

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

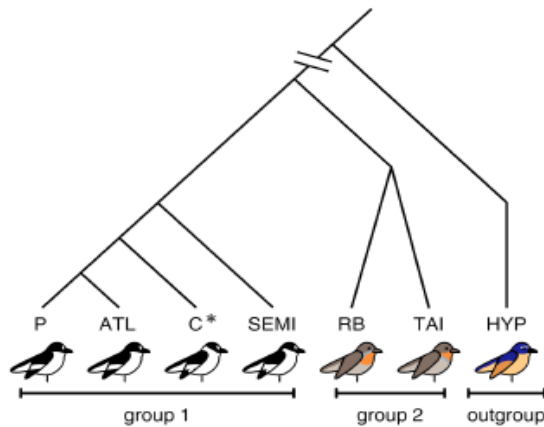


Figure: Phylogenetic tree of the flycatcher species under study

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. While it seems that host-pathogen co-evolutionary dynamics frequently result in the maintenance of genetic diversity (Ebert & Fields, 2020), the overall prevalence and targets of balancing selection are not fully elucidated yet, partly because it is quite hard to detect using within-species data only. Recently, multiple methods have been developed to take advantage of information across multiple species to identify the genomic regions under balancing selection (Fijarczyk & Babik, 2015; DeGiorgio et al, 2014; Cheng & DeGiorgio, 2019).

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 and filtered. A pipeline has then been developed, based on sequencing coverage, to detect collapsed regions in the genome, which can give rise to an artefactual enrichment of polymorphisms (resembling signatures of balancing selection). The internship will first consist in fine-tuning this pipeline to improve its sensitivity and specificity but also to make it publicly available. Then, the student will run an existing software (BalLeRMix) to detect balancing selection targets in the genome, followed by functional enrichment analyses. He/she will also investigate the underlying evolutionary mechanisms by exploring the sharing of signals between species and obtain phylogenetic trees for the top signals. This will overall inform us on the prevalence of this mode of genomic adaptation in these bird species.

References:

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- Soni V, Vos M, Eyre-Walker A. A new test suggests hundreds of amino acid polymorphisms in humans are subject to balancing selection. *PLoS Biol.* 2022 Jun 2;20(6):e3001645.

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. We also wish to present this project for a PhD thesis, so the candidate should be interested in pursuing in research. We would appreciate to receive the M1 grade of the candidate together with his/her CV.