

FINAL REPORT

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European Public Health Microbiology Training Programme (EUPHEM), 2021 Cohort
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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.

Both curriculum paths provide training and practical experience using the 'learning by doing' approach at acknowledged training sites across European Union (EU) and European Economic Area (EEA) Member States.

According to Article 9 (6), Article 5 (8) and Article 11a (1) of Regulation (EU) 2022/2370 of the European Parliament and of the Council of 23 November 2022 amending Regulation (EC) No 851/2004 establishing a European centre for disease prevention and control (the ECDC Founding Regulation):

Article 9 (6) 'The Centre shall, as appropriate, support and coordinate training programmes, in particular in relation to epidemiological surveillance, field investigations, preparedness and prevention, response to public health emergencies, public health research and risk communication. Those programmes shall take into consideration the need for training to be kept up-to-date, take into account the training needs of Member States and shall respect the principle of proportionality.'

Article 5 (8) 'By encouraging cooperation between experts and reference laboratories, the Centre shall foster the development of sufficient capacity within the Union for the diagnosis, detection, identification and characterisation of infectious agents that have the potential to pose a threat to public health. The Centre shall maintain and extend such cooperation and support the implementation of quality assurance schemes'.

Article 11a (1) 'The Centre shall establish a EU Health Task Force and ensure that there is a permanent capacity and an enhanced emergency capacity to mobilise and use it. The EU Health Task Force shall provide assistance with regard to requests for prevention, preparedness and response planning, local responses to outbreaks of communicable diseases and after-action reviews in Member States and in third countries, in cooperation with the WHO. The EU Health Task Force shall include the Centre's staff and experts from Member States, fellowship programmes and international and non-profit organisations'.

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.

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This final report describes the output of the fellow and the competencies they 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

Christina Merakou is a biotechnologist by training (integrated MSc degree in Agricultural Biotechnology and two-year MSc in Medical Biotechnology) and has extensive research experience in molecular biology, microbiology, infectious diseases, host-pathogen interactions, bacterial genetics, immunology, and vaccines. She was awarded a Marie Curie-funded PhD in Novartis Vaccines and Diagnostics in Siena, Italy, where she characterised the role of surface proteins in *Staphylococcus aureus* pathogenesis. Christina was a post-doctoral fellow at the Harvard Medical School, in the Priebe laboratory at Boston Children's Hospital in Boston, US, where she conducted research on *Pseudomonas aeruginosa* vaccines and on bacterial evolution in the human host. Before joining EUPHEM fellowship, she was a project manager of the pan-European project VACCELERATE, in the non-governmental organisation the Center for Clinical Epidemiology and Outcomes Research in Athens, Greece, and followed an online part-time Masters in Public Health at the European University of Cyprus.

Results

The objectives of these core competency domains were partly achieved through project and activity work and partly by participating in the training modules. Results are presented in accordance with the EPIET core competencies, as set out in the EUPHEM Fellowship Manual¹.

1. Epidemiological investigations

1.1. Outbreak investigations

Outbreak of COVID-19 in a summer camp in the Piedmont Region (2021): description, lessons learned and recommendations for future summer camps

Supervisors: Patrizio Pezzotti, Martina Del Manso

Category: Respiratory disease (including influenza and TB)

In August 2021, an outbreak of SARS-CoV-2 occurred in a summer camp in Piedmont region, Italy, affecting primarily campers aged ≤ 16 years. A retrospective cohort study was conducted to determine the attack rate (AR), evaluate possible transmission factors and recommend measures for the future camp organization. A de-identified database including demographic, role of attendees, cohorting, means of transportation to the camp, subgrouping, inter-camper interactions, SARS-CoV-2 testing results and symptomatology was provided by the camps' healthcare personnel. Attendees who had received a test after the first confirmed case were included in the analysis. The overall AR was 33.7% (63/187) and 72.0% (36/50) were asymptomatic at the time of testing. Only 17.1% of campers had direct contact with blood relatives from other subgroups. The AR of participants using a bus was 36.2% (59/163) with an RR of 1.18 (95% CI = 0.51-2.73,) and the AR of those belonging to a subgroup was 35% (62/177) with an RR of 3.5 (95% CI = 0.54-22.7). Prior to arrival, testing and campers' separation into low-contact subgroups was not sufficient to prevent an outbreak. No index case identification was feasible, nor was it possible to calculate whether the outbreak originated from the attendees who travelled on the same bus. The high AR observed in all subgroups suggests that there was frequent contact between attendees belonging to different subgroups. Sharing of common areas such as the canteen and contact between attendees are factors that could have contributed to the spread of the outbreak. The experience gained by the analysis of this data was used for the review of measures for the organization of summer camps in 2022 (1).

Role: Lead investigator. Christina was responsible for all communication with the healthcare personnel of the camp, collection of data and development of the line listing, wrote the STATA code for the analysis, performed the data analysis, prepared the data tables and figures, wrote the manuscript in English, helped with the translation and the final corrections of the manuscript in Italian. The manuscript was accepted in national a peer-reviewed journal (1).

¹ European Centre for Disease Prevention and Control. European public health training programme. Stockholm: ECDC; 2020. Available from: <https://www.ecdc.europa.eu/en/publications-data/ecdc-fellowship-programme-manual-cohort-2021>

*A urokinase-associated outbreak of *Ralstonia mannitolilytica* bloodstream infections in haemodialysis patients in North-Eastern Italy, January – April, 2023*

Supervisors: Patrizio Pezzotti, Claudia Lucarelli

Category: Healthcare-associated infections and antibiotic resistance

In January 2023, four patients undergoing haemodialysis at a tertiary care hospital in Trieste, Italy, were diagnosed positive for *Ralstonia mannitolilytica* bacteraemia. By the end of April, a total of 20 cases, all with tunneled central vascular catheter (CVC) access, were confirmed in four different hospitals in Friuli-Venezia-Giulia region, north-eastern Italy. Specifically, MALDI-TOF mass spectrometry identified *R. mannitolilytica* in 20 patient blood cultures. Environmental samples (including dialysis water, heparin, urokinase, saline solution, sodium citrate, chlorhexidine and epoetin alfa) were retrieved from the affected hospitals. *R. mannitolilytica* was identified in a batch of monodose urokinase vials (Batch n. NDY093B) administered to CVC patients in all four hospitals at different times between January and April 2023. All environmental samples were negative for *R. pickettii*. Illumina platform WGS was performed on all urokinase (n=3) and 19/20 human isolates. Genomic analysis confirmed that cases *R. mannitolilytica* isolates were closely related. Antimicrobial susceptibility testing was performed on all isolates by microdilution and EUCAST criteria for *Pseudomonas* spp. MIC interpretation was used. All isolates tested resistant to meropenem, piperacillin/tazobactam, ceftazidime, amikacin, colistin, aztreonam and ceftolozane/tazobactam. The MICs for cefepime and imipenem ranged from 4 to 16 mg/L. Fluoroquinolones (ciprofloxacin and levofloxacin) had low MICs for all isolates. All positive patients received ciprofloxacin as outpatient and cefepime plus ciprofloxacin as inpatient regime. In addition, 18/20 cases underwent prompt CVC removal. Sixteen cases had a full recovery, while *R. mannitolilytica* related sepsis was the probable cause of one death. Upon detection of contaminated urokinase vials, these products were replaced by other drugs. Discontinuation of the contaminated urokinase resulted in the termination of the outbreak. This is the first report of urokinase vials contamination with *R. mannitolilytica* and the first time to our knowledge that the source of infection was identified for this bacterium.

