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European Public Health Microbiology Training Programme (EUPHEM), Cohort 2022
Norwegian Institute of Public Health, Norway

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/2023/23 and ECDC/AD/2023/06 govern the EU-track and MS-track, respectively, of the ECDC Fellowship Programme, field epidemiology path (EPIET) and public health microbiology path (EUPHEM).

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

Arne M. Taxt is a medical doctor, certified clinical microbiologist and paediatrician in Norway. He holds a position as a senior medical officer at the Norwegian Institute of Public Health (NIPH), Department of Infection control, with responsibilities within infectious disease surveillance and vaccination. Arne holds a PhD from the Center for International Health at the University of Bergen, Norway. His PhD work focused on vaccine-development in a global health context targeting enterotoxigenic *E. coli* (ETEC) which resulted in several publications and a worldwide patent for an ETEC vaccine (2020). Other previous activities within the field of vaccinology and surveillance of epidemic diseases include participation in planning and implementing the Norwegian national immunisation program for COVID-19 at NIPH (2021–2022), and participation in the national coordination of testing and surveillance of COVID-19 as affiliated to the South-Eastern Norway Health Authority.

Results

The objectives of these 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 core competencies, as set out in the ECDC Fellowship Manual[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

Stockholm, 2025

1. Epidemiological investigations

1.1. Outbreak investigations

1.1.1 A large national outbreak of Serratia marcescens in Norway, 2022-2023

Supervisor: Thale Berg

Category: Healthcare-associated infections and antibiotic resistance

A national outbreak of *Serratia marcescens* cgMLST complex type 755 (ct755) occured in Norway between June 2021 and February 2023 with 74 cases identified. *S. marcescens* is a well-known cause of nosocomial outbreaks, often linked to neonatal wards or intensive care units. The bacteria tend to form biofilms and are capable of surviving on dry inanimate surfaces for weeks to months, and its distribution in the environment is considered ubiquitous. Primary objectives of the outbreak investigation were to characterise the outbreak, identify its source, and ultimately contain transmission. A secondary objective was later established; to rule out a nosocomial source. We defined a confirmed case as a person who tested positive for *S. marcescens* ct755 after 1 January 2021. Careful review of patient journals and interviews were performed, involving 33 hospitals throughout Norway. All hospitals performed whole genome sequencing of available clinical isolates of *S. marcescens* collected between January 2021 and February 2023 (n=455). Cases displayed a pattern of opportunistic infections, as usually observed with *S. marcescens*. No epidemiological links, common exposures or common risk factors were identified. The investigation pointed to an outbreak source likely present in the community. We suspect a nationally distributed product, possibly a food product, as the source. Phylogenetic analysis revealed a highly diverse bacterial population containing multiple distinct clusters. The outbreak cluster ct755 stands out as the largest and least diverse clone of a continuum, however a second cluster (ct281) also triggered a separate outbreak investigation. We were not able to identify the outbreak source, and the investigation was stopped in February 2023. This outbreak investigation encountered particular challenges related to the investigation of an outbreak caused by a low-grade opportunistic pathogen. Our results suggests that the presence of distinct clones of *S. marcescens* in clinical samples is more common than previously recognised.

Role: The fellow was part of the national outbreak investigation team and was main responsible for microbiology. As such he coordinated collection and analysis of microbiological data. He also had the role as national media spokesperson. He participated in data interpretation and contributed to the outbreak report. Furthermore, he coordinated and wrote (as first author) a manuscript submitted to a peer-reviewed journal.

Educational outcome

Participation in this large national prolonged outbreak investigation gave the fellow ample opportunity to gain knowledge on the various aspects of investigative work. He contributed to line listing, descriptive epidemiology, microbiological testing, national coordination and overall strategy for the outbreak work over the entire 16 month period. The fellow was main responsible for microbiology and for interpretation and integration of bioinformatic analysis in the outbreak investigation. Furthermore Arne was national media spokesperson for the outbreak and in the process gained valuable experience in communication with various media. As part of the national outbreak investigation team, with participants from all four Regional Health Authorities, the Norwegian Food Safety Authority and The Norwegian Medicines Agency, contributed importantly to national coordination of the outbreak response. Finally, he led the work with preparing, writing and submitting a manuscript to a peer-reviewed journal about the outbreak (ref nr 1 in list of publications).

