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EST-based identification of genes expressed in the several tissues of the black rockfish, *Sebastes schlegeli*

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Gene expression in five tissues of the black rockfish *Sebastes schlegeli* was investigated using an expressed sequence tag (EST) analysis. A total of 1,980 randomly selected clones were obtained from cDNA libraries constructed with intestine, liver, spleen, brain and head kidney. Using assembly program, the 1,980 ESTs coalesced into 178 contigs and 1,314 singletons. Of 1,492 clones analyzed, 1,314 clones (86%) in total turned out to share significant similarity with the sequences from NCBI GeneBank (less than 10^{-3} of e-value) and 178 clones (14%) appeared to be completely unknown and may represent newly described genes. Based an major function of their encoded proteins, the identified clones are classified into twelve broad categories. The putative identities of these clones reflected the expected tissue specificity. Among them, several immune-related genes were identified, e.g. hepcidin, LBP/BPI, transferin, and lysozyme from liver. Sequence analysis of ESTs revealed the presence of microsatellite-containing genes that may be valuable for further mapping studies. So, full scale EST collection is a valuable approach for the discovery of new genes of potential significance in various tissues, and the analysis of the gene expression pattern and gene function of black rockfish.

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