Role: Co-investigator. The fellow actively participated in all meetings of the multidisciplinary outbreak team, provided feedback, participated in the development of all necessary line lists with emphasis on the microbiological part, co-wrote the manuscript for a rapid communication (2) and participated in all internal communications on new isolates diagnosed in ISS. She was also in communication with Dr Michela Sabbatucci from the Ministry of Health regarding the preparation of a notification message on EPIS. All work performed at ISS was carried out in collaboration with the C2022 EU-track EPIET fellow Emmanouil-Alexandros Fotakis.

Investigation of a trichinellosis outbreak in Apulia region, Italy, February-March 2023

Supervisors: Patrizio Pezzotti, Martina Del Manso, María Ángeles Gómez Morales

Category: Food- and waterborne diseases

Trichinella spp. in domestic and wild reservoirs in Europe poses a risk for zoonotic disease transmission. European Centre for Disease Prevention and Control (ECDC) reported that in 2020 Italy was the European country with the second highest trichinellosis notification rate (0.13 cases/100.000). In February 2023, a *Trichinella* spp. outbreak was reported in San Marco in Lamis, Apulia region, Southern Italy, an area rich in wildlife. Demographic and clinical data, laboratory results, and risk factors were collected from symptomatic patients seeking healthcare, using a standard survey form. Serological samples were collected and tested for the presence of anti-*Trichinella* spp. IgGs by western blot. ECDC case definition was used for confirmed cases. From 11 February to 20 March 2023, 12 confirmed cases were reported. Nine patients were female, mean age was 47 years (range: 8–71). Mean time from symptom onset to laboratory diagnosis was 31 days (range: 19–71). All cases presented eosinophilia and myalgia. Five patients (42%) were hospitalised. All cases were prescribed with mebendazole which led to symptom improvement. None of them declared consuming wild game meat. All cases reported eating pork meat from a local butcher's shop. Most cases (67%) recalled consuming pork meat within one month prior to symptom onset. Consumed pork meat was not available for sampling, while *Trichinella* spp. was not detected in environmental samples from the butcher shop. The number of affected cases may be higher since only symptomatic cases were tested. Pork meat was suggested as the potential source of this outbreak, but to date no clear evidence of this association has been found. Past outbreaks of the same agent suggest that local populations may not follow hygiene rules of animal origin products for human consumption. Local community education on trichinellosis risks and the importance of proper handling and cooking of meat may help prevent future outbreaks.

Role: Co-investigator. The fellow attended all meetings with the outbreak team from Foggia, met in person with the microbiologist who performed the diagnosis of the cases at ISS and discussed on the technique used for diagnosis, wrote the material and methods and results for a potential manuscript and corrected the abstract, which was accepted as a poster at the International Conference on Trichinellosis (ICT-16) 2023 (16).

Educational outcome

The fellow gained practical experience of working in respiratory, hospital, food- and waterborne disease outbreak investigations both retroactively and prospectively in different settings (summer camp, hospital, community), with different national teams, and within multilevel organisations and strengthened her skills in management and communication with different stakeholders. She gained experience in data entry, handling and cleaning databases, description and analysis of epidemiological indicators while developing her skills working in excel and STATA. Moreover, she strengthened her knowledge on microbiological diagnostics in an outbreak setting. She became familiar with data acquisition from patients and health professionals involved. She wrote one manuscript, co-authored a rapid communication, and participated in the writing of two abstracts for international conferences.

1.2. Surveillance

Diagnosis of Dengue and Zika virus infections in Italy from November 2015 to November 2022: a National Reference Laboratory surveillance report

Supervisor: Giulietta Venturi

Dengue (DENV) and Zika (ZIKV) viruses are mosquito-borne human pathogens. In Italy, the presence of the competent vector *Aedes albopictus* increases the risk of autochthonous transmission from imported cases, and a national plan for prevention, surveillance and response (PNA 2020-2025) is in place. The aim of this study was to analyse all laboratory diagnosis data from suspected DENV and ZIKV cases received in National Reference Laboratory for Arboviruses (NRLA) from November 2015 to November 2022. Samples from 655 patients of suspected DENV and/or ZIKV cases were tested by molecular assays, NS1 antigen ELISA (only for DENV) and serological assays. Laboratory case classification was performed according to PNA criteria. Data analysis was performed using Excel and STATA 16.1. Of 524 cases tested for DENV, 146 were classified as confirmed, 7 as probable, while 288 were excluded. Of 619 cases tested for ZIKV, 44 were classified as confirmed, while 492 were excluded. All cases were imported. As much as 59% (86/146) of DENV and 50% (22/44) of ZIKV cases were confirmed by direct detection of the virus. High percentages of cross reactivity were observed between the two viruses. The median lag time from symptoms to sample collection was 7 days for DENV both molecular (range 0-20) and NS1 ELISA (range 0-48) tests, with high percentages of positivity also after 7 days (39% and 67%, respectively) whereas for ZIKV, it was 5 days (range 0-22), with 16% positivity after 7 days. Diagnostic performance was assessed in four IgM ELISA systems with negative predictive values ranging from 92% to 95% for the anti-DENV systems, and of 97% for the anti-ZIKV system. Lower positive predictive values were seen the tested population (DENV: 55% to 91%, ZIKV: 50%). DENV and ZIKV diagnosis by molecular test is the gold standard but the sample collection time is a limitation. Serological tests are thus necessary, including plaque reduction neutralization test. Co-circulation and cross-reactivity between the two viruses increase diagnostic difficulty. Continuous evaluation of diagnostic strategies is essential to improve laboratory testing.