1.2. Surveillance

1.2.1 Population dynamics, reservoirs and antimicrobial resistance in non-travel related **Salmonella** *Typhimurium and its monophasic variant, Norway 2018-2022*

Supervisors: Lin Brandal, Umaer Naseer

Category: Food- and waterborne diseases

Salmonella Typhimurium (*S.* Typhimurium) is an important cause of gastroenteritis and occasional cases of extra-intestinal disease. Recently, the serovar referred to as monophasic *S.* Typhimurium has gained attention due to several larger outbreaks and an association with antimicrobial resistance (AMR). Salmonellosis is a mandatory notifiable disease in Norway. We investigated samples of non-travel related *S.* Typhimurium and its monophasic variant in Norway from 2018 to 2022 using whole genome sequence (WGS) data. We sought to identify local reservoirs, analyse seasonality and AMR. We conducted a genomic epidemiologic analysis of 634 human and non-human *S.* Typhimurium and monophasic *S.* Typhimurium isolates that had been subject to WGS at the NIPH and at the Norwegian Veterinary Institute. The primary software tool used for this study was SeqSphere+. The population of *S.* Typhimurium is dominated by sequence type (ST) 19 and the temporal distribution of samples displays a pattern of seasonality with peaks in late autumn and early winter. Clustering of human and non-human samples is common, and the largest human cluster is consistent with transmission from a persisting local reservoir in the

western part of Norway, possibly hedge-hogs. The second largest human cluster is consistent with a food-borne outbreak. Among the monophasic *S.* Typhimurium samples ST34 dominates completely. No clear pattern is seen in the temporal distribution however a few distinct peaks stand out, one which is caused by a large human outbreak in 2022. Only a few small clusters consisting of human and non-human samples are identified, not providing any clear indication of a possible endemic reservoir. Both serovars of *S.* Typhimurium carry AMR, however the situation appears stable throughout the study period. A large proportion (70-90%) of monophasic *S.* Typhimurium carry AMR encoding genes consistent with resistance towards streptomycin, ampicillin, sulfonamide and tetracyline. These findings provide a genomic context that will improve surveillance of *Salmonella* and contribute to timely detection and prevention of future outbreaks.

Role: The fellow was the principal investigator, performed all data entry and data analysis, and wrote the report.

1.2.2 Surveillance of acute flaccid paralysis in Norway

Supervisor: Marianne Bergsaker

Category: Vaccine preventable diseases

Polio surveillance in Norway is an integral part of the global effort to eradicate poliomyelitis, a highly infectious viral disease that primarily affects young children. Norway has been polio-free for five decades, but continuous vigilance is essential to prevent reintroduction and protect public health. The primary aim of the surveillance in Norway is to detect any poliovirus importation early, monitor suspected outbreaks, and maintain polio-free status by ensuring high vaccination coverage and swift response to any suspected cases.

The cornerstone of polio surveillance in Norway is surveillance of Acute Flaccid Paralysis (AFP). This involves identifying and investigating cases of sudden onset of flaccid paralysis in children under 15 years old to rapidly clarify whether polio may be the cause. This approach is crucial for detecting poliovirus, as it targets symptoms directly associated with the disease. Recent results from these surveillance activities have shown no detection of wild poliovirus in Norway, reaffirming the country's polio-free status. High levels of population immunity have been maintained through robust vaccination programs, with routine immunisation coverage consistently exceeding 95%. The continuous absence of poliovirus highlights the effectiveness of Norway's polio vaccination and surveillance strategies. It also underscores the importance of maintaining these efforts to prevent potential outbreaks, especially considering global travel and the risk of virus importation from endemic regions.

Role: The fellow's role in the surveillance has been to participate in review of reported cases of AFP, prepare for and participate in the annual meeting with external experts to evaluate AFP-surveillance in Norway and contribute to reporting to international health authorities.

Educational outcome

The two surveillance projects have given the candidate valuable experience in various aspects of infectious disease surveillance. This includes genomic surveillance and microbial sequence analysis, the interplay between human infections and non-human reservoirs in a one-health context, national and international reporting systems and insights into the mechanisms engaged in a massive global effort of infectious disease eradication.

