INSTITUTIONEN FÖR BIOLOGI
OCH MILJÖVETENSKAP

Masters’ presentations in biology

Schedule & abstracts

Thursday August 28, 2025

At “Energin” (room 2123). The presentations can also be followed via Zoom.

Note! Times below are approximate (except for first presentation)

8.30 **Nayomi Edirisinghe** (MABI20, 60 hp, Nordic Master's programme in sustainable production and utilization of marine bioresources)

Underwater video–based habitat mapping in Swedish waters: Comparing trawled vs non-trawled areas for active restoration

Opponent: Elvira Hagman

Coffee break ca. 9.25

9.45 **Elvira Hagman** (Conservation biology, 30 hp)

Protecting biodiversity across land and sea: Opportunities for comparative life cycle assessment metrics

Opponent: Márcia Eriksson

10.30 **Márcia Eriksson** (Physiology & cell biology, 60 hp)

Identification of clinically relevant strains of the Str*eptococcus miti*s group based on sequences comparisons of housekeeping genes 16S rRNA, *groEL*, and *rpoB*

Opponent: Nayomi Edirisinghe

Welcome!

Abstracts

Underwater video–based habitat mapping in Swedish waters: Comparing trawled vs. non-trawled areas for active restoration

Kapugampatha Edirisinghe Arachchige Nayomi Edirisinghe (MABI20, 60 hp)

Supervisors: Laurenz Thomsen, Department of Marine Sciences, University of Gothenburg, Jonathan Roques, Department of Biological and Environmental Sciences, University of Gothenburg
Examiner: Kristina Snuttan Sundell

Underwater video transects (UWTV) from two sites in Swedish waters—deep offshore Bratten MPA (~250 m) and shallow Gullmarsfjorden (~30 m) were analysed. The objectives are to quantify species densities, habitats, and seafloor structure across trawled vs non-trawled areas, and to compare trainee–expert annotations for restoration-oriented, non-invasive monitoring. Three 15-min transects per area (Bratten-trawled, Bratten-non-trawled, Gullmarsfjorden-shallow; n = 9) were annotated in BIIGLE; counts were converted to densities (ind./0.1 ha) and compared with t-tests across trawling status, sites, and annotators. Expert vs. trainee annotations showed a significant difference in species-density estimates for non-trawled segments ($p < 0.05$), but not for trawled segments; OSPAR-listed taxa exhibited no trainee–expert differences across sites. In Bratten, sea pen *Funiculina quadrangularis* averaged ~4,098±594 ind./0.1 ha in non-trawled grounds vs ~323±457 ind./0.1 ha in trawled grounds; *Stylatula elegans* and *Ophiura sarsii* displayed similar depressions with trawling, whereas *Pectinidae* were relatively more frequent in trawled areas. In Gullmarsfjorden, sea-pen communities were present but patchy (*Pennatulacea* ~1,845 ± 1,660 ind./0.1 ha; *F. quadrangularis* ~120 ± 73 ind./0.1 ha), and there were organic-rich muds and weak bottom currents. OSPAR species densities were broadly similar between sites, though high variance and small sample sizes limit statistical power. Overall, trawled areas exhibited simplified community composition, while non-trawled areas held higher densities of sensitive taxa. This finding suggested that trawling bans would help with the recovery and active restoration. The workflow gives precise, updatable baseline data for MPA management and will add AI-ready labels to train object-detection models in the DIGI4ECO framework.

Keywords – Trawling, Non-trawling, Sea-pens, OSPAR, Benthic, REDRESS

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Protecting biodiversity across land and sea: Opportunities for comparative life cycle assessment metrics

Elvira Hagman (Conservation biology, 30 hp)

Supervisors: Sara Hornborg, RISE Research Institutes of Sweden and Thomas Dahlgren, Department of Marine Sciences, GU
Examiner: Karin Hårding

Biodiversity is invaluable to human well-being, yet it is declining at a rate faster than ever in human history, where one major driver is food production. Assessing the biodiversity impacts of foods is therefore critical, but current life cycle assessment methods focus mainly on terrestrial systems, limiting comparisons between agricultural products and seafood. This thesis explores if and how a leading terrestrial biodiversity assessment framework (Scherer et al., 2023) can be adapted for marine environments, and specifically to Norwegian Atlantic salmon farming as a case study. The methodological framework was broken down into eleven components and evaluated for applicability in marine environments through a narrative review. Insights on local salmon farm impacts were obtained through a systematic literature review and through analysing publicly available monitoring data. All components proved applicable, though several ecological differences need to be considered, and substantial needs for region-, species-, and activity-specific data were identified. The case study on Norwegian salmon farming informed six components of the framework, most importantly highlighting spatial aspects of species richness impacts and priority taxa for initial assessments. Although both the terrestrial framework and its potential marine adaptation simplify complex realities, applying them with the best available data may still generate valuable insights. Advancing these approaches is crucial for making biodiversity impacts visible and guiding more sustainable food production.

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Identification of clinically relevant strains of the *Streptococcus mitis* group based on sequences comparisons of housekeeping genes 16S rRNA, groEL, and rpoB

Márcia Eriksson (Physiology & cell biology, 60 hp)

Supervisors: Edward Moore, Liselott Svensson and Francisco S. Serra, Department of biomedicine, GU
Examiner: Henrik Nilsson

The *Streptococcus mitis* group (SMG) is considered to have closely related species, making it often difficult to distinguish them from each other. It represents a significant challenge for both taxonomy and the routines by clinical diagnostics laboratories. Precise identification of SMG members is crucial, once that it contains high pathogenic species, such as *S. pneumoniae* and *S. mitis*, which are major causes of invasive infections worldwide. Misidentification can lead to wrong antimicrobial therapy and contribute to the development of antimicrobial resistance. While single-gene sequencing methods, such as 16S rRNA gene analysis, are widely applied, it is not recommended for identification of species of the SMG because of their limited discriminatory power. In this study, 33 bacterial strains isolated from clinical samples, previously classified by the Culture Collection Gothenburg University (CCUG), as *S. mitis* or *S. mitis* complex or *S. mitis*-Group, were analyzed using multi-locus sequence analysis (MLSA) with three housekeeping genes: 16S rRNA, *groEL*, and *rpoB*. Of these, 31 strains produced high-quality 16S rRNA gene sequences, while 30 yielded reliable sequences for groEL and rpoB. Comparative analysis against GenBank references revealed that 16S rRNA gene alone was insufficient for species-level resolution due to the high sequence similarity among SMG members. In contrast, groEL and rpoB provided greater discriminatory power, particularly when used in combination. The results in this study highlight the importance of MLSA as a robust method for accurate SMG identification, demonstrating that the combination of multiple housekeeping genes significantly improves resolution compared to single-gene approaches. The implementation of such strategies in diagnostic microbiology can raise knowledge about SMG's functional structure, improve clinical decision-making in health care, strengthen epidemiological surveillance, and reduce the risks associated with antimicrobial resistance.

Keywords: Streptococcus Mitis-Group, MLSA, 16S rRNA gene, groEL, rpoB, bacterial identification, housekeeping genes, antimicrobial resistance.

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