THE EVOLUTIONARY HISTORY OF RABBITFISH (SIGANIDAE) BASED ON MORPHOLOGICAL AND MOLECULAR DATA

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A total of 18 nominal species in genus *Siganus* (Siganidae) is classified based on morphological features and colouration patterns. The remarkable morphological similarities and the intermediate morphological characters resulted in taxonomic confusion in Siganidae. Although a series of phylogenetic studies have been conducted, the research on divergence time and evolutionary history of rabbitfish are still lacking. This study was conducted to 1) determine the morphological characteristics of *Siganus* species collected from Terengganu Waters 2) show the patterns of phylogenetic diversification of siganids and 3) infer the time of divergence of the species by using the time-calibrated phylogeny. The phylogenetic tree of *Siganus* species was reconstructed based on mitochondrial DNA sequences of cytochrome oxidase I (COI) and nuclear DNA sequences of rhodopsin retrogene. The results were compared with morphological analysis outcomes. The Bayesian Inference (BI) and Neighbour-Joining (NJ) analyses of both genes produced phylogeny structure that are not identical due to the inconsistent placement of *S. argenteus*. The placement of *S. argenteus* as sister lineage to the other clades showed different patterns: 1) connected with the deep-bodied group (NJ analysis

of both genes), 2) recovered as sister lineage to both the slender-bodied and the deep-bodied group (BI analysis of COI) and 3) connected with the slender-bodied group (BI of rhodopsin gene). Molecular clock analysis defined an Eocene crown age for Siganidae (37.4 Mya). The major diversification of siganids into three clades was around 16.9 Mya during Miocene epoch. The evolution of siganids sister species is correlated with Plio/Pleistocene vicariance events. Speciation processes also occured between sister species at their overlapping zones. Siganid phylogeny and molecular clock are used to gain a deeper insights about the speciation processes and the influence of ecological and geographical distributions towards the diversification of marine reef fishes. In future, phylogenetic analysis using multiple genes is necessary to have a better resolution of phylogeny. Visual observation and physiological studies would also assist in understanding the ecological characteristics, habitat use and adaptation mechanism of siganids towards the current distribution ranges.