

## MOLECULAR PHYLOGENY OF CATFISHES (TELEOSTEI: SILURIFORMES) INFERRED FROM MITOCHONDRIAL MARKERS – IMPLICATIONS FOR LOWER MEKONG RIVER BASIN

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### ABSTRACT

Catfish species in the Order Siluriformes distribute widely in Mekong River Basin, where they are important economic species for aquaculture and fisheries, providing major food sources for local communities. However, phylogenetic relationships of Siluriformes have remained unresolved at high taxonomic level. In this study, phylogenetic trees of 30 catfish species belonging to nine families collected from Lower Mekong Basin (LMB) were constructed based on two mitochondrial gene sequences using Neighbor Joining (NJ), Bayesian inference (BI) and Maximum likelihood (ML) methods. The results obtained from the BI and NJ methods showed more similarity than those obtained from ML method. Monophyly of Siluriformes was strongly supported by all applied phylogenetic methods. Seven of nine studied families performed monophyletic clade, while other families including Pangasiidae (14 species, four genera) and Bagridae (11 species, three genera) displayed paraphyletic. All analyses indicated that: (i) Loricaridae was placed as basal and being a sister clade to remaining families; (ii) Among Silurioidei, Plotosidae showed as a sister clade to the rest of families. Interfamilial relationships of Siluriformes performed divergent between data sets, and methods used, and showing unmatched with traditionally and recently reported catfish phylogenies.

**Keywords:** Catfish, mitochondrial marker, molecular phylogeny, LMB, Siluriformes.