

An EST survey of genes expressed in liver of rock bream
(*Oplegnathus fasciatus*) with particular interests on the
stress-responsive and immune-related genes

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EST analysis was performed to identify stress-responsive and immune-related genes from rock bream (*Oplegnathus fasciatus*). cDNA libraries were constructed with liver and randomly chosen 624 clones were subjected to automated sequence analysis. Of 624 clones sequenced in total, approximately 15% of ESTs was novel sequences (no match to GenBank) or sequences with high homology to hypothetical/unknown genes. The bioinformatic sequence analysis including functional clustering, homology grouping, contig assembly with electronic northern and organism matches were carried out. Several potential stress-responsive biomarker and/or immune-related genes were identified in all the tissues examined. It included lectins, ferritins, CP450, proteinase, proteinase inhibitors, anti-oxidant enzymes, various heat-shock proteins, warm temperature acclimation protein, complements, methyltransferase, zinc finger proteins, lysozymes, macrophage maturation associated protein, and others. This information will offer new possibilities as fundamental baseline data for understanding and addressing their molecular mechanism involved in host defense and immune systems of this species.

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