

## Trans-Atlantic versus trans-Beringian migration routes – the role of biogeographical events during the largest avian radiation

Seminal biogeographical publications concern multiple colonisation events of the Nearctic and Neotropical regions. The trans-Beringian (from Asia), and the north (from Europe) and south (from Africa) trans-Atlantic pathways had important roles in the radiation of a wide variety of taxa, including less mobile insect groups (mostly trans-Beringian passage to North America) in comparison to e.g. birds. However, they have been studied mostly in focal avian lineages and thus, the general pattern of the aforementioned dispersal routes across birds is not yet fully understood. An increasing number of scientific publications examine the biogeographic origin of passerine birds (Aves: Passeriformes), and they have proposed several alternative hypotheses placing the major radiation hotspots in different biogeographical regions.

The major lineages, first, spread from Southeast Asia into the Palearctic and Afrotropical regions because the major orogenetic events in Central Asia, i.e. the uplift of the Eurasian mountains systems fundamentally drove these directional events. Then, the Nearctic and Neotropical regions were colonised from the north, through the Beringia, on the one hand, and from south, i.e. from Africa to South America, on the other hand. Previous studies found that the limitation in the distribution of closely related taxa (e.g. *Turdus* vs. *Catharus* genera) reflects these patterns, but they have never been tested in a diverse range of bird species. Moreover, long-term climatic constraints have led to the fixation of migratory behaviour compared to those species that were isolated on islands and underwent rapid allopatric diversification (increased number of subspecies/species).

During the varied periods in the last 40 million years, the common ancestor of Passeriformes and the basal clades of both the corvid and passeroid lineages originated in Australasia, around the Eocene-Oligocene boundary. The subsequent rapid diversification is likely related to convergent evolution by adaptation to diverse and available niches, also on different continents. Passerine species often replaced each other, which could have led to a more gradual occupation of niches. However, the phylogenetic patterns vary among the components of divergence (climatic, habitat, trophic niches) in different bird assemblages. Geographic changes and their climatic consequences had a great impact on the radiation of birds, also leading to variation in behaviour traits. The number of migratory passerine lineages increased during and after the Oligocene/Miocene boundary and the expansion of open habitats established the current bioclimatic zones, and provided new niches for bird species. Furthermore, the increasing seasonality facilitated the appearance of migratory behaviour related to niche switching in specific lineages (Tyrannidae, Sylvioidea, Muscicapidae, Passeroidea). Consequently, sister lineages appeared where species are widely distributed and migratory whilst other species are isolated (endemic or island species) and became non-migratory.

For the estimation of ancestral biogeographic and behaviour characteristics of birds, the selection of appropriate model groups should be based on the most complete phylogenetic datasets available. Nevertheless, the aforementioned factors caused significant changes in several aspects of avian life history, e.g. in their nest building behaviour or in their sex-specific contributions to reproduction. Furthermore, 10–20 million years ago, during the Miocene, the transforming topography of the Earth and the newly emerging habitats also had a significant effect on the radiation and diversification of different groups (e.g., *Sylvia* spp., *Turdus* spp., Accipitriformes) and on the adaptation to changes in climatic conditions, e.g. on the emergence of migration, as a consequence. Moreover, birds are also responding rapidly and ongoing climatic changes via their ecology and behaviour, meaning that this project has implications for the viability of birds in future climates, therefore, studying their evolution and historical biogeography can provide substantial information for more effective conservation programmes of protecting bird- and biodiversity.

The above examples form the basis of studies addressing important questions regarding the origin and evolution of the Eurasian avifauna. Research examining the evolution of avifauna at biogeographic scales is topical and has broad appeal for biogeographers, evolutionary biologists and ornithologists. Revising some alternative hypotheses for the origin of migration is also timely, specifically regarding patterns reflecting the distribution of species.

The work planned in this proposal will be mainly based on the application of phylogenetic, biogeographic and comparative methods, and thus, the knowledge in ecology and evolution, historical biogeography, statistics, the R language is advantageous but not exclusive.

For more information or application, please send a message to Jenő Nagy, Research Fellow, HUN-REN-UD Conservation Biology Research Group via [jenonagy.off@gmail.com](mailto:jenonagy.off@gmail.com).

