Dynamics and hypotheses of gene order shifts in mitochondrial genomes of Baikalian amphipods

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Picture 1. Amphipods *G.fasciatus, M.branickii* (with altered gene order)

Gene order in the mitochondrial genomes (mt genomes) of invertebrates is shown to be different. The dynamics of such changes are usually studied by analysis of different organisms' lineages. It is notable that in some animal lineages the mitochondrial gene order maintained the same for the long periods, whereas other lineages demonstrate a significant variation of this feature. Amphipods can be **a good model for studying mitochondrial gene order dynamics** because of a relatively large number of species with sequenced mt genomes (about 100) available and due to the **variability of their mt gene order**. Recent studies showed that endemic amphipods from Lake Baikal possess rearranged mt genomes in comparison to the non-Baikalian species.

Methods

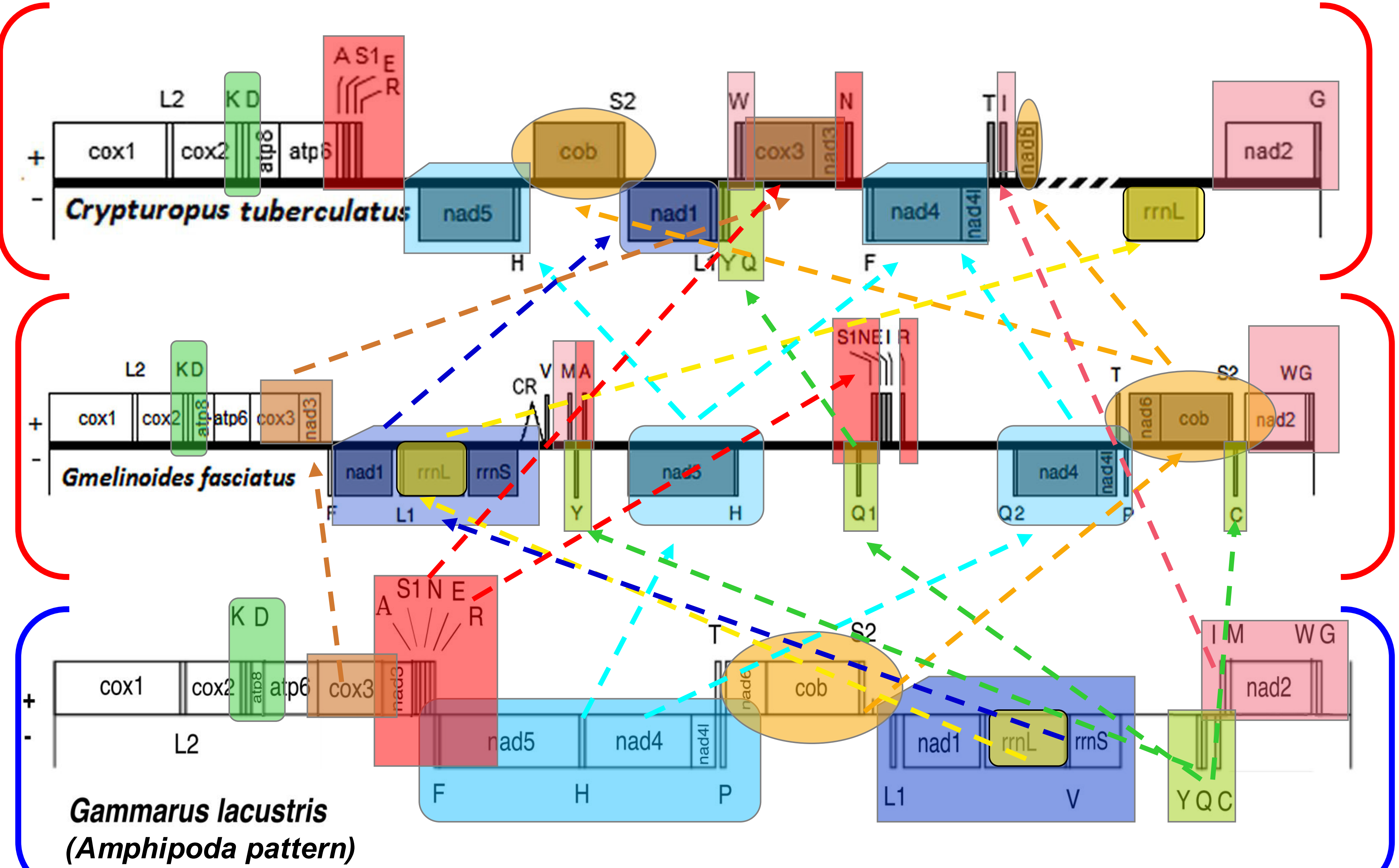
There are **two mechanisms** of the new gene orders emergence:

1) an erroneous duplication of the whole mt genome sequence during replication by “rolling ring” mechanism, associated with the DNA polymerase slippage on specific sites or repeats, and

2) a partial tandem duplication and random loss (TDRL) of a certain genome region. To measure such gene rearrangements quantitatively it is necessary to determine the number of mutational steps (permutations) from the ancestral gene order pattern to ones for the modern species. An ancestral gene pattern for any lineage is identified using phylogenetic reconstructions.

CREx
Common interval
Rearrangement
Explorer

We defined an **ancestral mt gene order pattern for all amphipods** performing phylogenetic inference based on amino acid sequences of 13 mt protein-coding genes. To estimate possible scenarios of gene order changing, including the minimum number of elementary gene permutations, we used CREx and SORT2. In some cases we assessed the changes manually by taking the number of displaced genes into account individually, and also counting the number of moved gene blocks grouped based on the proximity of their location



Picture 2. Mitochondrial gene orders of amphipods with extensive gene rearrangements comparing with Amphipoda pattern. Supposed TDRL areas are marked with colored blocks.

Results

The analysis showed that Pancrustacean pattern (the pattern common for all crustaceans and insects) generally used as a reference in mt gene rearrangements studies differ from deduced **Amphipoda pattern by the location of some tRNA genes**. The Amphipoda pattern deduced in our study turned out to be the same as one for gen. *Gammarus* species. The phylogenetic analysis showed that this pattern was ancestral for both lineages of Baikalian amphipods.

Thus the rearranged patterns of the majority of modern Baikalian amphipods were acquired during the evolutionary process in Lake Baikal. Notably, Baikalian amphipods from the second lineage (the one includes the majority of species which have very divergent morphological and ecological traits) possess gene order alteration **affecting mainly tRNA gene positions**. Whereas amphipods from the first lineage, which comprise much less number of species, having a smooth body and inhabiting mainly in shallow water, have **much more complex alteration in their mt gene order, affecting the positions of the protein-coding and ribosomal genes**.

We hypothesize that the fixation of highly rearranged mt genome becomes possible due to relaxed purifying selection in populations with low genetic diversity and low estimated effective population size. The shallow-water amphipod species in Lake Baikal could probably be more prone to the dramatic decrease of their population and consequently genetic diversity due to environmental changes in the Lake.