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Exploratory Profiling of Resistome Dynamics Along a Freshwater Gradient Influenced by Aquaculture Effluents

Inhalt

Aquaculture is expanding globally, yet antibiotic use raises concerns about antimicrobial resistance, posing risks to environmental, animal and human health. This study investigates the impact of a freshwater aquaculture farm in Brazil on microbial communities and ARG dissemination in water, sediment and algae-associated microbiomes. Samples were collected along a spatial gradient - from an upstream control site to locations up to 6 km downstream - and analyzed using shotgun metagenomics. Water and algae samples revealed distinct shifts in microbial community composition at pond effluent outlets and downstream sites, characterized by increased abundances of potential pathogens (e.g. *Flavobacteriaceae*) and elevated loads of antimicrobial resistance genes (ARGs). Algae represented an overlooked ARG hotspot and showed the highest ARG diversity. Detected ARGs included resistance to multiple antibiotic classes and were associated with diverse microbial taxa (e.g. members of Pseudomonadota). ARG mobilization potential was highest in water samples, where co-localization analysis identified linkage between a vancomycin resistance gene and phage-associated mobile genetic element. The findings demonstrate downstream effects of aquaculture on microbial communities and ARG dissemination in adjacent freshwater environments, emphasizing potential risks to environmental, animal and human health and the need to evaluate and manage veterinary antibiotic use through a One Health approach.

Keywords

Aquaculture; Freshwater microbiome; Antimicrobial resistance genes; Resistome; Mobile genetic elements; Shotgun metagenomics; One Health

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Yes, I am a Junior Scientist.

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