Jasmin S. Kutter

The European Public Health Microbiology Training Programme (EUPHEM), Cohort 2023

Instituto de Salud Carlos III, Madrid, Spain

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

Jasmin S. Kutter obtained a Master of Science in Molecular Biotechnology from the Technical University of Munich (2013–2015), where she conducted research at the Institute of Virology, Helmholtz Munich. Her work focused on characterising the Ebola virus glycoprotein and its interactions with Tetherin and tetraspanin-enriched microdomains. She then pursued a PhD in Virology at the Department of Viroscience, Erasmus Medical Center in Rotterdam, the Netherlands. Her doctoral research investigated the transmission of respiratory viruses, investigating key molecular determinants and developing experimental models to study transmission routes. Importantly, her work contributed to advancing the understanding of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission through air, providing valuable insights during the COVID-19 pandemic. After her academic training, Jasmin volunteered at a hospital in the Ecuadorian Amazon, where she supported laboratory and field operations, and contributed to the development of screening programmes, further broadening her expertise at the interface of virology, public health, and global health challenges.

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].

[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, 2025

1. Epidemiological investigations

1.1. Outbreak investigations

1.1.1. Increase of **Salmonella** *enterica serovar Chester cases in Spain, 2023*

Supervisor: Silvia Herrera León (Laboratorio de Referencia e Investigación en Enfermedades Bacterianas Transmitidas por Alimentos, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Category: Food- and waterborne diseases

Aim: To generate a hypothesis to explain and control the observed increase in *S.* Chester cases in Spain.

Methods: A descriptive analysis was performed of cases, defined as an individual diagnosed with *S.* Chester infection, in Spain between 1 January 2023 and 31 December 2023. A subset of 45 *S.* Chester isolates was further analysed using core genome multilocus sequence typing (cgMLST) EnteroBase scheme (≤7 alleles threshold), which included isolates obtained from humans (n=31) and isolates from chicken-derived food (n=14) that were whole-genome-sequenced (WGS) and deposited in public repositories by Spanish regional public health laboratories.

Results: We identified 179 cases across Spain, a five-fold increase from 2022; the male-to-female ratio was 1.1, the median age was 22 years (range: 0–92 years). cgMLST identified three clusters: cluster 1 comprised isolates from chicken-derived food (n=14) and human cases (n=14), while clusters 2 and 3 grouped 10 and two human isolates respectively. Clusters 1 and 2 were linked to the cases that were reported by Germany in August 2023.

Public health implications/Conclusions: Chicken-derived food was identified as a likely source of infection but could not explain all the cases. Nonetheless, a trace-back investigation to broilers and their origin should be conducted to identify the source of *S.* Chester-contaminated food products. *S.* Chester is not listed in the EU-regulation for *Salmonella* serotypes of public health significance. Yet, its continued detection in humans in 2024 suggests potential introduction, colonisation, and persistence within specific niches, warranting intensified surveillance and stricter control measures. WGS and cluster analysis should be integrated into these efforts, particularly where traditional epidemiological links cannot be established.

Role: The fellow conducted the descriptive analysis, interpreted data, drafted the outbreak investigation report, and presented the findings at the European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2024.

1.2. Surveillance

1.2.1. Nationwide retrospective study on the performance of the World Health Organization (WHO) mutation catalogue for genomic prediction of antibiotic resistance in the **Mycobacterium tuberculosis** *complex in Spain, 2022–2025*

Supervisor: Laura Herrera León (Laboratorio de Referencia de Micobacterias, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Type of project: Analysing data from a surveillance system

Aim: To assess the performance of the WHO mutation catalogue using an independent, real-world dataset collected over a three-year period from across Spain.

