Natalia Marta Zmarlak-Feher

The European Public Health Microbiology Training Programme (EUPHEM), Cohort 2023
Robert Koch Institute (RKI), Germany

Background

The ECDC Fellowship Programme is a two-year competency-based training with two paths: the field epidemiology path (EPIET) and the public health microbiology path (EUPHEM). After the two-year training, EPIET and EUPHEM graduates are considered experts in applying epidemiological or microbiological methods to provide evidence to guide public health interventions for communicable disease prevention and control. The Administrative Decisions ECDC/AD/2022/16 Rev.01 and ECDC/AD/2023/06 govern the European Union (EU)-track and Member State (MS)-track, respectively, of the ECDC Fellowship Programme, field epidemiology path (EPIET) and public health microbiology path (EUPHEM), Cohort 2023.

Both curriculum paths provide training and practical experience using the 'learning-by-doing' approach at acknowledged training sites across the European Union/European Economic Area (EU/EEA). This final report describes the experiences and competencies the fellow acquired by working on various projects, activities, theoretical fellowship training modules, other modules or trainings, and international assignments or exchanges during the fellowship.

Pre-fellowship short biography

Natalia Marta Zmarlak-Feher obtained her master's degree in Pharmacy at Medical University of Silesia, Poland (2010–2017) and bachelor's degree in Biotechnology at Jan Długosz University, Poland (2013–2015). She then completed her PhD in Molecular Biology at Sorbonne University, France (2017–2021). During her PhD and post-doctoral research (2017–2023), she worked at the Institut Pasteur in Paris, France where she studied the genetic basis of mosquito-vector competence in relation to malaria and arboviruses transmission. During her EUPHEM fellowship, she aimed to broaden her knowledge of how applied science is used in public health, with a focus on genomics. She was particularly interested in how the implementation of genomics is carried out in practice, how it aligns with epidemiology, and how molecular insights can enhance the understanding and investigation of infectious disease epidemiology. She is also interested in how public health institutes operate at both national and European levels.

Results

The objectives of the core competency domains were achieved partly through project and activity work, and partly by participating in the training modules. Results are presented in accordance with the EPIET/EUPHEM core competencies, as set out in the ECDC Fellowship Manual[1].

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[1] European Centre for Disease Prevention and Control (ECDC). Manual for the ECDC Fellowship Programme EPIET and EUPHEM paths. Stockholm: ECDC; 2025. Available at: https://www.ecdc.europa.eu/en/publications-data/ecdc-fellowship-programme-manual

Stockholm, 2026

1. Epidemiological investigations

1.1. Outbreak investigations

1.1.1. Outbreak of **Salmonella (S.)** *Strathcona, multi-country, 2011–2024*

Supervisors: Michael Pietsch and Sandra Simon (Unit for Enteropathogenic Bacteria and *Legionella* & National Reference Centre for *Salmonella* and other enteric pathogens, Robert Koch Institute, Wernigerode, Germany)

Category: Food- and waterborne diseases

Aim: To identify the suspected food vehicle for *S.* Strathcona cases in 2023 and describe the epidemiology of *S.* Strathcona infections in 17 European countries from 2011 to 2024. Furthermore, the genetic relatedness of *S.* Strathcona strains as of 2011 was investigated, hypothesising a common source for recurring outbreaks.

Methods: *S.* Strathcona isolates from the study period were whole genome sequenced (WGS). Cases were defined as persons within the study area (Europe) whose *S.* Strathcona isolate clustered with the outbreak reference strain in core genome MLST: within seven allelic distances (AD) for confirmed cases, 8–13 AD for possible cases, with an epidemiological link to a confirmed case for probable cases.

Results: Of 662 *S.* Strathcona infections in the study area since 2011, 469 were classified as confirmed cases, 161 as probable, 13 as possible cases and 19 non-outbreak cases. Median age of cases was 34 years (interquartile range (IQR): 19–58) and almost half (306/643, 47.6%) occurred in 2023/2024. Most isolates (469/496, 94.5%) showed a high genetic relatedness (≤7 AD) over time and across study area, compatible with a common source and vehicle. Epidemiological and traceback investigations from Austria identified small tomatoes from Sicily as the suspected food vehicle in 2023 (as did a Danish outbreak investigation in 2011).

Public health implications/Conclusions: Source investigations are recommended to identify and eliminate the cause of food contamination, thereby preventing future cases.

Role: The fellow was co-investigator of the outbreak along with the postgraduate training for applied epidemiology (PAE) fellow, Lena Böff. The role of the fellow was to conduct comprehensive molecular investigations of the outbreak. First, this included analysis of genomic data of human isolates of the outbreak cases in Germany (2023–2024), including core genome multilocus sequence typing (cgMLST) and single nucleotide polymorphism (SNP) and phylogenetic analyses. The fellow also took part in international communication and collaboration for the multinational outbreak investigation. Further, the fellow was responsible for collecting sequencing data from other countries, data preparation, cleaning, implementation of genomic data in the international line list, genomic analysis of recent international (2023–2024) and historical cases (2011–2022) by cgMLST and SNP analyses. The fellow contributed to the joint ECDC and EFSA Rapid Outbreak Assessment (ROA). A peer-reviewed manuscript (where the fellow is a joint first author) was accepted for publication by *Eurosurveillance* (see section 7.1, paper 1). The fellow also prepared and delivered an oral presentation of the project results at an internal seminar, and at a PAE meeting together with Lena Böff.

