

Statistical analysis of nucleotide sequences of a cytochrome c oxidase subunit 1 (CO1) mtDNA arctic (*Liopsetta glacialis*) and striped (*Liopsetta pinnifasciata*) flounder (Pleuronectidae) of the Sea of Okhotsk

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Within global project DNA- barcoding of animal species and plants (Hebert et al. 2003) in 2005 the program devoted to fishes (Fish Barcode of Life Initiative, FISH-BOL) (Ward et al. 2005). By July, 2011 from about 31 thousand types fishes the nucleotide sequence of a cytochrome c oxidase subunit 1 is known for 25% of species, and for order of the Pleuronectiformes - 30,2% (Becker et al., 2011).

Individuals of striped (*L.pinnifasciata*) and arctic (*L.glacialis*) flounder are caught during the winter period from 2010-2012 in the Amakhtonsky gulf of the Tauilip, northern part of the Sea of Okhotsk. The purpose of article carry out the statistical analysis of new nucleotide sequences of a gene cytochrome c oxidase two species. Statistical analysis is carried out by the program MEGA 5.1. (Tamura et al., 2011).

At 10 individuals of arctic flounder is revealed 6 haplotypes (Potapova et al., 2013). Replacements of nucleotides are most adequately described by Tamura's model, T92 (T92, Tamura, 92). It is possible to judge suitability of this model in size of Bayesian criterion (BIC, Bayesian Information Criterion, BIC=1882,5).

At 28 individuals of a striped flounder is revealed 11 haplotypes. For a striped flounder the most probable way of replacement of nucleotides is the one-parametrical model Jukes and the Cantor (JC, BIC=2464,37).

Table. Indicators of variability of nucleotide sequences of a gene cytochrome c oxidase 1 at arctic (*L.glacialis*) and striped (*L.pinnifasciata*) flounder

	N	m	s	p_s	π	D	model
<i>L.glacialis</i>	596	10	6	0,01008	0,00370	0,154	T92
<i>L.pinnifasciata</i>	599	28	15	0,02504	0,00446	-1,046	JC(K2)

N- length of gene, m- number of fish (sequences), s- number of polymorphic sites, $p_s = s/N$ – part of polymorphic sites, π – nucleotide diversity, D- test Tajima, «model» - model of nucleotide substitutions.

Nucleotide diversity of striped and arctic flounder differs slightly (table). Low level of differences of a nucleotide variety of two flounders is connected with that is the sibling species entering into one genus. Cytochrome c oxidase is considered a gene characteristic for each species (Shneyer, 2009), however results of our statistical analysis show that its variability isn't equal to zero.

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