Jana Grüttner

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

Statens Serum Institut (SSI), Denmark

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

Jana Grüttner holds a bachelor's degree in molecular and technical medicine from Furtwangen University, Germany, and a master's degree in infection biology from Uppsala University, Sweden. In the course of the degrees, Jana worked on research projects involving microbiological method development, genomics, infection dynamics, and microbial pathogenesis. She obtained a PhD in microbiology from Uppsala University, during which she studied host–pathogen interactions between the intestinal parasite *Giardia intestinalis* and intestinal epithelial cells, using different host model systems. Her work extensively used transcriptomics and proteomics methodologies to elicit host–parasite interactions and immune modulation by the parasite.

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, 2026

1. Epidemiological investigations

1.1. Outbreak investigations

1.1.1. Outbreak of Clostridium perfringens*, Capital Region, Denmark, 2024*

Supervisor: Luise Müller (SSI)

Category: Food- and waterborne diseases

Aim: To identify the source of the outbreak and the disease-causing pathogen, and to assess the extent of the outbreak.

Methods: A cohort study was conducted using an online questionnaire. A case was defined as any person who ate lunch that was prepared by the investigated catering company in week 36, 2024 in the Capital Region of Denmark and after consumption experienced at least one of these gastrointestinal symptoms, i.e. vomiting, diarrhoea, stomach aches, and/or nausea. Risk-ratios for the different meals during week 36 were calculated using univariate analysis. Faecal specimens and food samples were collected for polymerase chain reaction (PCR) and culture.

Results: The survey had 228 responders who ate food at their workplace in week 36 of which 91 cases (attack rate=40%) could be identified. Cases were detected in 18/27 (66.7%) of the participating companies. The onset of symptoms occurred for most cases on 6 September (Friday). Risk of illness was higher in individuals who ate lunch at their workplace on Friday (risk ratio (RR): 16.9, 95% confidence intervals (CI): 4.3–66.5, p<0.001), and in individuals who had 'flæskestegssandwich', the meat dish on Friday (RR: 5.4, 95% CI: 2.6–11.3, p<0.001). Out of the eight faecal samples collected, one tested positive for *Clostridium perfringens*. The one food sample collected (flæskestegssandwich) also tested positive for *Clostridium perfringens*.

Public health implications/Conclusions: Insufficient heating of the pork meat before delivery of the meals to different customers in the Capital Region was the suspected cause of the outbreak. The catering company received a fine for wrong handling of food, and food processing routines were revised by them.

Role: Jana was a co-investigator along with the EUPHEM fellow, Tine Larsen (Cohort 2023). Jana and Tine developed the questionnaire for the study, developed the analysis plan, analysed the data, and wrote an outbreak report. Both fellows followed the Danish Veterinary and Food Administration to the catering company for the control visit.

1.1.2. Outbreak of Chlamydia psittaci (C. psittaci) *in humans in Denmark, December 2023–March 2024*

Supervisor: Randi Føns Petersen (SSI)

Category: Food- and waterborne diseases

Aim: To assess the genotype of *C. psittaci* human cases of an outbreak in late 2023 to spring 2024 in Denmark, in order to help identify the source of the outbreak.

Methods: We performed multilocus sequence typing (MLST) and *ompA* gene typing on 15 human laboratory-confirmed *C. psittaci* cases between January and August 2024. MLST and *ompA* PCRs were sequenced using amplicon-based nanopore sequencing.

Results: Twelve samples were typed as sequence type (ST) 218 and *ompA* genotype A, and one additional sample had a partial match to ST218 (five of seven genes) for which we could not determine the *ompA* genotype. Two samples were typed as *ompA* genotype B with ST27 and one untyped ST. The untyped *ompA* genotype B sample had a partial match to ST212 (six of seven genes). The dominating genotype, ST218/*ompA* genotype A, could be found in samples taken between January and July 2024 in different parts of Denmark without any clear geographical pattern. Phylogenetic analysis of the *ompA* gene sequence showed three *ompA* variants within the ST218 population, each separated by one single nucleotide position (SNP). We could not detect a geographical or temporal pattern for the ST218 *ompA* variants.

