

The section header "Summary of work activities" in a bold, white, sans-serif font, set against a blue background.The author's name "Durdica Marosevic" in a white, sans-serif font, set against a blue background.The subtitle "European Public Health Microbiology Training Programme (EUPHEM), 2015 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 Durdica Marosevic, cohort 2015 of the European Public Health Microbiology Training Programme (EUPHEM) in the Department for Public Health Microbiology and Infectious Disease Epidemiology at the Bavarian Health and Food Safety Authority, Oberschleißheim, Germany.

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

Durdica Marosevic is a Croatian Molecular Biologist that prior to her EUPHEM fellowship had been working at the Veterinary Research Institute in Brno, and was completing her PhD in Microbiology. Her focus lied on the impact of antibiotics on the animal intestine and the transfer of MLS_B antimicrobial resistance genes between bacteria, employing metagenomics and next-generation sequencing techniques. Her Bachelor degree is in Molecular Biology, and later she pursued a Master degree in Molecular Biology in Zagreb and Bioindustrial Techniques at the University of Orleans. Durdica joined the EPIET/EUPHEM programme to broaden her competencies in public health microbiology and intervention epidemiology, gain hands-on experience on surveillance activities within public health institutions, and to actively engage in the exciting new area of implementing cutting-edge sequencing techniques in public health microbiology.

Fellowship assignment: Public health Microbiology (EUPHEM) path

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 guide¹.

1. Epidemiological investigations

1.1. Outbreak investigations

A. Outbreak of Norovirus after a company dinner

Supervisors: Katharina Schönberger, Anne Belting, Wolfgang Hautmann

After a company dinner on the 16.09.2016, Friday in a local restaurant with 140 participants, approximately 30 people reported ill on the following Monday 19.09.2016. The company medical officer immediately informed the local health authority (LHA) on the possible food related outbreak.

The LHA and Food Safety Authority (FSA) inspected the restaurant. The dinner was an open buffet, and a list of the served food (with pictures) was used for the questionnaire design with a total of 37 food items included. The questionnaire was distributed via the company mailing list (n=140). Stool samples were taken from the restaurant staff and the diseased participants and examined at the LGL with PCR for Norovirus, Rotavirus, Salmonella/Shigella, Campylobacter, EHEC, EPEC. Neither left-over food nor counter samples were available for laboratory testing. In Germany counter samples are only a recommendation for restaurants and cater companies, not a legal obligation. Counter samples are taken from the originally prepared food and kept frozen for two weeks for microbiological investigations. All hygienic legal requirements were in place in the restaurant. A total of 133 (95%) questionnaires were returned to the LHA and a cohort study and univariable analysis of the data was performed by the LHA using the RKI Line-list TOOL. The analysis revealed 48 cases with the highest risk ratio for Tomaten Mozzarella Salat, Tomaten Mozzarella, Nudel Salat, Eier Salat and Tomaten Salat. Additionally, the fellow performed at the LGL an univariable and multivariable logistic regression in order to try to narrow down the vehicle of transmission. In the multivariable logistic regression the best fit model included Tomaten Mozzarella Salat and Tomaten Mozzarella. When adjusting for Tomaten Mozzarella, the highest odds ratio 2.83 [1.28-6.30] had the Tomaten Mozzarella Salat and Tomaten Mozzarella had an odds ratio of 2.67 [1.12-6.35]. Considering that the questionnaire included only food intake, other possible ways of transmission cannot be dismissed, such as human-to-human transmission and

¹ European Centre for Disease Prevention and Control. European public health training programme. Stockholm: ECDC; 2017. Available from: <http://ecdc.europa.eu/en/publications/Publications/microbiology-public-health-training-programme.pdf>

transmission *via* contaminated surfaces (i.e. in the restroom). In total 11 samples from participants of the company dinner were tested positive for norovirus. Eight of the ten tested stool samples from employees of the restaurant were positive for norovirus. Two of the people working at the restaurant reported being ill starting with the 19.09.2016, the remaining 6 were asymptomatic, including the person that prepared the salads on the day of the dinner.

The recommendations included refreshment training in the importance of proper hygiene in restaurants for the personnel and the restaurant owner agreed to start using counter samples in the future in order to aid microbiological investigations if needed.

Durdica Marosevic was in contact with the LHA, provided support in the interpretation of the univariable analysis and performed the multivariable analysis. She was actively involved in the formulation of conclusions and recommendations and wrote the final report that was used as a base for the publication in the "Epidemiologisches Bulletin", a weekly epidemiological report of the German RKI.

B. Outbreak of Norovirus during a children school trip

Supervisors: Katharina Schönberger, Anne Belting, Wolfgang Hautmann

A cluster of 13 gastrointestinal ailments among a group of 45 schoolchildren housed in a youth hostel in Bavaria was notified on the 11.10.2016 to the local health authority (LHA) and LGL via the early warning system in place. This was the second instance of a gastrointestinal disease cluster in the same youth hostel within 3 months, therefore an outbreak investigation was initiated. A total of 46 (94%) of 49 persons answered the questionnaires and 23 (50%) of the responders met the case definition. None of the food items served at the youth hostel were significantly associated with the illness. However, group activities (eating together, sleeping in the same room or using the same toilette as an ill person) and daily excursions, were significantly associated with the illness, therefore a human-to-human transmission rather than food associated point source is most likely. Most interesting was the exposure "sitting next to an ill person on the bus on the way to the castle". The daily excursion to the castle took place on the 11th of October. The excursion to the Forest Adventure Centre that took place on the 12th of October was not significantly associated with developing the disease, although 15 persons who have already developed symptoms participated in the excursion. This is most probably due to the heightened hygiene awareness and precautions implemented by the LHA immediately upon the first notification on the 11th of October. Norovirus was detected in 3 stool specimen provided by the diseased. None of the personnel in the youth hostel was positive for norovirus. The outbreak was effectively controlled due to the fast implementation of recommended guidelines for cleaning and disinfection, and no further cases were reported to the youth hostel or the LHA during October, although a total of 130 persons were staying at the youth hostel at that time.

The EUPHEM fellow participated in all stages of the outbreak investigation in order to identify the source and the aetiology of the infections. She was in charge of the design and the implementation of the analytical cohort study, created the questionnaires in German, created a database using EpiData, entered data and performed the statistical analysis with the use of Stata. She was actively involved in the communication with the LHA, formulation of conclusions and recommendations and she wrote the final report that was distributed among the stakeholders.

