

DNA sequencing data analysis to uncover the role of the microbiome in the development of Red Mark Syndrome lesions in rainbow trout (Oncorhynchus mykiss)

treatments for animal health.

Home Institute: Technical University of Denmark (DTU) Aqua, Denmark

Mission hosting institute: Swedish University of Agricultural Sciences (SLLI) Sweden

of Agricultural Sciences (SLU), Sweden **Duration of mission:** 1 month

## **Summary**

The STM aimed to advance the participant's microbiome data analysis skills and to investigate the microbial dynamics underlying Red Mark Syndrome (RMS) in rainbow trout, an economically important disease in aquaculture whose causative agent has remained uncertain.

During the STM, advanced bioinformatic workflows were applied to 16S rRNA amplicon sequencing and shotgun metagenomics datasets. The activities covered the full workflow of microbiome data analysis, from raw sequencing reads to the interpretation of results and the initial drafting of a scientific publication. The analysis revealed that a Midichloria-Like Organism (MLO) was consistently and significantly enriched in active RMS skin lesions, strongly supporting its role as the primary pathogen. Metagenomic analyses of MLO-abundant samples facilitated the assembly of the first complete genome of this intracellular bacterium. Transient microbial shifts indicating opportunistic dysbiosis were also observed. These studies have led to significant progress in interpreting complex microbial community dynamics in RMS and identifying a likely primary pathogen. These findings have immediate relevance for aquaculture health research, but also have potential applications in the development of diagnostics, and disease prevention strategies.

The mission not only provided specialised training in sequencing data analysis, but also fostered a strong research collaboration between DTU and SLU, two existing EUP AH&W partners. The results obtained during the STM were presented at the international conference FEMS MICRO (July 2025, Milan, Italy) and will form the basis of two forthcoming scientific manuscripts, focusing respectively on 16S rRNA microbial dynamics and MLO genome characterisation. Overall, the STM contributed substantially to the achievement of the PhD research objectives, the strengthening of international scientific exchange, and ongoing efforts to advance microbial ecology research in support of aquatic animal health.

🇲 🇲 I am truly thankful to the EUP AH&W for supporting this mission, and to my host Fernando for the truly inspiring mentorship, constructive feedback, and for making me feel part of the team during my stay. This Short-Term Mission (STM) was one of the most useful and encouraging experiences in my PhD so far, significantly advancing my project and giving me the chance to reconnect with this exceptionally supportive and collaborative research group.

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