1.2. Surveillance

1.2.1. Advantages of integrated molecular surveillance to assess multidrug-resistant tuberculosis transmission in Germany, 2022–2023

Supervisors: Lena Bös (Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany), Stefan Kröger (Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany; German Center for Infection Research, Partner Site Braunschweig-Hannover, Germany)

Aim: This study aimed to assess whether integrated molecular surveillance can support epidemiological investigations in making a distinction between imported and locally transmitted rifampicin- and multidrug-resistant tuberculosis (RR/MDR-TB) cases, and in detecting transmission links not identified through routine epidemiology. In addition, WGS-based resistance prediction was analysed to evaluate the current RR/MDR-TB situation in Germany.

Methods: WGS data from 1 441 culture-positive *Mycobacterium tuberculosis* complex isolates collected in Germany between 2022 and 2023 were analysed together with linked epidemiological data. Among these, 127 were predicted as RR/MDR-TB. Genomic cluster analysis was performed using a ≤5 AD threshold, incorporating additional sequences from Ukrainian RR/MDR-TB cases to investigate potential cross-border transmission. Linked epidemiological data, including country of birth, date of entry, and case-finding method, were integrated to contextualise genomic findings.

Results: Of 127 RR/MDR-TB cases, 93.6% were foreign-born, with 54% originating from Ukraine. Genomic cluster analysis identified eight clusters suggestive of post-entry transmission; several of these were linked to Ukrainian sequences and indicated possible cross-border transmission. Epidemiological data revealed clusters representing imported cases, local transmission, and mixed origins. Notably, three genomic clusters were not detected through routine epidemiological investigations, underscoring the added value of WGS-based surveillance. Drug resistance prediction showed heterogeneity within clusters, including emerging pre-extensively drug-resistant tuberculosis (pre-XDR-TB) mutations.

Public health implications/Conclusions: Integrated molecular surveillance combining WGS and epidemiological data supports detection and enhances characterisation of RR/MDR-TB transmission, distinguishing importation from local spread. This approach supports targeted public health interventions, particularly in migration-influenced settings. Strengthening integrated molecular surveillance and international collaboration are critical to optimise TB control efforts in Germany and beyond.

Role: The fellow extracted TB data from the German electronic surveillance system, SurvNet, and analysed these together with WGS data from the National Reference Center (NRC) for Mycobacteria in Borstel, Germany. This work included developing an R script, merging epidemiological and genomic data, performing data cleaning, comparing the study sample with the study population, and contrasting RR/MDR-TB cases with drug-susceptible TB cases. The fellow also spent one week at the NRC, where RR/MDR-TB cases were analysed, including genomic cluster identification and comparison with sequencing data from patients in Ukraine. In addition, the fellow learnt *Mycobacterium tuberculosis* sequencing (MTB-Seq) bioinformatics pipeline from the NRC and applied it to the RR/MDR-TB study sample to conduct SNP and drug resistance analyses. A manuscript based on this work (the fellow is the first author) is in preparation for submission to a peer-reviewed journal (see section 7.1, paper 2).

1.2.2. Analysis of molecular footprints of integrase inhibitor-driven evolution of HIV-1 integrase at the interhost population level in Germany, 1986–2024

Supervisor: Karolin Meixenberger (Unit of Sexually Transmitted Bacterial Pathogens and HIV, Department of Infectious Diseases, Robert Koch Institute, Berlin, Germany)

Aim: This study investigated the molecular evolution of the HIV-1 integrase (INT) genomic region in relation to the introduction of integrase inhibitors (INIs) among antiretroviral therapy (ART)-naïve, newly diagnosed people with HIV (PWHIV) in Germany between 1986 and 2024. The aim was to identify potential interhost population-level footprints of INI use in circulating viruses and evaluate its impact on HIV-1 transmissibility.

Methods: HIV-1 integrase sequences from approximately 1 300 ART-naïve, newly diagnosed PWHIV in Germany (1986–2024) were analysed together with linked epidemiological data. Subtyping was performed using the HIVtype pipeline, with downstream analyses restricted to subtype B sequences. Integrase mutations were identified using the Stanford HIVdb Program, and amino acid frequencies were statistically evaluated with an R script. Descriptive analyses compared the prevalence of INI-associated variants between the pre-INI (1986–2006) and INI (2007–2024) eras. Maximum-likelihood phylogenies were constructed to detect transmission clusters, and analyses assessed whether variants of interest were enriched within clustered cases.