Methods: Culture-positive *Mycobacterium tuberculosis* complex (MTBC) isolates submitted to the Spanish National Reference Laboratory for Mycobacteria between 1 January 2022 and 15 February 2025 were included if WGS and phenotypic drug-susceptibility testing (pDST) data for at least one first- or second-line antibiotic were available. Genotypic drug-resistance profiles (gDST) were predicted by matching MTBseq-identified single nucleotide polymorphisms with variants in the catalogue. gDST profiles were subsequently compared with phenotypes (pDST). Catalogue performance was determined by computing sensitivity, positive predictive value (PPV), and specificity with binomial exact 95% confidence intervals (CI). gDST/pDST discrepancies were studied to investigate country-specific differences in resistance.

Results: We analysed 5 122 gDST/pDST associations from 1 223 tuberculosis (TB) strains. Sensitivity was highest for fluoroquinolones (100%; CI: 79.41–100) and PPV was highest for first-line drugs (92.12%; CI: 88.67–94.79). Specificity exceeded 94% for both drug categories. Analysis of gDST/pDST discrepancies revealed five phenotypically susceptible strains harbouring variants (*rpoB*_p.His445Asn, *rpoB*_p.Leu430Pro) associated with phenotypic borderline rifampicin-resistance. The variant *ethA*_p.Leu272Pro, classified as 'uncertain significance' was exclusively detected in phenotypically ethionamide-resistant strains (n=8).

Public health implications/Conclusions: The WHO catalogue is a valuable tool complementing pDST. Genomic prediction accelerates and substantially improves detection of drug-resistant tuberculosis (DR-TB), including resistance potentially missed by pDST. This enables more accurate diagnosis and patient-tailored treatment, ultimately advancing DR-TB control. Future research should validate the catalogue using real-world datasets from different locations to refine region-specific resistance profiling and strengthen national and global surveillance efforts.

Role: The fellow performed the data analysis and interpretation, presented results at ESCAIDE 2025, and submitted a manuscript to a peer-reviewed journal.

Routine surveillance activities

Coordination Centre for Health Alerts and Emergencies (CCAES) Rapid risk assessment: increase of shigellosis cases in Spain, 2023–2024

Activities and role: The fellow contributed to the analysis of microbiological data and drafted the microbiology section of the rapid risk assessment. Additionally, the fellow participated in meetings between the collaborating institutions.

Periodic review of Spanish national surveillance protocols: yersiniosis, typhoid and paratyphoid fever

Activities and role: The fellow reviewed the surveillance protocols for Yersinia and (para-)typhoid fever and drafted an updated version of both protocols. Additionally, the fellow participated in meetings between the collaborating institutions.

2. Applied public health microbiology and laboratory investigations

2.1. Unravelling norovirus GII.17[P17] transmission dynamics using whole-genome sequencing in two consecutive outbreaks at a hospital: implications for infection prevention and control, Spain, 2024

Supervisor: Maria Dolores Fernandez Garcia (Enterovirus and Viral Gastroenteritis Unit, National Centre for Microbiology, Instituto de Salud Carlos III, Madrid, Spain)

Category: Healthcare-associated infections and antibiotic resistance

Aim: To perform metagenomic next-generation sequencing (mNGS) to elucidate transmission dynamics of two consecutive norovirus outbreaks in February and May 2024 – Outbreak-1 and Outbreak-2 – that affected patients and healthcare workers in a Spanish hospital.

Methods: Norovirus-positive stool samples among 54 symptomatic patients in Geriatrics and Oncohaematology were identified by fluorescence immunoassay (FIA), genotyping reverse transcription polymerase chain reaction (RT-PCR), and LiquidArray®. mNGS was performed on 26 norovirus-positive samples. Transmission clusters were investigated using Bayesian phylodynamics, maximum-likelihood (ML) phylogeny, and single nucleotide variant (SNV) analysis. Genomic data were integrated with epidemiological information.

Results: FIA and RT-PCR detected 28.6% and 85.7% of norovirus-positive stool samples compared to LiquidArray®. All the cases were caused by a novel lineage of the globally re-emerging GII.17[P17] genotype. Genomic analyses identified three distinct transmission clusters (≥17 SNVs), two in Outbreak-1 (Geriatrics and Oncohaematology), and one in Outbreak-2 (Geriatrics). Transmission trees showed sustained human-to-human spread in both outbreaks, with 0–3 unobserved intermediate cases. In some cases, patients with identical norovirus sequences lacked epidemiological links, suggesting a potential role for fomite transmission.