Public health implications/Conclusions: The genotyping results supported the results obtained by a case–control study conducted by Roberto Croci (EPIET fellow, Cohort 2023). The case–control study found that indirect environmental transmission by wild birds could be the infection source. The dominating genotype, ST218/*ompA* genotype A, has previously been found in wild birds (great tits) and humans in Sweden.

Role: Jana was a co-investigator conducting microbiological analysis of the outbreak. She linked microbiological and epidemiological data, and analysed and interpreted the results. She has contributed, alongside an EU-track EPIET fellow at SSI, to a research paper about this nationwide outbreak.

1.2. Surveillance

1.2.1. Molecular characterisation and epidemiology of **Streptococcus pneumoniae** *meningitis isolates in Denmark, 2019–2024*

Supervisor: Hans-Christian Slotved (SSI)

Type of project: Analysis of data from a surveillance system.

Aim: To assess the genetic structure of pneumococcal meningitis isolates to understand the molecular epidemiology, and the occurrence of antimicrobial resistance (AMR).

Methods: All viable pneumococcal meningitis isolates, received by mandatory surveillance, were analysed (n=146, August 2019 to October 2024). Penicillin susceptibility was determined by oxacillin disc diffusion followed by minimal inhibitory concentration determination for cefotaxime, ceftriaxone, meropenem, vancomycin and levofloxacin. Acquired AMR genes, penicillin-binding proteins (PBP)-types, serotypes and Global Pneumococcal Sequence Clusters (GPSCs) were inferred from whole genome sequencing (WGS) data. Core-genome single-nucleotide polymorphism analysis was used to infer relatedness.

Results: In total, 56% of the sequenced isolates expressed a vaccine serotype. Thirty-five GPSCs and 23 serotypes were identified. Four GPSCs represented 42% of the total pneumococcal population: GPSC12/serotype 3 (15.8%), GPSC3/serotype 8, 11A, 11E, 33F (11%), GPSC19/serotype 22F (7.5%), and GPSC5/serotype 23A, 23B1 (7.5%). GPSC5, which comprises only of non-vaccine-serotypes, was 100% phenotypically resistant to penicillin and harboured penicillin resistance-associated PBP-types. Penicillin resistance in non-GPSC5 isolates was 9.4%. One isolate, GPSC59/serotype 35B, was resistant to all clinically relevant beta-lactams. No identified acquired AMR genes were relevant for meningitis treatment.

Public health implications/Conclusions: Denmark has a heterogeneous *S. pneumoniae* meningitis population with a high proportion of isolates representing vaccine serotypes. A penicillin-resistant, non-vaccine-serotype genetic cluster (GPSC5) was detected as the third most common GPSC in the study period. Continuous genomic *S. pneumoniae* surveillance is key to monitoring the occurrence and expansion of genetic clusters and AMR genes/mutations, thereby indicating possible treatment failures and consequences and effectiveness of vaccination programmes.

Role: Jana performed data analysis, interpreted results, drew conclusions, and wrote the report.

1.2.2. Phylogenetic analysis of rodent-adapted **Cryptosporidium** *species, Denmark, 2022–2023*

Supervisor: Rune Stensvold (SSI)

Type of project: Analysis of data from a surveillance system.

Aim: To conduct a comprehensive sequence analysis and phylogenetic investigation of rodent-adapted *Cryptosporidium* species.

Methods: As part of the national Danish *Cryptosporidium* surveillance system, positivity of *Cryptosporidium* DNA is confirmed, the *Cryptosporidium* species is identified, and molecular typing using gp60 is performed on voluntary submitted samples from the regional departments of clinical microbiology. All rodent-adapted *Cryptosporidium* species that caused an infection in humans were sequenced, including DNA sequences of SSU rDNA, actin and gp60 genes. Phylogenetic analyses of the sequences were done using the Neighbor-Joining algorithm to detect genetic diversity.