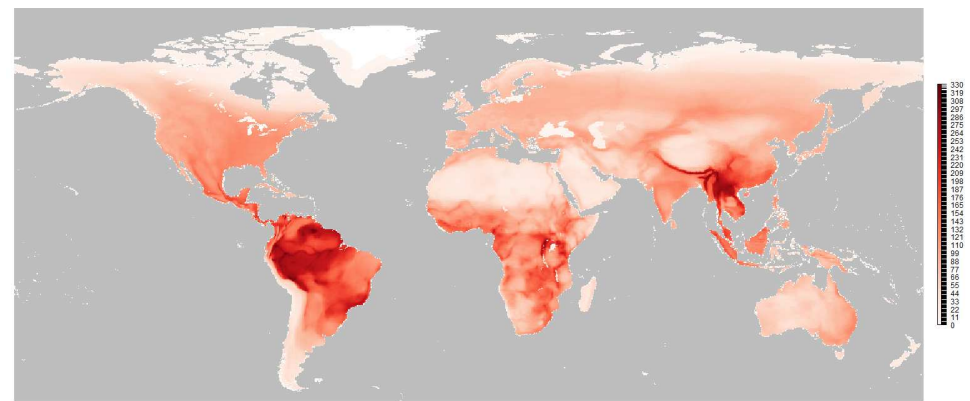
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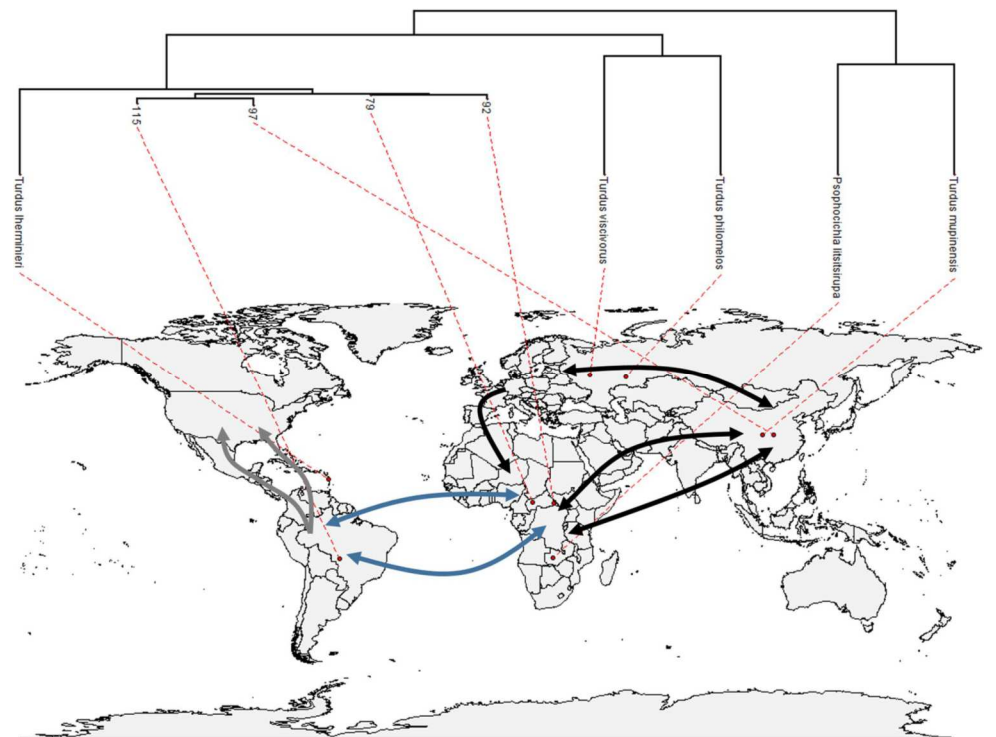
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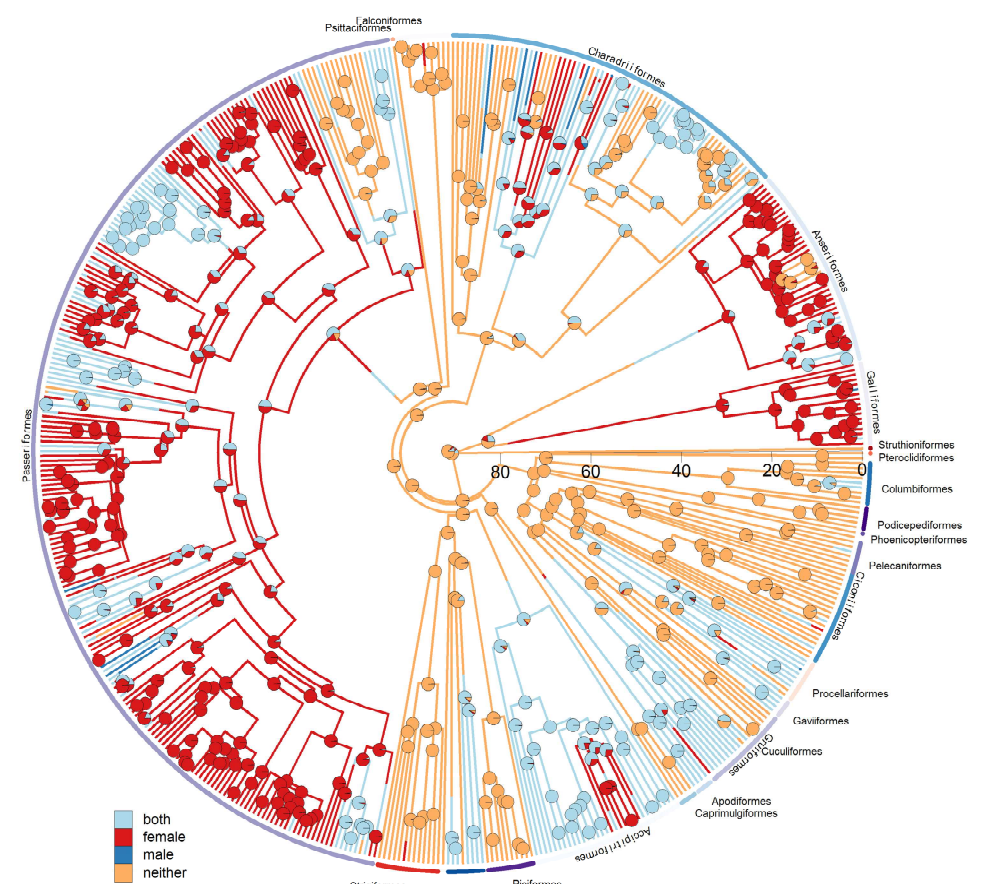
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Diversity map of Passeriformes (5870 species)



Mapped phylogeny of *Turdus* thrushes indicating the major dispersal routes during their evolution.



The phylogenetic hypothesis of the nest building sex(es) in 521 bird species