Public health implications/Conclusions: FIA showed low sensitivity highlighting the need of confirmatory molecular testing for accurate outbreak management. mNGS confirmed two separate introductions during Outbreak-1 that were simultaneously circulating in two units – a link previously missed by epidemiological investigations; and identified a separate introduction in Outbreak-2, underscoring the effectiveness of infection prevention and control (IPC) measures. These findings emphasise the value of genomic data to investigate transmission links and guide IPC strategies in healthcare settings.

Role: The fellow coordinated the project, liaised with hospital collaborators, conducted a site visit, drafted the ethics proposal, processed samples with various molecular techniques, and collected and analysed data. The fellow also presented the findings at the hospital and at the Congress of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID Global) 2025. She submitted a manuscript to a peer-reviewed journal.

2.2. Multicentre study on the prevalence of priority pathogenic fungi in intensive care units (ICU) of the Spanish national health system, 2024

Supervisor: Ana Alastruey-Izquierdo (Mycology Reference Laboratory, National Centre for Microbiology, Instituto de Salud Carlos III, Madrid, Spain)

Aim: To gain an improved understanding of fungal colonisation, prevalence of invasive fungal infections (IFIs) and antifungal resistance patterns in critically ill patients admitted to ICUs across Spain.

Methods: A systematic, biannual, multicentre, cross-sectional study was conducted in 22 Spanish ICUs. At two timepoints (30 January and 7 May 2024), skin swabs and either oral swabs or tracheal aspirates (for intubated patients) were collected and cultured at 30 °C for two weeks. IFIs were retrospectively recorded over a one-month follow-up. Fungal isolates were sub-cultured, identified by sequencing, and tested for antifungal susceptibility according to European Committee on Antimicrobial Susceptibility Testing (EUCAST) protocols.

Results: From 373 patients, 760 fungal isolates were identified: 90% yeasts (n=687) and 10% moulds (n=73), representing 37 species across 20 genera. Major genera included *Candida* (64%), *Nakaseomyces* (15%), and *Aspergillus* (8%). The most prevalent species were *Candida albicans* (*C. albicans*) (40%), *C. parapsilosis* (15%), *Nakaseomyces glabratus* (*N. glabratus*) (15%), and *Aspergillus fumigatus* (*A. fumigatus*) (7%). Secondary antifungal resistance was detected in *C. albicans* (8%), *C. parapsilosis* (38%), *N. glabratus* (20%), and *A. fumigatus* (8%). During follow-up, 54 IFIs were diagnosed: 30 invasive candidiasis, 19 invasive aspergillosis, three *Pneumocystis jirovecii*, one *Penicillium glabrum*, and one biomarker-positive case without culture confirmation.

Public health implications/Conclusions: Fungal colonisation is highly prevalent among ICU patients, with *Candida*, *Nakaseomyces*, and *Aspergillus* predominating. High resistance rates in *C. parapsilosis* and *A. fumigatus* emphasise the need for strengthened antifungal stewardship, improved diagnostics, and targeted therapies. These findings reinforce the importance of continued surveillance to address emerging fungal threats in critical care.

Role: The fellow supported the processing of clinical specimens for the second timepoint in May 2024 and wrote a study protocol.

2.3. **Mycobacterium leprae** *detection and antimicrobial resistance characterisation using a line probe genotyping assay in skin lesion exudates from a patient of Bolivian origin, Spain, 2023*

Supervisor: Laura Herrera León (Laboratorio de Referencia de Micobacterias, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Aim: To genetically identify *Mycobacterium leprae* (*M. leprae*) and potential mutations conferring antimicrobial resistance in skin lesion exudates that contained acid-fast bacilli (AFB) with the GenoType LepraeDR VER 1.0 kit (Hain Lifescience GmbH, Germany).