2. Applied public health microbiology and laboratory investigations

2.1 Molecular and epidemiological characterisation of **Streptococcus pneumoniae** *serotype 24F -an emerging serotype in Norway 2004-2022*

Supervisors: Vegard Eldholm and Brita Askeland Winje
Category: Vaccine preventable diseases

Streptococcus pneumoniae serotype 24F is not included in any licensed vaccines and is associated with serotype replacement following the introduction of pneumococcal conjugate vaccine (PCV13). In this study we investigated the genomic epidemiology of *S. pneumoniae* 24F in Norway and its relationship with the PCV13 vaccine's introduction in 2011. Invasive pneumococcal disease (IPD) is mandatory reportable in Norway. All cases of IPD are reported to the Norwegian Surveillance System for Communicable Diseases (MSIS) and bacterial isolates are sent to the national reference laboratory. We collected epidemiological data on all cases of IPD, regardless of serotype, reported to MSIS between 1 January 2004 and 31 December 2022 (n= 13 152). Furthermore, we analysed all available whole genome sequence data of *S. pneumoniae* serotype 24F (n= 124) to elucidate phylogenetic relationships in terms of Global Pneumococcal Sequencing Clusters (GPSCs) and their associations with virulence. Total cases of IPD have decreased substantially in Norway over the last two decades after the introduction of pneumococcal vaccines, from 1 124 in 2004 to 537 cases in 2022. The decrease was rapid and substantial in the first decade of the study period; total cases of IPD in 2014 was 569. Thereafter an increase in non-PCV13

serotypes have countered the effects of PCV13, giving little overall reduction in IPD after 2015. From the introduction of PCV13 in Norway (in 2011) and until the end of the study period serotype 24F is the most common cause of IPD in children. Cases of IPD due to 24F increased steadily from three cases in 2012 to a peak of 26 cases in 2016. Thereafter cases of IPD due to 24F showed a yearly decline, reaching an all-time-low during the pandemic in 2021. Cases of IPD due to 24F was 23 in 2022, approaching the record high level seen in 2016. Serotype 24F in Norway consists of four distinct sequencing clusters: GPSC6, GPSC7, GPSC16, and GPSC44. GPSC6 predominates, comprising 86% of the Norwegian dataset. *S. pneumoniae* serotype 24F is the most common cause of IPD in Norwegian children over the last decade and should be prioritised for vaccine development. GPSC6 accounts for the bulk part of 24F invasive cases and its genomic epidemiology should be closely monitored.

Role: The fellow was principal investigator and as such main responsible for developing and writing the research protocol and securing ethical approval. The fellow conducted all epidemiological analysis and participated in the bioinformatic analysis. He wrote the draft manuscript to-be-submitted.

2.2 Population structure analysis of **Serratia marcescens***: Outbreaks versus pseudo-outbreaks*

Supervisor: Vegard Eldholm
Category: Healthcare-associated infections and antibiotic resistance

Norway experienced a large national outbreak of *Serratia marcescens* that was investigated from October 2022 to February 2023. Two distinct strains of *S. marcescens* MLST complex type (ct) 755 and ct281 were detected across various health facilities, resulting in a total of 74 and 26 cases respectively. The epidemiological investigations, including patient data analysis and interviews, failed to pinpoint a common source of infection. The complexity and inability to identify the source of the outbreak warranted additional microbiological genomic investigation. A total of 455 genomes of *S. marcescens* were sequenced and analysed in the context of the outbreak investigation. Aligned whole-genome assemblies were used as a starting point to generate a genome-wide SNP-based phylogenetic tree. The median genetic distance within the main outbreak cluster (ct755) was seven SNPs with all samples included and five SNPs when nanopore sequenced samples were excluded, demonstrating limited sequence diversity within the cluster. Samples from every health region were found in the ct755 cluster with no apparent link between genetic relatedness and geographic origin. This might suggest that a product contaminated by a common source had been distributed repeatedly across the country. In addition to the ct755 outbreak cluster phylogenetic analyses also revealed the presence of two other relatively large clusters of isolates corresponding well with cgMLST classification as ct281 and ct833. These three largest clusters together accounted for 21% of all samples. In light of the population structure of all 455 sequenced *S. marcescens* genomes, ct755 appears less unique than initially perceived -the cluster rather emerges as the largest and least diverse clone of a continuum. Our observations suggest that the temporary presence of distinct clones of *S. marcescens* in clinical samples may be a relatively frequent phenomenon.

