

The main title "Summary of work activities" in a white, bold, sans-serif font, set against a blue background.The author's name "Natalia Redondo Sevillano" in a white, sans-serif font, set against a blue background.The subtitle "European Public Health Microbiology Training Programme (EUPHEM), 2016 cohort" in a white, sans-serif font, set against a blue background.The section header "Background" in a bold, blue, sans-serif font.

According to the European Centre for Disease Prevention and Control (ECDC) Advisory Group on Public Health Microbiology ('national microbiology focal points'), public health microbiology is a cross-cutting area that spans the fields of human, animal, food, water, and environmental microbiology, with a focus on human population health and disease. Its primary function is to improve health in collaboration with other public health disciplines, in particular epidemiology. Public health microbiology laboratories play a central role in detection, monitoring, outbreak response and the provision of scientific evidence to prevent and control infectious diseases.

European preparedness for responding to new infectious disease threats requires a sustainable infrastructure capable of detecting, diagnosing, and controlling infectious disease problems, including the design of control strategies for the prevention and treatment of infections. A broad range of expertise, particularly in the fields of epidemiology and public health microbiology, is necessary to fulfil these requirements. Public health microbiology is required to provide access to experts in all relevant communicable diseases at the regional, national and international level in order to mount rapid responses to emerging health threats, plan appropriate prevention strategies, assess existing prevention disciplines, develop microbiological guidelines, evaluate/produce new diagnostic tools, arbitrate on risks from microbes or their products and provide pertinent information to policy makers from a microbiological perspective.

According to Articles 5 and 9 of ECDC's founding regulation (EC No 851/2004) 'the Centre shall, encourage cooperation between expert and reference laboratories, foster the development of sufficient capacity within the community for the diagnosis, detection, identification and characterisation of infectious agents which may threaten public health' and 'as appropriate, support and coordinate training programmes in order to assist Member States and the Commission to have sufficient numbers of trained specialists, in particular in epidemiological surveillance and field investigations, and to have a capability to define health measures to control disease outbreaks'.

Moreover, Article 47 of the Lisbon Treaty states that 'Member States shall, within the framework of a joint programme, encourage the exchange of young workers.' Therefore, ECDC initiated the two-year EUPHEM training programme in 2008. EUPHEM is closely linked to the European Programme for Intervention Epidemiology Training (EPIET). Both EUPHEM and EPIET are considered 'specialist pathways' of the two-year ECDC fellowship programme for applied disease prevention and control.

This report summarises the work activities undertaken by Natalia Redondo Sevillano, cohort 2016 of the European Public Health Microbiology Training Programme (EUPHEM) at the Public Health Laboratory, Dublin, the Health Protection Surveillance Centre (HPSC) and others institutions of the consortium in Dublin, Ireland.

All EUPHEM activities aim to address different aspects of public health microbiology and underline the various roles of public health laboratory scientists within public health systems.

## Pre-fellowship short biography

Natalia Redondo Sevillano is a Spanish Molecular Biologist that prior to her EUPHEM fellowship was working at the Centro de Biología Molecular Severo Ochoa in Madrid (Spain). Her PhD was focused on the requirement of initiation factors for translation of mRNAs of picornaviruses. After, successfully completing her PhD, she worked as a postdoctoral scientist at the Max F. Perutz laboratories in Vienna (Austria) on the identification of cellular receptors for Rhinovirus group C virus. After several years working on basic research, she accomplished a Masters in Microbiology applied to Public Health organised by the Instituto de Salud Carlos III and Universidad de Alcalá. Natalia joined the EUPHEM programme in order to broaden her competences in public health microbiology as well as to gain experience in field epidemiology.

## Methods

This report accompanies a portfolio that demonstrates the competencies acquired during the EUPHEM fellowship by working on various projects, activities and theoretical training modules.

Projects included epidemiological investigations (outbreaks and surveillance); applied public health research; applied public health microbiology and laboratory investigation; biorisk management; quality management; teaching and public health microbiology management; summarising and communicating scientific evidence and activities with a specific microbiological focus.

The outcomes include publications, presentations, posters, reports and teaching materials prepared by the fellow. The portfolio presents a summary of all work activities conducted by the fellow, unless prohibited due to confidentiality regulations.

## Results

The objectives of these core competency domains were achieved partly through projects or activities (on-job services) and partly through participation in the training modules. Results are presented in accordance with the EUPHEM core competencies, as set out in the EUPHEM scientific guide<sup>1</sup>.

### 1. Epidemiological investigations

#### 1.1. Outbreak investigations

Supervisors: Eleanor McNamara and Anne Carroll

#### A. Investigation of an outbreak of *Salmonella* Brandenburg in a restaurant in Dublin

An outbreak of salmonellosis occurred among people attending different parties in Dublin, where the same Food Business Operator (FBO) provided the food on the weekend of 13<sup>th</sup>-14<sup>th</sup> May 2017. On Thursday 18<sup>th</sup> May 2017, the Health Service Executive Environmental Health Service (HSE EHS) was informed, and following notification to the regional department of public health of these cases and of further illness among staff, an inspection of the premises was conducted and consequently a closure order was served on the food business on 19<sup>th</sup> May 2017. A total number of 72 cases were reported. 35 (48.6%) were confirmed cases and 37 (51.4%) were probable cases. A case-control study resulted that consumption of cold turkey had an odds ratio (OR) =10.97 (4.71-25.55) with a p-value<0.0001, after stratification association between turkey and illness an OR=34.67(6.73-178.53) p-value ≤ 0.0001 (table 6) was found. Binary logistic regression showed that the OR for cold turkey was 14.31 (3.00-68.35) (p-value< 0.01). In addition to the analytical study, microbiological investigations were carried out. All clinical salmonella isolates were sent to the National *Salmonella*, *Shigella* and *Listeria* Reference Laboratory (NSSLRL)

<sup>1</sup> European Centre for Disease Prevention and Control. European public health training programme. Stockholm: ECDC; 2019. Available from: <http://ecdc.europa.eu/en/publications/Publications/microbiology-public-health-training-programme.pdf>

where they were identified as *Salmonella enterica* Brandenburg. A turkey food sample was also positive for *Salmonella enterica* Brandenburg, which pointed to the cold turkey as the most likely vehicle for this outbreak. Isolates were sequenced and compared using whole genome Multi-Locus Sequence Typing (wgMLST), which provided strong microbiological evidence that the cases of infection and the isolate from the food product were identical. The epidemiological, microbiological and environmental investigations concluded that the cooked turkey was the source of the outbreak. The fellow attended, prepared and collated the PHL results for the Outbreak Control Team (OCT) meetings, she was involved in the ten steps on outbreak investigation, she actively validated the laboratory results for the laboratory director and prepared an abstract for a conference presentation. The abstract failed to be disseminated due to legal issues that are still awaiting resolution.

