



Conference Abstract

Bacteria Communities in Swiss Fish Farms with Recirculating Aquaculture Systems

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Abstract

Recirculating aquaculture systems (RAS), often used in fish farming, rely on microorganisms to maintain healthy water quality, nutrient cycling, animal welfare, and disease control. However, many daily operations in fish farms (e.g., stocking) may negatively affect the microorganisms' community composition and create a favorable environment for opportunistic pathogens. Currently, understanding microorganisms' communities within RAS is scarce, which presents an obstacle for pro-active system management. To better understand microorganism communities' spatial and temporal structure within fish farms using a RAS, we collected samples of filtered water and biofilm swabs from two different Swiss fish farms and two different locations within each farm. Water was collected from within one tank and the biofilter, while biofilm swabs were collected from the same tank's wall where the water sample was collected. DNA was extracted using the Purelink Microbial DNA Purification kit, and then each sample was prepared with three different primer pairs, 341F/805R (V3V4 region), 515F/806R (V4), 27F/534R (V1-3), and ran on the MiSeq platform (v3 600 cycles). The pilot study aimed to understand 1) how the microbiota composition changes regarding spatial and temporal scales within and between farms, 2) the primer effect on detected taxa, and 3) the difference between commonly-used 16s pipelines.

Keywords

bacteria communities, 16S sequencing, RAS, aquaculture

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