

There is a common view that mitochondrial genomes of vertebrates are highly conserved in their gene content and order. Therefore, it is interesting that avian mitogenomes are characterized by different gene orders, which can include a duplication of control region and five neighbouring genes. Some species contain almost all duplicated elements but others kept only a few, which suggests the loss of copies. Since the number of mitogenomes without the duplicated elements exceeds those with duplication, many authors assume that the duplications occurred multiple times independently in the bird evolution and the single gene order was ancestral for all birds.

However, the lack of duplication may result from incorrect molecular techniques. The growing number of previously unidentified duplications implies that many avian mitogenomes without duplication, in fact can have it. Thus, a diligent searching for mitogenomic duplications is crucial to establish their true occurrence and evolution. Our results indicate that ancestors of many avian groups contained mitogenomic duplications, which were inherited or lost in their descendants. It cannot be excluded that the last common ancestor of all birds also contained the duplication. If this hypothesis occurred true, it would completely change the present scenario for the evolution of avian mitochondrial genomes.

The duplicated control regions are interesting from evolutionary point of view because their sequences can become similar or identical due to concerted evolution. Thus, it is interesting to trace the mitogenome evolution along avian phylogeny to find out how often the control regions were homogenized as well as in which lineages the duplication happened and in which degenerated. It is also interesting if the presence or absence of duplication is only a neutral trait or can provide a real selective advantage. Previous studies suggested that birds having mitogenomes with the duplicated control region are characterized by longer life-span as well as a greater metabolic rate and energy production.

Thus, the aims of this project is comprehensive examination of many avian mitogenomes as well as inferring their evolution and mechanisms of duplications. We are planning to infer if the ancestral gene order in the avian mitochondrial genome was single or duplicated and how mitogenomic duplicated elements evolved along the avian phylogeny and in various lineages. Finally, we will check whether mitochondrial duplications and their loss are associated with specific features of birds.

We are planning to sequence mitochondrial and nuclear genomes of at least 100 avian species representing ca. 20 avian orders. Duplication within mitogenomes will be searched using individually designed diagnostic amplification reactions. We will apply two strategies of sequencing. The new sequences and those available in GenBank database will be used to construct phylogenetic trees. We will compare phylogenies based on mitochondrial and nuclear markers to reconstruct evolution of the mitogenomes. We will map the identified avian gene orders onto the species phylogenetic trees based on nuclear markers to reconstruct evolution of mitogenomes and their duplication. Separate phylogenetic trees for control regions will reveal their evolution and determine when they were duplicated or homogenized. An interesting innovation will be correlation of the mitochondrial duplications or their loss with avian body mass and length, basal metabolic rate and the maximum life span.

Our project will be the first analysis done on such a large scale. If our results contradict that the standard mitochondrial gene order is the ancestral avian organization of the mitogenome, it will completely change the common view on the evolution of the bird's mitogenome. The results of this project will also provide a high-quality data that will be useful for reconstruction of avian phylogeny based on mitochondrial and nuclear sequences. Our results on the mitogenome evolution in birds can also help to understand the evolution of mitochondrial genomes in other vertebrates in which similar duplications were found. It can allow to discover common mechanism leading to the duplications and mitogenome organization.