## **B. Investigation of an outbreak of VTEC in a childcare facility in rural Ireland June 2017**

An outbreak of Verotoxigenic *Escherichia Coli* (VTEC) 0145 VT2 occurred in a childcare facility (CCF) in a small town in Ireland. 108 people, including children, their families and staff were at risk. In accordance with national guidelines on VTEC in CCFs immediately after the confirmation and notification of two cases of *E.coli* 0145 VT2 attending the same CCF contemporaneously, an outbreak was declared and an Outbreak Control Team (OCT) was convened.

Public health actions were implemented, which involved excluding all children and staff from the CCF, thereby affecting its closure. In addition, other people who might have been at risk were contacted by the public health personnel and given advice on how to recognise VTEC associated clinical symptoms and to seek medical assistance if they developed such symptoms. Cases were excluded from the CCF until they provided two negative faecal specimens 48 hours apart. Investigation of the CCF by Public Health Officers and Environmental Health Officers was carried out as well as microbiological investigation of clinical and environmental samples. In VTEC outbreaks usually multiple exposures are involved, making the investigation complicated because microbiological testing of suspected sources occurs after the event and therefore the original source may not be detected. Due to this, in this outbreak, an analytical study was not carried out.

As part of microbiological investigation validated whole genome Multi Locus Sequence Typing (wgMLST) analysis was performed in order to characterise the isolates and to decide on their relatedness. The results evidenced that all samples from the outbreak were closely related, with less than 8 allele differences, but were more distant from two samples corresponding to two previous outbreaks in the same region.

The fellow actively attended OCT meetings; she was involved in the analysis of samples in the laboratory, typing using wgMLST positive samples and writing a report. In addition, the fellow is collaborating in preparing a paper for peer-review publication.

## **C. Investigation of an outbreak of VTEC in a childcare facility in Dublin, September 2017**

An outbreak of VTEC 0145 VT2 was declared on 15th September 2017 after the notification of three cases linked to a childcare facility (CCF) in Dublin, Ireland. An outbreak control team was convened in order to control the outbreak and investigate the source.

On September 22nd 2017 the CCF closed under the Infectious Disease Regulations 1981, regulation 11. The Medical Officer of Health (MOH) and all staff and attendees were excluded and requested to send stool samples to the National Reference Laboratory of VTEC (NRL VTEC) for analysis with molecular and culture methods. The descriptive epidemiology showed that the median duration of illness for confirmed cases was 3 days (range 1-35). The most frequently reported symptoms were diarrhoea (15 cases) and abdominal pain (14 cases). The attack rate was 9% for females and 12% for males. There were no significant differences between male and female cases (Chi-square test).

In total 413 people (360 children, 48 staff and 5 household contacts) were screened for VTEC, meaning 1157 samples. Of these, 1134 were clinical samples (98%) and 23 were water samples (2%). 45 clinical samples were positive, among them, 25 cases (56%) were PCR plus culture positive and 20 (44%) were PCR positive and culture negative. All water samples resulted negative. In addition to microbiological investigation, environmental investigations were also carried out and some irregularities in the water supply and in the waste system of the CCF were found, being incriminated as possible source of the outbreak.

Moreover, due to the high number of VTEC 0145 detected over 2017, a phylogenetic analysis was done including all the samples belonging to the outbreak and all the 0145 VTEC positive samples diagnosed during 2017 in order to study the possibility of epidemiological links among the positive cases.

Two very well differentiated clusters, belonging to the outbreak in a rural area (explained above) and the present outbreak, were detected with less than 6 allele differences within the clusters. The remaining VTEC 0145 were associated with sporadic cases, with more than 6 allele differences with the rest of the samples.

The fellow attended OCT meetings, was involved in microbiological investigations and prepared a presentation on how to manage large outbreaks in the laboratory. As indicated above, the fellow is preparing a paper for peer-review publication.

## Training modules

Introductory course, Spetses, Sept-Oct 2016: this course provided participants with the basic concepts of logistical and analytical approach to outbreak investigations, including the ten steps of an outbreak investigation. Outbreak investigations Module, Berlin, December 2017: taught fellows how to perform analytical epidemiological studies within outbreak investigations using various software packages. During the module fellows performed all steps involved in outbreak analysis from creation of a data entry file to the stratified analysis using EpiData, Stata and Microsoft Excel. They were also given practical training in when and how to perform analytical studies for an outbreak investigation, including descriptive, cohort and case-control studies.

Multivariable Analysis Module, Cyprus, April 2018: this module provided a more comprehensive understanding of the principles of statistical analyses, and how to build an optimal model using linear, logistic, Poisson and Cox regression in STATA.

### Educational outcome:

Application of microbiological and epidemiological knowledge in outbreak situations. Standard Operating Procedures and guidelines in food-borne outbreaks. Participation in multidisciplinary outbreak control teams, risk assessments, infection control assessments, involvement in outbreak investigations, management of large outbreaks in the laboratory (staff, sample and waste management), application of new typing methods, writing of reports and scientific articles, implementation of prevention measures.

## 1.2. Surveillance

### A. Point prevalence survey 2017 of hospital-acquired infections & antimicrobial use in two Irish hospitals: comparison between paediatric and adult patients

Supervisors: Rob Cunney and Brian O'Connell

The European ECDC point prevalence survey (PPS) protocol is a standardised tool to collect information about the use of antimicrobial agents as well as the prevalence of healthcare-associated infection (HCAI) in acute health care facilities in European member states. We aimed to compare the data obtained in the 2017 Irish PPS in a paediatric and adult acute care hospitals with regard to the prevalence of HCAI, types of HCAI and associated risks as well as the use of antibiotics and profile of antimicrobial resistance using this protocol. We also endeavoured to assess any difference upon utilising this standardised PPS protocol in such different patient cohort settings. Collection of the data was performed in accordance with PPS audit tool.

Prevalence of HCAI was lower in paediatric setting (6%, 95%CI 2-14) than in adult hospital (12%, 95%CI 9-14), however, the antimicrobial use prevalence was higher in paediatric patients (54%, 95%CI 42-66) than in adult patients (43%, 95%CI 39-47). In both hospitals, peripheral vascular catheter was the most commonly detected risk factor.