Role: The fellow was main responsible for microbiology during the outbreak and participated in bioinformatic analysis and interpretations. He participated in writing the outbreak report and he wrote a manuscript on the outbreak and the laboratory investigation that has been submitted to a peer-reviewed journal (ref nr 1 in list of publications). The population structure analysis was also presented at two different scientific conferences as oral presentations: ECCMID 2023 (15-18 April, Copenhagen, Denmark) and National Consortium for Microbial Genomics Meeting 2023 (December 7th Oslo, Norway).

Educational outcome

The public health microbiology and laboratory investigations provided a framework for the fellow to deepen his knowledge and expand his skills on a wide range of topics. This included all the steps in the development of a research protocol and going through the entire process of gaining ethical approval for a clinical research study, conducting epidemiological analysis of a large dataset using R and familiarising himself with various bioinformatic tools including SeqSphere. Furthermore, the microbiological analyses involved interpretation of phylogenetic trees and application of various bacterial typing schemes such as cgMLST, GPSC and SNP-based approaches. On a more general level these projects contributed to a deeper understanding of public health research integrating the fields of epidemiology, microbiology and bioinformatics.

3. Biorisk management

Duty national preparedness laboratory (BSL-3/4)

The Norwegian Institute of Public Health operates a 24/7 duty function with national responsibility for managing highly pathogenic organisms at the National Preparedness Laboratory. This crucial function requires participants to be trained medical microbiologists or infectious disease specialists and serves as a third-line reference for diagnostic microbiological laboratories across Norway. Key responsibilities include conducting risk assessments, managing bio-risks, and performing practical arrangements and analyses of biological samples requiring BSL-3 or BSL-4 facilities. The duty also involves the critical task of communicating and managing situations when highly pathogenic microbes are identified or suspected, ensuring that accurate and timely information is provided to various stakeholders. The fellow has participated in the national preparedness duty during the fellowship, with week-long duties occurring every six to eight weeks.

Risk assessment multidrug resistant *Mycobacterium Tuberculosis*

This group exercise, part of the Biorisk and Quality Management module assignment, aimed to assess the biosafety risk of working with multidrug resistant tuberculosis (MDR TB) in a laboratory using the Biosecurity Risk Assessment Methodology (BioRAM) tool. Using information about the pathogen, the work type, and the laboratory environment from the provided scenario, the group discussed and completed the BioRAM sections. We assessed the risk to individuals performing in vitro work and to the broader community, including animals. The module's questions provided a quantitative estimate of transmission likelihood and infection severity. The group, including the fellow, submitted their risk assessment results after completing the exercise in an online meeting.

Educational outcome

The primary learning outcomes for the fellow were: Gaining expertise in bio-risk management and risk assessment for highly pathogenic organisms, developing practical skills in handling and analyzing biological samples under high-containment conditions, and sharpening communication skills for effectively managing and conveying information about highly pathogenic microbes to diverse audiences. Additionally, Arne further developed his ability to provide third-line reference support to diagnostic microbiological laboratories.

4. Quality management

A national External Quality Assessment (EQA) on HIV and Hepatitis E

Supervisor: Rikard Rykkvin

In Norway the *National Forum for Medical Microbiology* coordinates the country's clinical microbiological laboratories, organising biannual meetings and annual strategic sessions. They are responsible for national External Quality Assessments (EQAs) which complement international EQAs. In virology, Norway conducts two annual EQAs, one focusing on influenza and one on various serological tests. For 2024, the EQA will focus on Hepatitis E and HIV and be distributed to 22 laboratories. Hepatitis E is highlighted due to recent diagnostic assay developments in nine laboratories, while HIV is crucial for blood donor screening. The EQA's goal is to challenge the diagnostic procedures of participating laboratories and ensure national standardisation. It evaluates laboratory performance, standardises analytic results, and ensures consistent communication of results to clinicians. The Norwegian Institute of Public Health (NIPH) manages the EQA, where the fellow actively participated in organising the EQA in virologic serology for 2024. Samples are typically prepared by diluting strong patient samples to just above test cut-off limits and using potentially cross-reactive serums for negative controls. For instance, a negative Hepatitis E sample was prepared using serum positive for Epstein-Barr Virus (EBV) to test for potential analytical cross-reactivity. Laboratories receive 1ml of each test sample and have three weeks to report results to NIPH, including details on analytic instruments, assays, and kits used. NIPH evaluates the results, compiling a final report that includes performance analysis of each laboratory and analytic platform. This report helps identify trends and provides a gold-standard for test results. This EQA aims to be distributed in August/September 2024, promoting national standardisation and enhancing diagnostic accuracy for Hepatitis E and HIV in Norway's clinical microbiological laboratories.

