Rearing water treatment influences the microbiota and transcript profiles of cod larvae

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Microbial stability in aquaculture

In aquaculture facilities, fish share their environments with high loads of microorganisms. Negative microbe-fish interactions have been found to reduce both the growth and survival of marine fish larvae. More favourable and stable microbial environments can be obtained through well-designed water treatment systems.

Does the water treatment system influence cod larval microbiota and gene expression?

Results

Water treatments:
RAS and FTS

- Different water microbiota (DGGE)
- Different larval microbiota (pyrosequencing)
- Different transcript profiles

RAS

- *Vibrio* and *Marinomonas* abundant

FTS

- *Arcobacter* abundant
- Microbial-response genes upregulated

Microbial communities in cod larvae

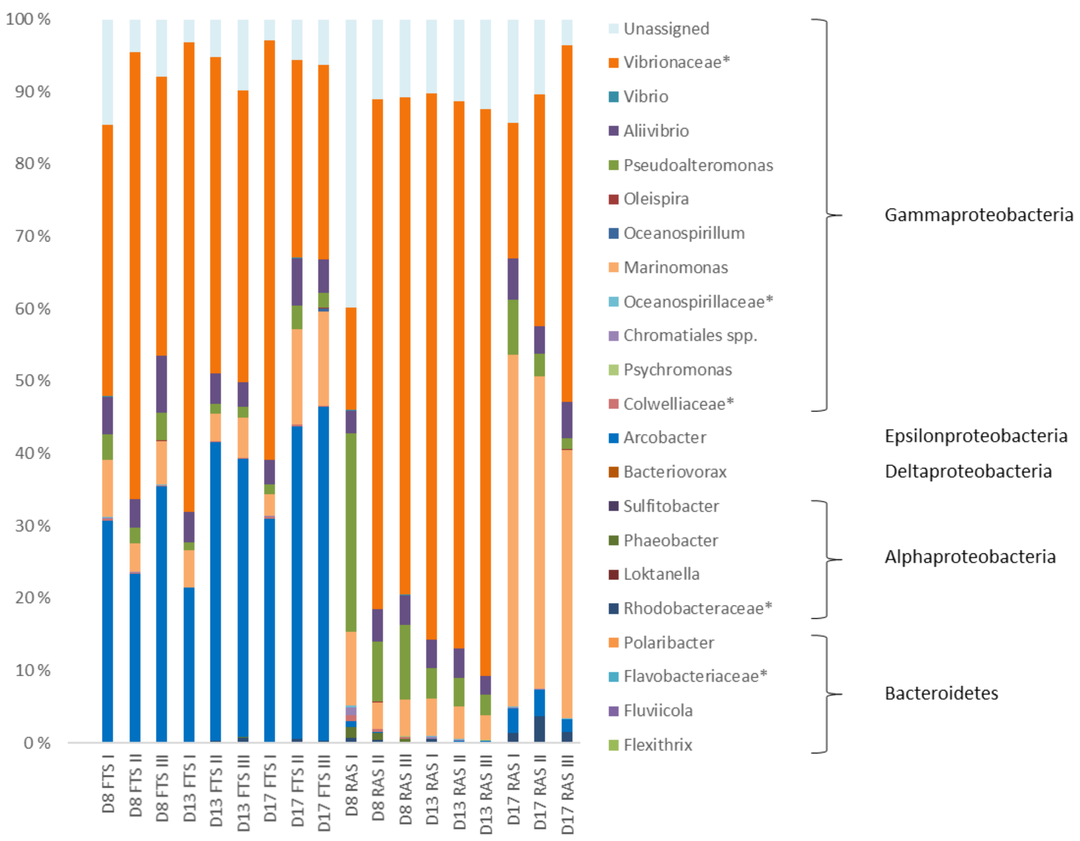

Figure 1: Microbiota associated with FTS and RAS cod larvae as assessed by 16S rRNA amplicon sequencing.

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Discussion and conclusion

- FTS promoted colonization of cod larvae by *Arcobacter* and upregulated microbial-response genes
- *Arcobacter* strains (*Epsilonproteobacteria*) has been recognized as enteropathogens
- We hypothezise that RAS counteracts the occurance of opportunistic bacteria in the rearing water and thus promotes good fish health

