



Cloning and characterization of major histocompatibility complex class II genes in the stone flounder *Kareius bicoloratus* (Pleuronectidae)

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ABSTRACT. Major histocompatibility complex (MHC) class II genes play important recognition roles in the immune system in vertebrates. We cloned the MHC class II genes *A* and *B* in the stone flounder (*Kareius bicoloratus*). The full-length cDNA and DNA sequences of both genes were obtained, and their characteristic motifs were analyzed. The DNA sequence of stone flounder MHC class II *A* consists of four exons, while gene *B* contains six exons. The extra intron in gene *B* might be a common feature in most of its Acanthopterygii orthologs. Several conserved motifs were identified by multiple deduced amino acid sequence alignments of the two genes and their orthologs. The peptide sequences of α chain and β chain shared identity of 86.0-30.1% and 69.8-31.3% with their orthologs, respectively. Bayes phylogenetic trees showed that the stone flounder is closely related to the spotted halibut (*Verasper variegates*), and the half-smooth tongue sole (*Cynoglossus semilaevis*). Real-time quantitative PCR showed that in the stone flounder, both genes *A* and *B* are highly or moderately

expressed in several tissues, including the intestine, spleen and gills, and less expressed or undetectable in the liver, kidney, brain, heart, and gonads. These expression patterns differed slightly from those in other teleosts. This might be a unique phenomenon in the stone flounder. This first study of MHC genes in stone flounder could provide reference data for comparative studies.

Key words: Major histocompatibility complex; Stone flounder; Cloning; Expression