C. VRE colonisation in a Neurorehabilitation hospital

Supervisors: Constanze Wendt, Katharina Schönberger, Christiane Höller

During the first half of 2017 an increase in vancomycin resistant enterococci (VRE) gastrointestinal colonisation without infection, was observed in a Neurorehabilitation Hospital in Munich. Cases were detected through routine monthly screening of all patients implemented in this hospital. No obvious epidemiological link, like sharing the room, was evident. The routine screening for other resistant pathogens did not exhibit a similar increase that could point to a general hygiene problem. Once being identified as VRE colonised, patients are preferably placed in single bedrooms or cohorted. All patients in this hospital exhibit prolonged hospital stay, antibiotic treatment, and older age, all described in the literature as risk factors for becoming colonised with VRE. A cohort study was suggested to try to identify other, specific risk factors that could promote VRE colonisation in this specific setting, where hygiene standards were kept very high and patients were already susceptible to VRE colonisation. PFGE analysis of all strains was performed at the LGL, revealing a diverse, non-clonal spread of the enterococci. This was expected, as due to frequent transfers from other hospitals, there is a high influx of diverse enterococcal subtypes in this setting, as evidenced also through the high proportion of VRE colonisations that are detected through admission screening. During that time additional training in hygiene was performed and awareness in personal hygiene among staff was strengthened even more. This was visible through the consumption rate of hand sanitizer during the first 5 months in 2017 that exceeded the average yearly consumption. By the end of May no new nosocomial transmission and VRE colonisation was observed, although several newly admitted patients were colonised with VRE.

The fellow was leading on writing the study protocol and communicating with the stakeholders, as well as developing the mask for data extraction and entry from the hospital information system. However, for internal reasons, the hospital eventually decided not to proceed with the study.

D. Training modules: Outbreak Investigation and Multivariable Analysis Module

During the EPIET/EUPHEM introductory course participants were familiarised with the methods and logistical aspects of outbreak investigations. Additional, training during the 'Outbreak investigation Module' taught essential data management skills (entering, validating and cleaning data), dataset management and how to perform case-control studies, descriptive and cohort studies, including stratified analyses. Building on these courses, during the 'Multivariable analysis Module', fellows discussed the principles, application and interpretation of multivariable analysis and its role in field epidemiology.

Educational outcome:

Understanding the need for a cooperative teamwork among laboratories, local and central authorities, including international collaboration; involvement in the outbreak investigations (case definitions, active case-finding, data collection, data analysis); integration of microbiological and epidemiological knowledge to investigate outbreaks.

1.2. Surveillance

A. Screening for infectious diseases among newly arrived asylum seekers in Bavaria, Germany, 2015

Supervisors: Nikolaus Ackermann, Katharina Schönberger, Andreas Sing

Since the beginning of 2010, many European Union/European Economic Area (EU/EEA) countries faced an ever increasing number of asylum seekers as a consequence of socio-economic and political crises including war and civil unrest in many parts of the world. The number of asylum seekers peaked in the year 2015 in Germany. The majority of asylum seekers tend to be in relatively good health, so that the risk of an outbreak of infectious diseases in host countries is low. Nevertheless, an established entry screening system for the presence of infectious diseases allows early diagnosis and consecutive timely treatment for the affected individual.

In the German Federal State of Bavaria foreigners applying for asylum have to undergo a medical examination including serological testing for a HIV and hepatitis B, a screening for tuberculosis, and until September 2015, a stool examination for salmonellae and shigellae. The HIV positivity and HBs-Ag positivity rate of tested samples from asylum seekers were 0.3 % and 3.3 %, respectively, while the detection rate of active tuberculosis was between 0.22 and 0.38 %. Importantly, the prevalence rates for HIV, hepatitis B, and tuberculosis among asylum seekers were in good concordance with the corresponding prevalence rates in most of their respective countries of birth. 53,085 stool samples were examined bacteriologically; only 47 salmonellae (0.1 %) were isolated: 45 enteric and 2 typhoid serovars. Beyond mandatory screening, a noteworthy disease that occurred was louse-borne relapsing fever (n=40), caused by *Borrelia recurrentis*. These results show that mandatory screening during 2015 in Bavaria yielded overall low positivity rates for all tested infectious diseases in asylum seekers and that there was no increased risk of importing infectious diseases. Therefore, mandatory screening might be limited to high-prevalence countries in order to facilitate diagnostics, as it was done in September 2015 for stool examination for salmonellae and shigellae. This could redirect resources to provision of treatment to affected individuals and providing appropriate health interventions.

The fellow was involved in the analysis and interpretation of the results of the mandatory screening for an oral presentation and drafted the manuscript. The data were presented at the EAN Mini Module 2016 "Migrant Health" in Brussels, and a manuscript with first shared authorship of the fellow is accepted for publishing in Eurosurveillance.

B. Bavarian Influenza Sentinel Season 2015/2016

Supervisors: Ute Eberle, Susanne Heinzinger, Nikolaus Ackermann, Andreas Sing

The Bavarian Influenza Sentinel (BIS) is an enhanced surveillance system, established in 2009 with the objective to monitor influenza virus activity and subtype distribution in order to elaborate on the data collected by the syndromic surveillance system. The sentinel is active only during the winter months and included in 2015/16 season 79 physicians. Nasopharyngeal swabs from first two patients presenting with symptoms of an acute respiratory illness (ARI) are collected per week and typed at the LGL.

During the Season 2015/16 a total of 2006 samples were analysed. In 425 samples influenza virus could be detected (21% average positivity rate), 213 (50.2 %) were Influenza A subtype H1N1, 188 (44.4 %) Influenza B and 6 were Influenza A subtype H3N2. The peak of the season with 48% positivity rate was in week 11. Interesting to note is the increase in Influenza B proportion among all identified cases, and the shift from dominating influenza A in the beginning to influenza B by the end of the season.

A significantly ($p < 0,001$) higher proportion of children aged 3-5 (26 %) and 6-18 (29 %) had an influenza infection compared to the other age-groups. This increase could be explained by a significant increase of influenza B infections among this age group. Similar observations were already noted in Australia in the influenza season 2015, where younger patients were affected more by the influenza B Victoria line. Our samples were not further subtyped, however, during the season 2015/16 96% of the Influenza B detected in Germany and subtyped at the NRC for

influenza belonged to the Victoria line, and therefore it can be assumed that a similar proportion of Victoria line was present in Bavaria as well.

