

INTERNSHIP PROPOSAL M2 2024-2025

TITLE: Characterization of the genetic diversity of European dark bees following a recent territorial change in the Cévennes national park

Supervisors, addresses, e-mails, URLs:

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Address of the internship location:

Musée de l'Homme, 17 place du Trocadéro et du 11 novembre, 75016 Paris

Possibility of a PhD proposal on/related to the internship subject:

YES NO

Publications of the supervisors related to the proposal (max. 5):

1. Guez J, Achaz G, Bienvenu F, Cury J, Toupance B, Heyer E, Jay F*, Austerlitz F*. (2023). Cultural transmission of reproductive success impacts genomic diversity, coalescent tree topologies and demographic inferences. *Genetics* **223**: iyad007. doi: 10.1093/genetics/iyad007
2. Fagny, M., Austerlitz, F. (2021). Polygenic adaptation: Integrating population genetics and gene regulatory networks. *Trends in Genetics*. **37**: 631-638. doi: 10.1016/j.tig.2021.03.005
3. Jay F, Boitard S, Austerlitz F 2019. An ABC method for whole-genome sequence data: inferring Paleolithic and Neolithic human expansions. *Molecular Biology and Evolution*. **36**: 1565-1579. doi: 10.1093/molbev/msz038
4. Quach, H., Quintana-Murci, L. (2017). Living in an adaptive world: Genomic dissection of the genus Homo and its immune response. *Journal of Experimental Medicine*, 214(4), 877-894. doi:10.1084/jem.20161942
5. Quach, H., Rotival, M., Pothlichet, J., Loh, Y.-H. E., Dannemann, M., Zidane, N., . . . Quintana-Murci, L. (2016). Genetic adaptation and Neandertal admixture shaped the immune system of human populations. *Cell*, 167(3), 643-656. doi: 10.1016/j.cell.2016.09.024

DESCRIPTION (2 PAGES MAX.):

INTRODUCTION, SCIENTIFIC CONTEXT:

As pollinators, honeybees play a critical role in ecosystem functions and human food security¹. Accordingly, the widespread bee decline observed over years threatens both biodiversity conservation and global food supplies. To preserve the existence and the genetic diversity of local honeybee populations, the association "Arbre aux Abeilles" is engaged in the conservation of the

European dark bee in the Cévennes area (Southern France). Four years ago, it launched a territorial development project aimed at rebuilding an abundant and diversified flora, favorable for both humans and pollinators, by cultivating local plant species that have been neglected by our agricultural system. However, the effect of these measures on the conservation of black bees and their genetic diversity has not been studied.

RESEARCH PROPOSAL/OBJECTIVES:

The aim of the internship will be to (i) characterize the genetic architecture at the genome-wide level of the European dark bees *Apis mellifera mellifera* sampled in different apiaries of the “Arbre aux Abeilles” association, (ii) highlight population structure and relatedness across honeybee populations, (iii) identify genes that have been selected for *Apis mellifera* survival and adaptation to changing environments and (iv) contrast the obtained population genetics metrics with those from populations collected in European black bee conservatories², for which genetic data is available.

DESCRIPTION OF DATA if applicable (Data must be available before the start of the internship):

The first data set, which will be available in November 2024, consists in the whole genome sequencing (at a minimum coverage of 10X) of 30 European dark bees collected in two apiaries from the association “Arbre aux Abeilles” located in the National Park of the Cévennes. The second data set consists in the whole genome sequencing data (at a minimum coverage of 10X) obtained from 40 honey bees collected in six different French European dark bee conservatories (data already available in the laboratory).

METHODOLOGIES:

Following the GATK best practices using high-throughput sequencing data³, the student will be responsible for the development of an analysis pipeline, which includes the quality check and cleanup of the sequencing data, the alignment of the reads to the *Apis mellifera* reference genome and the variant calling. The student will also perform exploratory analyses using population genomics tools such as “selscan” and “PCAdapt”^{4,5}. The investigation of the evolutionary history of native *Apis mellifera* in France is detrimentally missing in the literature, knowing that it informs on the genetic capacity of these bees to

persist when facing habitat and climatic changes. Therefore, we expect from the resulting analyses to gain original insights into *Apis mellifera mellifera* genetic adaptation, based on which effective strategies can be developed for constructing future sustainable apiculture managements and favoring the conservation of honeybees.

REFERENCES (max. 5):

1. Potts SG, Imperatriz-Fonseca V, Ngo HT *et al.* 2016; Safeguarding pollinators and their values to human well-being. *Nature* 540(7632): 220-9. [url](#).
2. Requier F, Garnery L, Kohl PL *et al.* 2019; The Conservation of Native Honey Bees Is Crucial. *Trends in Ecology & Evolution* 34(9): 789-98. [url](#).
3. Van der Auwera GA & O'Connor BD. 2020; Genomics in the Cloud: Using Docker, GATK, and WDL in Terra (1st Edition). O'Reilly Media.
4. Szpiech, Z. A. (2024). selscan 2.0: scanning for sweeps in unphased data. *Bioinformatics*, 40(1). [url](#).
5. Luu, K., Bazin, E., & Blum, M. G. (2017). pcadapt: an R package to perform genome scans for selection based on principal component analysis. *Mol Ecol Resour*, 17(1), 67-77. [url](#).