Transcript profiles of cod larvae

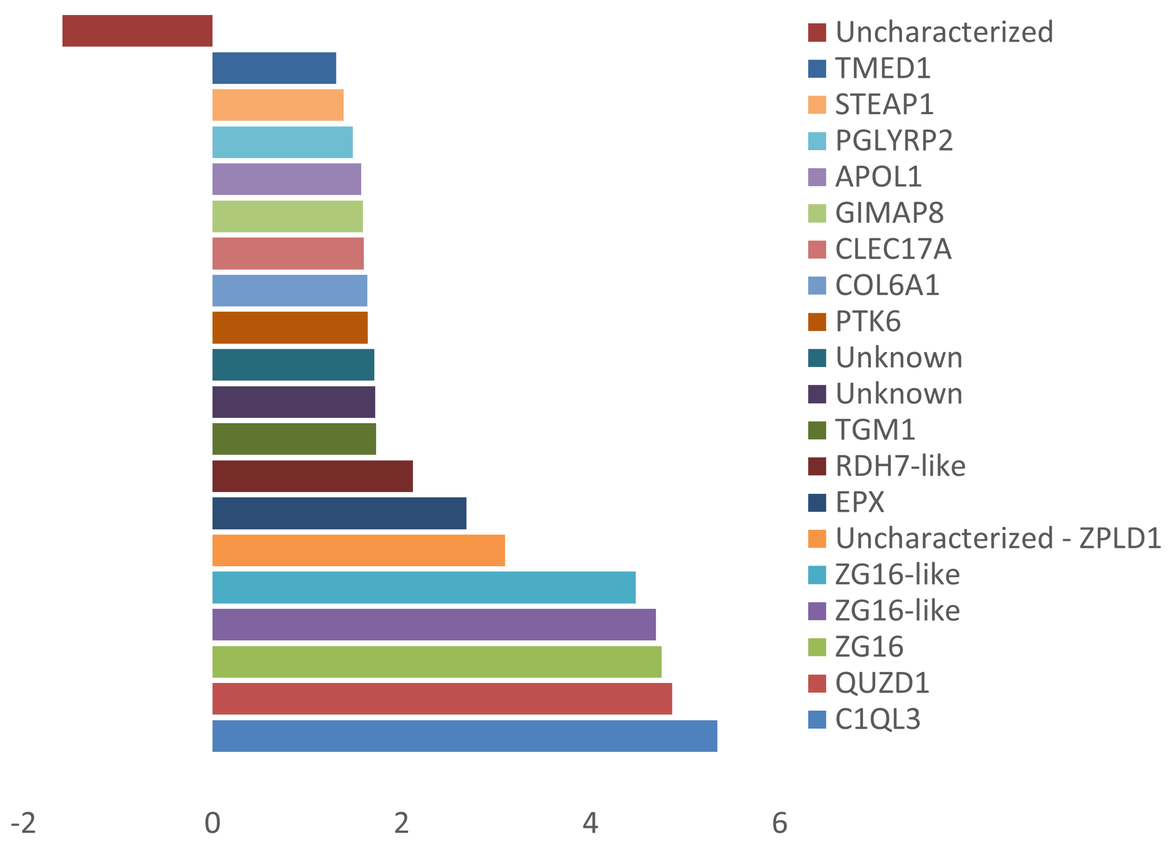

Figure 2: Summary of significantly up and down regulated genes in the FTS compared to the RAS.

Materials and Methods

A start feeding experiment with Atlantic cod (*Gadus morhua*) larvae was conducted in two different aquaculture systems.

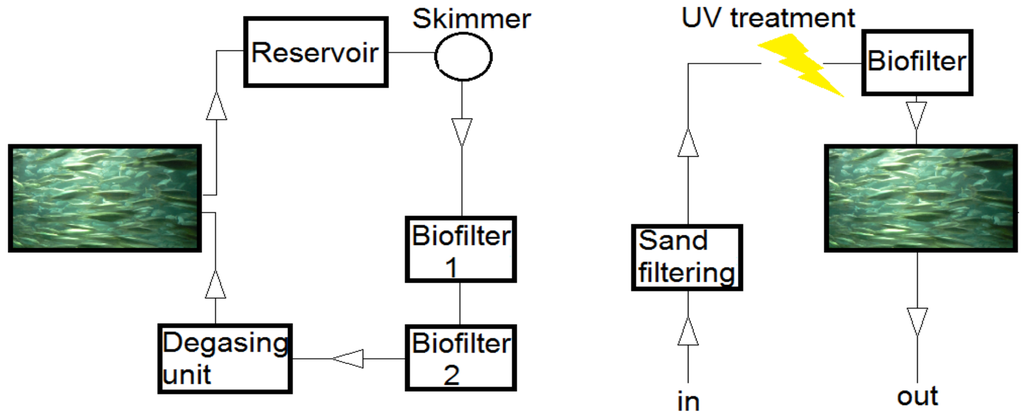

Figure 3: Schematic presentation of the experimental setup.

The microbial communities both in the water and associated with the larvae, were analyzed by pyrosequencing (8, 13 and 17 days post hatching) and DGGE. Transcript profiles of the larvae were analyzed using a custom 44k Agilent cod microarray (17 days post hatching).