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<AT>Impact of environmental bacterial communities on fish health in marine recirculating aquaculture systems

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<ABS-P><ST>Highlights</ST>

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The bacteria profiles of the water of a marine RAS with disease problems was significantly different from that of a healthy RAS.

The microbiota of the water in the healthy RAS was more diverse and balanced compared to the RAS with disease problems.

Some potential pathogenic bacteria were also found both in the water and in fish in the system with disease problems.

</LIST>

<ABS-HEAD>Abstract

<ABS-P>Marine cultured fish diseases caused by bacteria in recirculating aquaculture systems (RASs) greatly threaten fish aquaculture. To date, the dynamics of bacterial populations in RAS and their impacts to fish health remain largely unknown. In the present study, the bacterial communities in the water from two different marine RASs were analyzed using pyrosequencing technique. Fish disease syndromes and mortality had been reported from one RAS (RAS-d) while the fish in the other RAS remained healthy (RAS-h). The diversity of bacteria in each RAS and the abundance of each bacterium were identified based on sequencing the V4 hypervariable region of the 16S rRNA gene. A total number of 107,476 effective sequences were obtained from the pyrosequencing results. 640 and 844 operational taxonomic units (OTUs) were identified in RAS-d and RAS-h, respectively. In order level, tags annotation showed that *Vibrionales* and *Flavobacteriales* were the predominant strains in RAS-d with a relative abundance 50.5% and 36.5%, respectively. In contrast, the bacterial community in RAS-h contained 35.8% *Vibrionales*, 17.3% *Alteromonadales*, 10.7% *Rhodobacterales*, 7.43% *Kordiimonadales*, and 6.26% *Oceanospirillales*. In addition, the *Vibrionaceae* in the RAS-d represented 6.98% of the population which was significantly higher than that in RAS-h (0.40%). More potential pathogenic bacteria in fish, such as *Vibrio harveyi*, *Vibrio rotiferianus* were also found in the bacterial

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