Results: Through the Danish national *Cryptosporidium* surveillance system, seven new human cases of cryptosporidiosis involving rodent-adapted species (*Cryptosporidium ditrichi* (n=1), *Cryptosporidium mortiferum* (n=4), *Cryptosporidium tyzzeri* (n=1), and *Cryptosporidium viatorum* (n=1) were detected within a period of 12 months from 2022 to 2023. Phylogenetic analysis of SSU rDNA, actin and gp60 DNA sequences for the different species with reference sequences from different parts of the world showed the genetic diversity present for each species. Most cases of *C. ditrichi* and *C. mortiferum* were identified in northern countries, while *C. tyzzeri* and *C. viatorum* cases were identified primarily in warmer climates. All four *C. mortiferum* cases were the same subtype, XIVaA20G2T1, and phylogenetic analysis of actin also showed no genetic variation.

Public health implications/Conclusions: The identification of rodent-adapted *Cryptosporidium* species causing human infections in Denmark further support the role of *Cryptosporidium* as a cause of zoonotic disease. Analysing and assessing genetic variation help to identify potential infection sources and indicate outbreaks.

Role: Jana performed data analysis and contributed to the publication of a manuscript in a peer-reviewed journal (see section 7.1).

Routine surveillance activities

National surveillance of **Giardia intestinalis** *in Denmark, 2023–2025*

Activities and role: Throughout her fellowship, Jana actively participated in the national surveillance of *Giardia intestinalis,* which has been under surveillance in Denmark since October 2023. Surveillance activities included: regularly analysing and interpreting microbiological surveillance data, which included: genotyping *Giardia intestinalis* samples as part of the national surveillance system, data entry to the local surveillance database, organising and managing the samples needing genotype analysis, and monitoring the weekly *Giardia* case data from the Danish microbiology database to assess the epidemiological situation.

2. Applied public health microbiology research and laboratory investigations

2.1. Molecular epidemiology and antimicrobial resistance of invasive **Streptococcus dysgalactiae** *subsp.* **equisimilis** *isolates in Denmark, 2020–2022*

Supervisors: Marc Stegger (SSI), Steen Hoffmann (SSI)

Aim: To assess the prevalence of antimicrobial resistance (AMR) genes and explore the phylogenetic relationships of invasive *Streptococcus dysgalactiae* subsp. *equisimilis* (iSDSE) strains in Denmark between 2020 and 2022 using WGS surveillance data in order to understand the molecular epidemiology and occurrence of resistances that could lead to treatment failure.

Methods: All iSDSE isolates (n=1225, August 2020–September 2022) were whole-genome sequenced. Phenotypic antibiotic susceptibility to penicillin, erythromycin and clindamycin was determined. Core-genome single-nucleotide polymorphism analysis was used to infer relatedness, and phylogenetic clades were deduced using fast hierarchical Bayesian analysis of population structure (fastbaps). Acquired AMR genes, multilocus sequence typing and M protein gene (*emm*) types were inferred from WGS data. We describe key epidemiological characteristics of genetic clades and AMR genes.

Results: We identified 14 distinct genetic clades, of which four clades represented nearly 75% of the study population. The most prevalent sequence types (STs) were ST20 and ST17, which were the dominating STs in three of the four predominant genetic clades. The most dominant *emm*-type was *stG62647*, which is associated with higher virulence. All isolates were phenotypically susceptible to penicillin, the first-choice treatment option. Only two isolates harboured beta-lactam resistance genes. One clade showed a high prevalence of both phenotypic and genomic macrolide resistance (57% [n=39]), a second-choice treatment option.

Public health implications/Conclusions: Denmark has a heterogeneous iSDSE population with genetic clusters characterised by high proportions of AMR markers. Continuous genomic iSDSE surveillance can monitor the occurrence and expansion of genetic clades and AMR genes, e.g. beta-lactam resistance genes, and thereby indicate possible treatment failures and outbreaks of resistant clonal lineages.

Role: Jana wrote the study protocol; extracted data from the national surveillance database; analysed and interpreted genomic and phenotypic AMR data; analysed and interpreted the genomic structure of the bacterial population; and submitted a manuscript to a peer-reviewed journal (see section 7.1).

