



Internship available for a 2nd-year master student in population genomics to work on honeybee genomics (Toulouse, France)

Context:

The *Varroa destructor* mite is a major cause of colony loss in honey bees *Apis mellifera*. In order to find sources of resistance, several honey bee lines are measured by beekeepers for traits related to resistance to this parasite. These lines are monitored by genotyping DNA from a pool of males, representing the queen genome, with a SNP array containing 10 000 markers. These genotypes will allow us to characterize the genetic background present in these lines and to detect possible queen replacements in the colonies.

Available data:

- Genotyping of 700 bee lines using a 10,000 SNP array.
- Pedigrees of honey bee lines
- Genetic structure of reference populations (WGS data of subspecies *A. m. mellifera*, *A. m. ligustica*, *A. m. carnica* and *A. m. caucasica*)

Objectives :

The objective is twofold: 1) To determine in these lines the proportions of the different genetic backgrounds (subspecies) present in France, by comparison of the genotypes obtained with the 10k SNPs array with the data obtained from whole-genome sequencing of the reference populations. The analysis of the genetic structure will use different methods (PCA, Admixture software, etc). 2) Infer the kinship based on the data, in particular to detect queen replacements by comparing the genotypes obtained with the expected results based on the pedigrees.

Desired profile :

Master student in population genomics (or quantitative genetics), with a strong interest in the analysis of large data sets. Knowledge of the Linux environment (Bash) is desirable.

Hosting structure and location :

INRAE Toulouse (GenPhySE, team Cytogene, 31326 Castanet Tolosan)

Internship period and compensation:

January to June 2024 (flexible, depending on the student's availability); financial compensation : 4.05€/h (~550€/month)

Supervisors :

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References:

Wragg D, Eynard SE, Basso B, Canale-Tabet K, Labarthe E, Bouchez O, Bienefeld K, Bieńkowska M, Costa C, Gregorc A, Kryger P, Parejo M, Pinto MA, Bidanel JP, Servin B, Le Conte Y, Vignal A. Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. *Molecular Ecology Resources*. 2022 Nov;22(8):3068-3086.

Wragg D, Techer MA, Canale-Tabet K, Basso B, Bidanel J-P, Labarthe E, et al. Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. *Genome Biology and Evolution*. 2018 Jan 1;10(1):220-38.