On average, 15.7 samples per 100 000 population were sent in for analysis. The rate differed among different counties in Bavaria with the lowest in counties Schwaben and Mittelfranken. The low submission rate per 100 000 had two differing reasons: in the county Mittelfranken, a good sample submission rate per doctor was achieved, however, due to the fact that the county has high population numbers, the submission rate per 100 000 population was unsatisfactory; in the county Schwaben, only 50% of participating physicians were actively sending samples during the season 2015/16 (≤ 20 samples during the season). The Bavarian Influenza Sentinel is a valuable addition to the multi-layered influenza surveillance established in Germany. In order to remain a useful surveillance tool, geographic homogeneity and a steady and motivated submission behaviour has to be encouraged. Therefore recommendations include two different approaches: for county Mittelfranken, additional physicians have to be recruited, while for county Schwaben in addition to new physicians recruited, the objective of the sentinel has to be clearly communicated in order to improve the submission rate of already involved physicians.

Durdica Marosevic was involved in the weekly data analysis and communication with the participating physicians during the influenza season. This included preparation of updates published weekly on the LGL web-page and in the bulletin "LGL Monitor" distributed to all local health authorities in Bavaria, but also phone communication, logistical and technical support to participating physicians. The fellow was leading on analysing and writing the yearly report that was distributed among the participating physicians and in a shorter version also published in the Bavarian Medical Journal. Furthermore, the results were presented in October 2016 at the regional conference for infection prevention and hygiene "Erlanger-Nürnbergiger Hygienetage 2016".

C. HIV and syphilis co-infection in Bavaria 2010-2016

Supervisors: Katharina Schönberger, Ute Eberle, Nikolaus Ackermann

During 2010-2016 the incidence of HIV infections in Germany was stable, around 3.3 - 4.5 per 100,000. Concurrently, an increase in notification of syphilis cases was observed. Compared to 2014, in the year 2015 an increase of 19.4 % syphilis-cases was observed. Syphilis and HIV, are both associated with similar risk behaviors and exposures, and in addition to that, infection with syphilis can increase the risk of acquiring HIV through genital ulcers, while HIV affects the presentation, diagnosis, disease progression and therapy of syphilis.

In the German mandatory infectious disease notification system, both HIV and *Treponema pallidum* infections are notified directly and anonymously to the National Health Authority RKI and information on co-infections are included only on a voluntary basis. Due to the anonymity and voluntary inclusion of other infections, the proportion of 6.3 % co-infection with HIV among all notified syphilis cases in 2015 in Germany is presumed to be an underrepresentation. At the Bavarian LGL laboratory investigations and confirmation tests are performed as a support service for STD consultation offices at the local health authorities (LHA) and entrance screening of inmates in penitentiaries in Bavaria. The aim was to evaluate the proportion of co-infections of syphilis and HIV among patients tested at the Bavarian LGL during 2010-2016 in order to provide more detailed insights into the disease status of people suffering from sexually transmitted infections (STIs) in Bavaria.

Every year in the Bavarian LGL laboratories between 10,000-20,000 samples are investigated for STIs. Approximately 24 % of samples tested at the LGL for HIV were also tested for syphilis, *vice versa* all samples tested for syphilis were also tested for HIV. The LHA requested 54 % of the tests and 46 % of the samples are part of screenings in penitentiaries. There was no statistical difference in the positivity rate among the samples sent by the LHA or penitentiaries. Among all laboratory confirmed syphilis cases at the Bavarian LGL, 8.9 % had a coinfection with HIV. The coinfection rate differed among the years from 4.1 - 12.1 %, due to low case numbers.

This is an important public health investigation that addresses the limitations faced by the anonymous notification data collated at the RKI, and provides means of comparison and an estimate of the underestimation of the voluntary notified co-infections.

The fellow was involved in all stages of the study, from extracting the data from the laboratory database to the analysis in Stata 12, and formulating recommendations and conclusions. The results are being summarized in a manuscript and published in a peer-reviewed journal (in preparation).

D. Training modules: Introductory course & Rapid assessment and survey methods

The EPIET/EUPHEM introductory course familiarised participants with the main concepts of surveillance, including how to develop, validate, evaluate and operate a surveillance system. The "Rapid assessment and survey methods" module provided fellows with knowledge on how to contribute to the multidisciplinary response to complex emergencies as well as sampling techniques, and morbidity and mortality surveys.

Educational outcome:

Defining the components of a surveillance system, analyse and report data from surveillance systems, including defining recommendations for the improvement of the surveillance system. Identify health needs in complex emergency situations (CES) and define the role of the laboratory in CES, setting up a surveillance system during a CES.

2. Applied public health microbiology research

A. First insights in the variability of *Borrelia recurrentis* genomes

Supervisors: Gabriele Margos, Volker Fingerle

Recent migrations brought new attention to a disease that was nearly forgotten in Europe – louse-borne relapsing fever. It is the only relapsing fever transmitted by lice, and is caused by *Borrelia recurrentis*. Today it is endemic to the Horn of Africa, but due to the cosmopolitan nature of the vector, the pathogen still bears epidemic potential to spread globally among vulnerable populations. The highest number of cases (n=45) were reported among migrants in 2015 in Germany and sporadically from other European countries. So far only one genome was sequenced, hindering the development of specific molecular diagnostic and typing tools. The aim of this project was to examine the intraspecies genome variability of six strains isolated and cultured at different time-points in order to explore the possibility to identify new targets for typing and examine the molecular epidemiology of the pathogen.

Two historical strains from Ethiopia and four isolates from migrants from Somalia (n=3) and Ethiopia (n=1) isolated in 2015 were cultured. Whole DNA was sequenced. 29-38 SNPs were identified in the genome distributed on the chromosome and plasmids. In addition to that, plasmids of differing length, compared to the available reference genome were identified.