Methods: Prior to conducting the line probe assay, the extracted sample DNA was amplified by PCR. The hybridisation was performed according to the manufacturer's protocol. Results were evaluated using the corresponding evaluation sheet provided by the manufacturer. The banding pattern of the whole strip was analysed according to absence or presence of bands corresponding to either wildtype or resistant *M. leprae*. Only bands whose intensity was as strong or stronger than the controls were counted as present.

Results: The positive assay control displayed all the bands that were expected to be visible, demonstrating that the DNA strip assay was successful. The clinical sample showed bands for wildtype *M. leprae* and the three locus controls (*rpoB*, *gyrA*, and *folP1*). No bands were observed for the mutation probes. This binding pattern demonstrated that the clinical sample was positive for *M. leprae* and that this strain did not carry any resistance mutations and should therefore respond to standard multidrug therapy.

Public health implications/Conclusions: The use of GenoType LepraeDR VER 1.0 kit enables the rapid detection of *M. leprae* and associated resistance mutations directly from clinical samples, supporting timely and appropriate therapy. The absence of resistance mutations in this case indicates continued effectiveness of standard multidrug therapy, while highlighting the importance of ongoing surveillance to detect emerging resistance.

Role: The fellow performed the DNA amplification and the line probe assay, and was responsible for interpretation and documentation of the result. The activity was summarised in a report.

2.4. Molecular investigation of a malaria case in the context of a suspected hospital-acquired infection, Spain, 2024

Supervisor: Jose Miguel Rubio Muñoz (Malaria & Parasitic Emerging Diseases Laboratory, National Microbiology Center, Instituto de Salud Carlos III, Majadahonda, Madrid, Spain)

Aim: To investigate potential horizontal transmission after the detection of a malaria case in Spain without travel history to an endemic area, who presented at the same hospital concurrently with two other malaria cases, raising suspicion of a hospital-acquired malaria infection.

Methods: Molecular characterisation of *Plasmodium* species (nested multiplex malaria PCR), parasitaemia quantification (quantitative real-time reverse transcription PCR – qRT-PCR), and genotyping (nested PCR) were performed on three *Plasmodium*-positive blood samples from the three malaria cases.

Results: Molecular characterisation confirmed that all three cases were infected with *Plasmodium falciparum* (*P. falciparum*). qRT-PCR analysis showed differing parasite concentrations: Case 1 exhibited high parasitaemia, whereas Cases 2 and 3 had low parasitaemia. Genotyping further identified three distinct *P. falciparum* populations.

Public health implications/Conclusions: Based on the results, any relationship between the infections was excluded, and it was concluded that Case 1 was not hospital-acquired through horizontal transmission from either Case 2 or Case 3. Overall, these findings indicate no ongoing risk to the general population, as the likelihood of additional locally acquired cases or a larger outbreak has been ruled out. Therefore, no further public health measures are required.

Role: The fellow performed all three steps (molecular characterisation, parasitaemia quantification, genotyping) followed by data analysis and interpretation of the results. The results were summarised in a report.

2.5. Phenotypic determination of toxigenicity of a **Corynebacterium diphtheriae** *strain isolated from a child with cutaneous diphtheria returning from Senegal, Spain, 2024*

Supervisors: Silvia Herrera León (Laboratorio de Referencia e Investigación en Enfermedades Bacterianas Transmitidas por Alimentos, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain), Laura Herrera León (Laboratorio de Referencia de Micobacterias, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Aim: To determine the toxigenicity of a *Corynebacterium diphtheriae* (*C. diphtheriae*) strain isolated from a fully vaccinated child with cutaneous diphtheria returning from Senegal, and to assess the risk of transmission within the contacts.

Methods: An Elek test was performed on the *C. diphtheriae* strain isolated from the child's skin exudate to assess toxigenicity. Contact tracing was carried out, including a carrier study in which both nasal and pharyngeal samples were collected from each identified contact and tested for *C. diphtheriae*. Additionally, vaccination status was reviewed for all contacts.