Role: The fellow participated in the working group at NIPH that prepared the samples and the accompanying patient stories. The fellow summarised the work in a report.

Internal laboratory audit of the National Reference Laboratory for *Corynebacterium spp.* and *Streptococcus pneumoniae* at the NIPH

Supervisor: Ragnhild Bardal Roness

The audit was performed at Unit 5 (*Corynebacterium spp. and Streptococcus pneumoniae*) of the National Reference Laboratory (NRL) at the Norwegian Institute of Public Health after the Biorisk and Quality Management Module. The aim was to practice application of the BioRam tool, as well as increasing the fellows understanding of the procedures and documentation involved in a laboratory audit.

The assessment of the unit yielded good scores but indicated room for improvement in process management and quality Control as well as documentation. Internal quality control was assessed as 'no' for all analyses. This is because the inclusion of an internal quality control at the laboratory is assessed based on the frequency and type of analysis to be conducted. For some analyses, the internal quality control is performed weekly, whereas others are performed daily. In terms of sample documentation, no details on the time of sampling are recorded. This is because the NRL is not a primary laboratory and only works with referred samples. In terms of documentation, this exists only digitally, although this is readily available for printing when necessary. We identified that stock documentation does not exist. While the NRL has regular deliveries of material and all entry and use of material is recorded, the actual stock is unknown and is reported to be ordered by eyeballing its availability. We recommend the implementation of stock documentation to avoid unnecessary delays in sample processing or testing in times of increased workflow for Unit 5 pathogens. Only authorised persons have access to the laboratory, all rooms are well organised for laboratory work, and all activities in the laboratory are very well documented. Overall, the audit team concluded that the laboratory successfully passed the internal audit.

Role: The fellow conducted the internal audit together with the other C2022 EUPHEM fellow at the institute. Assessment, interview of laboratory personnel, evaluation and analysis using the BioRam tool was a collaborative effort.

Educational outcome

Through the EQA and the laboratory audit the fellow gained insights into the organisation of EQAs in Norway and in important aspects of laboratory quality assurance and quality management. This included an understanding of the goals of a national EQA and the strategy for making a good test. He gained knowledge about all the steps involved in planning and preparing a national EQA in virology, including the workflow and the methodology required to prepare positive and negative samples for further assessment by medical laboratories. Furthermore, he gained insights into the systems required for documentation and for maintaining accuracy, reliability and consistency in a clinical microbiological laboratory.

5. Public health microbiology management

Duty Epidemic Intelligence

The Norwegian Institute of Public Health has a duty function which receives, handles, organises and internally distributes all incoming alerts, warnings and reports concerning outbreaks and threats relating to infectious diseases. The incoming correspondence mainly originates from public health officers around Norway, ECDC and WHO. The duty also includes coordination tasks and drafting of a weekly report that summarises all relevant incidences and outbreaks. The duty lasts for a week at a time during regular working hours and is typically scheduled every 5-6 weeks for those involved. Arne received training and subsequently participated in the Epidemic Intelligence duty at NIPH for 9 months.

Main responsible for microbiology in a large national outbreak

During the investigation of the outbreak with *Serratia marcescens* (see section 1) which lasted for 16 months, the fellow was main responsible for microbiology. As such he coordinated collection and analysis of all microbiological data. This included strategy for collection of microbiological data from the 22 diagnostic laboratories in Norway and leading the interpretation of microbiological analyses and integration of bioinformatic analysis during the investigation. The national outbreak investigation team had participants from all four Regional Health Authorities, the Norwegian Food Safety Authority and The Norwegian Medicines Agency in addition to the participants from NIPH. As key member of the team at NIPH Arne contributed importantly to the national coordination of the outbreak response.