The observed low genetic variability of *B. recurrentis* strains is possibly due to the adaptation to a very conserved vector-host (louse-human) cycle, or influenced by the fastidious nature of the pathogen and their resistance to *in vitro* growth. Nevertheless, strains isolated in 2015 were bearing the same chromosomal SNPs and could be distinguished from the historical strains by means of whole genome sequencing, but not by hitherto used typing methods. This is the first study examining the molecular epidemiology of *B. recurrentis* and provides the necessary background for the development of better diagnostic tools.

Durdica Marosevic was the principal investigator and was involved in all stages of this project, from planning and performing the laboratory work and bioinformatical analysis, to writing a final manuscript as first author (accepted in PLOS Neglected Tropical Disease). The work was presented at the European Scientific Conference on Applied Infectious Disease Epidemiologically (ESCAIDE) in 2016 and at the 66. Scientific Congress of the German Association of Public Health Physicians – “Public health in the mirror of time” in 2016.

B. Whole genome sequencing of Bavarian *Salmonella enterica* ssp. *enterica* Serovar *Enteritidis* strains 2015

Supervisors: Regina Konrad, Alexandra Dangel, Anja Berger, Stefan Hörmansdorfer

The majority of Salmonella infections in Germany can be attributed to *S. Enteritidis* and *S. Typhimurium* which account for 60 and 20% of all cases, respectively. The absolute number of salmonellosis cases in Germany decreased from 77,000 to 14,000 per year since 2001, and approximately 10% of these cases are reported in Bavaria. In outbreak situations caused by the most common serotype such as *S. Enteritidis*, serotyping provides limited information and more discriminating methods have to be employed to distinguish and assign isolates to specific outbreaks, such as single locus typing, multilocus typing, multilocus variable number tandem repeat analysis, phage typing and PFGE. Recent advances in sequencing technologies and accompanying bioinformatics tools that have been developed enabled the introduction and application of whole genome sequencing (WGS) in public health laboratories. WGS provides the highest resolution and detection of single nucleotide differences (SNP) between strains and therefore also highly valuable information for outbreak investigations.

The aim was to expand the typing methods for *Salmonella* spp. with a state-of-the-art sequencing and whole genome analysis in order to improve outbreak investigation and assessment of clusters and/or transmission chains and identify the circulating *Salmonella enterica* ssp. *enterica* Serovar *Enteritidis* (*Salmonella Enteritidis*) strains in Bavaria collected from May to September 2015 in order to assess the variability of the most common gastroenteritis pathogen circulating in the Bavarian population.

The algorithms and conditions developed for SNP typing using CLC Genomic Workbench at the LGL were compared with the pipeline developed at Public Health England (PHE). The analysed strains clustered identically, therefore supporting the validity of the applied approach. The developed method was successfully applied to a food-borne outbreak in a home for the elderly, identifying strawberry pastry as the source of the infection.

The fellow was in London at the PHE Department for Gastrointestinal Diseases on a one-week hands-on training and introduction to the PHE bioinformatics pipeline. She participated in the development of the pipeline at the LGL and is involved in the manuscript preparation (in preparation).

C. Training modules: Bioinformatics and Phylogeny Module

During the ‘Bioinformatics and Phylogeny Module’ in November 2015, Stockholm, the fellows got familiarized with different tools for bioinformatics and phylogenetic analysis in order to allow them to deepen their knowledge and apply these practical skills further during the fellowship. Through short lectures and case-studies based on real-life examples fellows had the opportunity to practically test and apply the concepts of bioinformatic tools and phylogeny.

Educational outcome:

Introduction and use of various softwares for nucleotide and protein analysis (Bionumerics, CLC Genomic Workbench, SSE, MEGA, FigTREE, Galaxy, Clustal and Tablet); understanding and performing phylogenetic analysis (including sequence cleaning and alignment); evaluate NGS data; discussing the importance and future issues relating to bioinformatics and phylogeny in public health microbiology.

3. Applied public health microbiology and laboratory investigations

A. Measles genotyping at the Bavarian LGL

Supervisors: Nikolaus Ackermann, Ute Eberle, Bianca Treis

Measles (MeV) is a single-stranded, negative sense RNA virus, member of the *Morbilivirus* genus. Based on the sequence diversity of the 450 nt-sequence on the carboxyl-terminus of the nucleoprotein (N-450), the MeV can be divided into eight clades and 24 genotypes. The number of measles cases in Germany varies throughout the years, and the national incidence is still one of the highest in Europe. In order to proceed towards the measles elimination, genetic characterization of circulating wild-type measles viruses is critical. The rationale for this project was to establish and validate the new real-time PCR method for measles detection and additionally implement the genotyping method of N-450 at the LGL in order to get a better insight in the circulating genotypes in Bavaria, and support the NRC in the genetic characterisation of MeV. The implementation and availability of this method at the LGL enforced the overall laboratory preparedness of Germany for this pathogen. Strains that have been genotyped at the LGL in 2016, in combination with the epidemiological data, delivered first information about an ongoing measles outbreak among a migrant population from Chechenia; furthermore, cases diagnosed in Bavaria could successfully be assigned to an ongoing measles outbreak connected with music and arts festivals in Britain. The fellow received first hands-on training at the NRC for MMR at the RKI and implemented the methods at the LGL. This included initial laboratory work and management, development of in-house SOP-s, protocols and training for the technicians. Furthermore, the fellow was responsible for the communication with the Measles Nucleotide Surveillance (MeaNS) database and upload of MeV strains from Bavaria. First results were presented at the 67th. Scientific Congress of the German Association of Public Health Physicians: BVöGD – “Health for everyone” in 2017.