Results: The Elek test was positive, confirming that the child was an asymptomatic carrier and potential transmitter of toxigenic *C. diphtheriae*. A total of 29 contacts were identified: six family members, 14 classmates, two companions who shared a lunch table, and seven teachers. Among the classmates, 12 of 14 (85.7%) were appropriately vaccinated for their age. All contacts tested negative for *C. diphtheriae*. The index case was treated with antibiotics and re-tested to confirm treatment success. Vaccination was offered to all contacts who were not fully vaccinated according to the recommended schedule.

Public health implications/Conclusions: The absence of *C. diphtheriae* among contacts indicates a low risk of secondary transmission in this setting. The child's full vaccination likely reduced the severity of disease and the potential for transmission. Prompt diagnosis, vaccination status verification of contacts, and treatment of the case were effective in preventing further spread. Vaccination remains a critical public health measure, preventing disease, reducing severity, and limiting the spread of infectious pathogens within the community.

Role: The fellow prepared and performed the Elek test, followed by the interpretation of the results. Furthermore, the fellow participated in a meeting between the National Center of Microbiology (CNM), National Centre of Epidemiology (CNE), Coordination Centre for Health Alerts and Emergencies (CCAES), and the hospital that diagnosed the patient, in which further steps in relation to contact tracing, testing, and treatment were discussed. The results were summarised in a report.

3. Biorisk management

3.1. Previous experience in a BSL3+ laboratory

As part of her PhD, the fellow received extensive training in a biosafety level-3+ (BSL-3+) laboratory, where she conducted experiments with high-risk respiratory viruses. This provided her with hands-on experience in advanced biosafety procedures, strict containment practices, and adherence to rigorous protocols required for working with class 3+ pathogens.

3.2. External quality assessment (EQA) for **Mycobacteria** *diagnostics, Spain, 2024*

Supervisor: Laura Herrera León (Laboratorio de Referencia de Micobacterias, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Aim: As the Reference Laboratory for *Mycobacteria*, to participate in the following EQA schemes: I) identification of *Mycobacteria*, II) drug-susceptibility testing (DST) of nontuberculous *Mycobacteria*, III) DST of tuberculosis bacteria, IV) molecular DST of tuberculosis bacteria.

Methods: The EQA was organised by INSTAND e.V. For each scheme, a blinded panel of five samples was sent to the laboratory. Samples were processed as routine human specimens using accredited techniques for each scheme. Results were documented, submitted to INSTAND e.V., and subsequently evaluated. A certificate was issued for each EQA scheme in which at least 80% of the maximum score was achieved.

Results: The laboratory successfully met the requirements for all four EQA schemes, achieving 25/25 points (100%) for scheme I, 170/170 points (100%) for II, 255/300 points (85%) for III, and 165/175 points (94%) for IV. The overall success rate among all the laboratories that participated in the EQA was 93.6% (n=109) for scheme I, 96% (n=50) for II, 97.4% (n=153) for III, and 94.5% (N=110) for IV.

Public health implications/Conclusions: Participation in all EQA schemes confirmed the laboratory's high diagnostic accuracy in mycobacterial identification and DST. Participation in EQAs is essential to ensure the accuracy and comparability of laboratory testing across different laboratories. EQAs help identify potential errors, validate diagnostic methods, promote standardisation among laboratories, and ensure compliance with international quality standards.

Role: As a training activity, the fellow conducted EQA schemes II, III, and IV. Since handling nontuberculous and tuberculosis bacteria requires BSL-2+ and BSL-3 facilities, the fellow received training in these environments prior to performing the accredited techniques. The fellow was subsequently involved in result documentation and evaluation of reports and certificates after these were handed out by INSTAND e.V. The results were then summarised in a report.

3.3. Biological risk assessment as part of the 'Biorisk and Quality Management' module

As part of the 'Biorisk and Quality Management' module, the fellow, together with other EUPHEM fellows, conducted a biosafety and biorisk assessment of malaria diagnostic procedures: a) preparing thick and thin smears for microscopy with Giemsa staining, and b) centrifuging blood samples to collect plasma for serology. A risk assessment matrix was used to evaluate the biorisk associated with these procedures.