Our results suggested that comparing data from once-off surveys is very open to random variation, and we would probably need to compare serial data from repeated PPS surveys to be reliably able to make direct comparisons between hospitals. In addition, the prevalence in paediatric patients could be underestimated due to the low numbers of HCAIs detected. This observation can be the result of risk factors not considered in the protocol such as prematurity or low weight at birth; both might be implicated in HCAI acquisition in paediatric settings.

We would recommend the development of specific PPS protocols in paediatric hospitals in order to detect accurately problems associated with HCAI in these settings and also better implementation of prevention and control measures. Summarising, the PPS protocol should be adapted for different hospital population.

The fellow was involved in data collection helping different groups across different wards in St James's hospital and participated in the data collection for the PPS survey at Temple Street hospital. She carried out all the analysis of the data collected in the two hospitals and wrote a report. In addition, she wrote an abstract and presented a poster to the Irish Society for Clinical Microbiologists.

### B. Evaluation of the national surveillance system for pertussis in Ireland

Supervisors: Suzanne Cotter, Sarah Gee and Paul McKeown

Pertussis is a notifiable disease in Ireland since 1948 and individual case-based data notified since 1988 are on the national Computerised Infectious Disease Reporting (CIDR) system. All medical practitioners, including clinical directors of diagnostic laboratories must notify to the Director of the local Public Health Department i.e. Medical Officer of Health. Notifications can be made by writing, email or telephone. Laboratory notifications are made electronically to the CIDR and for the private laboratories not on CIDR these notifications are made by writing or email.

In Ireland, it is recommended that children be vaccinated with an acellular pertussis containing vaccine at two, four and six months of age and a booster dose at four to five years of age. A booster with low dose acellular pertussis vaccine was introduced in 2008 for children aged 11-14 years and in 2012 an additional booster was introduced for health workers and pregnant women. A cocooning strategy is recommended for close contacts of infants. The National Immunisation Advisory Committee (NIAC) has recommended that pregnant women should be offered tetanus and low dose diphtheria and acellular pertussis (Tdap) vaccine as early as possible after 16 weeks and up to 36 weeks gestation in each pregnancy, to protect themselves and their infant.

With this project we aimed to evaluate the national surveillance system for pertussis to determine, whether the current surveillance system collects appropriate, accurate and timely information to enable appropriate public health actions. The specific objectives were to describe the current Pertussis national surveillance system, to evaluate data quality/completeness and timeliness, identify areas for improvement and make recommendations.

As result of the evaluation, overall, the completeness of the system may be considered high; however there are some variables that require more attention. For instance, the variables "country of birth" and "Ethnicity", both collected under the "Patient Information" section, had a very low completeness; this information is important for assessing the access of minority groups to vaccination programmes so a higher completeness would be very helpful. The timeliness was also acceptable, with a median of three days between the diagnosis and the notification date. Based on the information gathered in the evaluation, some recommendations can be done in order to improve completeness and timeliness of the pertussis surveillance system in Ireland, such as promotion of completeness among CIDR users, which would help to better accomplish the objectives of the surveillance system. This could be done with training sessions or/and sensitization of the importance of collection accurate and reliable data. In addition, it is important to stress the importance of timely collection and reporting data, which highlight the need of recognition of pertussis cases and rapid notification in order to be able to detect cases or outbreaks, and implement adequate control and prevention measures. Further evaluation of other attributes of the pertussis surveillance system such as representativeness, simplicity or acceptability, as well as periodic evaluation of the pertussis surveillance system will be necessary in order to identify further gaps or data bottlenecks and to assess if improvements are evident following modifications implemented thanks to continue evaluation.

The fellow analysed the data using Excel and STATA software, attended and discussed results with vaccine preventable disease experts. She also wrote a report that will be shared with the regional Departments of Public Health in Ireland.

## Training modules

Introductory course, Spetses, Sept-Oct 2016: Fellows learned about the different types of surveillance systems and the attributes of a surveillance system. They also worked on how to set up and evaluate surveillance systems, as well as on the development of questionnaires in surveys.

**Educational outcome:** learning on surveys at European level; case definitions for health care associated infections, collection of data, describing and evaluating a surveillance system using attributes defined by the US Centre for Disease Control and Prevention (CDC) and ECDC such as data quality and timeliness, analysis with STATA and Excel, listing conclusions and recommendations

## 2. Applied public health microbiology research

### A. Risk factors associated with syphilis reinfections in Dublin from 2010 to 2017

Supervisors: Brendan Crowley and Paul McKeown

Persons with syphilis reinfections, including those who are asymptomatic, may play an important role in transmission of syphilis and other STIs. Since there was no specific information on syphilis reinfections in Ireland we aimed to describe the epidemiology of laboratory confirmed cases of syphilis reinfections among adults attending two STIs clinics in Dublin detected between 2010 and 2017.

A standardised review of the electronic medical records was made of all patients matching the syphilis reinfection definition: an episode of syphilis (symptomatic and/or asymptomatic) in a person who presents with a  $\geq 4$ -fold increase in RPR (Rapid Plasma Reagin) titre, at least 12 weeks after the completion of effective treatment for a previous syphilis episode that resulted in a  $\geq 4$ -fold decrease in RPR.

During a 8 year period, 1891 syphilis cases were laboratory confirmed, of which 217 were reinfections (11%; 95%CI 10-13%) most of them (53%) occurring in 2016 and 2017. The median age was 40 years (range 26-83) and majority (99%) were male, which it was a significant risk factor (OR=10.8 p<0.0001) compared to females. 64% were men reporting to have sex with men (MSM), 73% were HIV positive and 39% were diagnosed with at least one other STI. Other variables analysed were use of chemsex/drugs (22%), number of partners (45% had multiple partners), use of condoms (36% never/sometimes used condoms) and presence of symptoms (50% asymptomatic). Among the region of birth, almost 60% were born in Ireland, however there were individuals from other European countries, South America and a small proportion from Asia.

Syphilis reinfections are an increasing public health problem. This study is the first to provide data on syphilis reinfections in Ireland. Reinfections were diagnosed mainly in a population of males, who were also HIV positive. However further analysis will be needed in order to identify other risk factors and implement appropriate preventive measures to avoid transmission of syphilis and other STIs.

The fellow extracted the data from 191 medical charts, she performed all data analysis using Excel and STATA v12.0 software and presented a poster at ESCAIDE conference 2018. She is also preparing a short communication for peer-review publication.

