

TITLE:

Mutation and substitution rates in sexual and asexual forms: a clue to the persistence of sex in a model group of *Cobitis*?

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ABSTRACT:

Subject of this thesis is to test several hypotheses about the evolution of asexual reproduction in model group of fish family *Cobitis* and its mutual competition among sexual and asexual forms, which touches one of the oldest unresolved issues of biology. Specifically, the work deals with the accumulation of non-synonymous mutations, which accelerated accumulation in the genome of clonal lineages theoretically leads to increased extinction compared with sexually reproducing populations (so-called. The theory of Muller's ratchet and Kondrashov's hatchet). This thesis is based on a normalized cDNA sequencing data from oocytes and liver tissue, which has served as a base matrix (generated based on non-normalized cDNA data) for transcriptome sequencing (RNAseq). Consequently, the RNAseq data have served as validation for acquired polymorphisms, detection of differential expression of allele-specific expression (ASE) hybrid biotypes. This diploma thesis balances among the edges of vast spectrum of hypotheses regarding the evolution of the genus hybrid lineages, also consequences and the impact of polyploidisation, hybridization on transcription. Results concerning evolution of hybrid lines pointed out increased accumulation of non-synonymous mutations in the genome of the hybrid lineages in dependence on their age, which for the time being, however, does not lead to a noticeable degeneration in hybrid lineages. The overall view on the oocyte transcriptome between sexual asexual species reveals several differences either correlating with recent findings or points out unexplained phenomena, which may or may not have functionally positive or negative selective influence in gynogenetic individuals. ASE in hybrid genomes appear to be balanced, depending on the composition of the genome.

KEYWORDS:

Evolution of sex, gynogenesis, accumulation of deleterious mutations, next generation sequencing, allele specific expression, hybridization