Virulence-associated genes and antibiotic resistance patterns of Vibrio spp. isolated from cultured marine fishes in Malaysia

ABSTRACT

Background: Vibriosis is an important bacterial disease of cultured marine fishes worldwide. However, information on the virulence and antibiotic resistance of Vibrio spp. isolated from fish are scarce. This study investigates the distribution of virulence associated genes and antibiotic resistance patterns of Vibrio spp. isolated from cage-cultured marine fishes in Malaysia. Results: A total of 63 Vibrio spp. isolated from 62 cultured marine fishes in various geographical regions in Peninsular Malaysia were analysed. Forty-two of the isolates (66.7%) were positive for all chiA, luxR and vhpA, the virulence genes produced by pathogenic V. harveyi. A total of 62 Vibrio isolates (98%) had tlh gene of V. parahaemolyticus, while flaC gene of V. anguillarum was detected in 43 of isolates (68%). Other virulence genes, including tdh, trh, hlyA and toxRvc were absent from any of the isolates. Multiple antibiotic resistance (MAR) was exhibited in all strains of Harveyi clade, particularly against ampicillin, penicillin, polypeptides, cephems and streptomycin. The MAR index ranged between 0.06 and 0.56, and 75% of the isolates have MAR index of higher than 0.20. Host species and geographical origin showed no correlation with the presence of virulence genes and the antibiotic resistance patterns of Vibrio spp. Conclusions: The study indicates that majority of Vibrio spp. isolated from cultured marine fishes possess virulence genes, but were not associated with human pathogen. However, the antibiotics resistance is a real concern and warrants ongoing surveillance. These findings represent an updated knowledge on the risk of Vibrio spp. to human health, and also provides valuable insight on alternative approaches to combat vibriosis in cultured fish.

Keyword: Vibrio; Cultured fish; Virulence genes; Multiple antibiotics resistance