

Molecular characterization of *Hemibagrus nemurus* gonadotropin subunits: cDNA cloning and phylogenetic analysis

ABSTRACT

Hemibagrus nemurus is a valuable cultured catfish, but the production is limited due to problems associated with its reproduction, which are controlled by two pituitary gonadotropin (GtH) hormones, follicle-stimulating hormone (FSH) and luteinizing hormone (LH). This study reports the cloning, sequence analysis, and phylogenetic study of GtH subunits from *H. nemurus*. This work revealed that the cDNAs of Gp- β , FSH β and LH β were 656, 728, and 602 nucleotides in length and encoded for mature peptides of 92, 117, and 115 amino acids, respectively. The amino acid sequence identities of *H. nemurus* mature subunits Gp- β , FSH β and LH β in comparison with other fishes were 51-100%, 23-89% and 44-88%, respectively; while in comparison with tetrapods were 64-73%, 12-30% and 26-52%, respectively. The cysteine residues of the mature protein were conserved in comparison with other fishes, which were 10, 13 and 12 cysteines in Gp- β , FSH β and LH β , respectively. Meanwhile, all potential N-linked glycosylation sites were fully conserved with other vertebrates. The Gp- β , FSH β and LH β of *H. nemurus* resembled most to those of Siluriformes, Cypriniformes, and Anguilliformes implying a close phylogenetic relationship. This study demonstrates that Malaysian *H. nemurus* can be utilized as a good model for investigating GtH functions in other catfish species throughout the Indo-Pacific region.

Keyword: *Hemibagrus nemurus*; Gonadotropin; LH; FSH; Phylogenetic analysis