## B. Analysis of *Mycobacterium abscessus* isolates collected from 2006-2017 using Next Generation Sequencing

Supervisors: Tom Rogers, Margaret Fitzgibbon

Nontuberculous mycobacteria (NTM) are ubiquitous environmental organisms that can cause mainly chronic pulmonary infections, particularly those with pre-existing inflammatory lung diseases such as cystic fibrosis (CF), but also can cause infections outside the respiratory tract in susceptible individuals. The major NTM infecting CF individuals around the world are the microorganisms including in the *Mycobacterium abscessus* complex (MABC). Three subspecies have been described: *M. abscessus subspecies abscessus*, *M. abscessus subspecies bolletii*, and *M. abscessus subspecies massiliense*. Ireland has the highest incidence rate of CF in Europe and therefore there are a significant number of people at risk of MABC infection.

With this project we aimed to use next generation sequencing on clinical isolates from CF patients and non-CF patients collected in the Irish Mycobacteria Reference laboratory (IMRL) in order to extend the knowledge of *M. abscessus* circulating in Ireland.

72 isolates from 37 patients, 27 CF patients and 10 non-CF patients, submitted to the IMRL from different hospitals and clinics across Ireland, were sequenced using MiniSeq (Illumina) following single-nucleotide polymorphism (SNP) analysis using BioNumerics and Geneious pipelines. Detection of antimicrobial resistance markers associated with clarithromycin and amikacin resistance as well as a phylogenetic analysis were carried out. Out of 72 isolates, 70 were satisfactorily sequenced. A maximum likelihood tree showed a clear differentiation between the three subspecies and it was possible to assign 57 isolates to *M. abscessus* subsp. *abscessus*, 10 to *M. abscessus* subsp. *massiliense* and 3 to *M. abscessus* subsp. *bolletii* supporting the three previously recognized *M. abscessus* subspecies as monophyletic. Very interestingly was that most of the infections in CF patients were due to *M. abscessus* subsp. *abscessus*, found in 49 isolates whereas only 3 isolates was infected with *M. abscessus* subsp. *massiliense* (OR=14.3 p<0,001). One patient was infected with both subspecies. The phylogenetic analysis also showed the presence of 4 clusters within *M. abscessus* subsp. *abscessus* isolates with no SNPs differences, which could indicate patient-to-patient transmission or acquisition from a common source. Regarding the antimicrobial markers, the mutation T28C in the *erm(41)* gene, leading to an inducible clarithromycin resistance, was detected in 15 isolates, all *M. abscessus* subsp. *abscessus*. In the 10 isolates of *M. abscessus* subsp. *massiliense* the *erm(41)* gene was truncated, which is an intrinsic characteristic of this subspecies as previously described and it is related with clarithromycin susceptibility. The mutation at positions 2058 or 2059 in the *rrl* gene of the 23S rRNA was not detected and only one isolate harboured the mutation at position 1404 in the gene *rrs* of the 23S rRNA. Further analysis will be focused on comparison of the genotypic with the phenotypic antimicrobial profiles in order to elucidate if genomic markers can be used as an antimicrobial resistance-screening tool in clinical laboratories.

In Ireland, *M. abscessus* infections are not notifiable, however the presence of clusters indicating very close related strains highlight the possibility of patient-to-patient transmission, as it has been previously described; or presence of common sources of transmission. These, along with the challenges that treatment of *M. abscessus* infections poses due to multidrug-resistance mechanisms could indicate the need for monitoring and surveillance in order to be able to implement prevention and control measures and avoid further spread of the disease.

The fellow performed all steps of the project, from laboratory (DNA extraction and library preparation) to data analysis. She also wrote a research protocol and she is preparing a peer-review publication.

## Training modules

Introductory course, Spetses, Sept-Oct 2016: In this course, fellows were taken through a review of the basis of epidemiology and microbiology. In addition, fellows were trained in writing a study protocol and discussing study designs. Fellows performed exercises on scientific writing.

Outbreak investigation module-EUPHEM specific sessions, Berlin, December 2017: This part of the module focused on sequence analysis and phylogenetic analyses. Fellows were introduced to different software such as SSE or as well as concepts of phylogeny. An introduction to next-generation sequencing was also delivered in this module.

Biorisk and Quality management, Stockholm, February 2018: During this module, fellows were introduced to quality management practices and trained in performing risk assessment and on how to propose mitigation measures.

Management, Leadership and Communication in Public Health, Stockholm, February 2018: The module covered aspects such as time and person management or communication, which are important aspect in research activities.

**Educational outcome:** Preparation of a study protocol, adherence to ethical principles, gaining expertise in data analysis with STATA, troubleshooting and analysis of next generation sequencing data, phylogenetic analyses, presentations at conferences and writing scientific publications.

### 3. Applied public health microbiology and laboratory investigations

#### A. Retrospective study to analyse and detect changes in molecular epidemiology trends of *Campylobacter* sp. in Ireland from 2006 to 2016

Supervisors: Eleanor McNamara and Anne Carroll

Campylobacteriosis is the commonest bacterial cause of gastroenteritis in Ireland. Recent national introduction of polymerase chain reaction (PCR) as the sole diagnostic test for campylobacter could lead to a loss of epidemiological data on campylobacteriosis. Using whole genome sequencing (WGS) we aimed to retrospectively review molecular epidemiology of *Campylobacter* sp that could influence clinical treatment and public health actions. Stored *Campylobacter* spp isolates cultured from stools of symptomatic sporadic cases submitted to the regional Public Health Laboratory (PHL) over 10-year period (2006-2016) were included. WGS was performed using MiSeq System (Illumina) and analysis with BioNumerics pipeline. Typing was determined by core genome MultiLocus Sequence Type (cgMLST).

A total of 122 *Campylobacter* isolates were sequenced. Pathogenic genes associated with cytotoxins production (*cdtA* 88%, *cdtB* 89%, *cdtC* 89%), adherence and colonization (*flaA* 10%, *cadF* 99%, *dnaJ* 99%, *racR* 98%) and invasion (*iam* 99%, *virB11* 1%, *ciaB* 80%) were detected. Genotypic markers associated with resistance to quinolones, beta-lactams and tetracycline were present in 43%, 71% and 25% of isolates, respectively. The *cmeABC* operon had a prevalence of 94%. No macrolide or aminoglycoside resistance markers were detected. Phylogenetic analysis showed that 92% of the isolates were assigned to 29 sequence types grouped into 17 clonal complexes. In addition, one cluster and three pairs with no allele differences were detected, although further analysis did not show obvious epidemiological link. The most prevalent clonal complex (CCs) (CC21, CC48, CC828, and CC257) accounted for 55% of isolates and the most prevalent sequence type (STs) were ST48, ST21 and ST257.