4. Quality management

4.1. Implementation of the EUCAST protocol for the antifungal susceptibility testing of dermatophytes

Supervisor: Ana Alastruey-Izquierdo

Affiliation: Mycology Reference Laboratory, National Centre for Microbiology, Instituto de Salud Carlos III, Madrid, Spain.

Aim: To implement the EUCAST protocol for antifungal susceptibility testing (AFST) of dermatophytes at the Spanish Mycology Reference Laboratory, enabling identification and characterisation of antifungal resistance in Spain.

Methods: AFST was performed using the EUCAST broth microdilution protocol, which determines minimum inhibitory concentrations (MICs) based on 50% fungal growth inhibition in wells with serial dilutions of antifungals. Assay validation included two EUCAST quality control strains, *Trichophyton indotineae* (*T. indotineae*) and *Trichophyton rubrum* (*T. rubrum*), with published MIC ranges available for itraconazole, voriconazole, and terbinafine. In addition, the antifungals amphotericin B, flucytosine, fluconazole, posaconazole, and isavuconazole were included in the assay. The MICs of these antifungals were compared with documented results from the Mycology Reference Laboratory, Radboud University Medical Center (the Netherlands).

Results: Initial assays were successful for *T. rubrum*, with MICs for itraconazole, voriconazole, and terbinafine falling within EUCAST ranges. MIC values for the other antifungals were consistent with results of the Mycology Reference Laboratory in the Netherlands. In contrast, the assay did not yield valid results for *T. indotineae*.

Public health implications/Conclusions: Further repetitions are required to optimise performance for *T. indotineae* and ensure reproducibility across both strains before routine implementation. Establishing AFST for dermatophytes will support more accurate treatment selection, reducing inappropriate therapy, minimising toxicity, and preventing resistance development. Ultimately, these efforts will provide critical data on antifungal resistance patterns among dermatophytes in Spain, strengthening public health surveillance and clinical management.

Role: The fellow visited the Mycology Reference Laboratory, Radboud UMC, in Nijmegen, the Netherlands, where AFST of dermatophytes is routinely performed, to acquire the skills required for testing and result interpretation. The fellow then implemented the assay at the Spanish Mycology Reference Laboratory and drafted a standard operating procedure (SOP).

4.2. Annual internal audit of the quality system of the Reference Laboratory for Enterobacteria, Spain, 2024

Supervisor: Silvia Herrera León (Laboratorio de Referencia e Investigación en Enfermedades Bacterianas Transmitidas por Alimentos, Centro Nacional de Microbiología, Instituto de Salud Carlos III, Madrid, Spain)

Aim: To assess the quality management system as part of the 2024 internal audit in accordance with the CNM Quality Manual, the Internal Audit Procedure, and the Spanish National Accreditation Body (ENAC) Guides and Reference Notes.

Methods: First, a documentary audit was conducted remotely in which the documentary requirements for the laboratory were inspected. This was followed by an in-person audit in the laboratory in which the requirements regarding the management system (e.g. records, non-conformities and corrective actions), resources (e.g. personal qualifications, reagent and media control, reference material and strains) and processes (e.g. sample management, technical logs, laboratory reports) were evaluated. Afterwards, an audit report was prepared including the non-conformities and necessary corrective actions.

Results: Three non-conformities (NC) were identified during the audit. NC1 involved missing documentation of actions taken for missed deadlines for a test in 2023. NC2 concerned reagent control records, which were not under document control. NC3 included uncontrolled documents related to reference strains accessible to laboratory personnel. All NCs correspond to the requirement of UNE-EN ISO 15189:2023 concerning quality indicators, record control, and document control. Corrective actions were promptly implemented.

Public health implications/Conclusions: Regular audits are essential for ensuring the effectiveness of a laboratory's quality management system. By identifying gaps, nonconformities, or deficiencies, audits enable laboratories to correct errors, and maintain compliance with ISO standards. A reliable quality management directly supports accurate diagnostic results, as well as strengthens surveillance systems and infectious disease control.