Results: HIV-1 subtyping identified 1 038 subtype B sequences. Analysis of 278 amino acid positions in the integrase gene associated with INI resistance revealed 3/1 038 (0.3%) isolates with predicted resistance to bictegravir and 9/1 038 (0.9%) isolates with predicted resistance to raltegravir. Comparative analysis of amino acid variation between the pre-INI and INI eras identified 11 mutations with an absolute frequency difference of ≥10% for further analysis.

Public health implications/Conclusions: Analysing the presence and patterns of major INI resistance mutations and accessory/compensatory mutations will help assess whether the use of INI-containing ART gives rise to virus variants with increased transmissibility.

Role: The fellow conducted all relevant bioinformatics analyses of integrase sequences, including viral subtyping, resistance mutation analysis, and phylogenetic reconstruction. In addition, the fellow developed an R script and performed statistical analyses to detect accessory and compensatory mutations following the introduction of INI. The fellow also reflected on her experience in a report.

1.2.3. Comparative genomic analysis of bla$_{KPC}$ plasmids from environmental and clinical Enterobacterales

Supervisor: Martin Fischer (Department of Infectious Diseases, Division of Nosocomial Pathogens and Antibiotic Resistances, Robert Koch Institute, Wernigerode, Germany)

Aim: The project aimed to investigate the occurrence, diversity, and structural characteristics of *bla*$_{KPC}$-containing plasmids in bacteria from environmental and clinical sources. These plasmids, which encode for carbapenem resistance, pose a major public health threat due to their mobility across bacterial species. Another goal was to familiarise the fellow with a complete bioinformatics workflow for plasmid analysis, including hybrid assembly of Illumina- and Oxford Nanopore-derived sequence data.

Methods: Bacteria isolated from wastewater samples collected near hospitals with *bla*$_{KPC}$ outbreaks were sequenced using Illumina (short reads) and Oxford Nanopore Technologies (long reads). Reads were quality-filtered, assembled, and final contigs were annotated. Following plasmid reconstruction, resistance gene detection and genus identification were carried out. Comparative plasmid visualisations assessed structural diversity. Clinical *bla*$_{KPC}$ plasmid sequences were downloaded from the National Center for Biotechnology Information (NCBI) platform, and processed using the same workflow. A custom R script integrated the results and enabled descriptive analyses of 104 environmental and 416 clinical plasmids, including plasmid type prevalence and associations with genus and plasmid size.

Results: Hybrid assemblies successfully reconstructed complete plasmid structures, capturing both sequence accuracy and structural complexity. Analyses revealed diverse plasmid types carrying *bla*$_{\text{KPC}}$ across genera in both environmental and clinical datasets. Comparative assessments identified shared plasmid backbones and recurrent resistance determinants, highlighting potential overlap between clinical and environmental reservoirs.

Public health implications/Conclusions: The project demonstrated the value of combining short- and long-read sequencing for plasmid epidemiology. Findings suggest that *bla*$_{\text{KPC}}$ plasmids circulate in both healthcare and environmental settings, underlining the need for integrated 'One Health' surveillance to prevent the dissemination of carbapenem resistance beyond clinical boundaries.

Role: The fellow performed the full plasmid analysis workflow, including read quality control, hybrid assembly of Illumina and Oxford Nanopore Technologies data, genome annotation, plasmid reconstruction, and resistance gene detection. She extended the workflow to clinical datasets from NCBI and wrote a custom R script to merge tool outputs, filter *bla*$_{\text{KPC}}$ plasmids, and conduct descriptive analyses. This included assessing plasmid types, sizes, and host associations. The fellow also generated comparative visualisations, contributing to the identification of similarities between environmental and clinical plasmids, and supporting the project's goal of understanding cross-sectoral transmission of carbapenem resistance. Lastly, the fellow wrote a reflective note.

2. Applied public health microbiology research and laboratory investigations

2.1. *Country-wide assessment of tick-borne pathogens collected in ticks between 2021 and 2024 in Germany, with a focus on* **Francisella***: A One Health pilot study*

Supervisors: Kristin Köppen and Klaus Heuner (Working group: Cellular Interactions of Bacterial Pathogens, Centre for Biological Threats and Special Pathogens, Highly Pathogenic Microorganisms (ZBS 2), Robert Koch Institute, Berlin, Germany)

Aim: The aim of this study was to perform a pilot study addressing the presence of tick-borne pathogens in ticks across Germany, with a special focus on *Francisella* in order to better understand its distribution.

Methods: A total of 339 *Dermacentor reticulatus* ticks and 353 *Ixodes ricinus* ticks were collected in Germany between 2021 and 2024. DNA was extracted and analysed individually by multiplex quantitative polymerase chain reaction (qPCR) assays detecting *Francisella tularensis* subsp. *holarctica*, *Francisella*-like endosymbionts, *Rickettsia* spp., *Borrelia burgdorferi sensu lato* complex, *Borrelia miyamotoi*, *Anaplasma phagocytophilum*, *Ehrlichia* spp., *Coxiella burnetii*, *Bartonella* spp., *Babesia* spp., and tick-borne encephalitis virus.

