# Molecular phylogeny of some Malaysian groupers (subfamily: Epinephelinae, family: serranidae) inferred from mitochondrial and nuclear gene sequences

## ABSTRACT

Groupers are known as one of the important marine and estuarine fishes they are widely distributed in the tropical and subtropical open water. Nevertheless, the taxonomy and phylogenetic relationships among wild groupers in Malaysian waters are still poorly studied and need to be further clarified. Thus, this study aimed to elucidate the phylogenetic relationship of wild grouper using samples collected from eight coastal areas in Peninsular Malaysia. Samples were identified manually based on their morphological characteristics. Molecular phylogeny was inferred for subfamily Epinephelinae using a combined analysis of the mitochondrial cytochrome b and nuclear Recombination activating gene-1 (RAG-1) genes from 12 species representing three genera of subfamily Epinephelinae. Results from all methods of analyses (Neighbour-joining (NJ), maximum parsimony (MP), maximum likelihood (ML), minimum evolution (ME), and Bayesian analyses (BI)) produced similar tree topologies and strong supported the monophyletic status of the three genera within the subfamily Epinephelinae with genus Plectropomus was basal to the other genera. Phylogenetic analyses also divided genus Epinephelus into two different clades similar to other previous findings. Nevertheless, several relationships remain unresolved particularly among morphologically similar species (e.g between E. fario and E. longispinis) and species with limited number of individuals (E. coioides). Overall, the findings of this study have managed to provide new insights on the taxonomy, phylogeny and genetic diversity of grouper fishes in Peninsular Malaysia, which are important for their appropriate sustainable management, either for conservation or aquaculture purposes.

**Keyword:** Epinephelinae; Molecular phylogeny; Cytochrome *b* gene; Mitochondrial DNA