B. Antimicrobial resistance of toxigenic and non-toxigenic *C. diphtheriae* and *C. ulcerans* in Germany 2010-2016

Supervisors: Anja Berger, Andreas Sing

Respiratory or cutaneous diphtheria is caused by diphtheria toxin (DT) producing strains of *C. diphtheriae*, *C. ulcerans* and *C. pseudotuberculosis*. Due to high vaccination coverage, diphtheria is nowadays a rare disease in Europe and other developed countries. During 2016 a total of 9 toxin-producing diphtheria cases have been notified in Germany. In the last 10 years, majority (50-100%) of the notified cases were caused by DT producing *C. ulcerans*. Similar trends have been seen in other developed countries. Reports of NT strains have been increasing over the past 30 years and cause infections such as endocarditis, discitis, septic arthritis, pharyngitis and tonsillitis. The case fatality rates of invasive NT *Corynebacteria* are significantly higher than reported case fatality rates for DT *Corynebacteria* nowadays. The empirical choices of antibiotics for treatment are benzylpenicillin or macrolides. Antibiotics are administered also to non-symptomatic carriers, to prevent further spread. Timely antibiotic treatment and exhaustive antibiotic susceptibility criteria will be critical in preventing significant morbidity and mortality associated with both DT and NT *Corynebacteria* infections. The European Committee on antimicrobial susceptibility testing (EUCAST) guidelines and the Clinical and Laboratory Standards Institute (CLSI) guideline for Infrequently Isolated or Fastidious Bacteria provide limited and sometimes inconsistent information for antibiotic susceptibility testing of this important pathogen. Therefore the rationale of this project was to examine the antibiotic susceptibility profiles of current and historical *Corynebacterium* strains available at the Consultant laboratory for Diphtheria in Germany, in order to fuel information for the harmonization of international guidelines and facilitate diagnosis and prescription of appropriate therapy.

Data from 234 NT and 122 DT *Corynebacterium* spp. isolates show that 33 % (n=77) and 76 % (n=93) were penicillin resistant, respectively. Erythromycin resistance was observed for 2.6 % (n=6) and 2.5 % (n=3) NT and DT isolates. *C. ulcerans* a common pathogen found in wound infections, either alone or in combination with other microorganisms was in 69% of tested isolates (n=93) clindamycin resistant. This is worrying as clindamycin is the recommended antibiotic for these infections. No resistance against vancomycin or linezolid was observed, and resistance against other classes was rare.

These preliminary data point to developing resistance against the most commonly used antibiotics, therefore performing antibiotic susceptibility testing should be recommended for all clinical strains in order to facilitate treatment.

The fellow was the principal investigator in this study and involved in all stages of this project, from planning and performing the laboratory work and data analysis, to writing a final manuscript as first author (in preparation). The

results of this project were shared with EUCAST in order to update and expand the current guidelines for *Corynebacterium* spp. The work has been presented as an e-poster during ESCAIDE 2017.

4. Biorisk management

A. Study on laboratory preparedness of Germany towards emerging and re-emerging diseases

In early 2016 the fellow did a study on the preparedness of Germany towards emerging and re-emerging diseases. The results were presented to the Director, the Chief Microbiologist, and the Chief Scientist of ECDC during the Module on Initial Public Health Management.

B. PPE training at the airport

Supervisors: Friedrich Pürner, Siegfried Ippisch

At the LGL is located the "Task Force Infektionsepidemiologie - Flughafen" (TFIF). They are responsible for the crisis management in case of infectious diseases and contact tracing at the airport. During a one-day induction, the fellow had hands-on training and the practical application of personal protection equipment (PPE) at the airport and a theoretical introduction and explanation of SOPs and legislation.

C. Biosafety and Biosecurity assessment

The BioRAM Biosafety and Biosecurity Tool was used to assess and mitigate possible shortcomings in a simulation considering given laboratory setup, and the laboratory setup in our host country. This was part of the homework post the 'Biorisk and quality management module'.

5. Quality management

A. Preparation of audit paperwork for measles genotyping

Supervisors: Ute Eberle, Nikolaus Ackermann, QS office at LGL

As part of the measles genotyping project at the Bavarian LGL, the fellow was responsible for the development of all SOPs for the laboratory and computer analysis of samples processed at the LGL. This includes internal laboratory protocols, as well as sample submission guidelines for physicians and sequence submission guidelines for the MeaNS database.

B. Internal audit of the Virology Laboratory at the Bavarian LGL, 2016

Supervisors: Nikolaus Ackerman, QS office at LGL

Internal audit of the Virology laboratory was performed as an assignment post biorisk and quality management module. The audit inspected process management and quality control indicators as well as documentation.

The Virology laboratory at the Bavarian LGL processes 100-200 thousand of samples per year (in 2015 95 thousand samples were processed as part of the asylum seeker entering screening), it has 10 laboratory technicians working on 20 laboratory tests. The accommodation and environmental conditions of the laboratory are up to all standards, with all laboratory sections effectively separated and access to the laboratory building is controlled *via* a chip-based system. The whole analytical process (including pre- and post-analytical process) is handled according to all recommendations. No standardized and regularly performed survey to assess client feedback and satisfaction is in place, however, there are standard operation procedures in place for recording complaints. These complaints are handled on a case by case basis and corrective actions implemented. Regarding the documentation and document handling at the Virology laboratory, all indicators are met. The lowest score is recorded for the standardized report format because specific time is not recorded and reported for the sample collection, sample receipt in the lab, or report release. The laboratory has summary reports on a three-month basis. Collated is the number of performed tests and results. The lab is also reporting weekly to the authorities the numbers of performed HIV and Hepatitis B tests and the respective results by county, performed as part of the § 62 AsylVfG health examination of asylum seekers in Bavaria. SOP's for maintenance are available for some equipment in paper form, for others it is a click-through guide available as part of the software. The location for the procedure is not explicitly stated in the SOP (i.e. room number) however, it is self-explanatory, as the necessary equipment for the procedure is located only in one specific room. No explicit review period for the procedures is indicated and it is performed upon request and in case of need (e.g. change in the kit and reagents provided by the producer, change of equipment in the laboratory).

The audit yielded a general indicator percentage of 95%, with lowest scores for quality improvement (67%). The laboratory was advised to implement a client feedback and prevention planning system in the form of a yearly client satisfaction survey in order to review client feedback and address possible non-conformities.

The fellow completed the audit by interviewing laboratory technicians, going through protocols and methods

descriptions and workflows in the laboratories.

C. Training modules: Biorisk and Quality Management Module

The module provided training on topics related to quality management in biomedical and public health laboratories according to ISO 15189 norm, training for international shipping of infectious substance and the biosafety assessment and mitigation techniques in biomedical laboratories and a visit to a biosafety level 4 (BSL4) facility.

Educational outcome:

Understanding biosafety regulations, applying biorisk mitigation methods in theory and practise in laboratory and field settings, learning appropriate measures for the safe transport of hazardous substances and pathogenic specimens completed with a WHO certificate of International Transport of Infectious Substances.

