

Internship proposal (Master 2)

Detection of balancing selection in *Ficedula* flycatchers

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Keywords:

evolution, population genetics, natural selection, genome-wide polymorphisms, flycatchers

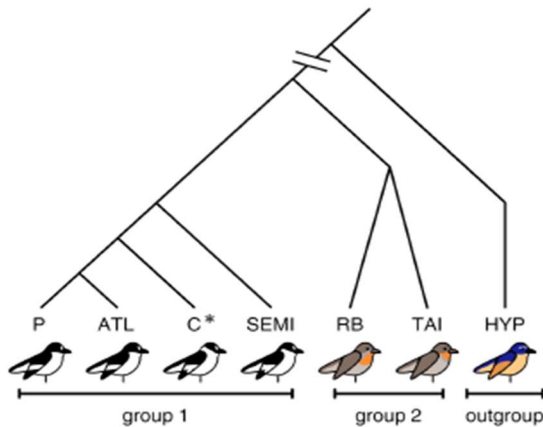


Figure: Phylogenetic tree of the flycatcher species under study

Project:

Understanding how species adapt to their environment is a central question in evolutionary biology. Notably, it is still unclear how much of the observed phenotypic diversity in nature can be explained by neutral versus selective processes. The study of the genomic variation within and between species can allow us to reconstruct their evolutionary history, and to trace back adaptive events. Among the different adaptive forces, positive and negative selection are characterized by a reduction of genetic diversity within species, while balancing selection is defined as a process that maintains genetic diversity. There are different mechanisms that result in balancing selection: heterozygote advantage (higher fitness of heterozygotes); negative frequency-dependent selection (higher fitness of rare alleles); fluctuating selection in time or space (Charlesworth, 2006). In addition, host-pathogen co-evolutionary dynamics also seem to result in maintenance of genetic diversity (Ebert & Fields, 2020). However, it is at present not known which of the different mechanisms is prevailing in nature, since balancing selection is hard to detect within species. To overcome this limitation, multiple methods have been developed to take advantage of information across multiple species (Fijarczyk & Babik, 2015).

The aim of this internship is to look for regions of the genome experiencing balancing selective pressures across multiple species of *Ficedula* flycatchers, migratory birds in the family *Muscicapida*. For this purpose, the student will take advantage of an assembled polymorphism dataset across 280 individuals belonging to seven *Ficedula* flycatcher species that have been previously sampled and sequenced in two separate sequencing efforts (Burri et al. 2015; Chase et al. 2021). The genomic data have then been collated, mapped to the same reference genome and the resulting single nucleotide variants (SNVs) have been called, filtered and transformed into a vcf (*variant calling format*) file. The internship will consist in using this vcf file to first obtain the ancestral state for all polymorphisms (using parsimony) and then apply existing statistics (DeGiorgio et al, 2014; Cheng & DeGiorgio, 2019; Soni et al, 2022) to investigate the prevalence of balancing selection in those bird species and to identify and characterize genomic regions that have been affected by it.

References:

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Skills of the candidate:

The student should have a strong interest in molecular evolution and population genetics, notably in data analysis. He/she should have skills in bioinformatics or be willing to acquire such skills.