

Comparative study of gut microbiota in wild and captive Malaysian Mahseer (*Tor tambroides*)

ABSTRACT

Aims: The aim of this study was to identify and compare the gut microbial community of wild and captive *Tor tambroides* through 16S rDNA metagenetic sequencing followed by functions prediction.

Methods and results: The library of 16S rDNA V3-V4 hypervariable regions of gut microbiota was amplified and sequenced using Illumina MiSeq. The sequencing data were analyzed using Quantitative Insights into Microbial Ecology (QIIME) pipeline and Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt). The most abundant bacterial phyla in both wild and captive *T. tambroides* were Firmicutes, Proteobacteria, Fusobacteria and Bacteroidetes. *Cetobacterium* spp., Peptostreptococcaceae family, *Bacteroides* spp., Phosphate solubilizing bacteria PSB-M-3, and *Vibrio* spp. were five most abundant OTU in wild *T. tambroides* as compared to *Cetobacterium* spp., *Citrobacter* spp., Aeromonadaceae family, Peptostreptococcaceae family and *Turicibacter* spp. in captive *T. tambroides*.

Conclusion: In this study, the specimens of the wild *T. tambroides* contain more diverse gut microbiota than of the captive ones. The results suggested that *Cetobacterium* spp. is one of the core microbiota in guts of *T. tambroides*. Besides, high abundant *Bacteroides* spp., *Citrobacter* spp., *Turicibacter* spp., and *Bacillus* spp. may provide important functions in *T. tambroides* guts.

Significance and impact of the study: The results of this study provide significant information of *T. tambroides* gut microbiota for further understanding of their physiological functions including growth and disease resistance.

Keyword: 16S rDNA; Gut microbiota; Illumina MiSeq; Metagenetic sequencing; Next-generation sequencing; *Tor tambroides*