Role: Lead investigator. The fellow manipulated the data, performed all descriptive analysis, created all graphs and table outputs, wrote all the command line for clean-up of data and analysis in excel and STATA, wrote the manuscript, wrote two abstracts from this work and prepared and presented an e-poster (17) in an international conference. Wrote manuscript (3) and presented this project in both introductory course and first year PRM module.

Diagnosis of Chikungunya virus (CHIKV) infection at the Italian National Reference Laboratory for Arboviruses, in the period November 2015 to December 2021

Supervisor: Giulietta Venturi

Chikungunya virus (CHIKV) is a mosquito-borne alphavirus and is widespread worldwide. This arthropod-borne virus represents a major public health challenge in tropical and subtropical regions. CHIKV is mainly transmitted to humans by the bites of infected female mosquitoes within the *Aedes* spp., specifically *Aedes aegypti* and *Aedes albopictus*, common vectors also for Dengue virus and Zika virus. Up to today, two outbreaks of this virus have been recorded in Italy. The first, in 2007 in Northern-Eastern Italy, was the first known autochthonous CHIKV transmission in Europe by the vector *A. albopictus*. The second occurred in 2017 in the centre of Italy, with a subsequent secondary outbreak in the South of Italy. For this reason, surveillance of *Aedes* spp. transmitted arboviruses, among which CHIKV is included in the five-year National Plan for Prevention, Surveillance, and Response to arboviruses is in place (PNA 2020-2025), issued by the Italian Ministry of Health. In the framework of the laboratory investigation project 'Diagnosis of Chikungunya virus (CHIKV) infection at the Italian National Reference Laboratory for Arboviruses, in the period November 2015 - December 2021', the fellow analysed the data of all IgM and IgG ELISA systems used by the laboratory for diagnosis using STATA. Sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) were evaluated. Evaluation of performance of available or new diagnostic assays is critical for the correct diagnosis of suspected cases and thus prevention of outbreaks.

Role: Co-investigator. The fellow extracted, cleaned, wrote the script, and analysed the data using STATA for the assessment of two commercially available ELISA (IgM/IgG) systems by calculating sensitivity, specificity, positive

predictive value (PPV) and negative predictive value (NPV). A report was produced (6). These data are also included in a manuscript in preparation (4).

Educational outcome

The fellow gained extensive knowledge of the laboratory surveillance of arboviruses in Italy, specifically of DENV, ZIKV and CHIKV. She learned about case classification based on the integration of clinical, epidemiological and laboratory data, data cleaning and data manipulation using both excel and STATA. She manipulated all data, produced tables and graphs for visualisation and wrote a manuscript and participated as co-author in a second one. She wrote and submitted two abstracts for international conferences and prepared an e-poster in an online international conference.

2. Applied public health microbiology and laboratory investigations

A retrospective genomic analysis by Whole Genome Sequencing (WGS) of zoonotic Hepatitis E virus (HEV) genotype 3 (HEV-3) clinical strains that sustained a 2019 outbreak in Abruzzo, Italy

Supervisors: Anna Rita Ciccaglione, Roberto Bruni, Michele Equestre

Hepatitis E virus (HEV) is one of the most common causative agents of acute hepatitis worldwide, with four major genotypes (HEV-1 to HEV-4) affecting humans. In Europe (EU), hepatitis E is a zoonosis mainly transmitted via contaminated pork meat. HEV-3 is prevalent in animal reservoir and in humans. A nationwide study conducted at the National Health Institute of Italy (ISS) and the National Blood Center (NBC) showed that from 2017 to 2019 the prevalence of anti-HEV IgG ranged from 1.3% to 27.20% in different regions with extremely high rates (exceeding 40%) in Sardinia and Abruzzo. In Italy, notification of acute hepatitis E is included in the surveillance system for acute viral hepatitis (SEIEVA) since 2007. From 8 June to 6 December 2019, 47 cases of HEV infection were observed in Abruzzo and Lazio regions with the cases of the latter showing an epidemiological link to the former. The aim of this study was to develop a protocol for the whole genome sequence (WGS) of 20 human samples from this outbreak. The use of WGS will provide details of the circulating genomes for design of a PCR test for rapid detection of future outbreak strains, provide information on subtype distribution in humans, correlated human isolates to food and environmental specimens, identify sources of infection, transmission routes, and implementation of future interventions to avoid dissemination. Moreover, geographic origin of epidemic strains is for the moment limited due to the low number of complete HEV genomes available in other countries.

Role: Lead-investigator. The fellow revised WGS and HEV literature, developed pre-WGS library preparation protocols, performed laboratory experiments (RNA extraction, genome library preparation by SISPA or primer specific protocols) to test these protocols and produced a public health research study protocol (6) to be followed in the incident of future HEV outbreaks.

*Genomic surveillance of methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections in Italy: a cross-sectional observational pilot study*

Supervisors: Monica Monaco, Giulia Errico, Maria Del Grosso, Paolo D'Ancona

Methicillin-resistant *Staphylococcus aureus* (MRSA) invasive infections are a serious public health issue in Italy. The percentage of MRSA 30% in 2021, monitored by the national antibiotic-resistance surveillance, is one of the highest in Europe. We conducted a cross-sectional observational pilot study, collecting case notifications and isolates from MRSA bloodstream infections (BSI), as a baseline for the establishment of a national MRSA-BSI surveillance system based on epidemiological, clinical and WGS data. From July-October 2022, 32 hospital laboratories from 17 Regions/autonomous provinces were asked to notify the first ten MRSA-BSI cases, including demographics, clinical, and microbiological data on a web platform. Sent strains to ISS, were characterised by whole genome sequencing (WGS). The 32 laboratories notified 202 MRSA-BSI cases (median: 7, IQR: 4--8) and sent all the associated strains. Most cases were reported in males (65%) and in patients aged 65 or older (66%). The onset of symptoms occurred mainly in hospital (65%) and were associated with use of central or peripheral venous catheter (44%). Additionally, 82% of cases presented comorbidities. Furthermore, the isolates were found to be resistant to levofloxacin (78.3%, 123/157), erythromycin (45.9%, 90/196), and less frequently to other antibiotics. All isolates were susceptible to ceftaroline, linezolid, tigecycline and vancomycin. In 58 isolates ResFinder analysis showed that all harbored the *mecA* gene, 55.2% carried macrolide resistance genes, 22% aminoglycoside resistance genes, and 10% tetracycline resistance gene. Point mutations conferring resistance to quinolones were detected in 82.8% of the isolates. MLST analysis showed that the isolates belonged to 9 different Sequence Type (ST)s (ST22 (72%), ST5 (7%) and ST1 (5%)). Further WGS analysis is ongoing. This pilot study suggests that the establishment of a new MRSA-BSI surveillance, implemented by epidemiological, clinical, and WGS data, may be sustainable at national level in Italy.

