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GENETIC SIMILARITY OF BACTERIAL STRAINS ISOLATED FROM ULCERATIVE SYNDROME IN *ELOPS MACHNATA* AND SUSCEPTIBILITY TO DIFFERENT DRUGS

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ABSTRACT

Nowadays there are a large number of antibiotic resistant pathogenic bacteria were identified in captive fish culture, which indicated that the risk of ineffective antibiotic treatment without laboratory susceptibility test in infected fishes. In the present study, ten bacterial isolates were derived from the ladyfish, *Elops machnata* (n=10) in captive condition which showed ulcerative syndrome. The ten isolated bacterial strains were putatively identified by morphological characters and gram staining under microscope. They were confirmed by 16S rRNA gene sequence and the majority of the isolates were *Bacillus* sp (7/10). Based on the genetic similarity study, 16S rRNA gene UPGMA tree topography showed *Bacillus, Staphylococcus* and *Halomonas* species were clustered clearly with >90% bootstrap confidence value. Among these three genus, *Bacillus* and *Staphylococcus* were more closely related than *Halomonas.* The antibiotics susceptibility testing was performed by disc diffusion method, using 12 types of antibiotic discs. In the susceptibility study, *Bacillus* sp. (TRLB3) and *Bacillus vietnamensis* (TRLB6) stains were highly sensitive to all the antibiotics. Whereas the gram negative bacterial strains such as *Bacillus cereus* (TRLB4) and *B. cereus* (TRLB8) were resistant to Amoxyclav and Penicillin and gram positive strains, *Halomonas* sp (TRLB7) and *Halomonas* sp (TRLB9) were resistance to Nalidixicacid and Nitrofurantoin respectively. As per the observed results the two Halomonas isolates are genetically different in their patterns of antibiotic resistance. The remaining all the bacterial strains were intermediately sensitive to all the tested antibiotics.