Our results have shown that most isolates demonstrated the presence of virulence-associated genes related with adherence, colonization, invasion and cytotoxin production. With regard to antimicrobial resistance, the high prevalence of quinolone resistance markers would preclude the use of these antimicrobials for empiric treatment of gastroenteric infections by *Campylobacter* while awaiting antimicrobial susceptibility results. In addition, it is worth noting that the most prevalent STs found in the clinical isolates in this study correlated with the most prevalent ST found in poultry isolates in Ireland, suggesting an active transmission of *Campylobacter* through the food chain over time.

In this study, the use of WGS and cgMLST analysis has provided valuable data on the presence of virulence genes, antimicrobial resistance markers and molecular epidemiology of *Campylobacter* in clinical isolates in Ireland, showing that would be a useful surveillance tool compared to the classic typing methods (Pulse Gel Field Electrophoresis). WGS could be utilized in a National Reference Laboratory for *Campylobacter* to advance One Health campylobacter reduction strategies.

The fellow took the lead in all the steps carried out for the completion of this project. She performed all laboratory procedures from culture to validation and sequencing of isolates, troubleshooting, data analysis and communication of results. An abstract was accepted as an oral presentation at ECCMID 2018 and delivered at that conference in Madrid. A publication has been submitted.

## B. Pilot project on detection of erythromycin resistance markers in group B streptococcus using Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry

Supervisors: Rob Cunney and Richard Drew

*Streptococcus agalactiae* or group B streptococcus (GBS) is a leading cause of invasive bacterial disease in neonates. GBS is an opportunistic commensal constituting a part of the intestinal and vaginal physiologic flora and maternal colonization is the principal route of GBS transmission. GBS is also an important pathogen for pregnant women, elderly and immunocompromised adults. Benzylpenicillin is the first line antibiotic in non-allergic women for intrapartum antimicrobial prophylaxis, and clindamycin is the first line for women with anaphylaxis reactions to penicillin. However, an increase in macrolide resistance has been documented in different studies, with 50.7% of prevalence of erythromycin resistance in some cases. Thus it would be valuable to rapidly identify such macrolide resistant organisms in order to provide alternative prophylactic options in penicillin allergic patients.

During recent years, the use of Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry (MALDI-TOF MS) has emerged as a potential tool for microbial identification and diagnosis, being a rapid, sensitive, and economical process in terms of both, labour and consumable costs involved. The aim of this project was to investigate the possibility of detecting erythromycin resistance markers in GBS isolates using MALDI-TOF MS. To accomplish this, twenty GBS isolates (10 erythromycin sensitive and 10 erythromycin resistant, and all previously typed as ST17) were cultured from frozen stocks and run on the MALDI-TOF in quadruplicates. For the analysis, Mass-up v1.0.13 software was used. Three biomarkers (spectrometry peaks) were significantly different between the resistant and sensitive isolates. These are preliminary but promising results, demonstrating the potential for rapid identification of macrolide resistance in GBS. Further analysis will include the analysis of GBS isolates with different STs and it will be necessary to analyse if the peaks detected correlate with erythromycin resistance mechanisms. This project will be continued by master students in order to validate the application of MALDI-TOF for erythromycin resistance detection.

The fellow was involved in culturing the isolates, running and acquiring the data with MALDI-TOF, analysing the data and writing a report.

## C. Is it necessary to request a second serum sample for diagnosis of Zika virus?

Supervisor: Maria Paz Sánchez-Seco Fariñas

During an internship at the Instituto de Salud Carlos III (ISCIII), the fellow reviewed and analysed the current serological algorithm used for Zika virus infection laboratory diagnosis. To accomplish this, the fellow was introduced to OpenLab Software, which is the database where all the specimen information (patient information, analysis, results) is stored, analysed and shared with clinicians and hospitals.

Currently, if there is a positive IgG and negative IgM, a neutralization assay (NT) is performed. This test allows the detection of neutralizing antibodies against Zika virus, however it is a very tedious technique with implied biorisk since it involves the manipulation of the virus. In the case of pregnant women, if the result of the NT is indeterminate (values between 1/32 and 1/512), the patient is asked for a second serum sample and a new NT test is performed. The aim of this activity was to review all Zika cases from 2016 to 2018 in order to check if the current laboratory algorithm for Zika diagnosis is adequate or some modifications can be applied. From the OpenLab database, all Zika cases from 2016 to 2018 (until 6/11/2018) were exported to an Excel sheet. Then, the paired serum samples with Zika neutralization results were analysed. In total, 2881 serum samples were submitted and a NT assay was performed at the arbovirus reference laboratory. Out of these, 630 were paired samples (in some cases more than two samples were submitted from one patient) collected from 308 patients, mostly pregnant women. A total of 53 patients (17%) showed a different result between the first and the subsequent samples. The NT assay results of these 53 patients were carefully reviewed. Out of these, 5 patients (9%) were found to have differences of  $\geq 4$ -fold increase or decrease in the titre of neutralizing antibodies between the first and subsequent NT assays. This means that if a pregnant woman has a positive IgG and/or positive IgM and a neutralization assay is performed with an indeterminate result, it might be unnecessary to request a second sample for the confirmation of the presence of neutralizing antibodies since this patient will be considered as a probable case, and therefore the same clinical follow-up will be indicated as that for a confirmed case. However, if the result of the neutralization assay is indeterminate with a previous positive IgG and negative IgM, a second sample might be necessary for confirmation. These results could influence and/or update the current clinical management of Zika cases.

The fellow was involved in analysis of all the data and writing a report.



## Training modules

Outbreak Investigation Module - EUPHEM specific sessions, Berlin, December 2017: This part of the module oriented to EUPHEM fellows focused on sequence analysis and phylogenetic analyses. Fellows were introduced to different software such as SSE or as well as concepts of phylogeny. An introduction to next-generation sequencing was also delivered in this module.

Biorisk and Quality Management module, Stockholm, February 2018: During this module, fellows were introduced to quality management practices, which were applied when the fellow undertook laboratory investigations.

**Educational outcome:** Application of virology, bacteriology and molecular biology concepts to the public health discipline; understanding the use and limitations of diagnostic and typing methods and their interpretation; developing expertise in analysis of next generation sequencing data and microbiome analysis; development and assessment of laboratory methods to improve surveillance and diagnostics procedures.

## 4. Biorisk management

### A. Risk assessment working with *Mycobacterium abscessus* isolates

As part of the project (section 2.B), the fellow had to assess the biorisks involved when working with this pathogen. She wrote reports on a variety of issues concerning biosafety and biosecurity prior to starting the project. She was also introduced to the biosafety workflow of the IMRL in the BSL-3 laboratory in the reception of samples, culture, microscopy and identification using classical and molecular tools.

