

A study of polymorphism in the MHC class II genes of Atlantic salmon and brook trout

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Salmonids include some of the most important species in aquaculture. Domestication has resulted in a number of weaknesses mainly related to infectious diseases due to intensive selective breeding and drastic changes in the environment. Studies of major histocompatibility complex (MHC) genes give information about polymorphism and possible changes in variability as a result of selective breeding and disease resistance or susceptibility associated with specific alleles or haplotypes. Variation in the highly polymorphic peptide-binding region of MHC class II gene was surveyed in two salmonid species, Atlantic salmon (*Salmo salar*) and brook trout (*Salvelinus fontinalis*). A total of 37 Atlantic salmon and 24 brook trout were collected from four different locations in Newfoundland, Canada. Fin clips were cut and preserved in 95% ethanol. Genomic DNA was extracted and MHC class IIB1 exon was amplified using polymerase chain reaction (PCR) and the alleles were identified using denaturing gradient gel electrophoresis (DGGE) by their sequence specific melting properties. A total of 13 alleles were identified in Atlantic salmon with an expected heterozygosity of 0.76 and a total of 7 alleles were identified in brook trout with an expected heterozygosity of 0.78. These alleles were verified by nucleotide sequence analysis. Sequences were corrected and aligned with Sequencer 3.0 and analyzed with MEGA. All the sequences that differed in nucleotide sequence also differed in amino acid sequences. Moreover, non-synonymous substitutions were observed more frequently than synonymous substitutions in both species. These results indicate that a high level of polymorphism, both at the allelic level and at the amino acid level, is maintained in Atlantic salmon and brook trout populations used in this study.

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