

The analysis of mitochondrial genome evolution in parrots on the example of genus *Amazona*

In 1973, a famous geneticist and evolutionary biologist Theodosius Dobzhansky said that “nothing in biology makes sense except in the light of evolution”. This well-known statement is still topical. In order to understand the diversity of the organisms that surround us, we need to study them from the evolutionary point of view. Basic evolutionary changes take place at a molecular level. That is why, a lot of important and interesting information is provided by the analysis of. In this type of study, mitochondrial genomes are especially popular.

The sequences of such genomes evolve at a very fast pace, compared to nuclear genomes, and are passed through the mother's line. This features make the mitochondrial DNA sequences especially useful in evolutionary and phylogenetic analyses. What is interesting, despite the quick pace of evolution of the sequences, mitochondrial genomes of vertebrates seem to be very conservative in terms of their length and structure. It is believed that the stable size of the genomes, the gene composition and arrangement, as well as the lack of introns and intergenic sequences, indicate that mitochondrial genomes evolve towards reduction of their size or have already reached a steady state. These features also suggest that such phenomena like duplications and gene rearrangements should occur extremely rarely, and if the duplications take place, they should be quickly eliminated. Along with the development of sequencing techniques and a growing number of published mitochondrial genome sequences, it turned out that these events actually take place in some genomes and may be much more frequent than it was originally supposed.

One of the groups of organisms that is appropriate for investigating such phenomena are the parrots of genus *Amazona*, in which an unprecedented rearrangement of mitochondrial genes was found. What is more, a case of duplication of the control region, along with the duplication of adjacent genes was described for the very first time. Interestingly, both copies of the sequences seem to perform biological functions. The *Amazona* genus is the richest in species among all parrot genera. It comprises 30 species that are diversified morphologically and ecologically. The Amazon parrots inhabit mainly the mainland, two American continents, but some of them are endemic and live on small islands of the Caribbean Sea. The presence of those unusual mitochondrial genome features as well as the amount of species and their diversity in this genus make it possible to analyse the evolution of mitochondrial genomes and the mechanisms of duplication in them.

Although duplications and rearrangements in mitochondrial genomes are described in various groups of vertebrates, still very little is known about the mechanisms of their formation and sustaining in the genome. It is not clear what benefits the duplicated sequences may bring. Are they, for example, related with the effectiveness of respiratory processes and energy release occurring in mitochondria? It is especially important for organisms with high metabolism rate, such as birds

It is also an open question whether the duplications occur independently in the individual evolutionary lineages or their presence is the original state and the copies of sequences are eliminated in during evolution in these lineages. The proposed analysis based on the complete mitochondrial genomes can help to answer these questions. The proposed analyses will let us determine when and at what pace those phenomena take place and whether they were related to migrations and settling new regions by parrots. It is possible that a more detailed phylogenetic analysis of genomes investigated in terms of rearrangement and duplication will lead to a revision of *Amazona* taxonomy, as it is not very clear. The proposed analyses are to determine the grade of heteroplasmy in the mitochondrial genomes, i.e. a simultaneous existence of different molecules of mitochondrial DNA. This phenomenon is connected with ageing and diabetes, along with many other human mitochondrial diseases. For example, centenarians tend to have the heteroplasmy level higher than average. Recognition of the grade of heteroplasmy in birds can bring a broader insight into these processes in humans.