### B. Risk assessment working with arboviruses and biohazard alert drill

As part of the internship carried out at the ISCIII, in Madrid, Spain, the fellow received theoretical instruction on the biological risks working with arboviruses such as dengue, chikungunya, yellow fever and Zika, among others. All of them require BSL-3 facilities except Zika virus. A visit to the BSL-3 facilities was organized to enable the fellow to understand the complete workflow of the vector-borne diseases reference laboratory.

In addition, the fellow had the opportunity to attend a national drill on biological alert as an observer, chaired and organized by the "Centro de emergencias y alertas sanitarias" (part of the Ministry of Health). In this regard, the fellow was able to understand how management and communication is organised when different institutions, media and politicians are involved under very stressful circumstances. The fellow also gained insight into the Early Warning and Rapid Response System (SIAPR for its Spanish name, Sistema de alerta precoz y respuesta rápida), which is a communication tool for alert situations.

### C. Biorisk and Quality Management Module, Stockholm, 2018

During this module, fellows were introduced to quality management practices and trained in performing risk assessment and proposing mitigation measures. Fellows used an assessment tool to assess process management, quality control and documentation available. Fellows were also introduced to procedures for laboratory accreditation and certification. During this module, fellows also received training in international regulations and good practices for biological specimen shipment and obtained the WHO certificate for International Transport of Infectious Substances. The module included a visit to the Biosafety Level 4 Laboratory of the Folkhälsomyndigheten Institute (Stockholm, Sweden). During this visit, fellows were able to observe the rooms, equipment and to discuss practices of the level 4 laboratory.

**Educational outcome:** Understanding biosafety regulations, applying biorisk mitigation methods, learning appropriate measures for the safe transport of hazardous substances and pathogenic specimens completed with a WHO certificate of International Transport of Infectious Substances. In addition, the fellow learned about the risks working with arboviruses and how to respond to a biohazard alert at national level.

## 5. Quality management

Supervisors: Anne Carroll, Lucy Devlin

### A. Whole-genome sequencing validation in the VTEC National Reference Laboratory (VTEC NRL), Ireland

Following the ECDC roadmap for integration of molecular and genomic typing into surveillance and epidemic preparedness, the VTEC NRL in Ireland undertook a programme of validation and verification to acquire the capability and capacity to incorporate whole-genome sequencing on clinical isolates of VTEC into their routine VTEC NRL service and workflow. Prior to the launch of the service in January 2018, the technique was externally validated in collaboration with Public Health England (PHE). A set of 100 isolates previously characterized using Pulse Field Gel Electrophoresis (PFGE) was selected for sequencing. Once the isolates were sequenced using Illumina platform, the BioNumerics software (Applied Maths, Belgium) was used for the analysis of the data. A complete correlation with previous typing results was found. In addition, the fastq files were shared with PHE for comparison with their platform. A 100% correlation was obtained between the 2 site results and the VTEC NRL started the full service of WGS on January 2018.

The fellow collaborated with NRL scientists during all stages of the validation process and in the Standard Operating Procedures preparation for the delivery of this new NRL service.

## B. Quality audit of the VTEC reference laboratory

The fellow performed an internal audit of the national reference laboratory for VTEC at the PHL by interviewing the quality manager, going through protocols and methods descriptions and workflows in the laboratories. The audit focused on process management, quality control indicators and documentation. The audit yielded a general indicator percentage of 96%. The overall quality was high and no deviations affecting the quality of the results were identified. The laboratory was advised to encourage the clients to use standardized request forms to order laboratory tests.

## Training modules

Biorisk and Quality Management Module, Stockholm, February 2018: During this module, fellows were introduced to quality management practices. Fellows used an assessment tool to assess process management, quality control and documentation available. Fellows were also introduced to procedures for laboratory accreditation and certification.

**Educational outcome:** The fellow learned the concepts of accreditation procedures, quality audits, and validation of laboratory methods.

## 6. Teaching and pedagogy

### A. Outbreak management exercise for Microbiology Specialist Registrars

The fellow, along with the EPIET fellow Lois O'Connor, provided an overview of outbreak investigation and some basic epidemiological skills to medical clinical microbiologists in postgraduate training during two sessions of 3 hours each. At the first session a presentation was delivered with information on basic epidemiology and the 10 steps in an outbreak investigation using several outbreak examples. In the second session, we used a previously developed outbreak investigation exercise, which was modified for the session. The microbiology specialist doctors in training were required to calculate attack rates and relative risks in a food-borne outbreak scenario. After both sessions, evaluation questionnaires were distributed among participants. The sessions received very good feedback.

### B. Whole-genome sequencing user group for laboratories working on food and water-borne diseases

The objective of this activity was to set up a whole-genome sequencing user group for people/researchers working on Food and Waterborne diseases in Ireland. Several organizations were invited to participate such as the relevant national reference laboratories, laboratories in the Department of Agriculture, Food and the Marine, University College Dublin and Ashtown food research centre. The aim of the user group was to help in troubleshooting, technical issues when setting up this technology within the laboratories. Validation and accreditation of WGS, data analysis and quality, sharing data and data protection, storage and IT issues, training and research advice were addressed. During the fellowship, the Fellow chaired and organised three teleconferences. Different issues were discussed such as quality parameters, advantages and disadvantages of different kits and protocols for library preparation, potential accreditation by the Irish National Accreditation Body (INAB) or data storage and data sharing in the context of the new European law of the General Data Protection Regulation (EU) 2016/679 ("GDPR"). The user group will be continued, chaired by the new EUPHEM fellow of Cohort 2018 place at PHL.

The role of the fellow was to facilitate communication between users by organising teleconferences (TC) every 3-4 months. Emails were sent in order to find a suitable week first and then the Doodle platform was used to agree a date and time. Agendas were sent to each member prior to the meeting and minutes were taken. The participants

were enthusiastic about this development as it provided a forum to discuss the challenges about implementing this technology for either service delivery or research. The fellow wrote a final report describing the activity, the topics discussed and conclusions.

### C. Training in library preparation for Whole-Genome Sequencing

The fellow provided hands on training for several scientists and masters students in library preparation and sequencing at St James' s hospital. She guided the trainees across all steps of the library preparation according to Illumina protocol, giving advice on implementation for routine diagnosis and laboratory research.