Results: qPCR testing revealed a varying frequency of these pathogens depending on the tick species. The most frequently identified bacteria were *Francisella*-like endosymbionts (18–97%), *Rickettsia* spp. (32–74%), and *Borrelia burgdorferi sensu lato* complex (0–16%). The occurrence of *Francisella tularensis* subsp. *holarctica*, *Borrelia miyamotoi*, *Anaplasma phagocytophilum*, *Babesia* spp., and tick-borne encephalitis virus was observed at a low frequency in ticks (less than 10% in either tick species). *Coxiella burnetii*, *Ehrlichia* spp., and *Bartonella* spp. were not detected in the investigated ticks. More than 70% of *Dermacentor reticulatus* ticks and 19% of *Ixodes ricinus* ticks were positive for at least two pathogens. There was a significant co-occurrence of *Francisella*-like endosymbionts and *Rickettsia* spp. in both tick species.

Public health implications/Conclusions: This pilot study offers a framework for the surveillance of common, rare, and newly emerging tick-borne pathogens in Germany.

Role: The fellow conducted laboratory work, including DNA extraction from ticks and qPCR for pathogen detection. In addition, the fellow contributed to tick line list creation and updates, developed an R script for data analysis and visualisation, and drafted the study protocol. The study results were presented as an oral presentation (online) at the European Conference on Tick-Borne Diseases in Paris in 2025. A peer-reviewed manuscript (the fellow is a joint first author) was published by *One Health* (see section 7.1, paper 3).

2.2. *Revealing disinfectant tolerance in* **Candida (C.) auris** *biofilms: a challenge to current testing standards*

Supervisors: Anja Richter (Hospital Hygiene, Infection Prevention and Control, Department Infectious Diseases, Robert Koch Institute, Berlin, Germany), Mardjan Arvand (Hospital Hygiene, Infection Prevention and Control, Department Infectious Diseases, Robert Koch Institute, Berlin, Germany; Institute for Medical Microbiology and Hygiene, Department of Infectious Diseases, University of Heidelberg, Heidelberg, Germany)

Aim: This study aimed to adapt a biofilm assay that uses porous glass beads as a surface for microbial attachment and biofilm formation. Originally developed for bacteria, the method was modified to reproducibly cultivate *Candida auris* and *Candida albicans* biofilms. The assay was further applied to evaluate the efficacy of disinfectants from four active substance classes commonly employed in clinical settings.

Methods: *Candida* biofilms were grown using the adapted bead assay, and their presence was confirmed by scanning electron microscopy. Four disinfectants – alcohol-, quaternary ammonium compound (QAC)-, peracetic acid-, and glutaraldehyde-based – were tested. Efficacy was measured by the reduction in viable biofilm cells, with ≥4 $\log_{10}$ colony-forming unit (CFU) reduction considered effective.

Results: Consistent biofilm formation was achieved for both species. Following current disinfection standards, alcohol- and QAC-based disinfectants showed insufficient reduction of viable biofilm cells. In contrast, peracetic acid and glutaraldehyde achieved ≥4 $\log_{10}$ CFU reductions but required relatively high concentrations. Notably, *C. auris* biofilms exhibited different tolerance profiles compared to *C. albicans*, suggesting that using *C. albicans* as sole reference yeast species in disinfectant testing may underestimate resistance in clinical settings.

Public health implications/Conclusions: Current disinfectant efficacy standards rely on planktonic *C. albicans* and fail to account for biofilm-associated resilience, particularly to emerging pathogens like *C. auris*. These findings highlight the need to update disinfection protocols and testing models to include biofilm-forming yeasts and potential species-specific responses. This will better inform infection prevention strategies and regulatory standards, improving clinical outcomes and public health safety.

Role: The fellow conducted laboratory work, including protocol optimisation for *Candida* biofilm cultivation and testing of disinfectants against *Candida* in this form. Data were analysed using GraphPad software. The study results were presented as a poster at the Congress of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID Global) Conference in Vienna in 2025. In addition, the fellow prepared and delivered an oral presentation of the project results at an internal seminar. A peer-reviewed manuscript (the fellow is the first author) has been submitted to *Microbiology Spectrum* (see section 7.1, paper 4).

3. Biorisk management

3.1. Safety Level 3 laboratory (S3) laboratory training: handling **Mycobacterium (M.) tuberculosis-***complex pathogens, Germany, 2025*

Supervisor: Astrid Lewin (Unit 16 Mycotic and Parasitic Agents and Mycobacteria, Robert Koch Institute, Berlin, Germany)

Aim: To familiarise the fellow with S3 laboratory safety regulations, the appropriate use of personal protective equipment (PPE), and the workflow for the manipulation of high-risk pathogens, specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis*.

