

Molecular characterization of 16S rRNA and internal transcribed spacer (ITS) regions of *Aeromonas* spp. isolated from cultured freshwater fishes in Malaysia

ABSTRACT

The *Aeromonas* spp., which are found mostly in freshwater fishes are known to cause uncontrolled disease outbreak in aquaculture system. In the present study, twenty-two of *Aeromonas* spp. strains isolated from diseased freshwater fishes were identified using the 16S ribosomal RNA (rRNA) and internal transcribed spacer (ITS) regions gene amplification where they produced a 1500 bp and 1000-1200 bp amplicon each. Phylogenetic analysis with BLASTn and 16S rRNA neighbor-joining bootstrapping methods revealed that all strains were identified up to genus level with 15 strains were classified as *Aeromonas hydrophila* (*A. hydrophila*) and the rest were *Aeromonas veronii* (*A. veronii*). Further ITS gene analysis disclosed strains identification up to species level; *A. hydrophila* (14 strains) and *A. veronii* (8 strains). These rapid DNA-based detection methods are simple, easy to perform and faster in identifying *Aeromonas* spp., thus are absolutely efficient for regular monitoring of *Aeromonas* spp. in a potential outbreak situation.

Keyword: Hepatitis B; Core antibody; Occult hepatitis B infection; Polymerase chain reaction; Surface antigen