6. Teaching and pedagogy

A. Organisation and teaching Interdisciplinary Workshop on epidemiological investigation of food-borne outbreaks, Bad Alexandersbad, 14-16.02.2017

The fellow was co-organizing the "Interdisciplinary Workshop on epidemiological investigation of food-borne outbreaks" – 14-16.02.2016. This included the preparation and delivery of 4 lectures of 45 min on "First steps of an outbreak investigation", "Descriptive analysis", "Analytical studies" and "Sources of error and interpretation". Preparation and facilitation of a Case study in German "Outbreak after a company dinner". The workshop was aimed at people working at the Local Health Authorities (doctors and hygiene inspectors) and at the Local Veterinary Authorities (veterinarians and food inspectors) and the objective was to facilitate the cooperation and understanding of the mutual needs from all participating stakeholders. Therefore a big focus of the workshop was on cooperation, communication and management.

B. Teaching at the Ludwig-Maximilians University (LMU), Munich, February 2016 and 2017

The fellow adapted and delivered two lectures and facilitated a case study at the Ludwig-Maximilians University in Munich to Master students of the master programme for Public Health. The lectures were organized both years in the winter semester February 2016 and 2017 for two different cohorts. The lectures were entitled "Surveillance systems" and "Outbreak Investigations" and the practical example was the case study "An outbreak of trichinosis in France".

C. Teaching at the Technical University Munich, May 2017

Given the interest and success of the long-term cooperation with the LMU (since 2009), in 2017 a new cooperation was initiated with the TUM and their newly established Masters program "Health Science & Diagnostics and Training". The fellow gave a lecture on "10 steps of an outbreak investigation" and facilitated a case study "Outbreak after a company dinner" as part of the "Infectious Disease Epidemiology" module.

D. Development of case study "Outbreak after a company dinner"

Supervisor: Katharina Schönberger, Anne Belting, Wolfgang Hautmann

The food-borne outbreak of Norovirus after a company dinner that the fellow was actively involved in was re-written into a case study in German for the participants at the Interdisciplinary workshop. The case study covers: The ten step of an outbreak investigation, the importance of collaboration of different disciplines (veterinarians, doctors, hygiene and food inspectors at the local authorities, epidemiology, microbiology at the state authorities and laboratories), epidemiological analytical cohort study, importance of BELA-questionnaires for food-borne outbreaks.

E. Case study facilitation at the OIM, Berlin, December 2016

The fellow participated in the facilitation of two bioinformatics and phylogeny case-studies during the 'Outbreak Investigation Module' for Cohort 2016 in Berlin.

F. Molecular Biology Techniques at the LGL, September 2016

The fellow developed and delivered a lecture on molecular biology techniques in nucleic acid detection and analysis as part of the further education programme for laboratory technicians at the LGL.

F. Quality Management Systems Lecture, Stockholm, February 2016

The fellow adapted and delivered a lecture on quality management systems in biomedical laboratories during the biorisk and quality management module in February 2016 in Stockholm.

Educational outcome:

Identify training needs, define course objectives, develop curriculum, plan and organise a course, design and facilitate case studies, prepare and deliver presentations aimed at a range of health-care professionals, re-evaluate delivery and content.

7. Public health microbiology management

A. 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. For numerous of projects the fellow communicated with different supervisors, technical assistants and other collaborators both within the LGL, RKI and LHAs. During the establishment of the measles genotyping at the LGL she communicated with the NRC, as well as LHA to encourage sampling and heighten the awareness for the new methods available and their importance for public health. For the VRE colonisation outbreak in a hospital, the fellow was leading in the study protocol development and coordinating the communication with the LHA, hospital staff and the LGL laboratory. During the one week induction at PHE and their bioinformatics department, the fellow strengthened the collaboration and facilitated knowledge transfer. As part of the BIS project, the fellow also participated in communication with the public and answering media questions about influenza season. The fellow was also actively involved in the "Outbreak café", a regular monthly interdisciplinary meeting between the epidemiology, public health microbiology, veterinary microbiology and food microbiology departments at the LGL in order to facilitate cooperation, information exchange and coordinated outbreak investigations. Throughout the fellowship the fellow practiced effective time management, organised and participated in meetings, communicated through scientific writing and presentations, and gave and accepted feedback.

B. Training modules: Initial Management in Public Health Microbiology

During the Initial Management in Public Health Microbiology Module, the participants were introduced to the roles and responsibilities of effective management and how to assume different management and leadership styles. Assessment of the levels of self and team motivation and team development by applying and developing effective communication and structured feedback with peers, stakeholders and media/public. The role of different agencies were defined and described. Stress recognition and management was also tackled.

Educational outcome: understanding of what Initial Management is within a Public Health environment, maximise the impression on others and how a more principled approach to managing situations, contributes to developing personal relationships and Public Health success; different motivational needs and styles necessary for the functioning of a diverse team.

8. Communication

Publications

1. Ackermann N*, Marosevic D*, Hörmansdorfer S, Eberle U, Rieder G, Treis B, Berger A, Bischoff H, Bengs K, Konrad R, Hautmann W, Schönberger K, Belting A, Schlenk G, Margos G, Hoch M, Pürner F, Fingerle V, Liebl B, Sing A; Screening for infectious diseases among newly arrived asylum seekers in Bavaria, Germany, 2015; (Eurosurveillance accepted) * shared first authorship.
2. Marosevic D, Margos G, Wallich R, Wieser A, Sing A, Fingerle V; First insights in the variability of *Borrelia recurrentis* genomes; PLoS Negl Trop Dis. 2017 Sep 13. doi: 10.1371/journal.pntd.0005865.
3. Marosevic D, Eberle U, Heinzinger S, Ackermann N, Schönberger K, Hautmann W, Liebl B, Sing A; Bericht zur Influenzaüberwachung in Bayern Saison 2015/16; <http://www.bayerisches-aerzteblatt.de/inhalte/details/news/detail/News/bericht-zur-influenzaueberwachung-in-bayern-saison-201516.html>
4. Norovirus-Ausbruch im Landkreis Amberg-Sulzbach, Bayern, September 2016; DOI 10.17886/EpiBull-2016-069.
5. Margos G, Hepner S, Mang C, Marosevic D, Reynolds SE, Krebs S, Sing A, Derdakova M, Reiter MA, Fingerle V; Lost in plasmids: next generation sequencing and the complex genome of the tick-borne pathogen *Borrelia burgdorferi*; (2017) 18:422 DOI 10.1186/s12864-017-3804-5
6. Margos G, Marosevic D, Cutler S, Derdakova M, Diuk-Wasser M, Emler S, Fish D, Gray J, Hunfeldt KP, Jaulhac B, Kahl O, Kovalev S, Kraiczky P, Lane RS, Lienhard R, Lindgren PE, Ogden N, Ornstein K, Rupprecht T, Schwartz I, Sing A, Straubinger RK, Strle F, Voordouw M, Rizzoli A, Stevenson B, Fingerle V; There is inadequate evidence to support the division of the genus *Borrelia*; Int J Syst Evol Microbiol 2017;67:1081–1084; DOI 10.1099/ijsem.0.001717

