

Analyses of phylogenetic relationships and evolutionary history of parrots based on new molecular markers

A famous epigraph by Jay M. Savage said that “Nothing in evolutionary biology makes sense except in the light of a phylogeny.” This motto highlights significance of phylogenetic studies (i.e. reconstructing evolutionary relationships between species) in understanding of all evolutionary processes and mechanisms, e.g. origin of species (speciation) and their diversification and spreading. Such studies are also necessary for modern natural taxonomy and systematics, which try to describe and classify species according to their evolutionary relationships.

One of animal groups, which is suitable to study these subjects are parrots. These birds constitute the order *Psittaciformes*. Parrots represent one of the most species-rich groups of birds, with 92 genera and 394 species. At present, they inhabit almost all continents, South and Central America, Australia and Oceania, Africa as well as South and Southeast Asia. Parrots are diversified to many morphologically and ecologically distinct forms. They are of great ecological importance, playing a significant role in the dispersion of seeds of many tropical plant species. According to the International Union for Conservation of Nature, *Psittaciformes* are the most endangered order among all birds. Currently, at least 111 parrot species are threatened with extinction, whereas at least 18 taxa are already considered extinct or extinct in the wild. The main reason of this situation is the degradation of natural habitats of these birds, which results from expansively growing agricultural economy, deforestation and poaching. Still disputed and constantly changing systematics of parrots is a problem for their active protection. Many taxa belonging to *Psittaciformes* has an unresolved status of the species or subspecies, which makes that it is difficult to carry out conservation programs. The systematics and nomenclature of many genera is undergoing dynamic changes.

Many aspects of their origin, phylogeny, evolution and taxonomy are still unsolved due to the lack of sufficient number of molecular data. Therefore, the aim of this project is the search for new nuclear molecular markers (genes and retrotransposons) bearing a suitable phylogenetic signal. Next, the markers, together with complete mitochondrial genomes, will be applied in extensive phylogenetic analyses of parrots. The studies will be associated with molecular dating (determining time of split of lineages) and phylogeographic analyses (connecting split of lineages with geography).

The proposed phylogenetic analyses based on the large number of molecular markers and board taxon sampling of *Psittaciformes* help to determine controversial taxonomic status of many parrots and select representatives of particular evolutionary lineages for special conservation and protection including rare species. The results will be also important for the crowd of parrot keepers and breeders for whom the knowledge about the precise identification of species is important for their breeding and reproduction. The proper classification of parrots is also crucial for the struggle against smuggling and trade of the endangered species.

Our studies enable to find the closest relatives of parrots among other birds' orders as well as determine when parrots originated, diversified into particular lineages, migrated and inhabited new continents and regions. The will studies connect evolution of parrots with climate fluctuations and vegetation changes as well as geological events such as the break-up of Gondwanaland, uplift of Andes, the emergence of Panama isthmus and other migratory routes.

The planning analyses will explain complex evolutionary history of parrots and untangle still controversial systematics problems on different taxonomic levels, from families to species, including interspecies crosses and cryptic species (which are difficult to recognise morphologically or indistinguishable). Our results will enable to assess the role of dispersal (differentiation associated with spreading to new regions) and vicariance (differentiation resulting from the emergence of physical or biotic barriers between populations) in parrots' diversification and evolution. Analyses will show if the diversification of Neotropical parrots was associated with changes in Amazonia habitats and their fragmentation into potential refugia (small isolated region in which species could survive).

Our multi-faceted analyses will allow reconstruction of comprehensive evolution and biogeographical history of parrots. Well-resolved phylogenies will be important in proper interpretation of different comparative studies of parrots concerning vocalization, comparative anatomy, longevity, breeding behaviour, invasive species and biodiversity. Based on reliable phylogenetic trees it will be possible to check if these features evolved independently or were inherited from common ancestors. The tested usefulness of markers and phylogenetic methods and evolutionary models will have an important influence on phylogenetic analyses of other organisms. The results can be a good reference and model for other groups of birds and also mammals, which rapid evolution and diversification associated with spreading to new regions have started since Cretaceous and Paleogene boundary.