Shotgun metagenomic approach for studying microbiome in shrimp aquaculture in Vietnam

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Abstract (less than 250 words)

Vietnam is one of the world's leading shrimp-producing and exporting countries. Despite the economic value as a key aquaculture species, the production of Pacific white shrimp (*Penaeus vannamei*) faces significant challenges from intensive farming practices. High stocking density and excessive feeding can lead to the accumulation of harmful substances, frequently deteriorating water quality, shifting environmental microbiota in shrimp ponds with the emergence of pathogens, resulting in overuse of antibiotics and/or economic losses. In this study, we employed a shotgun metagenomic approach to characterize microbial communities and antibiotic resistance profiles in intensive and extensive shrimp farming systems in north-central and southern Vietnam. At the phylum level, the dominant phyla in environmental samples were Pseudomonadota, Actinomycetota, Bacteroidota, and Bacillota. Microbial diversity in feces of intensively cultured shrimp was clustered together with that in water samples of growth-out ponds. There was a significant difference between the microbial composition in water and sediment samples in the extensive farming system. At the genus level, *Streptomyces* and *Xanthomononas* tended to be enriched in the sediments, while *Synechococcus* was highly abundant in the water samples. Notably, higher antibiotic-resistance genes (ARGs) are found in intensive farming system than in extensive farming system. Our findings may be helpful in comprehensive understanding of the compositional characteristics and functions of microbiota in shrimp ponds and the dissemination of ARGs in aquaculture environments. Shotgun metagenomic approach can be further used for developing management strategies to sustain shrimp aquaculture and contribute to the improved ecological management of aquatic ecosystems.

Keywords: *microbial diversity; microbiome; shrimp aquaculture; and less than 5 words.*

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