7. Teutsch B, Berger A, Marosevic D, Schönberger K, Lâm TT, Hubert K, Beer S, Wienert P, Ackermann N, Claus H, Drayß M, Thiel K, van der Linden M, Vogel U, Sing A; *Corynebacterium* species nasopharyngeal carriage in asymptomatic individuals aged 65 years in Germany; *Infection*, 2017 Apr 20. doi: 10.1007/s15010-017-1017-0. [Epub ahead of print]
8. Marosevic D, Berger A, Sing A; Antimicrobial resistance of toxigenic and non- toxigenic *C. diphtheriae* and *C. ulcerans* in Germany (in preparation)
9. Marosevic D, Schönberger K, Ackermann K, Eberle U, Sing A; HIV and syphilis co-infection rate in Bavaria 2010-2016 (in preparation)

Reports

1. „Noroviren-Ausbruch in Jugendherberge“ Outbreak report of norovirus during a children school trip

Conference presentations

1. Marosevic D, Margos G, Wallich R, Wieser A, Sing A, Fingerle V; Gesamtgenom-Sequenzierung von *Borrelia recurrentis*; Oral presentation at BVÖGD Congress 2016
2. Marosevic D, Margos G, Wallich R, Wieser A, Sing A, Fingerle V; First insights in the variability of *Borrelia recurrentis* genomes; E-poster presentation at ESCAIDE 2016
3. Marosevic D, Eberle U, Heinzinger S, Ackermann N, Sing A; Bayerisches Influenza Sentinel Saison 2015/16; Oral presentation at Erlanger-Nürnberger Hygienetage 2016
4. Marosevic D, Ackermann N, Treis B, Rieder G, Eberle U, Sing A; Masern-Genotypisierung in Bayern; Oral presentation at BVÖGD Congress 2017
5. Berger A, Meinel DM, Marosevic D, Konrad R, Margos G, Egli A, Sing A; Molekulare Epidemiologie toxigener Corynebakterien Infektionen in Deutschland at BVÖGD Congress 2017
6. Marosevic D, Berger A, Sing A; Antimicrobial resistance of toxigenic and non- toxigenic *Corynebacterium diphtheriae* and *Corynebacterium ulcerans* in Germany 2011-2016 at ESCAIDE 2017

Other presentations

1. Marosevic D, Emerging and re-emerging diseases Laboratory preparedness Germany, oral presentation to ECDC Director, Chief Microbiologist and Chief Scientist during the IPHMM, ECDC, Stockholm, February 2016.
2. Marosevic D, Introduction- Laboratory Quality Management System, lecture given during the Quality Management Module. February 2015.
3. Marosevic D, HIV, Hepatitis B and TBC on arrival screening of asylum seekers in Bavaria, oral presentation at the EAN MiniModule "Refugee and Migrant Health", Brussels, July 2016.
4. Marosevic D, Molecular biology techniques for the detection and analysis of nucleic acids available at the LGL, lecture given at the LGL as part of the continuous lifelong learning program for laboratory assistants, September 2016.
5. Marosevic D (adapted from Haußig J), Labor-Methoden im Überblick, oral presentation during Lab Modul for Epidemiologist, RKI Berlin, February 2017.
6. Marosevic D, Masern-Genotypisierung in Bayern, oral presentation during IfSG Quality circle, an event organized by the LGL for local health authorities to present and discuss ongoing and important public health topics in Bavaria, May 2017.

SOPs

1. Measles Laboratory SOP
2. Measles Computer SOP
3. Measles Sampling requirements; part of the GE 2 Laboratory Performance Catalogue

Training modules

1. The fellow co-organized the training module: "Interdisciplinary Workshop on epidemiological investigation of food-borne outbreaks", 14-16.02.2016, Bad Aleksandersbad, Germany
2. Development of case study "Outbreak after a company dinner" based on the outbreak the fellow was involved in

9. EPIET/EUPHEM modules attended

1. EPIET/EUPHEM Introductory course, 28.September – 16. October 2015, Spetses, Greece
2. Bioinformatics and Phylogeny Module, 16.-18. November 2015, Stockholm, Sweden
3. Outbreak Investigation Module, 07.-11. December 2015, Berlin, Germany
4. Biorisk and Quality Management Module, 01.-05. February 2016, Stockholm, Sweden
5. Initial Management in Public Health Microbiology, 08.-12. February 2016, Stockholm, Sweden
6. Multivariable Analysis Module, 14.-18. March 2016, Vienna, Austria
7. Rapid Assessment and Survey Methods, 20.-25.June 2016, Athens, Greece
8. Project Review Module, 22.-25. August 2016, Lisbon, Portugal
9. Project Review Module, 28. August – 02. September 2016, Lisbon, Portugal

10. Other training

1. Hands-on training in measles genotyping at the NRC for Measles, mumps and rubella at the RKI, 14.-15. December 2015, Berlin, Germany
2. London Salmonella bioinformatics training, PHE Department for Gastrointestinal Diseases 26.-30. October 2016, London, UK
3. Phylogenetic and population genetic tools for vectors and vector-borne pathogens, Instituto De Higiene E Medicina Tropical, 23.-27. January, Lisbon, Portugal
4. PAE Jour Fixe, 4 meetings (every 6 months) at the RKI with the PAE fellows to present and discuss ongoing projects during the fellowship.