Methods: The training included theoretical instruction and practical observation. Safety modules covered biosafety and biocontainment principles, the S3 hygiene and emergency plans, fire safety, PPE donning and doffing, entry/exit procedures, infectious material storage, alarm systems, disinfection, and waste disposal via autoclaving. Practical sessions included observation of laboratory procedures for culturing *M. tuberculosis* and *M. bovis* under biosafety cabinet conditions, emphasising unidirectional workflow and contamination prevention. Molecular procedures, such as DNA extraction from mycobacterial cultures, were demonstrated under containment. Roles of operating and assisting personnel were also explained, highlighting safety responsibilities and adherence to protocols.

Results: The fellow acquired theoretical knowledge of biosafety measures and observed microbiological and molecular workflows in the S3 environment. The training emphasised strict safety practices, correct PPE use, and containment strategies essential for preventing laboratory-acquired infections.

Public health implications/Conclusions: Training in S3 laboratory safety is essential to ensure high biosafety standards in research and diagnostics involving high-risk pathogens. By strengthening biosafety competencies, such training supports safe laboratory practices and contributes to the prevention of accidental pathogen release.

Role: The fellow observed S3 laboratory workflows, reviewed biosafety protocols, and received hands-on instruction in PPE use and workflow organisation for high-risk pathogen handling. The fellow also wrote a protocol for the DNA extraction of *Mycobacterium* in an S3 laboratory and a reflective note.

4. Quality management

4.1. Annual European Antimicrobial Resistance Surveillance Network (EARS-Net) external quality assessment (EQA) in Germany, 2024

Supervisor: Franziska Layer-Nicolaou (Department of Infectious Diseases, Division of Nosocomial Pathogens and Antibiotic Resistances, Robert Koch Institute, Wernigerode, Germany)

Aim: The aim was to analyse the 2024 European Antimicrobial Resistance Surveillance Network (EARS-Net) external quality assessment (EQA) results from Germany and prepare a national report for participating laboratories, with a focus on species identification and antimicrobial susceptibility testing (AST).

Methods: A total of 22 laboratories in Germany participated in the 2024 EQA, receiving six bacterial strains relevant for EARS-Net surveillance: *Acinetobacter baumannii*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*. Species identification and AST results were reported and evaluated against expected consensus results. AST interpretations were scored according to EUCAST v14.0 breakpoints, taking into account error severity, including very major errors (VMEs, false susceptibility) and major errors (MEs, false resistance).

Results: All 22 laboratories (100%) submitted results for species identification and AST. Overall, 97.7% of identifications (129/132) were correct. Complete accuracy was achieved for four of the six strains, while minor discrepancies occurred for *E. faecium* (90.9% correct) and *P. aeruginosa* (95.5% correct). AST performance showed a high degree of concordance with expected results, although isolated VMEs and MEs were observed. Mandatory antimicrobials were reported by all laboratories in line with EUCAST requirements.

Public health implications/Conclusions: The high level of agreement in species identification and AST results demonstrates strong laboratory performance in Germany. However, the occurrence of VMEs and MEs underlines the need for continuous quality monitoring of testing performance. Ensuring reliable and comparable AST data is essential for accurate surveillance of antimicrobial resistance and for guiding clinical decision-making at both national and European levels.

Role: The fellow summarised national EQA results, prepared the German report, and examined AST performance, including very major errors (VMEs), in relation to the methodologies applied for AST testing.

5. Public health microbiology management

5.1. Update on the national polio incident and Enterovirus *surveillance in Germany, 2024*

Supervisor: Kathrin Keeren (Commission for Polio Eradication in Germany, Robert Koch Institute, Berlin, Germany)

Poliomyelitis (polio) is a highly contagious disease caused by poliovirus, mainly affecting children under five. Of the three wild poliovirus (WPV) serotypes, only WPV type 1 remains endemic in Pakistan and Afghanistan, while types 2 and 3 have been eradicated. Circulating vaccine-derived polioviruses (cVDPVs) have recently caused outbreaks in areas with low vaccination coverage. This activity focused on understanding poliovirus circulation within the Global Polio Eradication Initiative (GPEI) in Germany, the national enterovirus surveillance system, and updating Germany's annual World Health Organization (WHO) polio eradication report.

Role: The fellow reviewed the literature and updated the German annual progress report on polio eradication. The fellow also wrote a reflective note.

5.2. Update on the national Neisseria gonorrhoeae *surveillance in Germany, 2024*

Supervisors: Regina Selb (Unit 'HIV/AIDS, STI and Blood-borne Infections', Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany), Hana Tlapák (Unit of Sexually Transmitted Bacterial Pathogens and HIV, Department of Infectious Diseases, Robert Koch Institute, Berlin, Germany)

Antimicrobial resistance in *Neisseria gonorrhoeae* poses a major public health challenge, threatening treatment effectiveness, especially with resistance to ceftriaxone, the last remaining first-line therapy in Europe. To monitor trends, ECDC established the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP), in which Germany has participated since 2014, collecting isolates annually for antimicrobial susceptibility testing, molecular typing, and whole genome sequencing (since 2018). The fellow contributed to preparing and harmonising the German genomic and epidemiological data for 2024 for uploading to The European Surveillance System (TESSy), ensuring compliance with Euro-GASP protocols.