### D. Open day at Public Health Laboratory, HSE Dublin for users

In order to further develop the communication network that exists between the Public Health Laboratory, HSE DML and its clients, the laboratory organized an Open Day for laboratory users. The aim was to provide an insight for the clients into the laboratory services that are provided and to facilitate valuable feedback. Two sessions were organized, one for Public Health Doctors and other for medical scientific laboratory chiefs. The sessions had slightly different focus, but covered a brief introduction to the laboratory scope, an overview of the enteric screening methodologies using molecular techniques, an introduction to whole-genome sequencing and an introduction to outbreak management in the lab. The fellow took a lead role along with PHL staff in the coordination of the event, writing the invitations, organizing the agenda, providing a welcome presentation and managing the time for each session. The fellow formulated and invited the attendees to complete a post visit questionnaire, which will be analysed.

**Educational outcome:** Identify training needs, define course objectives, develop curriculum, plan and organise a course, prepare and deliver presentations aimed at a range of health-care professionals, re-evaluate delivery and content.

## 7. Public health microbiology management

### A. 'Management, Leadership and Communication in Public Health, ECDC, Stockholm, Sweden

This one-week module focused on understanding roles and responsibilities in public health management. Topics included the identification of different management styles, team roles and team evolution, the delegation of tasks and the provision of structured feedback.

### B. Public health microbiology management components as part of regular projects

Public health microbiology management was an integral component of all projects and activities during the fellowship. This included laboratory management, ethical and integrity considerations, team building and coordination, research collaboration, time management, management of cultural differences in international contexts and working in a multidisciplinary team with microbiologists, physicians, laboratory technicians, epidemiologists, statisticians, government officials, public health officers and logisticians.

**Educational outcome:** Working in a multidisciplinary public health team; understanding team management; planning, scheduling and organising research projects. Understanding the role and responsibilities of a people manager within a public health environment, understanding different management styles; understanding team roles and team evolution to ensure team success; motivation of teams; conflict management: structured feedback to improve performance and minimise disruption in a conflict; communicating with authorities, the public and the media.

## 8. Communication

### Publications

1. **Natalia Redondo**, Anne Carroll, Eleanor McNamara. Molecular characterization of clinical isolates of *Campylobacter* using whole-genome sequencing: virulence, antimicrobial resistance and phylogeny. (Manuscript submitted to PLoS One)
2. **Natalia Redondo**, Simone Mock, Margaret Fitzgibbon, Thomas Rogers. Molecular epidemiology of *Mycobacterium abscessus* in Ireland. (Manuscript drafted)
3. Anne Carroll, **Natalia Redondo**, Eleanor McNamara. An unexpected increase of Verotoxigenic *Escherichia coli* 0145 in Ireland during 2017 (Manuscript in preparation)
4. **Natalia Redondo**, Brendan Crowley. Syphilis reinfections in Dublin: challenging public health? (Short communication in preparation)

## Reports

1. **Redondo N.** Report on an outbreak of Salmonella Brandenburg in a restaurant in Dublin
2. **Redondo N.** Report on an outbreak of VTEC in a childcare facility in a rural area of Ireland, June 2017
3. **Redondo N.** Report on an outbreak of VTEC in a childcare facility in Dublin, September 2017
4. **Redondo N.** Report on Point Prevalence Survey 2017 of Hospital-Acquired Infections & Antimicrobial Use in two Irish hospitals: comparison between paediatric and adult patients.
5. **Redondo N**, Gee S, Cotter S. Report on the evaluation of the pertussis surveillance system in Ireland
6. **Redondo N.** Report on whole-genome sequencing user group in Ireland
7. **Redondo N.** Zika virus diagnosis at the vector-borne diseases reference laboratory at ISCIII
8. **Redondo N.** Detection of erythromycin resistance markers in group B streptococcus using Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry

## Conference presentations

1. **Redondo N**, Cunney R, O’Connell B, McNamara E. ECDC Health Care Associated Infections Point Prevalence Survey 2017: adequate protocol for both paediatric and adult hospitals? Irish Society of Clinical Microbiologists Spring 2018, Dublin. Ireland. Poster presentation.
2. **Redondo N**, Carroll A, McNamara E. Whole-genome sequencing; a proposal for future campylobacter surveillance in Ireland. ECCMID 2018, Madrid, Spain. Oral presentation (Funded by Health Service Executive-Public Health Laboratory)
3. **Redondo N**, McKeown P, Crowley B. Descriptive analysis of syphilis reinfections in Dublin, 2010-2017. ESCAIDE 2018. St Julian’s, Malta. Poster presentation

## Other presentations

1. 3 min presentation introductory course
2. Management of large outbreaks. PHL, October 2017
3. WGS in Ireland. 3 min presentation. Management, Leadership and Communication in Public Health, Stockholm, 2018

## 9. EPIET/EUPHEM modules attended

1. Introductory Course, Spetses, Greece, 26<sup>th</sup> September - 14<sup>th</sup> October 2016
2. Rapid Assessment module, Athens, Greece, 8<sup>th</sup> - 13<sup>th</sup> May 2017
3. Project Review module, Lisbon, Portugal, 26<sup>th</sup> - 30<sup>th</sup> August 2017
4. Outbreak Investigation module, Berlin, Germany, 4<sup>th</sup> - 8<sup>th</sup> December 2017

5. Biorisk and Quality Management module, Stockholm, Sweden, 5<sup>th</sup> - 9<sup>th</sup> February 2018
6. Management, Leadership and Communication in Public Health, Stockholm, Sweden, 12<sup>th</sup> - 16<sup>th</sup> February 2018
7. Multivariable Analyses module, Nicosia, Cyprus, 16<sup>th</sup> - 20<sup>th</sup> April 2018
8. Project Review Module, Lisbon, Portugal, 27<sup>th</sup> August - 31<sup>st</sup> August 2018

## 10. Other training and scientific meetings attended

1. Training in Clinical Microbiology at Public Health Laboratory. 19<sup>th</sup> -23<sup>rd</sup> September 2016
2. Legal Framework Seminar at PHL, Dublin, Ireland. 18<sup>th</sup> October 2016
3. Vaccinology. MOOC by Institute Pasteur, January 2017
4. Seminar: AMS Insight. Antimicrobial Stewardship: A Multi-disciplinary Team Initiative. Dublin, Ireland. 12<sup>th</sup> June 2017
5. Tutorial on Public Health Microbiology in Ireland at PHL. 28<sup>th</sup> June 2017
6. Next generation sequencing in Clinical Microbiology Forum. St James's Hospital. 19<sup>th</sup> July 2017
7. Training in Serology lab at St James's Hospital on diagnosis of syphilis. Dublin, Ireland. 10<sup>th</sup> August 2017
8. Training course with MALDI-TOF VITEK MS In Vitro Diagnostic System (IVD) software (BioMerieux) at Temple Street Hospital and Rotunda Hospital. Dublin, Ireland. 27<sup>th</sup> September 2017
9. Training course with MALDI-TOF VITEK MS Research Use Only (RUO) (BioMerieux) at Rotunda Hospital. Dublin, Ireland. 9<sup>th</sup> October 2017
10. Attendance "5 Nations Public Health Microbiology meeting" at HPSC. Dublin, Ireland. 3<sup>rd</sup> November 2017
11. Whole genome sequencing in food safety and public health. One day conference. Dublin, Ireland. 27<sup>th</sup> November 2017
12. Training course with SARAMIS Premium (BioMerieux) Software (MALDI-TOF VITEK MS) (continuation) at Rotunda Hospital. Dublin, Ireland. 12<sup>th</sup>-13<sup>th</sup> July 2018
13. Visit to the EPIET Training site in Belfast, Northern Ireland. 16<sup>th</sup> July 2018
14. Internship at Instituto de Salud Carlos III at the vector-borne diseases reference lab, Madrid, Spain. 5<sup>th</sup> November 2018-16<sup>th</sup> November 2018