Discussion

Coordinator's conclusions

Durdica Marosevic, DJ (cohort 2015) developed her EU track Fellowship at the Department for Public Health Microbiology and Infectious Disease Epidemiology, at the Bavarian Health and Food Safety Authority, Oberschleißheim (Germany), by actively participating in a wide number of projects that reflect the "learning by doing" philosophy of the training programme. Her participation in projects in the area of epidemiological investigations evidenced an increased ability to actively get involved at all stages of the outbreak investigations and to liaise and closely collaborate with external agencies, and diverse stakeholders. Her involvement with a project in screening for the presence of infectious diseases among newly arrived asylum seekers in Bavaria in 2015 contributed data to advise the formulation of public health policy directives on prioritisation and effective allocation of resources to appropriate health interventions. Through these projects, as a Fellow, Durdica refined her analytical skills which led to project investigating the molecular epidemiology of *Borrelia recurrentis* infections, where she was the principal investigator. In addition, the site provided excellent opportunities for exposure to state of the art surveillance applications by encouraging her participation in the sentinel influenza surveillance system in Bavaria in 2015, where DJ had hands on experience on surveillance systems using data collected in real time. Further involvement in projects at the forefront of technology saw her validate the Whole Genome Sequencing (WGS) SNP typing protocols for *Salmonella enteritidis* at LGL in collaboration with colleagues who developed the WGS pipeline at Public Health England. Durdica was also able to contribute her molecular microbiologist experience to the site by successfully transferring and validating a real time PCR method for measles detection with further implementation of genotyping which allowed the characterisation of MeV outbreaks in Bavaria in 2016. Contribution to international guidelines on antimicrobial resistance of toxigenic and non-toxigenic *C. diphtheriae* and *C. ulcerans* through site expertise was achieved by AMR testing of banked strains at LGL in a project also lead by the Fellow.

The impressive body of work developed over the past two years was supported by a solid training provided by the Fellowship programme, which contributed to the development and refinement of Durdica's skills in public health microbiology. The excellent leadership skills developed are also reflected in the numerous presentations, capacity development activities and associated materials developed. The publications listed in peer reviewed journals are testimony to her dedication, hard work and professionalism. The coordinator team concludes that Durdica has fulfilled

the Fellowship requirements with highest quality and wishes her all success in her future career as a Public Health Microbiologist.

Supervisor's conclusions

During her EUPHEM training, DJ has further strengthened her skills as an expert public health microbiologist. She has gained comprehensive practical and theoretical knowledge in various fields of both microbiology and infectious diseases epidemiology. Her most impressive and extremely diverse project matrix involving basic research including Next Generation Sequencing which was quite recently introduced in our PHM labs, applied laboratory science, as well as epidemiological outbreak investigations and surveillance activities clearly testify to her motivation and ability to assimilate new knowledge in excellent manners. Due to her broad knowledge in both lab and epi, enthusiastic and inspiring character, her refreshing team spirit as well as her interest in teaching she instantly became a very valuable team member and bridge-builder between lab and epi people fostering mutual understanding of both disciplines not only in our weekly PHM & ID epidemiology team meetings of our department, but also far beyond in the much broader LGL arena during outbreak meetings with veterinary and food safety specialists. Most importantly, in her lab work she implemented molecular techniques for measles genotyping, WGS of Salmonella and Corynebacterium antibiotics susceptibility testing thus having a really sustainable impact on our PHM labs for the future; without her initiative, the introduction of these new methods in our routine methods portfolio would not have been possible to get achieved in a reasonable time period by our lab team. Due to her powerful and dedicated initiative and her broad interest in all aspects and fields of PHM it was very easy and rewarding to supervise DJ during her fellowship; she independently planned and implemented both lab analytical and epidemiological studies, engaged herself in teaching public health experts, MPH students and at special occasions the broader public. Very importantly, DJ was able to adapt very fast to the German public health system; due to both her German language and social skills she was a great communicator both within our team as well as outside the LGL on a regional, national and international level. In conclusion, we have to thank both the EUPHEM program and DJ as an extraordinary fellow for their sustainable impact on our PHM capacities. To state that DJ was a fantastic and enthusiastic EUPHEM fellow actually would be a gross understatement.

Personal conclusions of fellow

As a young scientist, in the early phases of my career I was very grateful to get the opportunity to participate in the EUPHEM Programme and to get hands-on experience outside of the laboratory and with a focus on applied epidemiology and infectious diseases. The multidisciplinary work that is crucial to public health is well reflected in the Programme, both in the selection of the fellows, as well as in the projects we are working on. Very valuable were the "peer-to-peer" learning sessions that tapped into this diverse background of fellows during modules and the "learning-by-doing" aspect of the fellowship which allowed through the application of specific tasks and involvement in different projects the personal development of the fellow. It was a rewarding experience personally and professionally, as through the EPIET and EUPHEM Programme we got to build relationships and develop a scientific multidisciplinary network that is crucial to successfully tackle public health challenges of a united Europe and an ever more connected world.

The diverse and intensive involvement in projects at the LGL allowed me to gain knowledge on previously unfamiliar topics such as surveillance and outbreak investigations. The fellowship also broadened my view on topics of international importance and our involvement as public health specialist in this area. During these two years I developed skills necessary to function in this diverse field, not only state-of-the-art microbiological methods and basic epidemiological skills, but also communication, interdisciplinary collaboration and management. I hope to implement these skills and continue to contribute to public health microbiology in the future.

Acknowledgements of fellow

I would like to thank my supervisor at the LGL, Prof. Dr. Andreas Sing, for his supervision, support and introduction to German culture and humor. He was always encouraging, insightful, motivating and gave me the opportunity to develop and pursue my own ideas. A special thank you goes to all my project supervisors on site, for their valuable guidance, fruitful discussions and heartfelt acceptance in the team. It was a pleasure to work and learn with you.

I am especially grateful to be blessed with three amazing public health professionals as coordinators: Androulla Efstratiou, Aura Andreassen and Silvia Herrera-Leon. Thank you for the mentoring, constructive feedback and guidance through the fellowship. It was both a challenging and enriching experience. I am also highly appreciative to Aftab Jasir, who provided guidance and support by all means and in all opportunities. I am pleased and proud to be part of the EPIET/EUPHEM family and hope to cherish the friendships made during these two years for a lifetime. Special thanks also to my office-buddies and colleagues from the "Villa", all the late afternoon coffee-breaks and brainstorming sessions that have led to some of the best and most productive outputs. Last but not least, I would like to thank my family for supporting me in all my endeavours, bearing with me through the stressful times and celebrating all joyous moments.