Role: The fellow reviewed the literature and prepared epidemiological and genomic data for uploading to TESSy. The fellow also wrote a reflective note.

5.3. Assessing and increasing vaccine readiness in sub-Saharan Africa: pilot survey in Guinea, 2024

Supervisor: Charbel El Bcheraoui (Evidence-based Public Health, Centre for International Health Protection, Robert Koch Institute, Berlin, Germany)

The Robert Koch Institute (RKI), through the project, 'Assessing and increasing vaccine readiness in sub-Saharan Africa' (VRSA), supported Guinea's 'Expanded Program on Immunization' (EPI) in strengthening readiness for new vaccines. Following an external evaluation that informed Guinea's national vaccination strategy, the project entered its second phase in 2024. Activities included preparing a nationally representative household and seroprevalence survey to assess vaccination coverage, acceptance of new vaccines, and hepatitis B immunity among children. In September 2024, the team trained data collectors in survey methods, dried blood spot (DBS) sampling, and data management.

Role: The fellow participated in the preparation and implementation of the training for data collectors and the two-day pilot survey, as well as post-deployment tasks related to data quality reporting. The fellow also wrote a reflective note.

5.4. Assessing and Building Capacities: Madagascar's public health system (ABCM) – setting up the arboviruses surveillance system for **Aedes** *mosquitoes in Madagascar, 2024*

Supervisors: Essia Belarbi and Sabrina Weiß (Public Health Laboratory Support, Centre for International Health Protection, Robert Koch Institute, Berlin, Germany)

Madagascar is a hotspot for vector-borne diseases such as chikungunya and dengue, transmitted by mosquitoes. Limited surveillance capacity hampers accurate disease tracking and delays interventions, allowing outbreaks to spread. To address this, the German Federal Ministry of Health initiated the Global Health Protection Programme (GHPP) with the RKI playing an important role in its implementation through the project, 'Assessing and Building Capacities: Madagascar's public health system (ABCM)'. In collaboration with the Ministry of Public Health of Madagascar, the project aimed to strengthen arbovirus surveillance in *Aedes* mosquitoes through field collection, laboratory diagnostics, and capacity building.

Role: The fellow participated in the preparation and implementation of the mosquito vector and pathogen surveillance setup during a three-week deployment to Madagascar. The tasks included mosquito collection in the capital city, Antananarivo, and the coastal city of Tamatave, as well as visual and molecular identification of mosquito species, followed by arbovirus detection by a molecular assay. The fellow also wrote a reflective note and a postcard-from-the-field for ECDC website.

5.5. Organisation and implementation of the Laboratory Module (Lab4Epi) for fellows of the PAE and EPIET programmes based in Germany, 2024

Supervisors and co-organisers: Astrid Lewin (Unit 16 Mycotic and Parasitic Agents and Mycobacteria, Robert Koch Institute, Berlin, Germany), Jennifer Bender (Department of Infectious Diseases, Division of Nosocomial Pathogens and Antibiotic Resistances, Robert Koch Institute, Wernigerode, Germany), Veronica Briesemeister (Public Health Laboratory Support, Centre for International Health Protection, Robert Koch Institute, Berlin, Germany), Juliette Zunk, Katharina Alpers (German Fellowship PAE (EPIET Associated Programme), Robert Koch Institute, Berlin, Germany)

The training module for German PAE/EPIET fellows (described in more detail in section 6, 'Teaching and pedagogy') required drafting the PAE module agenda, communication with invited speakers, as well as planning laboratory activities. The structure of the module, timeline and preliminary schedule (including demonstration of laboratory activities) were discussed extensively with other PAE team organisers. Once the training module content was agreed upon, the final version of the agenda was shared with RKI presenters and participants. After the module, an evaluation was conducted and analysed.

6. Teaching and pedagogy

Organisation and implementation of the Laboratory Module (Lab4Epi) for fellows of the PAE and EPIET programmes based in Germany, 2024

Supervisors and co-organisers: Astrid Lewin (Unit 16 Mycotic and Parasitic Agents and Mycobacteria, Robert Koch Institute, Berlin, Germany), Jennifer Bender (Department of Infectious Diseases, Division of Nosocomial Pathogens and Antibiotic Resistances, Robert Koch Institute, Wernigerode, Germany), Veronica Briesemeister (Public Health Laboratory Support, Centre for International Health Protection, Robert Koch Institute, Berlin, Germany), Juliette Zunk (German Fellowship PAE (EPIET Associated Programme), Robert Koch Institute, Berlin, Germany), Katharina Alpers (German Fellowship PAE (EPIET Associated Programme), Robert Koch Institute, Berlin, Germany)

The PAE Laboratory Module (Lab4Epi) is organised annually by the current EUPHEM fellow at the RKI in collaboration with multiple institute units. In 2024, the course was delivered as a five-day, face-to-face module in Berlin and Wernigerode. It included plenary lectures, unit presentations, hands-on laboratory activities, and an outbreak scenario to contextualise diagnostic methods. The module's main objectives were to familiarise PAE fellows with RKI laboratory work, projects, and microbiological methods, while fostering cooperation and knowledge exchange between epidemiologists and microbiologists.

