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Publication date:
2012

Document Version
Publisher's PDF, also known as Version of record

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The gut microbiota in rainbow trout changes after first feeding and is dependent on the type of diet

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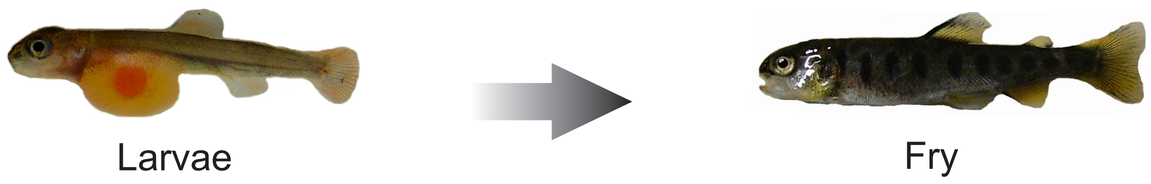
INTRODUCTION

In the very first life stage of most fish species nutrition only comes from a yolk sac originating from the egg. During this larval phase the intestine is being formed and becomes functional as the amount of yolk sac protein is used up and feeding from external sources then slowly takes over. Thus, this developmental window is a good model to study the influence of feeding on the gut microbiota dynamics. Further, the origin of the feed sources may also influence the microbial community.
In this study we examined this in the commercially produced species rainbow trout (*Oncorhynchus mykiss*) using next-generation sequencing.



External food intake initiates during the metamorphosis from larvae to fry when yolk sac is depleted

OBJECTIVES

i) To examine the microbiota in the intestine of rainbow trout before first feeding.

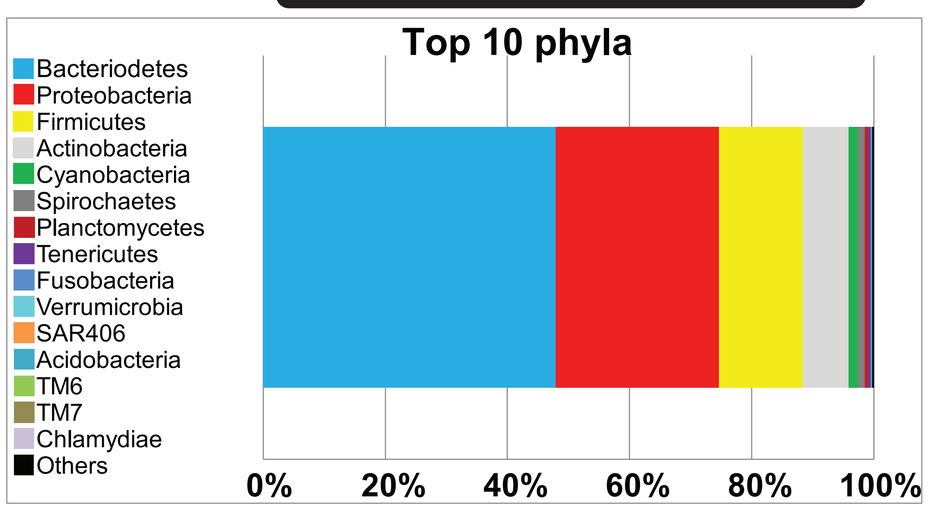
ii) To study the impact on the intestinal microbiota after giving feed to the fish of either marine or plant origin.

