Evaluation of Molecular Makers for Species Phylogeny of Genus *Acropora* (Cnidiaria; Scleractinia; Acroporidae)

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Acropora is the most speciose genus in coral reef with 113 species currently described. Diversified morphology and potential of cross-species hybridization have drawn our attention in defining the species boundary, constructing species-level phylogeny, and inferring mechanism of speciation for this genus. Although endeavours have been taking in developing molecular markers in the last decade, several unique features such as slow evolution of mitochondrial genome and abundant ribosomal pseudogenes of Acropora neither provide little resolution for phylogenetic inference, nor equivocal conclusions in contrast to phylogenies based on fossil records and morphological characters. In this study, we evaluated 4 molecular markers, including mitochondrial cytochrome b gene (Cytb), mitochondrial integenic spacer spanning between Cytb and ND gene (mtigs), mini-collagen intron 2 (mci2), and nuclear histone 2a and 2b gene (H2ab), for constructing species phylogeny of genus Acropora. All the 4 loci supported the two subgenera, Isopora and Acropora, as two distinct evolutionary lineages, and relocated Acropora togianensis as the fifth species in the subgenus Isopora. However, Cytb, mtigs, and mci2 suffering from either low variability or sharing unsorted polymorphisms between the Caribbean and Indo-Pacific species provided no further resolution in resolving phylogeny in subgenus Acropora. In contrast, phylogeny constructed based on h2ab gene using Bayesian approach supported, in part, to Wallace (1999) that A. humilis group and A. austera form the basal clades of morphological phylogeny. The utility of nuclear coding genes in resolving species phylogeny of Acropora is highlighted.