

## ABSTRACT

As global demand for aquaculture products are increasing annually, the mortality of fish by bacterial diseases need to be put to an end. However, current method of overcoming this issue, which is antibiotic treatment of the fishes are proved to be more of a problem than solution taking into consideration the rise in multidrug-resistant bacteria. Alternatively, probiotics are considered one of the more prominent solutions for treating bacterial infectious diseases and maintaining overall health of the fishes in aquaculture industries. To identify potential probiotics, understanding the gut microbiota compositions and the possible factors contributing to the differences in the gut microbiota composition are important in determining the possible role of the gut microbiota in contributing health benefits to the host fishes. In line with this, gut microbiota of economically important fishes, *Oxyeleotris marmorata* (Marble Goby) and *Pangasius sutchi* (Pangasius catfish) in Malaysia was identified using 16S rRNA metagenomic approach. Gut microbiota from both wild and captive marble goby as well as captive Pangasius catfish were studied. DNA from the fish gut content were extracted using MN NucleoSpin soil kit. The clustering and classification of Operational Taxonomical Unit (OTU) of the gut microbiome was done using MOTHUR based on Silva Bacterial 16S rRNA database. Subsequently, the data from Marble Goby and Pangasius catfish was compared to 16S rRNA metagenomic data that were available in the database. Based on the analysis, 18 phyla were present in wild Marble Goby, 20 phyla in captive Marble Goby, and 26 phyla were present in captive Pangasius catfish, with Chao1 index of 232.36, 127.50, and 372.23 respectively. Unifrac distance among the OTUs from each fish was analysed and the outcome indicated that gut microbiota diversity of wild Marble Goby and captive Pangasius catfish which were collected from the same region were more similar than captive Marble Goby from a different locality. This suggest that habitat (wild and captive) and diet of the fishes plays an influential role in determining the gut microbiota composition of the fish. In addition, a few probiotics candidate were found based

on our *in silico* analysis. Those organisms are possible probiotics candidate as suggested by previous literature. However, this study does acknowledge that the sample number and sampling condition may be a limitation to conclude on the possible role of the indentified probiotic candidates. This study is a preliminary study that would pave the path for future studies to identify probiotics for these two species of fish. Further analysis of gut microbiota composition among 4 other fishes revealed the influence of feeding behaviour (predatory, opportunistic feed, etc.) in determining the gut microbiota composition of the fishes. In summary, the differences in the gut microbiota profile are more apparent according to the locality (habitat) and diet preference, than the type of fish species.