2.2. Culture-independent detection assay for routine surveillance of poliovirus in wastewater at Statens Serum Institut

Supervisors: Lasse Dam Rasmussen (SSI), Sofie Elisabeth Midgley (SSI), Kristina Trætholt Franck (SSI)

Aim: To develop and implement a culture-independent detection assay of poliovirus in wastewater at SSI for routine surveillance.

Methods: Wastewater was concentrated using a two-phase separation method, followed by viral RNA extraction using a magnetic-bead RNA purification method. Quantitative real-time reverse-transcription PCR amplification with poliovirus specific primers (PanPolio qRT-PCR) received from commercial vendors or the United States Centers for Disease Control and Prevention (CDC) were used to detect poliovirus in the wastewater extracts. To distinguish between poliovirus strains, a VP1 gene fragment was amplified by nested PCR and sequenced by amplicon nanopore sequencing. The workflow was tested using different dilutions of spiked wastewater samples.

Results: The wastewater concentration and RNA purification method tested showed insufficient sensitivity for all spiked wastewater dilutions and was too labour-intensive to be used for routine surveillance. The PanPolio qRT-PCR was successfully optimised and validated on non-wastewater poliovirus extracts of Sabin-like poliovirus (SL) 1 and SL3 strains. Only PanPolio primers received from the CDC had an appropriate sensitivity and robustness. The VP1 gene nanopore sequencing could distinguish the tested poliovirus strains, SL1 and SL3.

Public health implications/Conclusions: Environmental surveillance of poliovirus will be important for the final stages of poliovirus eradication. The recent detection of vaccine-derived poliovirus type 2 in multiple countries in Europe highlights the need for a fast, simple and culture-free method to detect poliovirus in wastewater. The tested PanPolio qRT-PCR can be used to screen samples for poliovirus. Amplicon sequencing of the VP1 gene fragment can be used for routine surveillance to distinguish between poliovirus strains. However, another method needs to be established to concentrate wastewater and purify viral RNA.

Role: Jana performed the testing and validation of the methods; analysed and interpreted the PCR and sequencing data; formulated conclusions; wrote a protocol and a report.

2.3. Improving the efficiency of genotyping of **Chlamydia psittaci** *strains*

Supervisor: Randi Føns Petersen (SSI)

Aim: To improve the efficiency and thereby sensitivity of the currently used *Chlamydia psittaci* multi-locus sequence typing (MLST) and *ompA* gene typing method.

Methods: MLST and *ompA* PCR conditions were optimised. PCR products were sequenced using nanopore sequencing. The sequencing strategy included primary fragment amplification with primers containing barcoded adaptors (BCA). The primary PCRs were purified using magnetic bead-purification followed by barcoding PCR. Sequencing library preparation was done with Oxford Nanopore Technologies SQK-LSK114 and EXP-PBC096 ligation sequencing and PCR barcoding kits. The libraries were sequenced on an Oxford Nanopore Technologies GridION sequencer using R10.4.1 (FLO-FLG114) flow cells. The two-step PCR method was validated using dilutions of a positive control and a panel of primary samples positive for *C. psittaci* determined by species-specific real-time PCR used during diagnosis at SSI.

Results: The primary PCR achieved the best performance using HotStarTaq Master Mix Kit (Qiagen). The two-step PCR procedure of primary PCR with tailed BCA primers followed by barcoding PCR yielded efficient amount of product for sequencing if DNA concentrations corresponding to cycle threshold (Ct) value of 33 or below with the diagnostic species-specific real-time PCR were used. The method was validated for sequencing the PCR products individually or pooled per sample (pooling all seven MLST PCRs and *ompA* PCR) before the barcoding PCR. The PCR clean-up steps and DNA concentration measurements were further successfully run with an automated liquid handling workstation (Biomek) for easier handling of many samples.

Public health implications/Conclusions: The optimised method for MLST and *ompA* genotyping can be implemented in the future for routine surveillance as well as for processing large number of samples during an outbreak.

Role: Jana designed the method; optimised the different steps of the method; analysed the laboratory and sequencing data; wrote a laboratory protocol.