Role: The fellow observed the audit process, reviewed documentation and the final audit report, and wrote a report on the activity.

4.3. Quality management assessment as part of the 'Biorisk and Quality Management' module

As part of 'Biorisk and Quality Management' module, the fellow performed an assessment of the laboratory quality management at the host institute. The institute maintains a comprehensive quality management system coordinated by a central Quality Core Unit and supported by designated quality managers in each laboratory. Quality activities include maintaining SOPs, monitoring indicators, managing equipment and reagents, and ensuring staff qualification. Processes are supported by a digital platform for documentation, non-conformity tracking, and corrective actions. Laboratories undergo continuous internal quality assessments, quarterly blind sample testing, and annual internal audits, complemented by EQAs. Annual external audits by the Spanish National Accreditation Body (ENAC) further ensure compliance. This system ensures reliable, standardised, and accredited laboratory performance.

5. Public health microbiology management

5.1. Project management, Spain, 2023–2025

The fellow gained extensive experience in project and public health management throughout the fellowship. During the norovirus outbreak investigation, she coordinated the project and collaborated with multiple hospital units, highlighting the importance of cross-sectoral communication. Project management skills were further developed through various projects and teaching activities, requiring coordination with different teams, stakeholders, and institutions at regional and national levels. She also participated in the internal audit of a reference laboratory, gaining insight into laboratory management. These diverse experiences strengthened her coordination, organisational, and leadership capacities.

5.2. Epidemic intelligence, Coordination Centre for Health Alerts and Emergencies (CCAES), Spanish Ministry of Health

The fellow completed a one-week rotation at the CCAES, gaining insight into its organisational structure, functions, and coordination with national and international partners. Through thematic lectures, active participation in coordination meetings, and daily round tables, the fellow acquired knowledge and skills in epidemic intelligence, rapid risk assessment, and surveillance coordination. This provided valuable experience in applying international and national legislation to public health practice, culminating in the fellow leading one of the daily round-table sessions presenting epidemic intelligence results.

6. Teaching and pedagogy

Facilitation of an exercise on descriptive analysis of surveillance data for students of the 'Microbiology Applied to Public Health and Research in Infectious Diseases' master's programme, University of Alcalá, Spain, 2024

As part of the Microbiology and Public Health section of the master's programme, the fellow participated as facilitator in a practical group activity. The objective of this activity was to teach master's students how to conduct descriptive analyses in a practical context using real-world surveillance databases. At the end of the module, students presented their findings in a peer group and supervisors through PowerPoint presentations.

Facilitation of a case study for students of the 'Microbiology Applied to Public Health and Research in Infectious Diseases' master's programme, University of Alcalá, Spain, 2024

As part of the Waterborne and Food-borne Infectious Diseases section of the master's programme, the fellow facilitated the ECDC case study, 'An Outbreak of Gastroenteritis in Kalundbourg, Denmark'. The activity aimed to train master's students in outbreak investigation and highlight the importance of a multidisciplinary approach. The fellow was responsible for teaching the case study and guiding the students' learning experience. This included reviewing and updating the case study materials and leading a four-hour interactive session with the students.

7. Communications related to the EPIET/EUPHEM fellowship

7.1. Manuscripts published in peer-reviewed journals

- **Kutter JS**, Cuevas Lobato O, Fernandez-Pacheco Gonzalez-Echavarri BE, Gomila CM, Garcia Ibañez N, Camacho J, et al. Unravelling GII.17[P17] norovirus transmission dynamics using whole-genome sequencing in two consecutive outbreaks at a Spanish hospital: implications for infection prevention and control. [Submitted]
- **Kutter JS**, Saiz-Vega P, Ramiro R, Casas J, Herrero M, Abascal Saiz E, Herrera-Leon L. Retrospective study on the transmission dynamics and drug-resistance profiles of *Mycobacterium tuberculosis* complex in Spain, 2022–2025. [In preparation]