Role: Lead-co-investigator. The fellow analysed all demographical and risk factor related data received through the questionnaires by the participating laboratories, using STATA 16.1. Created and inserted all antibiotic susceptibility data in an excel database. Cleaned, adjusted according to EUCAST standards and analyses the data. Performed all laboratory procedures (culturing strains and DNA extraction for WGS) together with a colleague and set up and contributed to the analysis of the sequencing data. The fellow wrote an abstract submitted to an international conference (18), co-authored an abstract accepted in a national conference (19), produced a report (8), and has a manuscript in preparation (5).

Norovirus whole genome sequencing using a metagenomics approach

Supervisor: Maria Dolores Fernandez Garcia (Instituto de Salud Carlos III, Madrid, Spain)

Noroviruses belong to the Caliciviridae family and can cause gastrointestinal illness to humans. The incubation period ranges between 12 and 48 hours and the infection can cause vomiting, diarrhea, and stomach pain. Recovery occurs usually in one or two days. Mode of transmission is primarily through the faecal-oral route, either by consumption of contaminated food or water, or by spreading directly from person to person. In Spain, during the period 2012-2020, Norovirus has been the predominant etiologic agent for waterborne outbreaks and the third one in foodborne outbreaks. The fellow attended a two-weeks period of training at the Instituto de Salud Carlos III, Madrid, Spain, where she received training on RNA extraction from human stool samples, next generation sequencing (NGS) library preparation for viral metagenomics, library quantification and quality, viral library enrichment by capture, sequencing of libraries using an Illumina MiSeq Reagent kit v2 Nano on a MiSeq sequencer (300 cycles), and analysis of FASTQ Illumina raw reads using online platforms Genome Detective and IDSeq. Phylogeny and clustering of the genus were discussed.

Role: The fellow received training by observation of the laboratory techniques and analysis and wrote a report (9).

Development of a whole genome sequencing (WGS) analysis pipeline for mpox virus (MPXV)

Supervisor: Giulietta Venturi

A pipeline using Galaxy platform tools and workflows was developed in order to analyse raw paired-end Illumina reads of MPXV. This pipeline includes quality check of raw reads, taxonomy of raw reads, removal of human reads, paired-end read mapping, variant calling, genetic analysis reporting by samples and by variant, allele-frequencies, built of consensus sequence, cluster and sub-cluster identification, build of Maximum Likelihood bootstrapping phylogenetic and visualization of the tree. This pipeline was developed for future use for MPXV WGS analysis for capacity building of the NRLA laboratory in ISS.

Role: Lead-investigator. The fellow review the literature, followed hands-on tutorials on the Galaxy platform and participated in a 'do at your own pace' one week workshop organised by the Galaxy platform. Taking into consideration the goals and objectives of an EQA on MPXV dry analysis developed from scratch a WGS pipeline starting from raw Illumina reads to phylogenetic analysis using tools found on the Galaxy platform. The fellow produced a report (10).

Educational outcome

The fellow deepened her understanding of public health aspects of an endemic disease such as hepatitis E, its surveillance system and the importance of an in-place study protocol in case of an outbreak. She obtained knowledge in laboratory techniques for NGS and analysis including clustering. She became aware of the importance of EU and world study networks which monitor circulating strains in order to prevent or successfully resolve possible outbreaks. Furthermore, the fellow gained understanding of the current Italian surveillance system of hospital-acquired bloodstream infections and the necessity of integration of genomic data. She furthered her knowledge about genetic determinants and the public health impact of AMR, learned about representative sample selection and preparation of clinical isolates for sequencing. She extended her background in bioinformatics workflow for NGS and available tools to detect different genetic markers of AMR and became proficient in mastering relevant tools in the Galaxy platform and Center for Genomic epidemiology and interpretation. Furthermore, she learned how metagenomic whole genome sequencing is done, how this is adjusted for use for viral detection, how data are analysed, how viruses are clustered and what information can be extracted by phylogenetic analysis.

3. Biorisk management

Certificate BSL-3 Biosafety and Biosecurity training on Arboviruses

Supervisor: Giulietta Venturi

The fellow received a three-week full-time training given by the EUPHEM co-supervisor Giulietta Venturi at the virology dedicated BSL-3 of the department of Infectious diseases, at ISS. The training included both theoretical and practical courses, covering the review of biosafety principles and levels, risk assessment, waste management, laboratory management, safety procedures, emergency management, biosafety cabinet practices and procedure and biosecurity. Furthermore, the fellow observed the sample processing of a suspected mpox virus case. After receiving the full training, the fellow performed RNA isolation under supervision, of Dengue and West Nile virus samples.

*Biorisk management, species identification and diphtheria toxin gene detection on a suspected *Corynebacterium diphtheriae* isolate by molecular and phenotypic methods*

Supervisors: Giulia Errico, Maria Del Grosso and Monica Monaco

Diphtheria is a potentially fatal infection principally caused by the toxigenic *Corynebacterium diphtheriae*. The disease, if untreated, is one of the most severe bacterial infections in humans. Even though diphtheria is a vaccine preventable disease and despite available clinical treatment, it has a case fatality rate of approximately 10%. *Corynebacterium* spp. are Gram-positive, mostly aerobic bacilli, belonging to the *Corynebacteriaceae* family. The genus *Corynebacterium* comprises of 111 species. *C. diphtheriae* is genetically heterogeneous and has three main biovars (*Mitis*, *Gravis*, and *Belfanti*). In October 2022, an increase in diphtheria cases was noted in Europe by the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization Regional Office for Europe (WHO/Europe). A 53-year-old male presented with skin lesions visited the hospital in a northern Italian region, in November 2022. At the local hospital laboratory, a cutaneous sample was collected, microbiologically cultured and was diagnosed by MALDI-TOF to have a *C. diphtheriae* infection. The patient had a record of vaccination against this bacterium and had no history of travelling abroad recently. The isolate was sent to the national reference laboratory for diphtheria in ISS, for the confirmation of the species, further investigation on the biovar, the presence/absence of the toxin gene (*tox*), and its antibiotic susceptibility. The fellow became familiar with the diagnosis of a *C. diphtheriae* case, learned and practiced biorisk management for safe handling and disposal of a suspected toxin producing bacteria, read the protocols and observed the experiments.

Role: Observer. The fellow reviewed diphtheria disease relevant literature and was updated on the current ongoing EU-outbreak of *C. diphtheriae* pathogen, reviewed laboratory safety manuals for work with a toxin producing bacterium, read all related laboratory diagnostic protocols, observed how molecular, biochemical and AMR genomic and phenotypic assays are performed and analysed. The fellow produced a report on this activity (11).