2.4. Group B **Streptococcus** *in silico genotyping using whole-genome sequencing data*

Supervisor: Hans-Christian Slotved (SSI)

Aim: To determine and implement an appropriate bioinformatics tool for genotyping *Streptococcus agalactiae*, (Group B *Streptococcus* – GBS). The tool needed to be able to serotype GBS and identify the presence of selected virulence factors and surface protein genes.

Methods: In Denmark the surveillance of GBS is conducted by the national Neisseria and Streptococcus Reference (NSR) laboratory at SSI, and includes phenotypic serotyping using GBS latex agglutination test (SSI Diagnostica, Denmark). From 2019 onwards, voluntarily submitted isolates to SSI were whole-genome sequenced. Different *in silico* analysis tools, including SRST2, were tested to perform molecular serotyping and detect surface protein and virulence genes using whole-genome sequencing data. The reference gene database chosen for the molecular serotyping was published previously (Tiruvayipati et al., 2021). A custom reference gene database for surface protein gene and virulence gene typing was created for surveillance purposes.

Results: SRST2 was determined to be a suitable tool for molecular serotyping as well as for surface protein and virulence gene typing of GBS, using the reference and custom-made database. The SRST2 output was successfully integrated into the WGS analysis pipeline after running bifrost (https://github.com/ssi-dk/bifrost), which SSI uses for routine bacterial WGS surveillance. Further, an R script was developed to easily create and add possible new genes to the SRST2 reference gene database in the future.

Public health implications/Conclusions: The newly established genotyping tool for GBS using WGS data will facilitate routine surveillance and is easily customisable. Integrating the typing output of SRST2 in the bifrost summary result output as a species-specific workflow, will reduce the workload for genotyping GBS.

Role: Jana validated the genotyping tools and created gene databases for routine surveillance; wrote an R script for gene database creation; analysed and interpreted sequencing data; wrote a report.

2.5. Characterisation of gp60 gene sequence of Cryptosporidium suis

Supervisor: Rune Stensvold (SSI)

Aim: To characterise *Cryptosporidium suis* gp60 gene obtained from human and suid faecal samples.

Methods: Phylogenetic analysis was performed of *Cryptosporidium (C.) suis* gp60 gene sequences with other selected *Cryptosporidium* species (n=12) serving as references. The amino acid sequences of *C. suis* and other reference *Cryptosporidium* species were characterised by multiple sequence alignment. The gp60 amino acid sequences were further analysed by predicting and annotating signal peptides, transmembrane domain regions, furin cleavage sites, O- and N-glycosylation sites. Human and suid samples were subtyped using a novel subtyping assay targeting the post-repeat region of *gp60*.

Results: The complete ORF of *gp60* comprised 1 635 base pairs (bp), encoding 544 amino acids (aa). The highest sequence similarity at the aa-level was to a *C. ubiquitum* gp60 sequence (64% identity). Phylogenetic analysis of the *gp60* DNA sequence also showed clustering with *C. ubiquitum*. Sequencing of the *C. suis gp60* gene identified a novel type of tandem repeat within the gene, consisting of a 21-bp repeat, occupying almost half of the gene. Subtyping of samples from Norway, Denmark, Spain and Sweden using the novel subtyping method resulted in three different subtypes: XXVa-1, XXVa-2, and XXVa-3. Subtype XXVa-1 was detected in the human sample.

Public health implications/Conclusions: Sequencing of the *gp60* gene of *C. suis* revealed a unique multiple 21-bp repeat region. The novel subtyping assay targeting the post-repeat region facilitates *gp60* typing of this *Cryptosporidium* species for the first time.

Role: Jana analysed the gene sequences and assessed the phylogeny of the samples included; contributed to the publication of a manuscript in a peer-reviewed journal (see section 7.1).