Co-supervisor PhD on *Leishmania spp.*

Starting in 2020 and continuing throughout the entire fellowship Arne has served as co-supervisor for a PhD candidate -a colleague who is a medical doctor, infectious disease specialist, and medical microbiology specialist. The PhD project is entitled *Point of care detection, molecular typing and antimicrobial resistance in Leishmania in high endemic countries.* The fellow has been involved in the project since its early stages, contributing to the planning and writing of the project proposal and securing funding from the South-eastern Norway Health Authority. As the main applicant for funding, Arne was the formal project leader until summer 2023, when this responsibility was transferred to the candidate's main supervisor. The formal tasks as project leader included budgetary responsibilities and all formal communication with the funding agency, including yearly progress reports. The scientific tasks as co-supervisor include maintaining close contact through regular meetings with the candidate, providing feedback and supervision on laboratory experiments, guiding the preparation of an abstract and poster for ECCMID 2023, advising on the development of the first manuscript (ongoing), and participating in establishing international collaboration with partners in Ethiopia and India. The PhD project is now at a stage where a LAMP assay has been successfully developed for quantification of Leishmania parasites, an achievement that has not previously been reported. The first manuscript to be part of the PhD is currently under preparation and a field visit to project partners in India autumn 2024 is being planned.

Educational outcome

Overall, the above-mentioned activities have provided the fellow with broad management experience at the institutional level, at the national level and in academia. He has participated in the management of critical outbreak-related information and efficiently coordinated communication among public health officers. Furthermore, he has engaged in internal epidemic intelligence coordination tasks at the NIPH, thereby exposing him to outbreak work, communication, and risk assessments one a wide range of infectious diseases. Finally, Arne has engaged in a supervising role for a PhD candidate, thereby gaining experience and insights regarding planning, managing and follow-up of a scientific project with partners in two developing countries.

6. Teaching and pedagogy

Co-supervisor PhD on *Leishmania spp.*

Starting in 2020 and continuing throughout his fellowship, Arne has co-supervised a PhD candidate, a medical doctor and infectious disease specialist, on a project entitled *Point of care detection, molecular typing, and antimicrobial resistance in Leishmania in high endemic countries*. Arne has been integral to the project's development, contributing to planning, proposal writing, and securing funding from the South-eastern Norway Health Authority. His supervisory role includes regular meetings, feedback sessions, and addressing the candidate's learning needs in experimental setup, molecular assays, and research methodologies. The candidate is currently drafting her first manuscript, focusing on structuring the paper, scientific figure creation, and clear scientific writing. Arne has provided scholarly articles, laboratory protocols, and tailored guidance to support the candidate. Regular meetings and virtual discussions have facilitated active participation, encouraging the candidate's engagement and leadership in experimental design and international collaboration.

Eradication of infectious diseases through vaccination: Smallpox and Polio

Linked to his participation in surveillance of acute flaccid paralysis (AFP) in Norway (see section 1.2) Arne prepared and held a lecture on eradication of infectious diseases through vaccination for senior staff at the NIPH. The lecture focuses on the historical context, strategies employed, and challenges faced in the eradication of smallpox and the ongoing efforts to eradicate polio. The lecture highlights differences between the two pathogens and the particular challenges associated with eradication of each disease the goal of extinction of the two pathogens. For polio in particular the various vaccines were discussed, pros and cons of live attenuated vaccines, and the impact of circulating vaccine-derived polio viruses in the global eradication effort.

Educational outcome

Supervision of the PhD candidate allowed Arne to engage actively in teaching and training, both to facilitate the development of advanced laboratory skills and to provide guidance and mentorship in project planning, research proposal writing, writing of abstracts and manuscript preparation. The interaction, feedback and continuous dialogue with the PhD-candidate allowed Arne to enhance and refine his supervision skills. Lecturing senior staff at NIPH provided a unique opportunity to gain deep knowledge on the complex topic of infectious disease eradication and the successes and pitfalls of the various vaccination strategies employed to target smallpox and polio.

7. Communication

7.1 Media spokesperson in a large national outbreak

From October 2022 and onwards the fellow participated in a national outbreak team investigating a large outbreak of *Serratia marcescens* in Norway. He was part of the coordinating investigative team at the Norwegian institute of public health, was main responsible for microbiology and served as national media contact person. This involved the preparation of two national press-releases with information about the outbreak and interview with one national newspaper. Additionally, the fellow had close collaboration with the public relations department at the institute to shape and quality check the communication between the institute and the regional health authorities and their respective public relations offices. Furthermore, Arne was responsible for two alerts about the outbreak posted in ECDC's Early Warning and Response System (EWRS). The outbreak has been summarised in an outbreak report, and a manuscript is under preparation.