Educational outcome

The fellow was trained with a practical understanding of the work environment in BSL-3 and working with a toxin producing bacterium in BSL-2. Specifically, she understood the importance of biorisk management, the identification and mitigation of risks, the use of personal protective equipment, performance of waste management and safe handling of infectious materials.

4. Quality management

European Union Reference Laboratory for Parasites (EURLP) quality management plan review of the year 2021

Supervisor: Alessia Possenti

The Unit of Foodborne and Neglected Parasites has been designated as Reference Laboratory for Parasites by the European Commission (EURLP since July, 2006). The Unit is accredited as a competent testing laboratory according to the international standard ISO/IEC 17025:2017 since 2006 and as Proficiency Testing Provider (PTP), in conformity with the ISO/IEC 17043:2010 international standard since 2013. Accreditations and audits are provided by ACCREDIA, the Italian accreditation body. The main mission of the EURLP is to support the National Reference Laboratories (NRLs) of the EU member states in the field of foodborne parasites, such as *Trichinella*, *Echinococcus* and *Anisakis*. This is accomplished through the development, validation and accreditation of analytical methods and the organization of proficiency testing. The fellow received training from the supervisor on the management plan of the EURLP laboratory by reviewing every section in comparison to the ISOs in place. This training led to the observation of a two-hour planning unit meeting on the 21st of January 2022. The aim of the online meeting was the review and discuss the quality management plan of the Unit during the previous year

(2021) and to review the current plan to ensure continuous suitability, effectiveness and adequacy for the unit functions. Furthermore, results of internal audits, corrective actions, external validation of laboratory procedures, client's and personnel's feedback and complains were discussed, as well as effectiveness of the previous year improvements, risk identification, review of results from adopted activities for insurance of laboratory test validity, and other planning factors. In addition, plans for the coming year laboratory activities were discussed.

Role: The fellow, together with the supervisor, review the laboratory management plan document and deep dived into the details concerning all involved activities, in Italian. The fellow participated as an observer to the annual meeting (online). The fellow wrote a report on this (12).

European Union Reference Laboratory for Parasites (EURLP) external laboratory audit witness report

Supervisor: Alessia Possenti

The Unit of Foodborne and Neglected Parasites as a designated European Commission Reference Laboratory for Parasites (*Trichinella*, *Echinococcus* and *Anisakis*) is accredited as competent of testing laboratory according to the international standard ISO/IEC 17025:2017 and as Proficiency Testing Provider (PTP), in conformity with the ISO/IEC 17043:2010 international standards. The fellow observed a two-day external audit at ISS on the 5th and 6th of May 2022. Two certified auditors from ACCREDIA (the Italian accreditation body) visited the laboratory and performed the audit following the quality management system developed according to the ISO 17025:2017. The aim of the audit was to start the fifth cycle of accreditation of the laboratory. The lead auditor was focusing on reviewing all documents implemented to demonstrate that the laboratory operates in accordance with the referring ISO. The technical auditor observed, throughout the two-day visit, the performance of the personnel in applying two-sampled accredited methods together with all registrations of instruments and reagents needed to perform the following laboratory methods: a) Western blotting of *Trichinella* spp. protein specific IgG from infected swine serum samples, b) Indirect ELISA for the detection of anti-*Trichinella* antibodies in swine serum, c) PCR identification of *Opisthorchis* spp. eggs, d) Artificial digestion for the detection of *Trichinella* muscle larvae in striated muscle tissue from animals. Overall, the audit confirmed that employees are technically competent, that do have the knowledge of the management system procedures and that all quality management criteria are followed. Zero non-conformities were detected nonetheless there were 10 observations and two comments. The fellow also participated as an observer to an after audit online meeting during which the results of the external audit were presented and discussed, analyse the origin of the causes of the observations and comments received and plan the corrective actions and their implementation.

Role: The fellow observed the two day external audit, kept notes, correlated steps and findings to the management plan, participated as an observer to the after-audit meeting and in a later time discussed on both the audit and the meeting her observations and questions with the supervisor. The fellow wrote a report on this (13).

Eighth External Quality Assessment on Antimicrobial Susceptibility Testing (EQA8-AST) for *Salmonella* spp. and *Campylobacter* spp.

Supervisors: Claudia Lucarelli, Aurora García-Fernández

Over 200 diseases are caused by eating food contaminated with bacteria, viruses, parasites or chemical substances posing a considerable socioeconomic impact contributing significantly to the global burden of disease and mortality. A subcategory of foodborne diseases is that of the foodborne zoonotic diseases, which are caused by food or water contaminated by pathogenic microorganisms. The most common of these diseases are caused by *Campylobacter* spp., *Salmonella* spp., *Yersinia* spp., *Escherichia coli* and *Listeria* spp. The ENTER--NET laboratory participated from 20 June to 31 August 2022, to the Eighth External Quality Assessment on Antimicrobial Susceptibility Testing (EQA8-AST) for *Salmonella* spp. and *Campylobacter* spp. The aim of the EQA8-AST was to follow the recommended EU protocol at the highest extent possible for antimicrobial monitoring of human *Salmonella* and *Campylobacter* isolates and assess the quality of the data reported to TESSy of ECDC. Specifically, for *Salmonella* spp. serological O-typing and H-typing was performed on eight isolates, by slide agglutination according to the WHO 2007 Antigenic formulae of the *Salmonella* serovars by Grimont and Weill. Determination of antimicrobial resistance was performed by disk diffusion (DD). For *Campylobacter* spp., molecular identification was performed by multiplex PCR and antibiotic susceptibility by disk diffusion. For *Campylobacter*, the evaluation report showed 100% correct species identification and DD results. For *Salmonella*, serotyping was 100% accurate for all isolates whereas for DD some antibiotics mm values were off (more than +/- 3 mm). These have been noted and taken into consideration for future improvements.

Role: The fellow reviewed all related literature and protocols used during the quality assessment, observed all laboratory assays and reviewed and discussed with supervisors the results of the assessment and the actions needed for corrections. The fellow wrote a report (14).