3. Biorisk management

3.1. Biosafety level (BSL)-3 theoretical training, Statens Serum Institut, Denmark, 2025

Supervisor: Kirsten Marie Bay Tjørnehøj (SSI)

Jana received BSL-3 theoretical training organised by the department of Virology and Microbial Preparedness at SSI. The BSL-3 training objective was to get an overview of working in a BSL-3 laboratory. The training included an overview of guidelines and rules of working in a BSL-3 environment in Denmark as well as internationally. Jana also received more detailed information about regulations and workflows implemented at the different BSL-3 laboratories at SSI. Biorisk classification and risk assessment for different pathogens and procedures were discussed. Furthermore, she received detailed information about the Danish legislative framework for working with high-containment pathogens, including discussion of the 'Executive Order on Biological Agents and the Working Environment (Bekendtgørelse 1270 af 20/11/2024)'. The training contributed to the fellow's development on how to work with high-risk agents.

3.2. Nordic Biopreparedness Forum's annual workshop at the Norwegian Institute of Public Health, Oslo (September 2024)

Supervisor: Aoife Ronayne (SSI)

Between 2023 and 2025, Jana was part of the steering committee of the Nordic Biopreparedness Forum (NBF), which is a network between the Nordic countries to strengthen preparedness diagnostics for biological agents and biosecurity for enhanced joint capacity (see section 5). NBF holds an annual on-site workshop for two half-days, which took place in 2024 at the Norwegian Institute of Public Health in Oslo. Jana attended the workshop on-site. The NBF workshop covered different topics of biopreparedness and strong focus was placed on collaboration between countries including civil and military institutes. She gained insights during the workshop on topics such as methods for microbiological analysis, biosecurity and biosafety, laboratory support for international bioweapon investigations, and high-containment and mobile laboratories for civil and military use. Jana strengthened her knowledge on biopreparedness from a civil and military perspective and on collaborations between European national agencies.

4. Quality management

4.1. External Quality Assessment (EQA) to support diagnosis of HIV in Denmark, 2025

Supervisor: Anders Frische (SSI)

Aim: To assess and analyse the results of an EQA scheme for HIV diagnostics.

Methods: The HIV EQA scheme is organised twice a year by the Virologi & Mikrobiologisk Specialdiagnostik department at SSI for regional diagnostic laboratories and departments for clinical microbiology in Denmark including Faroe Islands and Greenland. For the 69th round of the EQA scheme, samples were sent out to 11 participating laboratories in May 2025, which included six samples of HIV-1, HIV-2 and negative samples.

Results: SSI received the HIV EQA scheme results by the end of June. All but one participating laboratory submitted their testing results back to SSI. The participating laboratories used a total of three different primary diagnostic (screening) methods. All laboratories correctly diagnosed the EQA samples using their screening assays and no difference could be detected between methods.

Public health implications/Conclusions: The EQA scheme for HIV primary diagnostics ensures accurate test results from the regional departments of microbiology in Denmark. A high standard in diagnostic testing also enhances surveillance capacity and possible outbreak detection.

Role: Jana performed data analysis; evaluated laboratory results; updated and revised the summary report.

4.2. DANAK accreditation visit at Statens Serum Institut, 2025

Supervisor: Ismira Crneta (SSI)

In June 2025, DANAK, the Danish accreditation fund, audited the different accredited laboratories at SSI according to ISO/IEC 17025 (international standard for testing and calibration laboratories). Prior the accreditation visit, Jana prepared herself for the audit by getting familiar with the standards and documentations, which would be evaluated during the three-day accreditation visit. She attended one of the days, which included meetings with DANAK accreditors and SSI personnel, and visit of the parasitology laboratory for accreditation. Jana followed the technical assessor during the inspection of the parasitology laboratory and observed the different steps and procedures during the audit.

Role: Jana prepared for the accreditation visit, observed the accreditation and wrote a reflective note.

5. Public health microbiology management

Member of the steering committee of the Nordic Biopreparedness Forum (NBF), 2023–2025

Jana was part of the steering committee of the Nordic Biopreparedness forum (NBF), which is a network between the Nordic countries to strengthen preparedness diagnostics for biological agents and biosecurity for enhanced joint capacity. Jana participated in the meetings, which took place every two months, between November 2023 and August 2025. As part of this role, Jana took meeting notes during 2024, the year Denmark chaired the steering committee. She also prepared a reflective note about her time on the committee.

