

Mitochondrial genetics of amphipods: revealing mechanisms of diversity

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Abstract — We performed a thorough analysis of mitochondrial (mt) genomes of amphipods with the focus on endemic Baikalian species. Possible causes and mechanisms explaining an unusually high variability in mt genomes of Baikalian amphipods in comparison to that of non-Baikalian species are discussed.

Keywords — mitochondrial genomes, amphipods, Lake Baikal

Motivation and aim

Motivation

Mitochondrial (mt) genome sequences are widely used in evolutionary and phylogenetic studies. The architecture of mt genomes (i.e. their shape, length, gene order) can significantly vary in different organisms' groups [1]. The studying of the lineages with different mt genome architecture can help to reveal causes and mechanisms leading to such diversity.

Aim

In our previous study, we sequenced mt genomes of nine endemic amphipod (Crustacea) species from Lake Baikal [2]. We further sequenced mt genomes of Holarctic species *Gammarus lacustris* and pelagic Baikalian species *Macrohectopus branickii*. Amphipods is the most numerous and diverse group of Baikalian animals [3]. Genetic studies showed that modern Baikalian amphipod diversity (about 350 species) in the lake appeared by means of adaptive radiation of gammaroidean ancestors which had two independent invasions in the lake [3, 4, 5]. We showed that mt genomes of Baikalian amphipods significantly vary in length, gene order and gene number in comparison to the modern amphipods of gen. *Gammarus*, which are their nearest relatives. Thus we applied different bioinformatics approaches to discover the mechanisms of mt genome architecture diversity in Baikalian amphipods.

Methods

We had performed phylogenetic inference of amphipod species with available mt genomes (100 species in total) based on amino acid sequences of their mt protein-coding genes [6]. The scenarios of mt gene order rearrangements

were estimated using CREx [7]. The prediction of tRNA genes was made by MitFi [8]. For this analysis, we developed amphipod-specific models which showed a better performance than the default metazoan models implemented in MitFi. The non-coding parts of amphipod mt genomes were tested to contain repeated sequences and open reading frames. We used a custom R script to assess rates of molecular evolution in Baikalian amphipods and the group of gen. *Gammarus*.

Results

Phylogenetic analysis allowed us to deduce an ancestral mt gene pattern for both lineages of Baikalian amphipods, which appeared to be the same as one for species of gen. *Gammarus* group. Baikalian species show a drastic diversity in their mt genome lengths (from 14370 to 42256 bp.). A pelagic species *M. branickii* has the longest mt genome. The largest part of this genome consists of the numerous repetitive non-coding regions, which, presumably arose due to the proliferation of ribosomal genes. Mt genome sequences of seven out of twelve Baikalian amphipods species possess from one to four additional tRNA genes. Four species have tRNA genes that underwent to remodeling (changing tRNA gene identity through a mutation in their anticodon sequences) [9, 10]. Among 88 non-Baikalian amphipod species, only five species have additional tRNA genes in their mt genomes and four of them have tRNA remodeling cases. The frequent changes of gene number and order as well as other "peculiarities" in mt genomes of Baikalian amphipods in comparison to species of gen. *Gammarus* may be explained by the frequent sequence duplication and loss events happening in the former group. Thus we may assume that the specific environmental conditions in Lake Baikal allow the appearance and maintenance of such mt genomes without loss of species fitness.

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