RingTrial2 of the FWD AMR-RefLabCap project

Supervisor: Silvia Herrera Leon (Instituto de Salud Carlos III, Madrid, Spain)

The European Food- and Waterborne Diseases and Zoonoses (FWD) AMR-RefLabCap project organises an annual External Quality Assessment (EQA) since 2022, for the analysis of whole genome sequences of *Salmonella* and *Campylobacter* in order to detect genes and point mutations that confer antimicrobial resistance. The Reference Laboratory for Food- and Waterborne diseases (FWD) of the Instituto de Salud Carlos III (ISCIII) was invited to participate as member of the FWD network. Five *Salmonella* and five *Campylobacter* raw Illumina reads were analysed for molecular typing and detection of genes and point mutations conferring antimicrobial resistance, using online platforms/tools such as Enterobase, PubMLST and ResFinder. Findings were submitted. Evaluation results are expected.

Role: The fellow performed the analysis with the guidance of the supervisor, participated in the submission of the results, reviewed the evaluation results and wrote a report (15).

3rd United Nations Secretary-General's Mechanism (UNSGM) for Investigation of Alleged Use of Biological Weapons Dry Lab EQA Exercise, focused on the mpox virus

Supervisor: Giulietta Venturi

The UNSGM organises an annual dry lab EQAE focused on different pathogen per year, for the build of UN's investigative capability on future possible alleged biological weapon attacks. This year the EAQE was focused on MPXV. Participants were given a real-life scenario and were asked to identify MPXV virus in the datasets, perform metagenomic analysis for presence of additional viruses, genome characterization, strain identity and phylogenetic placement, identification of mutations and genetic engineering, answering of specific questions for solving the investigation. Tools in Galaxy platform, nextstrain.org and tablet sequence visualizer were used. Findings were submitted. Evaluation results are expected.

Role: The fellow performed the analysis, answered the questions, produced a EAQE report which was submitted for evaluation, and wrote a report (16).

Educational outcome

The fellow learned in depth how a European accredited reference laboratory is organised and works. She read in detail, discussed, and implemented in an internal audit based on international standards (ISO17025), followed the whole procedure from preparation to evaluation and action taken after an external accreditation audit, and can describe, evaluate and analyse results of an EQA. She also studied how the EUCAST AST system works depending on the bacterium and how you use it as guidance for phenotypical assessing of AMR. In parallel, she learned how to use WGS data to assess AST from a genomic point of view, the tools that can be used, the approach and how to verify comparing these with what is found as phenotypes. Furthermore, she performed WGS analysis using different tools and platforms for pathogen identification, metagenomics, genome characterisation, strain identity, and phylogenetic placement.

5. Public health microbiology management

5.1 Management during outbreak investigation and other projects

SARS-CoV-2 outbreak in an Italian summer camp

During the retrospective investigation of the outbreak, the fellow was responsible for organising meetings between the ISS and the private company, having one-on-one meetings with the company's medical personnel, presenting the progress of the project to the team, helping with the submission of the manuscript and replying to reviewers' comments.

Trichinellosis outbreak in Apulia region, Italy

During the investigation of a *Trichinella* spp. outbreak in a village in the Apulia region, the fellow participated in all meetings consisting of epidemiologists, microbiologists and medical doctors, had a close collaboration for learning the approach of microbiological diagnosis, wrote the material and methods and results section of the outbreak report, and corrected the abstract for an international conference.

Ralstonia mannitolilytica outbreak in hemodialysis units, in the North of Italy

During the investigation of a bacteremia *Ralstonia* spp. outbreak in hemodialysis patients caused by a contaminated urokinase vial batch, the fellow participated in the team meetings involving clinicians, surgeons, renal hemodialysis experts, microbiologists and epidemiologists, informed the team on what was necessary for a rapid communication, wrote the manuscript in collaboration with the ISS EPIET fellow, corrected and integrated comments on the draft from the working team and was responsible for communicating new manuscript versions

to all. Together with the other members of the ISS team, she was in communication with Dr Michela Sabbatucci of the Italian Ministry of Health and produced together a short communication for the ECDC Epidemic Intelligence Information System (EPIS).

Genomic epidemiology mini-module by EAN

The fellow was part of the team managing and organising a mini-module on genomic epidemiology taking place in November before the ESCAIDE 2023 conference in Barcelona, Spain. This includes aim and objectives, decisions on the program, the preparation of teaching material for both in person and online pre-and after-modules, the audience, evaluation of the courses, and administration preparation.

Presentation to ECDC's Director and Chief Scientist

During the Management, Leadership and Communication module in Stockholm, the fellow and her group gave the oral presentation 'When you look back to two years of the pandemic, and keep in mind the period ahead of us... What competences, skills, and personal characteristics (and why) would you consider most important for a public health leader to be successful in such a crisis period? ECDC Director, Andrea Ammon', to discuss with the highest authorities of ECDC, including the ECDC Director (22).

Educational outcome

The fellow further developed her project management skills and learned to adapt communication to different levels of authority and knowledge base. She gained experience in communicating data for action and formulate recommendations in public health. She increased her skills in communication with scientific experts from a multidisciplinary background and the authorities. She also improved communication through scientific writing and oral presentations. Lastly, the fellow enforced her project management, organisational and administrative skills.

6. Teaching and pedagogy

'Mpox virus WGS-from Illumina reads to phylogenetic analysis using the Galaxy platform'

A two-hour training was prepared with a focus on the use of Galaxy platform and tools for the analysis of whole genome sequencing (WGS) Illumina reads of the MPXV. The training included a presentation, learning material and hand-on exercises with examples for analysis. The objectives of the training was to teach/explain the galaxy platform and the available tools, upload of raw reads, quality check, use of workflows, cleaning of reads from human contaminants, taxonomic report, mapping, variant calling, reporting, consensus sequence production, alignment, phylogeny, and visualisation. Short hands-on exercises were included. The target audience were laboratory virologists with little to more advanced knowledge on WGS, with little experimental experience on mpox who have never or partially worked with the galaxy platform, as well as some invited EUPHEM fellows from C2021. A pre-course evaluation questionnaire was created for audience knowledge assessment and a post-course evaluation questionnaire for the impression of the training to participants, both created in Google forms. The seminar took place at Aula Marotta of the Istituto Superiore di Sanità and online.

Educational outcome

The fellow learned how to assess training needs and identify knowledge gaps for an audience of different backgrounds and career levels. Prepared a two-hour seminar including hands-on exercises and participated in the organization and material preparation of a mini-module. She was exclusively responsible of planning the seminar, preparing the seminar flyer, develop the training material and presentation, prepare a pre- and after seminar knowledge assessment, and create and analyse an evaluation form. Collaborated with other current and past fellow on the preparation of educational material. The fellow wrote a reflective note on the experience gained from the seminar.

