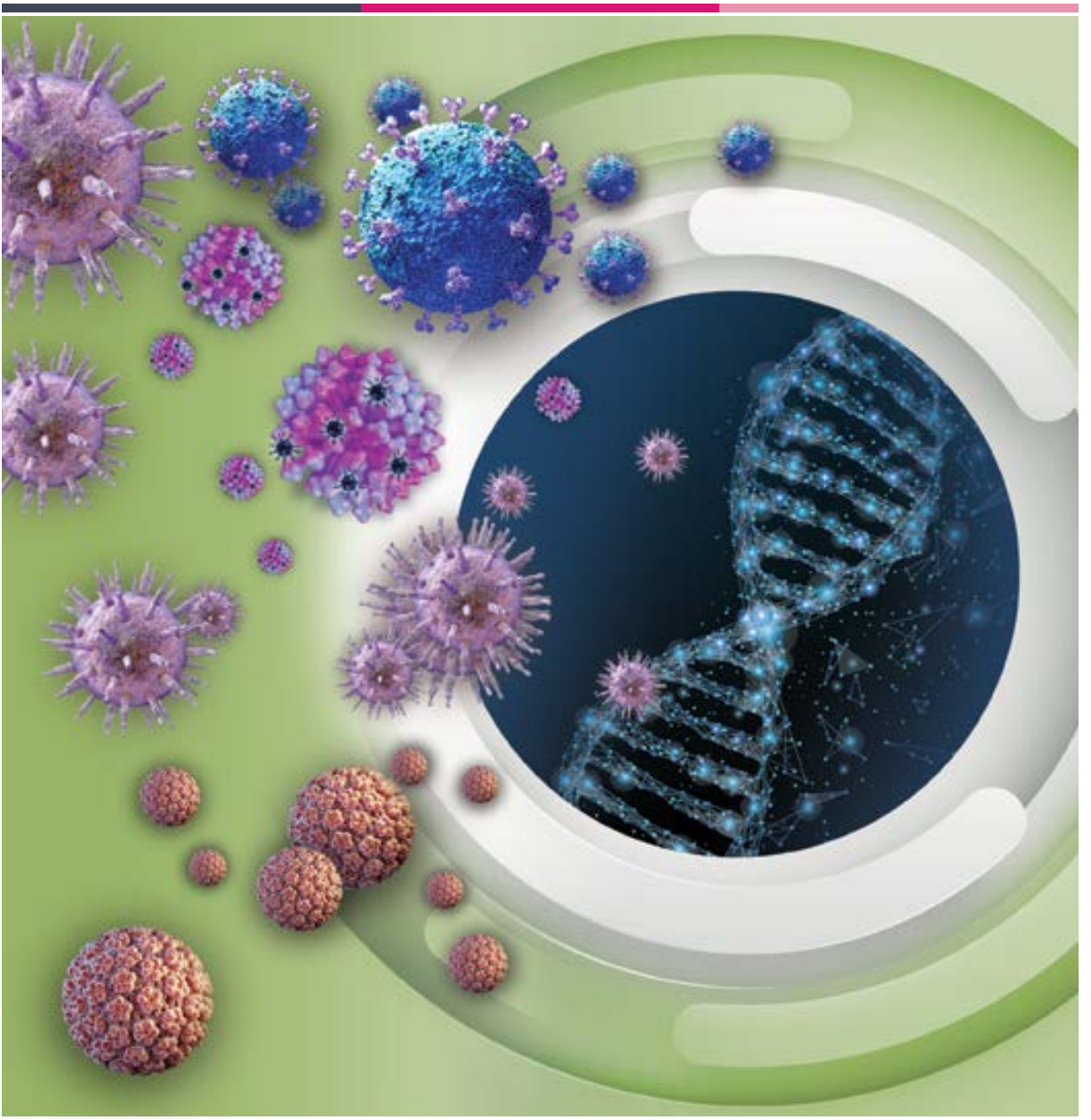

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