

Cleaning the cleaner fish: Managing the microbiome of lumpfish in hatcheries

Supervisory team:

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Project description:

Sea lice represent a severe commercial burden to salmon farming world-wide. These ectoparasites can cause damage to fins, gills, and skin, which leave the fish more vulnerable to other infections. Moreover, lice infestations in farmed salmon pose a risk to wild stocks, primarily through the dispersal of eggs and larval stages. As there are limited effective therapeutics to control salmon lice, there is increasing emphasis on biocontrol using cleaner fish, in particular wrasse and lumpsucker, which efficiently graze on the lice. However, cleaner fish health and welfare has recently itself also become a focus of attention. Microbial diseases represent one of the main threats to the sustained use of cleaner fish, and significant problems have been found with use of wild-captured wrasse and lumpfish attributable to bacteria. This has led to a strong move to rear lumpfish from eggs in hatcheries to reduce dependence on wild stocks. A particularly important issue is survival during larval rearing of lumpfish, where losses can often be both unpredictable and high. This PhD will help to characterise the development of the microflora of developing lumpfish, with the aim of identifying potential pathogens and beneficial microbes in the lumpfish rearing environment. By seeking to understand how these bacteria interact with each other, and with the fish host, we will develop and trial various microbial control strategies (probiotics or prebiotics) to improve lumpfish health. We will also characterise these bacterial communities at a genetic level using next-generation sequencing technology in order to identify key species / strains or individual genes which may either contribute to disease in the host, or else have beneficial (protective) qualities. The project will also consider recent evidence that the microbiome influences host behaviour by examining how whether feeding patterns are impacted by microbial flora. The data will be incorporated into a mathematic model aiming to describe and predict likely interactions between different bacteria within the microbial community, and between bacterial communities and the hosts (including disease onset) under different husbandry conditions.