7. Communication

7.1 Publications related to the EUPHEM fellowship

7.1.1 Manuscripts published in peer-reviewed journals

1. **Merakou C**, Del Manso M, Lucarelli C, Petrone D, Bandini L, D'Ancona PF, et al. Focolaio di COVID-19 in un campo estivo nella Regione Piemonte (2021): descrizione, lezioni apprese e raccomandazioni per futuri campi estivi. *Boll Epidemiol Naz.* 2022 Nov;3(3):1–9. https://doi.org/10.53225/BEN_048
2. Fabricci M, Trinca A, Talotti L, Busetti M, Fotakis EA, **Merakou C**, et al., A urokinase-associated outbreak of *Ralstonia mannitolilytica* bloodstream infections in haemodialysis patients in north-eastern Italy, January to April 2023. *Euro Surveill.* 2023;28(28):pii=2300328. <https://doi.org/10.2807/1560-7917.ES.2023.28.28.2300328>
3. **Merakou C**, Fortuna C, Amendola A, Marsili G, Argentini C, Fiorentini C, Benedetti E, Riccardo F, Del Manso M, Bella A, Caporali MG, Pezzotti P, Venturi G. Diagnosis of Dengue and Zika virus infections in Italy from November 2015 to November 2022: Laboratory Surveillance Data from a National Reference Laboratory (**submitted to Viruses' special issue 'Arbovirus diagnostics', in the processes of revision**).
4. Errico G, Amendola A, **Merakou C**, Fortuna C, Marsili G, Argentini C, Fiorentini C, Benedetti E, Riccardo F, Del Manso M, Bella A, Caporali MG, Pezzotti P, Venturi G. Diagnosis of Chikungunya virus infection at the Italian National Reference Laboratory for Arboviruses, in the period November 2015 - December 2021. (**in preparation**).
5. **Merakou C**, Errico G, Pagnotta M, Del Grosso M, Maggio Cavallaro G, D'Ambrosio F, Iacchini S, Creti R, Pantosti A, D'Ancona F, Monaco M. Genomic surveillance of methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections in Italy: a cross-sectional observational pilot study (**in preparation**).

7.1.2 Other reports

6. **Merakou C**. Diagnosis of Chikungunya virus (CHIKV) infection at the Italian National Reference Laboratory for Arboviruses, in the period November 2015 - December 2021 – Calculation of sensitivity, specificity and predictive values for IgM and IgG ELISA systems.
7. **Merakou C**, A retrospective genomic analysis by Whole Genome Sequencing (WGS) of zoonotic Hepatitis E virus (HEV) genotype 3 (HEV-3) clinical strains that sustained a 2019 outbreak in Abruzzo, Italy.
8. **Merakou C**, Genomic surveillance of methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections in Italy: a cross-sectional observational pilot study.
9. **Merakou C**, Norovirus whole genome sequencing using a metagenomics approach.
10. **Merakou C**, Development of a WGS analysis pipeline for mpox.
11. **Merakou C**, Biorisk management, species identification and diphtheria toxin gene detection on a suspected *Corynebacterium diphtheriae* isolate by molecular and phenotypic methods.
12. **Merakou C**, European Union Reference Laboratory for Parasites (EURLP) quality management plan review of the year 2021.
13. **Merakou C**, European Union Reference Laboratory for Parasites (EURLP) external laboratory audit witness report.
14. **Merakou C**, Eighth External Quality Assessment on Antimicrobial Susceptibility Testing (EQA8-AST) of *Salmonella* and *Campylobacter* in 2022.
15. **Merakou C**, RingTrial2 of the FWD AMR-RefLabCap project report.
16. **Merakou C**, 3rd United Nations Secretary-General's Mechanism for Investigation of Alleged Use of Biological Weapons (UNSGM) Dry Lab EQAE focused on MPXV virus.

7.2 Conference presentations

17. **International Conference on Trichinellosis (ICT-16) 2023**, 30 August-1 September 2023, Belgrade, Serbia. Accepted as short flash oral poster presentation. E. Di Maggio, M. Meola, V. Bramante, M. Nesta, M. Corritore, F. Fortunato, R. Prato, D. Martinelli, E. A. Fotakis, M. Del Manso, P. Pezzotti, **C. Merakou**, A. Ludovisi, M. Á. Gómez Morales. Investigation of a trichinellosis outbreak in Apulia region, Italy, February-March 2023.
18. **International Congress on Infectious Diseases (ISID) 2022**, 17-20 November 2022, Kuala Lumpur, Malaysia and online. Accepted as e-poster. **C. Merakou**, C. Fortuna, A. Amendola, G. Marsili, C. Argentini, C. Fiorentini, E. Benedetti, F. Riccardo, M. Del Manso, A. Bella, M. Grazia Caporali, P. Pezzotti, G. Venturi. Diagnosis of Dengue virus infections in Italy from November 2015 to November 2021: a National Reference

Laboratory surveillance report. (Abstract number: 388 - Published in International Journal of Infectious Diseases, 130, Supplement 2, p. S117. <https://doi.org/10.1016/j.ijid.2023.04.289>).

19. **National Congress of the Italian Society of Microbiology (SIM) 2023**, 24-27 September 2023, Cagliari, Italy. Accepted as poster. M. Pagnotta, G. Errico, **C. Merakou**, F. D'ambrosio, S. Giancrisofaro, R. Camilli, M. Del grosso, M. Monaco. Genomic analysis of methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections in Italy: a pilot study.

7.3 Other presentations

20. C. Merakou. Diagnosis of Dengue (DENV) and Zika (ZIKV) virus infections in Italy from November 2015 to November 2021: a National Reference Laboratory surveillance report; ECDC Introductory course, 2022, oral presentation, 20/04/2022, Spetses, Greece.
21. C. Merakou. A retrospective data analysis study of laboratory tests performed for the diagnosis of Dengue (DENV) suspected cases by the National Reference Laboratory for Arboviruses (NRLA) at Istituto Superiore di Sanità (ISS) over the period from November 2015 to November 2021; ECDC Project Review Module, 2022, oral presentation, 30/08/2022, Lisbon, Portugal.
22. Oral Presentation at the MLCPH module entitled 'When you look back to two years of the pandemic, and keep in mind the period ahead of us... What competences, skills, and personal characteristics (and why) would you consider most important for a public health leader to be successful in such a crisis period? ECDC Director, Andrea Ammon', Presentation to the ECDC Director and Chief Scientist during the Management, Leadership and Communication module, 12/05/2023, Stockholm, Sweden.
23. C. Merakou. A urokinase-associated outbreak of *Ralstonia mannitolilytica* bloodstream infections in haemodialysis patients in north-eastern Italy, January to April 2023; ECDC Project Review Module, 2023, oral presentation, 31/08/2023, Lisbon, Portugal.