Management and communication of outbreaks, Denmark, 2023–2025

During the fellowship, Jana was part of the food-borne outbreak team at SSI, which comprises people from different departments at SSI and different areas of expertise. She gained experience on how the team operates during outbreaks, including internal communication, as well as communication with other agencies and the public. Being part of the team, Jana further gained insights into public health measures applicable in different situations and responsibilities of the different national agencies. She applied these experiences while investigating a food-borne outbreak.

Project management and communication with collaborators, Denmark, 2023–2025

Jana led several projects independently during the fellowship and worked with collaborators within SSI and different organisations, e.g. Danish Veterinary and Food Administration and regional departments of clinical microbiology. As part of optimising *Chlamydia* typing methodologies (see section 2), Jana led and supervised laboratory technicians in optimising laboratory assays. For the *Streptococcus dysgalactiae* subsp. *equisimilis* research project, she was the contact person for investigating the diagnostic procedures used over the past decade at the 10 regional departments of clinical microbiology (DCMs) (see section 2).

Participation in the 2nd EU Health Taskforce Stakeholder meeting, Stockholm, 2024

Jana participated in the 2nd EU Health Taskforce (EUHTF) Stakeholder meeting, which took place on 18–19 November 2024 in Stockholm, Sweden. Recently established by ECDC, the EUHTF provides operational outbreak response and crisis preparedness support to EU/EEA countries as well as supports wider global health security. The participants included representatives from EU/EEA Member States, EU agencies, the European Commission, and partner organisations – World Health Organization (WHO), Global Outbreak Alert and Response Network (GOARN), Doctors Without Borders (Médecins Sans Frontières – MSF) and the International Federation of the Red Cross (IFRC).

6. Teaching and pedagogy

R training for epidemiologists and public health experts, 2025

Jana prepared for and delivered an R training session for public health professionals focusing on analysing outbreak and surveillance data and producing descriptive epidemiological illustrations. The material developed for the training included preparation of a new case study of mock measles case-based data. The case study focused on data cleaning, data analysis and data illustrations through figures and tables. Jana also delivered an R training session at a weeklong on-site course for epidemiologists from Rwanda Biomedical Centre (RBC) and the Africa Centres for Disease Control and Prevention (Africa CDC). The training included lectures and facilitating group work.

Parasitology training for master's students at Copenhagen University, Denmark, 2025

Jana prepared and delivered a parasitology training session for master's degree students of the Human Parasitology course, Copenhagen University. As part of a site-visit to the parasitology unit at SSI, the students attended a three-hour session about parasitology diagnostics and surveillance procedures for parasites relevant in a Danish context. Jana delivered a 30-minute lecture about *Giardia intestinalis*, focusing on symptoms, epidemiology, and diagnostics. She prepared the lecture's content and the presentation.

7. Communications related to the EPIET/EUPHEM fellowship

7.1. Manuscripts published in peer-reviewed journals

- Lebbad M, **Grüttner J**, Beser J, Lizana V, Dea-Ayuela MA, Oropeza-Moe M, et al. Complete sequencing of the *Cryptosporidium suis* gp60 gene reveals a novel type of tandem repeats-Implications for surveillance. Infect Genet Evol. 2024 Aug;122:105614. doi: 10.1016/j.meegid.2024.105614. Available at: https://www.sciencedirect.com/science/article/pii/S1567134824000650?via%3Dihub
- Stensvold CR, Larsen TG, **Grüttner J**, Nielsen L, Engberg J, Lebbad M. Rodent-adapted Cryptosporidium infection in humans: Seven new cases and review of the literature. One Health. 2024 Jan 20:100682. doi: 10.1016/j.onehlt.2024.100682. Available at: https://www.sciencedirect.com/science/article/pii/S2352771424000089?via%3Dihub
- **Grüttner J**, Ronayne A, Lindegaard M, Hoffmann S, Stegger M. Emerging Trends in Invasive Streptococcus dysgalactiae subsp. equisimilis Infections in Denmark: A Nationwide genomic and Registry-Based Study. [Submitted].
- **Grüttner J**, Ronayne A, Kristensen Lomholt F, Slotved H. Molecular characterisation and epidemiology of *Streptococcus pneumoniae* meningitis isolates in Denmark, 2019–2024. [In preparation].
- Croci R*, **Grüttner J***, Espenhain L, Kjelsø C, Holm Hansen C, Trier Møller F, et al. Psittacosis outbreak linked to wild birds, Denmark, 2023–2024: a One Health, collaborative investigation. [In preparation]. *Joint first authors.

