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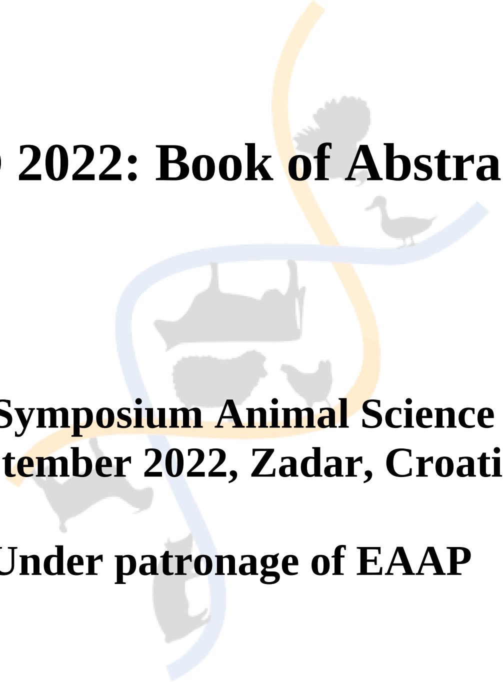

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EXPLORING MICROBIAL COMMUNITIES IN HALOPONIC SYSTEMS AT DIFFERENT WATER SALINITY

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ABSTRACT: Haloponics is a form of aquaponics, a multi-trophic production system based on the dynamic integration among fish, plants, and microorganisms in brackish water. To understand the role of water salinity on bacteria structure in a low-tech haloponic system, we performed a 16S rDNA multi-amplicon sequencing to compare microbial community profiles in nine tanks where rainbow trout and catfish were kept at three water salinity concentrations (0.5‰, 3‰, and 6‰).

The overall microbial profile was represented by different functional groups, involved in plant growth and protection, and nitrification processes, but also bacteria found in the guts of freshwater fish. Potential fish and human pathogens such as *Pseudomonas*, *Vibrio*, and *Aeromonas* were detected. The core microbiomes revealed the absence of beneficial and plant-associated bacteria such as *Bacillus*, *Lactobacillus*, *Massilia*, and *Thermomonas*, in the tanks at 6‰ salinity. Principal Coordinate Analysis showed no significant separation between bacterial communities according to salinity, suggesting a common structure among samples. These results enhance our understanding of the composition of bacterial populations in haloponic systems and their relationships with water salinity. Brackish water up to 6‰ did not severely impact the microbial ecosystem, resulting in an alternative source for the establishment of sustainable and healthy aquaponic systems.

Keywords: Aquaponics, Next-generation sequencing, Microbial communities, Salinity

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