7.4 Other communications

24. EAN Twitter account curation, presenting the project of a EUPHEM working in ISS, Rome. (<https://twitter.com/EANBoard/status/1615293577285828610>)

8. EPIET/EUPHEM modules attended

1. Introductory course (part I), 20 September 2021 to 8 October 2021, online.
 - a. IC Inject Day – Phylogeny, 20 October 2021, online.
 - b. IC Inject Day – Operational Research, 27–28 October 2021, online.
 - c. IC Inject Day – Data Management, 10–11 November 2021, online.
2. Introductory course (part II), 20–29 April 2022, Spetses, Greece.
3. Biorisk and Quality Management (BQM) module, 17–18 January 2022, online.
4. Management, Leadership and Communication in Public Health (MLCPH) module, 8–12 May 2023.
5. Multivariable analysis, 14–18 March 2022, online.
 - a. MVA Inject Day, 30 March 2022, online.
6. Outbreak investigation, 6–10 December 2021, online.
7. Project Review Module 2022, 29 August 2022 to 2 September 2022, Lisbon, Portugal.
8. Rapid Assessment & Survey Methods (RAS) module, 6–10 June 2022, Stockholm, Sweden.
9. Time Series Analysis (TSA) module, 7–11 November 2022, Bilthoven, the Netherlands.
10. Qualitative Research (QR) module, 31 January 2023 to 3 February 2023, online.
11. Vaccinology, 13–17 February 2023, online.
12. Management, Leadership and Communication in Public Health (MLCPH) module, 8–12 May 2023, Stockholm, Sweden.
13. Project Review Module 2023, 28 August 2023 to 1 September 2023, Lisbon, Portugal.

9. Other training

1. ESCAIDE 2021, 16–19 November 2021, Stockholm, Sweden.
2. Certified online course: Safety prevention protection - General training, Sector: ATECO 207:M72, Risk type: B, organised by the Directorate General of the Istituto Superiore di Sanità, 25 January 2022.
3. Certified online course: Specific training course for workers, Pursuant to Article 37 of Legislative Decree 81/08 'Consolidated Law on Health and Safety of Workers', State-Regions Agreement of 21 December 2011, organised by the General Directorate of the Istituto Superiore di Sanità, 8, 9, and 11 February 2022, online.

4. 'EUPHEM lectures' series, Virology, 12 May 2022, online.
5. 'EUPHEM lectures' series, Immunology, 12 May 2022, online.
6. Mass gathering WHO course (partial), 3 June 2022, online.
7. Certified online course: BSAFE, United Nations Department of Safety and Security (UNDSS), 3 June 2022.
8. 'EUPHEM lectures' series, WGS, 30 June 2022, online.
9. Intensive Italian language course, 18–28 July 2022, Rome, Italy.
10. ESCMID seminar: 'Genomic surveillance of viral pathogens: are we prepared for emergent global threats across One Health' with Vítor Borges, 20 September 2022, online.
11. Field Epi Response to the Climate and Health Crisis: Vector-borne Diseases organised by TEPHINET Climate and Health Working Group's webinar series, 'Field Epi Response to the Climate and Health Crisis', 28 September 2022, online.
12. ESCMID online seminar: 'Using genomics for antimicrobial resistance at the public health and clinical interface', 10 October 2022, online.
13. WHO Public Health Laboratories knowledge sharing webinar series: SARS-CoV-2 variants circulation and examples of genomic surveillance strategies, 10 October 2022, online.
14. Microbial symbiosis in insect vectors, Guido Favia, Ciclo di Seminari di Parassitologia Molecolare 2022–2023 (ISS and Sapienza Università di Roma) (How the microbiome of insects facilitate their capacity of carrying different diseases), 14 October 2022, online.
15. New roles of microbiology laboratories in public health surveillance and epidemic response. Organised by ESGPHM, 27 October 2022, online.
16. Seminar organised by Microbiology society (UK) with the title: 'Mosquito immunity shapes arbovirus evolution and emergence' given by Dr Kevin Maringer (Flavivirus Transmission & Pathogenesis Group, Pirbright Institute, UK), 17 November 2022, online.
17. In-person course: Media and Infodemics course, EPIET Alumni Network, 21–22 November 2022, Stockholm, Sweden.
18. ESCAIDE 2022, 23–25 November 2022, Stockholm, Sweden.
19. ECDC press conference on World AIDS Day – latest ECDC/WHO Europe report, 30 November 2022.
20. Certified online course: Introduction to Infectious Disease Preparedness micro learning, ECDC virtual academy, 16 December 2022.
21. Certified online course: Introduction to R, Datacamp, 29 December 2022, online.
22. 'Cholera outbreaks: The current situation and what are doing to address it', seminar by the WHO, 15 March 2023.
23. 'Review of recent emerging and re-emerging virus outbreaks' - talks on 1. Borna disease virus 1 situation in Germany; 2. Multi-country outbreak of Monkeypox virus: genetic clustering and transmission dynamics; 3. Ngari virus circulation in Kenya, a seminar organised by EVD-LabNet and ECDC, 20 March 2023.
24. In person observer of the three-day workshop on 'Strengthening Preparedness and Response to West Nile Virus through identifying and acting upon lessons learned' organised by ECDC and ISS, in ISS, Rome, Italy, 22–24 March 2023.
25. Spring European testing week, online event organised by ECDC with the title: 'HIV, Hepatitis B and C and Sexually Transmitted Infections: why is testing important and what can be done to increase testing access and uptake?', 17 May 2023, online.
26. GTN Smörgåsbord 3. The course consisted of a week of online, asynchronous training which enabled participants to work at their own pace and on their own schedule. The workshops consisted of a blend of seminars and hands-on practical work. This course was organised by the Galaxy Training Network, in collaboration with the Gallantries Project, Galaxy Project, CINECA, BY-COVID, RO-Crate, Bioconductor. The course infrastructure was provided by Galaxy Europe, Galaxy Australia and the Australian BioCommons, and TACC Instruction provided by the global instructor community of Galaxy. Subjects completed: 1) Intro to Galaxy; 2) Rule-based Uploader; 3) Quality Control; 4) Mapping; 5) Genome Annotation with Prokka; 6) From NCBI's Sequence Read Archive (SRA) to Galaxy: SARS-CoV-2 variant analysis; and 7) Pox virus genome analysis from tiled-amplicon sequencing data, 22–26 May, 2023, online.
27. EPI-WIN Webinar, organised by WHO's Information Network for Epidemics (EPI-WIN) with the title: 'Managing Dengue: a rapidly expanding epidemic', 2 August 2023, online.

10. Missions

None undertaken.

11. Other activities

None undertaken.

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