Research-oriented Master 2 internship:

Metagenomic analysis of honeys as a tool for traceability and monitoring of the infestation level of the varroa parasite

Background :

The host lab has extensive experience in the genomic characterization of honey bees (*Apis mellifera*) used by French beekeepers. As part of the MALLAURIE project - Honey and bees: the contribution of sequencing based solely on hive products to more international and ethical sampling - we aim at obtaining honey bee genetic data via a non-lethal strategy, through sequencing DNA extracted from honey.

Objective of the internship :

The aim of the internship will be to develop a metagenomic approach for the characterisation of DNA present in honey, other than belonging to honey bees. The focus will be on two other major types of organisms: plants and the varroa parasite. Thanks to a collaboration with the UMR *Abeilles & Environnement* (INRAE Avignon), we have set up a pilot study following hives that were migrated on different floral resources over the course of the season, including different species of varying pollen and nectar content, and with a general expectation of an increase in varroa infestation during the season. In addition, we have extracted DNA from a large number of honey samples of various origins. All the samples are anonymized before sequencing. The student will lead the investigation in order to propose a potential geographical origin of the honeys using the sequencing reads from the plants. Some additional questions may be investigated depending on the progress made during the internship.

Available data :

At the start of the internship, we will have around 80-100 honey samples sequenced at relatively low coverage on 2 to 3 MiSeq runs (~50 of which will come from the pilot study carried out with INRAE in Avignon), as well as a full NovaSeq run for high-coverage sequencing of 10-20 samples.

Ideal candidate :

The master student will have a certain taste for exploring large datasets and bioinformatics, with the use of a command-line computing softwares, ideally with a good knowledge of at least a scripting language (R, python, bash). Scientific knowledge in genomics and/or population genomics would be appreciated.

Hosting structure and location :

You will be hosted in the Cytogene team of the UMR GenPhySE at the INRAE Occitanie-Toulouse center (Castanet-Tolosan, France). The laboratory is easily accessible from downtown Toulouse (metro line B + "L6" express bus).

Internship period and compensation :

The internship will ideally be between January and June 2024, with the possibility of adjustment depending on the student's availability (e.g. March to September period). A stipend is associated with this internship (contractual amount at INRAE: 4,05€/hour, i.e. ~550€/month on a 35-hour per week basis).

Supervisors:

Thibault Leroy, thibault.leroy@inrae.fr (main supervisor)
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References (more available upon request):

Bovo, S., Utzeri, V.J., Ribani, A. *et al.* Shotgun sequencing of honey DNA can describe honey bee derived environmental signatures and the honey bee hologenome complexity. *Sci Rep* **10**, 9279 (2020). https://doi.org/10.1038/s41598-020-66127-1

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