Role: The fellow organised and managed all stages of the training module. She also delivered a lecture on molecular genetic methods, including PCR and next-generation sequencing (NGS), and conducted an evaluation of the module using online questionnaires. The fellow also wrote a reflective note.

7. Communications related to the EPIET/EUPHEM fellowship

7.1. Manuscripts published in peer-reviewed journals

- Paper 1: Brait V*, Böff L*, **Zmarlak-Feher NM***, Jourdan-Da Silva N, Mazzilli S, Pardos de la Gandara M, et al. Insights into international, recurring outbreaks of *Salmonella* Strathcona associated with tomatoes, 2011–2024. Eurosurveillance. 2025 Oct 16;30(41):2500224. doi: 10.2807/1560-7917.ES.2025.30.41.2500224 *Joint first authors
- Paper 2: **Zmarlak-Feher NM**, Bös L, Dreyer V, Houwaart T, Walz T, Tietjen M, et al. Integrated genomic surveillance: an essential tool for enhancing the understanding of rifampicin- and multidrug-resistant tuberculosis transmission. [Manuscript in preparation for submission]
- Paper 3: Köppen K*, **Zmarlak-Feher NM***, Dörre A, Hagedorn P, Kohl C, Heuner K. Country-wide assessment of tick-borne pathogens collected in ticks between 2021 and 2024 in Germany, with a focus on *Francisella*: A one health pilot study. One Health. 2025;Sep 5:101190. Available at: https://doi.org/10.1016/j.onehlt.2025.101190 *Joint first authors
- Paper 4: **Zmarlak-Feher NM**, Finke A, Konrat K, Schaudinn C, Arvand M, Richter AM. Revealing disinfectant tolerance in *Candida auris* biofilms: a challenge to current testing standards based on *Candida albicans*. [Manuscript submitted to *Microbiology Spectrum*]

7.2. Other reports

- Postcard from the field 1: Arbovirus and mosquito vector surveillance in Madagascar. Available at: https://www.ecdc.europa.eu/en/news-events/postcard-field-arbovirus-and-mosquito-vector-surveillance-madagascar
- Rapid Outbreak Assessment: European Centre for Disease Prevention and Control (ECDC), European Food Safety Authority (EFSA). Prolonged multi-country outbreak of *Salmonella* Strathcona ST2559 linked to consumption of tomatoes in the EU/EEA and the UK. Stockholm/Parma: ECDC/EFSA; 2024. Available at: https://www.ecdc.europa.eu/sites/default/files/documents/salmonella-strathcona-ST2559-tomatoes-rapid-outbreak-assessment-november-2024.pdf
- Report 1: Quality Management: Annual European Antimicrobial Resistance Surveillance Network (EARS-Net) external quality assessment (EQA) in Germany, 2024
- Report 2: Public Health Management: Assessing and increasing vaccine readiness in sub-Saharan Africa – pilot survey in Guinea
- Report 3: Public Health Management: Assessing and Building Capacities: Madagascar Public Health System (ABCM) – setting up the arboviruses surveillance system for *Aedes* mosquitoes in Madagascar
- Reflective note 1: Teaching: PAE Laboratory Module- Lab4Epi 2024
- Reflective note 2: Bio-risk Management: S3 Laboratory Training – handling *Mycobacterium* pathogens
- Reflective note 3: Public Health Management: Update on the national Polio incident and *Enterovirus* surveillance in Germany, 2024
- Reflective note 4: Public Health Management: Update on the national *Neisseria gonorrhoeae* surveillance in Germany, 2024
- Reflective note 5: Surveillance: Molecular footprints of integrase inhibitor-driven evolution of the HIV-1 integrase at the interhost population level in Germany, 1986–2024
- Reflective note 6: Surveillance: Comparative genomic analysis of $\mathit{bla}_{\mathrm{KPC}}$ plasmids from environmental and clinical Enterobacterales: insights into resistance and mobility

7.3. Conference presentations

- Conference 1: **Zmarlak-Feher NM**, Richter AM, Finke A, Schaudinn C, Arvand M. Tolerance of *Candida auris* biofilms to disinfectants (onsite poster presentation). Presented at: ESCMID Global 2025, 15 April 2025; Vienna, Austria.
- Conference 2: **Zmarlak-Feher NM**, Köppen K, Dörre A, Hagedorn P, Kohl C, Heuner K. Country-wide assessment of pathogen presence in ticks collected in 2021–2024 in Germany, with a focus on *Francisella*: A One Health perspective (online oral presentation). Presented at: European conference on Tick-Borne Diseases (ETBD), 10 March 2025; Paris, France.