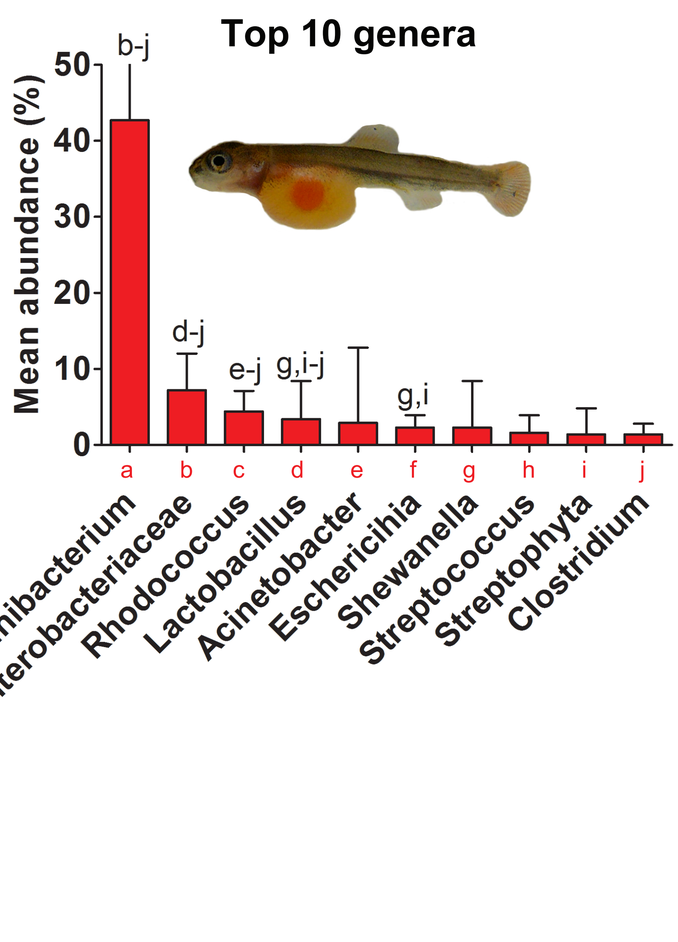
CONCLUSIONS

i) The intestinal community changed from a Bacteriodetes dominated towards a Proteobacteria and Firmicutes dominated microbiota in connection to first feeding. The bacterial flora before first feeding may reflect the one present in the surrounding water.

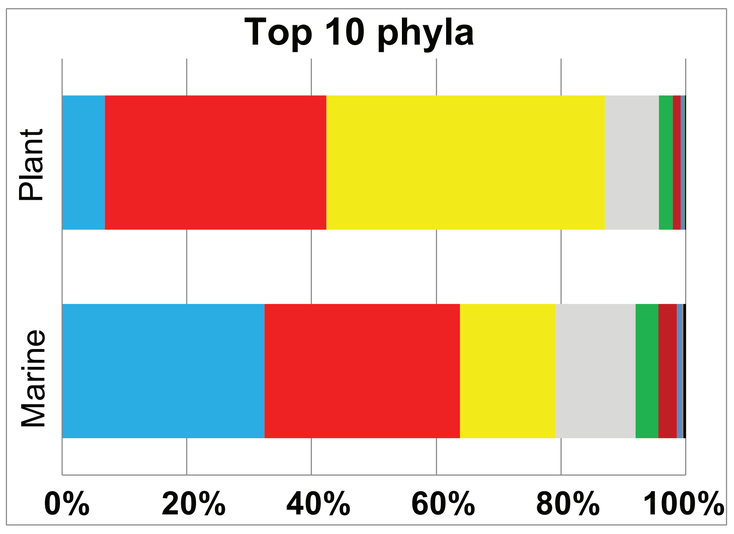
ii) Fish fed a plant based diet had a higher ratio of Firmicutes relative to marine fed fish. Among these, there was a higher amount of the genera *Streptococcus*, *Leuconostoc* and *Weissella* in fish fed a plant based diet compared to a marine diet.