# Discussion

## Coordinator's conclusions

This portfolio encompasses the work of Natalia Redondo Sevillano (Cohort 2016), as the first EU track fellow to undertake the EUPHEM fellowship at the Public Health Laboratory, Health Service Executive (HSE) in Dublin, Ireland. Natalia initiated her two year journey into the fellowship as an accomplished molecular virologist, searching to widen her competences in Applied Public Health Microbiology.

In line with the fellowship objectives, her site supervisors provided a broad variety of quality projects and activities addressing current public health challenges in The Republic of Ireland, and by increasing the network of collaborations, Natalia was able to widen and refine her competences in field microbiology. She covered three outbreak investigations, which gave her the opportunity to understand the delicate balance between successful outbreak control and effective public health management. In addition, by working in a point prevalence survey of HCAI and antimicrobial use, and on the evaluating the National pertussis surveillance system, she became skilled at identifying not only the strengths but also the gaps in protocols and procedures, and as a result, was able to provide useful suggestions for specific interventions in both cases.

The "learning by doing" philosophy of the fellowship was evidenced when undertaking an activity introducing novel approaches for detection of AMR using MALDI-TOF in Group B streptococcus, and by leading projects on applications of WGS for the characterisation of *Campylobacter* and *M. abscessus* isolates. Thus, Natalia's work has contributed to setting the basis for the introduction of WGS as a tool to clarify the epidemiology of both organisms

in The Republic of Ireland. Modules provided by the ECDC Fellowship training programme and multiple high quality teaching activities complemented her training programme at the site.

During her time at the PHL Dublin, supported by ECDC, Natalia grew in confidence and was prised for her positive attitude, initiative, and leadership and through the development of multidisciplinary projects and activities Natalia achieved her objective of acquiring competences in public health microbiology and field epidemiology. In addition, interaction with colleagues from different cohorts and a deployment at Instituto de Salud Carlos III in Madrid have provided her with the contacts to build valuable future collaborations. These are assets that will serve her well in her future career as a public health professional. The EUPHEM Coordinator team has concluded that Natalia Redondo Sevillano has fulfilled the fellowship requirements to a high standard and in a professional manner and wishes her all success in her future career.

## Supervisor's conclusions

Natalia Redondo has completed a comprehensive and fulfilling 2 year EU funded EUPHEM Fellowship in public health microbiology based at Public Health laboratory, HSE, Dublin along with a consortium of national reference laboratories and the health protection surveillance centre in Dublin from September 2016 to February 2019.

All supervisors found Natalia to be a very bright engaging and committed fellow. She was an enthusiastic learner, availing of the broad opportunities afforded to her by undertaking and completing a variety of different projects covering the competencies required by the fellowship. Her supervisors were impressed with her ability to address the public health microbiology challenges posed in each project. This involved clarification of the project proposals to showing initiative when trouble shooting technical issues and resolving other logistical problems to complete the task in hand. She was successful with her excellent communication skills in presenting many of these project results at international meetings and is still involved in writing up associated papers to peer reviewed journals. She received significant exposure to communicable disease outbreak management and is now competent to undertake and lead such investigations herself. She displayed significant ability to prioritise and multitask while utilising good organisational skills. She has grown professionally during this fellowship and is now a competent public health microbiology specialist who will contribute to the European capability in this field. Ireland is proud to have facilitated her specialist development.

## Personal conclusions of fellow

Joining the EUPHEM programme has provided me with valuable knowledge and experience in public health applied to different fields such as microbiology, epidemiology or virology. I have acquired skill and competencies in a variety of topics that without any doubt will contribute to continue my professional career in the field of public health. One of the things that I consider most useful was the learning by doing approach. I was very lucky to broaden my knowledge by working on excellent projects and to develop invaluable technical and analytical expertise. I enjoyed working in different institutes and laboratories across Dublin and to collaborate with many people to accomplish the excellent projects they proposed me. For the short-term future I'm really looking forward to apply what I learned in these two years focus on the prevention and control of infectious diseases. In addition, I am glad to have expanded my personal and professional network and wish to continue to contribute to strengthen public health at European level and beyond.

## Acknowledgements of fellow

I would like to thank my EUPHEM supervisor Eleanor McNamara for her excellent supervision and encouragement during the last two years and to my co-supervisor Robert Cunney. Special thanks go to Anne Carroll for her support and guidance and to all staff at PHL for the amazing team spirit and atmosphere in the laboratory. Also a big thanks to all my local project supervisors who gave me the opportunity to work on a variety of interesting and exciting projects, for their great supervision and confidence and thanks to all the staff who help me and supported me across different departments and institutes: the Irish Mycobacteria Reference Laboratory and Serology Department at St James's Hospital, the Health Protection Surveillance Centre, the Irish Meningitis and Sepsis Reference Laboratory at Temple Street University Hospital and the Microbiology Department at Rotunda Hospital for their valuable insights in their respective institutions and for great collaborations.

I would like to express my gratitude to my frontline coordinator Aura Andreassen for her guidance and continuous support during our long calls. Thanks to all other EUPHEM and EPIET coordinators, heads of programme and members of the fellowship office for their enthusiasm, administrative support, scientific input and leadership.

A big thank you to the amazing C2016 fellows, for the great company and fun times during the modules and who made these two years a fantastic experience. A special thanks to Carina Brehony, the new EUPHEM fellow from C2018 at PHL, for their help, support and friendship in the hard last months of the fellowship. Last but not least, a huge thank you to my family because without them this could have not been possible. And finally, my special thanks to my beautiful daughter, who is the sunshine of my life and has accompanied me during this adventure.