7.2 Publications related to the EUPHEM fellowship

7.2.1 Manuscripts published in peer-reviewed journals

1. **Arne M. Taxt,** Vegard Eldholm, Nicola Isabelle Kols, Maria Schei Haugan, Niclas Raffelsberger, Anne Mette Asfeldt, André Ingebretsen, Anita Blomfeldt, Kristin Stenhaug Kilhus, Paul Christoffer Lindemann, Horst Bentele, Jeanette Stålcrantz, Liz Ertzeid Ødeskaug, Thale Cathrine Berg and The Norwegian Serratia study group. A national outbreak of *Serratia marcescens* complex: investigation reveals genomic population structure but no source, Norway, June 2021 to February 2023. Euro Surveill. 2025;30(5):pii=2400291. https://doi.org/10.2807/1560-7917.ES.2025.30.5.2400291 Available at: https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2025.30.5.2400291

2. **Arne M. Taxt,** Vegard Eldholm, Caroline Knudsen, Brita Askeland Winje, Magnus Osnes. Molecular and epidemiological characterization of *Streptococcus pneumoniae* serotype 24F – an emerging serotype in Norway 2004–2023. Manuscript in preparation.

3. Magnus Osnes, **Arne M. Taxt**, Caroline Knudsen, Vegard Eldholm. Genomic Epidemiology of *Streptococcus pneumoniae* serotype 24F in Norway and Global Pneumococcal Sequencing Cluster 6 internationally. Manuscript in preparation.

7.3 Conference presentations

1. ECCMID 2023, 15-18 April, Copenhagen, Denmark: A national outbreak of Serratia marcescens in Norway: Genomic epidemiology reveals population structure but no source (Oral presentation).
2. National Consortium for Microbial Genomics Meeting 2023, December 7th Oslo, Norway: A national outbreak of Serratia marcescens in Norway: Genomic epidemiology reveals population structure but no source (Oral presentation).

7.4 Other presentations

Infectious Disease Surveillance seminar Norwegian Institute of Public Health, Oslo, Norway: Behov for infrastruktur for mikrobielle gensekvenser (Oral presentation, in Norwegian).

8. EUPHEM modules attended

1. Introductory Course, 26 September to 14 October 2022, Spetses, Greece
2. European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2022, 23–25 November 2022, Stockholm, Sweden
3. Outbreak Investigation, 5–9 December 2022, Berlin, Germany
4. Biorisk and Quality Management, 16–17 March 2023, virtual
5. European Congress of Clinical Microbiology and Infectious Diseases (ECCMID) 2023, 15–18 April 2023, Copenhagen, Denmark
6. Multivariable Analysis, 22–26 May 2023, Frankfurt, Germany
7. Project Review Module 2023, 28 August to 1 September 2023, Lisbon, Portugal
8. European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2023, 22–24 November 2023, Barcelona, Spain
9. Time Series Analysis, 11–15 December 2023, Rome, Italy
10. Rapid Assessment and Survey Methods, 15-19 April 2024, Dublin, Ireland
11. Public health microbiology III – Whole Genome Sequencing & Bioinformatics, 3–7 June 2024, Vienna, Austria
12. Management, Leadership and Communication in Public Health, 24–28 June 2024, Stockholm, Sweden
13. European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) 2024, 20–22 November 2024, Stockholm, Sweden

9. Other training

Not applicable.

10. International assignments

The fellow did not participate in any international assignment during the fellowship.

11. Other activities

During the fellowship the fellow has participated in the following additional activities at NIPH:

- National vaccination and surveillance of invasive pneumococcal disease
- Mapping needs for a national IT-infrastructure for microbial sequence data

Acknowledgements

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Throughout the two years excellent guidance has been provided by ECDC frontline coordinators Aftab Jassir and Aura Aguirre-Beltran. Thank you for good discussions, pointing me in the right direction, keeping an eye on my progress and always being available and supportive when needed. Also, to the project supervisors and collaborators: Thale Berg, Lin Brandal, Umaer Naseer, Brita Winje, Vegard Eldholm, Magnus Osnes, Caroline Knudsen, Camilla Sekse and Bjarne Bergsjø. I very much appreciate your scientific input and the novel insights that arise within cross-sectoral projects. Hopefully we will continue our collaborative effort well beyond the fellowship.