



The effects of marine farm-scale sequentially integrated multi-trophic aquaculture systems on microbial community composition, prevalence of sulfonamide-resistant bacteria and sulfonamide resistance gene *sul1*

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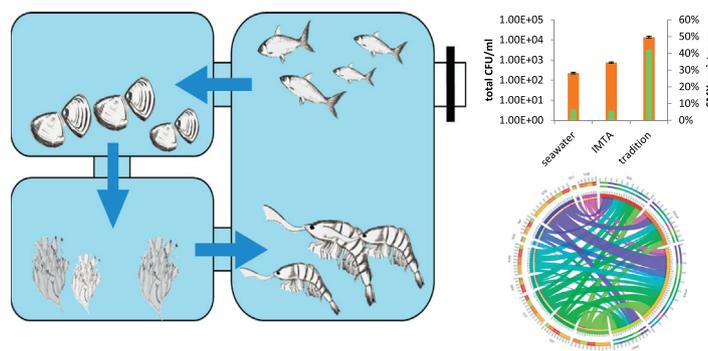
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HIGHLIGHTS

- IMTA system maintained microbial community structure and prevalence of sulfonamide resistance in marine environments.
- *Vibrio* was the most frequently isolated *sul1*-possessing genus in marine fishponds.
- High *sul1* sequence similarity was observed in marine bacteria of distinct phylogenetic taxa.
- Sulfonamide resistance was accompanied by streptomycin resistance in bacteria isolated from marine aquaculture systems.

GRAPHICAL ABSTRACT



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ABSTRACT

Aquaculture, one of the most important food production practices worldwide, faces serious challenges of mitigating the detrimental impacts of intensive farming on the environment and increased prevalence of antibiotic resistance. To develop an environment-friendly aquaculture system, a land-based and farm-scale sequentially integrated multi-trophic aquaculture (IMTA) system was established for farming *Chanos chanos* in southwestern Taiwan. In this system, fishes are cultured in combination with organic extractive shellfish and inorganic extractive seaweed. This study aimed to evaluate the prevalence of sulfonamide-resistant bacteria, microbial community structure, and occurrence of sulfonamide resistance genes in the IMTA and traditional aquaculture systems. Water and sediment samples were collected before raising and after harvesting *C. chanos*. Our results showed that the occurrence of sulfonamide-resistant phenotypes in the IMTA system was comparable with that in influent seawater, while the traditional system exhibited a high sulfonamide resistance rate. Additionally, the traditional system resulted in a deviation of the bacterial community structure from that of seawater. In the water samples from the IMTA system and influent seawater, Proteobacteria and Bacteroidetes were the two dominant phyla, representing approximately 75% and 15% of the community, respectively. In the traditional system, Actinobacteria, constituting 39% of the community, was the dominant bacterial phylum. Thirty-one sulfonamide-resistant bacterial species were isolated. In conclusion, a sequentially IMTA system showed superior

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