7.4. Other presentations

- **Feher-Zmarlak NM**. Genetic variation of transcriptional enhancers and mosquito vector competence. Oral presentation. Presented at: RKI FG16 internal seminar, January 2024; Berlin, Germany.
- **Feher-Zmarlak NM**, Schmidt K. Outbreak Scenario. Oral presentation. Presented at: PAE Laboratory module, March 2024; Berlin, Germany.
- **Feher-Zmarlak NM**. Polymerase Chain Reaction (PCR) methods. Oral presentation. Presented at: PAE Laboratory module, March 2024; Berlin, Germany.
- Böff L, **Feher-Zmarlak NM**. *Salmonella* Strathcona outbreak presentation. Oral presentation. Presented at: PAE meeting, July 2024; Berlin, Germany.
- **Feher-Zmarlak NM**. Country-wide analysis of pathogens transmitted by ticks in Germany 2022–2023, with a focus on *Francisellaceae.* Oral presentation. Presented at: Project Review Module, August 2024; Lisbon, Portugal.
- **Feher-Zmarlak NM**. Spread of rare *Salmonella enterica* serotype Strathcona across Europe: Investigation of a multinational outbreak, 2023. Genomic approach. Oral presentation. Presented at: RKI FG16 internal seminar, November 2024; Berlin, Germany.
- **Feher-Zmarlak NM**. Tolerance of *Candida auris* biofilms to disinfectants. Oral presentation. Presented at: RKI FG16 internal seminar, April 2025; Berlin, Germany.
- **Feher-Zmarlak NM**. The Molecular Detective: Investigating Pathogens in Public Health Across Continents during EUPHEM Fellowship. Oral resentation. Presented at: RKI internal seminar, September 2025; Berlin, Germany.

8. EPIET/EUPHEM modules attended

- Introductory Course, 25 September−13 October 2023, Spetses, Greece
- Study Protocol and Scientific Writing, 26−27 October and 7−8 November 2023, virtual
- European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2023, 22–24 November 2023, Barcelona, Spain
- Multivariable Analysis, 19−23 February 2024, Berlin, Germany
- Vaccinology, 4−8 March 2024, virtual
- Writing Abstracts for Scientific Conferences, 14–20 March 2024, virtual
- Public Health Microbiology II – Biorisk and Quality Management, 21−23 May 2024, virtual
- Public Health Microbiology III – Whole Genome Sequencing & Bioinformatics, 3−7 June 2024, Vienna, Austria
- Project Review Module, 26−30 August 2024, Lisbon, Portugal
- European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2024, 20−22 November 2024, Stockholm, Sweden
- Social and Behavioural Sciences 2025, 24–25 March 2025, virtual
- European Society of Clinical Microbiology and Infectious Diseases Congress (ESCMID Global) 2025, 11−15 April 2025, Vienna, Austria
- Leadership and Communication, 1−3 September 2025, Lisbon, Portugal.

9. Other training

- Introduction to R, Applied Epi, 19–23 September 2023, virtual
- Joint NFDI & de.NBI Metagenomic Training Course, 6–8 February 2024, Bielefeld, Germany
- 'Sealing the Leaky Pipeline' workshop on Gender Equity in Global Health Research Leadership, 26–27 June and 16 October 2024, Berlin, Germany
- Epidemiology in Health Care Associated Diseases Module (UK FETP and German PAE module), 3–5 July 2024, Berlin, Germany
- GOARN Tier 1, 5 training, 10 October 2024, Berlin, Germany
- GenEpi-BioTrain – Building bioinformatics workflows, 19 and 21 March 2025, virtual

- GenEpi-BioTrain – Empowering AMR Research through R: Analysis and Visualisation, 18 and 25 June 2025, virtual
- GenEpi-BioTrain – Genomic Tools in Outbreak Investigations – Case Study Cholera Outbreak, 27 August and 3 September 2025, virtual

10. International assignments

- Assessing and increasing vaccine readiness in sub-Saharan Africa – pilot survey in Guinea, Conakry, Guinea, 12–18 September 2024.
- Assessing and Building Capacities: Madagascar Public Health System (ABCM) – setting up the arboviruses surveillance system for *Aedes* mosquitoes in Madagascar, Antananarivo, Tamatave, Madagascar, 27 November–19 December 19 2024.

11. Other activities

- *Aedes* mosquito surveillance training with Andreas Larem at Hessische Landesamt für Gesundheit und Pflege (HLFGP), 28–30 October 2024, Darmstadt, Germany
- Linux and HPC Workshop, 12–13 February 2025, Berlin, Germany
- Genomics of RR/MDR-TB at Research Center Borstel – Leibniz Lung Center, Molecular and Experimental Mycobacteriology, 17–21 February 2025, Borstel, Germany

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