7.2. Other reports

- Centro de Coordinación de Alertas y Emergencias Sanitarias, Ministerio de Sanidad, Evaluación rápida de riesgo. Aumento de casos de shigelosis en España, 2023–2024. 20 de diciembre 2024. Available at: https://www.sanidad.gob.es/areas/alertasEmergenciasSanitarias/alertasActuales/shigella/docs/20241220_ERR_Shigelosis.pdf

7.3. Conference presentations

- **Kutter JS**, Pino-Rosa S, Rodríguez-Paredes V, Herrera-Leon S. Increase of *Salmonella enterica* serovar *Chester* cases in Spain, 2023 (poster presentation). Presented at: European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE), 20–22 November 2024; Stockholm, Sweden.
- **Kutter JS**, Rodríguez-Paredes V, Pino-Rosa S, Guerrero-Vadillo M, Peñuelas M, Saravia-Campelli G, Guzmán-Herrador BR, Varela-Martinez C, Herrera-Leon S. Surge of shigellosis cases in Spain: Retrospective analysis of *Shigella* cases in 2023 (accepted poster presentation). European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE), 20–22 November 2024; Stockholm, Sweden.
- **Kutter JS**, Cuevas-Lobato O, Fernandez-Pacheco-Gonzalez-Echavarri BE, Gomila CM, Garcia-Ibañez N, Camacho J, et al. Unravelling GII.17[P17] Norovirus transmission clusters in two consecutive outbreaks in a Spanish hospital: a retrospective whole-genome analysis with implications for infection prevention and control (poster presentation). Presented at: European Society of Clinical Microbiology and Infectious Diseases (ESCMID global), 11–15 April 2025; Vienna, Austria.
- **Kutter JS**, Saiz-Vega P, Ramiro R, Casas J, Herrero M, Abascal-Saiz E, Herrera-Leon L. Nationwide Retrospective Study on the Performance of the WHO Mutation Catalogue for Genomic Prediction of Antibiotic Resistance in the *Mycobacterium tuberculosis* Complex in Spain, 2022–2025 (poster presentation). Presented at: European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE), 19–21 November 2025; Warsaw, Poland.

7.4. Other presentations

- Kutter JS. Unravelling GII.17[P17] Norovirus transmission clusters in two consecutive outbreaks in a Spanish hospital: a retrospective whole-genome analysis with implications for infection prevention and control (oral presentation) presented at: Preventive Medicine Department and Microbiology Department, University Hospital of Getafe, 17 October and 6 November 2024; Madrid, Spain.

8. EPIET/EUPHEM modules attended

- Introduction to R, 19–22 September 2023, virtual
- 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 March–20 March 2024, virtual
- Rapid Assessment and Survey Methods, 15–19 April 2024, Dublin, Ireland
- 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
- Public Health Microbiology I – Basic phylogeny, 17–18 June 2024, virtual
- 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
- Time Series Analysis, 9–13 December 2024, Utrecht, the Netherlands
- Social Behavioural Sciences, 24–28 March 2025, virtual
- One-Health, 12–15 May 2025, virtual

9. Other training

- Spanish B1, Inhispania Escuela de Español, 17 October–12 December 2023, Madrid, Spain
- ECDC GenEpi-Biotrain Virtual Training 5: Bacterial genome assembly and quality control, 4–7 December 2023, virtual.
- WHO E-learning: Public Health Preparedness for Mass Gathering Events, 22 May 2024, virtual.
- ECDC E-learning: Rapid Risk Assessment, 23 May 2024, virtual.
- Spanish B2, Inhispania Escuela de Español, 10 June–14 October 2024, Madrid, Spain
- ECDC E-learning: Understanding vaccine acceptance and strategies to increase vaccine uptake, 7 February 2025, virtual.

10. Other activities

- Laboratory visit to the National Reference Laboratory of Mycology, Radboud University Medical Centre, 22–24 July 2025, Nijmegen, the Netherlands

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