

CHARACTERISATION OF THE GUT MICROFLORA IN RAINBOW TROUT FRY (*ONCORHYNCHUS MYKISS*) USING DEEP-SEQUENCING

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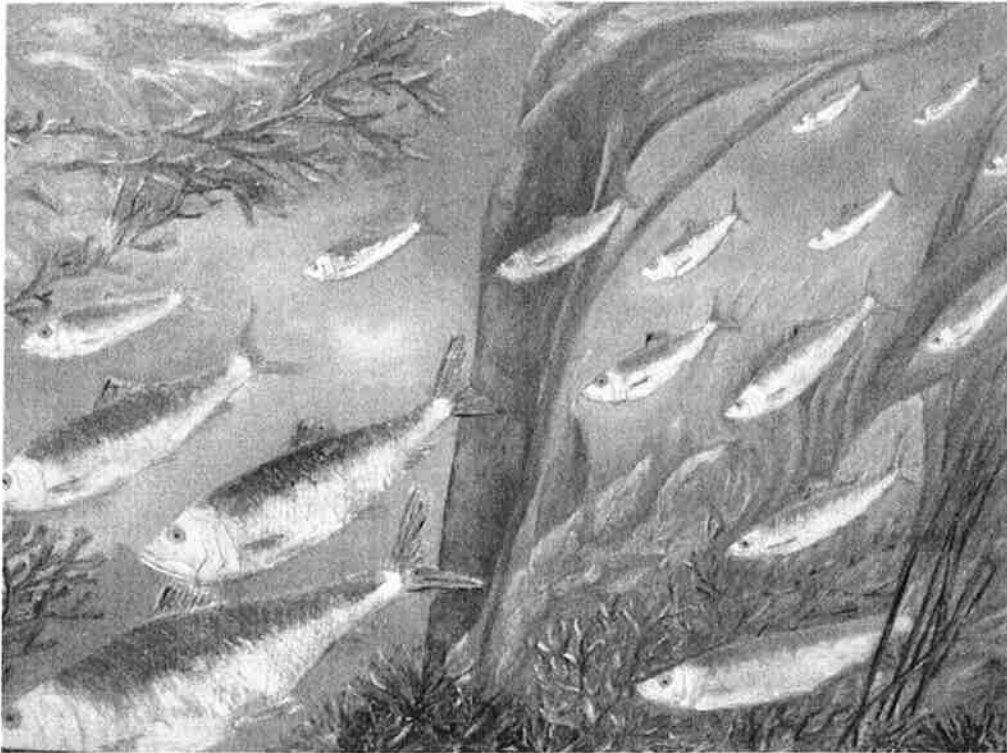
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For many years it has been known that the bacterial microflora in the gut of warm-blooded animals exists in harmony with the host and exert various beneficial effects on the health by their metabolic activities. Hence, the gut microbiota has a high importance for the animal. In many studies from *e.g.* humans and the pig mapping of the bacterial flora from the gut have shown dominance by some specific bacterial groups, and this bacterial profile is termed as a 'core microbiota'. For lower vertebrates like fish mapping of the bacterial flora in the gastrointestinal system is to date a relatively new research field and previous studies have mainly been done on bacterial species that can be cultured or by classical molecular techniques like T-RFLP and DGGE. In the last recent years deep-sequencing techniques have enabled sequencing and mapping of entire microbial communities from for instance an environmental sample or a tissue / fecal sample from an animal. These metagenomic studies have provided new and deeper insight into the microbial ecology and the influence of the microbiota in warm-blooded animals.

In this study next-generation sequencing of the 16S rDNA gene on the Illumina HiSeq platform was used to examine the composition of the microbial flora in the gut of rainbow trout (*Oncorhynchus mykiss*) fry. The fish were examined before and after first-feeding and after administration by commercial probiotic lactobacilli to the feed.

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