

The evolution of cod protein coding genes: intra- and interspecies levels

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Atlantic cod (*Gadus morhua*) is a large, cold-adapted bony fish with important commercial value. Two ecotypes of cod, «migratory» and «coastal stationary», were described by researchers. The ecotypes differ from one another by the depth of habitat, migration and feeding strategy; they reproduce separately. Also were identified genetic loci that are most likely related to such adaptation and were found strong genetic differentiation between ecotypes.

The availability of cod genome and genomes of related species allows us to study in detail molecular evolution of coding elements. In current study were estimated evolutionary rates, selection coefficients for different functional classes of cod protein coding genes, this data were compared (where it is possible) with level of divergence of corresponding genes between cod ecotypes.

Cod proteins from the Ensembl Genome Browser were grouped by hierarchical clustering by identity, for every group were found their homologues from 10 fish genomes (amazon molly, cave fish, coelacanth, fugu, medaka, platyfish, stickleback, tetraodon, tilapia, zebrafish).

Functional gene annotation was performed using the Gene Ontology database. Amino acid sequences were transformed to original CDS nucleotide sequences, then substitution rates were estimated and selection tests were used. Finally, for loci associated with adaptation of ecotypes (or list of genes worth paying attention to) were calculated correlations between the obtained estimates and F_{st} values from previous research of ecotype genetic characteristics

1. B.O. Karlsten et al. (2013) Genomic divergence between the migratory and stationary ecotypes of Atlantic cod. *Molecular ecology*, 22(20): 5098-5111.
2. J. Hemmer-Hansen et al. (2013) A genomic island linked to ecotype divergence in Atlantic cod. *Molecular Ecology*, 22(10): 2653-2667.