

Master Internship offer M2

Detection of balancing selection in *Ficedula* flycatchers

Supervisors:

Laure Ségurel (CR CNRS), laure.segurel@univ-lyon1.fr

Carina Farah Mugal (CR CNRS), carina.mugal@univ-lyon1.fr

Host laboratory:

LBBE – Laboratoire de Biométrie et Biologie Evolutive, UMR5558

Batiment Mendel, 43 boulevard du 11 novembre 1918, Villeurbanne

Team BPGE « Bioinformatique, Phylogénie et Génomique Evolutive »

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: if heterozygotes are favored in the population, if there is negative frequency-dependent selection (the rarer forms have a higher fitness) or if selection fluctuates in time or space (Charlesworth, 2006). Host-pathogen co-evolutionary dynamics seem notably to often result in such maintenance of genetic diversity (Ebert & Fields, 2020). However, balancing selection is hard to detect within species, and 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 assemble a polymorphism dataset across 280 individuals belonging to seven *Ficedula* flycatcher species that have been previously sampled and sequenced in two separate efforts (Burri et al. 2015; Chase et al. 2021). The internship will consist primarily in collating the data, performing read mapping and SNP calling in order to have a large dataset that we can further analyze. In a second step, we will 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 identify and characterize genomic regions that have been affected by it.

References:

- Burri R, Nater A, Kawakami T, Mugal CF, Olason PI, Smeds L, Suh A, Dutoit L, Bureš S, Garamszegi LZ, Hogner S, Moreno J, Qvarnström A, Ružić M, Sæther SA, Sætre GP, Török J, Ellegren H. Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers. *Genome Res.* 2015 Nov;25(11):1656-65
- Charlesworth D. Balancing selection and its effects on sequences in nearby genome regions. *PLoS Genet.* 2006 Apr;2(4):e64.
- Chase MA, Ellegren H, Mugal CF. Positive selection plays a major role in shaping signatures of differentiation across the genomic landscape of two independent *Ficedula* flycatcher species pairs. *Evolution.* 2021 Sep;75(9):2179-2196
- Ebert D, Fields PD. Host-parasite co-evolution and its genomic signature. *Nat Rev Genet.* 2020 Dec;21(12):754-768.
- Fijarczyk A, Babik W. Detecting balancing selection in genomes: limits and prospects. *Mol Ecol.* 2015 Jul;24(14):3529-45.
- DeGiorgio M, Lohmueller KE, Nielsen R. A model-based approach for identifying signatures of ancient balancing selection in genetic data. *PLoS Genet.* 2014 Aug 21;10(8):e1004561.
- Cheng X, DeGiorgio M. Detection of Shared Balancing Selection in the Absence of Trans-Species Polymorphism. *Mol Biol Evol.* 2019 Jan 1;36(1):177-199.
- 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.