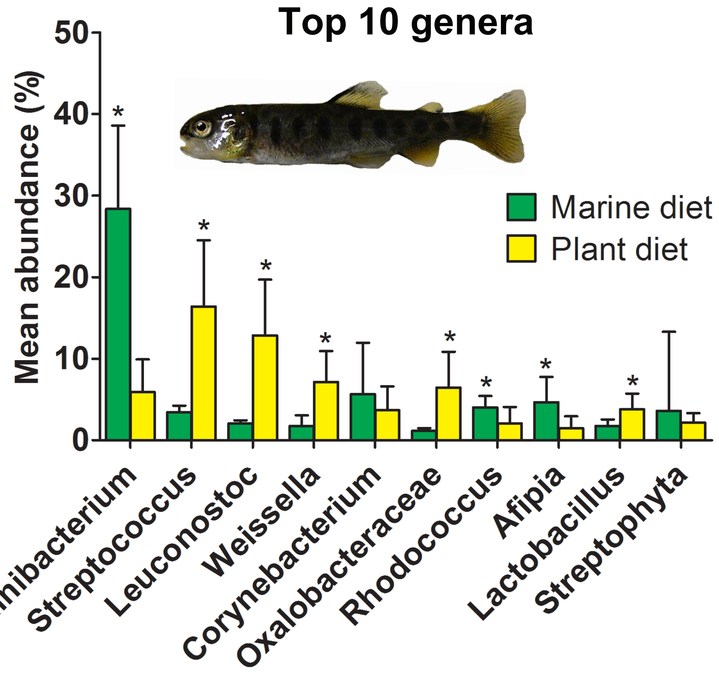
1 day before first feeding



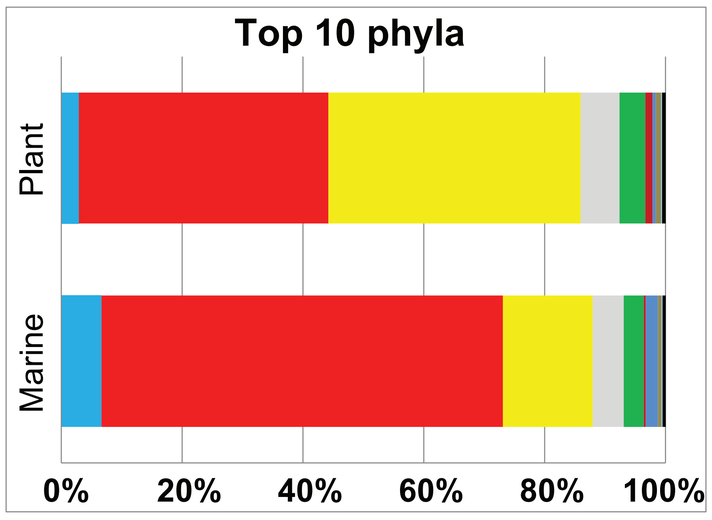


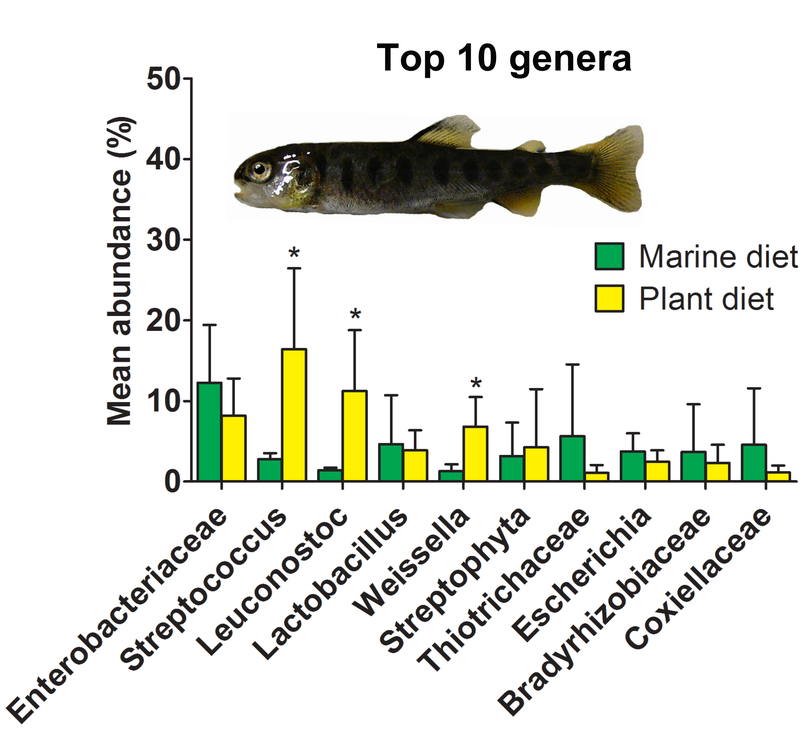
26 days post first feeding





49 days post first feeding





MATERIALS & METHODS

Intestines from experimental fish were collected for analysis 1 day before first feeding (n=31), 26 (n=40) and 49 (n=43) days post first feeding. Mean size of sampled fish was 0.12 g, 0.31 g and 1.08 g at the three sampling points, respectively. The fish collected at days 26 and 49 had been fed a) commercial diet of marine origin (Inicio, Biomar A/S) or b) tailormade diet containing plant parts; rapeseed oil (instead of fish oil as in Inicio) plus pea proteins. DNA was extracted from the intestines and subsequently used for PCR by universal barcoded primers targeting the V5 region of the 16S rDNA gene. Sequencing was conducted on the Illumina HiSeq 2000 platform. Obtained sequences were sorted and normalised by BION-meta software[1]. Taxonomic classification was according to the Greengene database.

REFERENCES

1. Larsen N., Ingerslev H.-C., Molbak L., Ahrens P. and Boye M. ftp://genomics.dk/pub/BION. BION-meta, a 16S/23S sequence classification pipeline. *In preparation*.

This project was funded by The Danish AgriFish Agency, Ministry of Food, Agriculture and Fisheries. The project (OPTIFISH) is a part of the research programme Organic RDD, which is coordinated by ICROFS (Project ID: 3405-10-OP-000128).