7.2. Other reports

- **Grüttner J** and Graakjaer Larsen T. *Clostridium perfringens* Outbreak investigation report.; October 2024.
- **Grüttner J**. Method development for routine surveillance of poliovirus in wastewater at Statens Serum Institut.; 2024.
- **Grüttner J**, Group B *Streptococcus in silico* genotyping using whole-genome sequencing data; 2025.

7.3. Conference presentations

- **Grüttner J**, Ronayne A, Lindegaard M, Hoffmann S, Stegger M. Molecular epidemiology and antimicrobial resistance of invasive *Streptococcus dysgalactiae* subsp. *equisimilis* isolates in Denmark, 2020–2022 (poster presentation). Presented at: ESCAIDE; 21 November 2024; Stockholm, Sweden.
- **Grüttner J**, Ronayne A, Kristensen Lomholt F, Slotved H. Molecular characterisation and epidemiology of *Streptococcus pneumoniae* meningitis isolates in Denmark, 2019–2024. Submitted to ESCAIDE 2025.

7.4. Other presentations

- **Grüttner J**, Molecular characterisation and epidemiology of *Streptococcus pneumoniae* meningitis isolates in Denmark, 2019–2024. Project review module, 26 August 2025, Lisbon, Portugal
- **Grüttner J**, Molecular epidemiology and antimicrobial resistance of invasive *Streptococcus dysgalactiae* subsp. *equisimilis* isolates in Denmark 2020–2022. BPS department seminar, 12 June 2025, Copenhagen, Denmark
- **Grüttner J**, Molecular characterization and epidemiology of *Streptococcus pneumoniae* meningitis isolates in Denmark, Nordic Mini Project Review Module. Folkhälsomyndigheten, 13 March 2024; Stockholm, Sweden
- **Grüttner J**, Molecular epidemiology and antimicrobial resistance of invasive *Streptococcus dysgalactiae* subsp. *equisimilis* isolates in Denmark 2020–2022. Project review module, 28 August 2024, Lisbon, Portugal
- **Grüttner J**, Comparative genomics and antimicrobial resistance of invasive *Streptococcus dysgalactiae* subsp. *equisimilis* strains in Denmark (2020–2022). Nordic Mini Project Review Module. Finnish Institute for Health and Welfare; 29 February 2024; Helsinki, Finland.

8. EPIET/EUPHEM modules attended

- Introductory Course, 25 September–13 October 2023, Spetses, Greece
- Study Protocol and Scientific Writing, 26–27 October and 7–8 November 2023, virtual
- European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2023, 22–24 November 2023, Barcelona, Spain
- Time Series Analysis, 11–15 December 2023, Rome, Italy
- 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
- 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
- One-Health, 12–15 May 2025, virtual
- Project Review Module, 25–29 August 2025, Lisbon, Portugal
- Public Health Leadership, 1–3 September 2025, Lisbon, Portugal.
- European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2025, 19–21 November 2025, Warsaw, Poland

9. Other training

- Nordic Mini Project Review Module (NMPRM), 29 February–1 March 2024; Helsinki, Finland
- Public Health Preparedness for Mass Gathering Events, WHO, 7 April 2024, virtual
- Nordic Mini Project Review Module (NMPRM), 13–14 March 2024; Stockholm, Sweden.

10. International assignments

- One-week R training facilitation for epidemiologists from the Rwanda Biomedical Centre (RBC) and Africa CDC, organised by the epidemic intelligence team at ECDC, Kigali, Rwanda, July 2025.
- Two-week remote assignment preparing course materials for an R training for epidemiologists and public health experts from Africa CDC, organised by the epidemic intelligence team at ECDC, Copenhagen, Denmark, January 2025.

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