Poste d'ingénieur·e d'études
Lead Research Technician position

Haplotagging for the study of genetic architecture of complex traits

ERC-funded 54-months position,
ISYEB, Paris, France

Offer Description

Summary

We offer a 4.5 years (54 months) position, working as Ingénieur·e d'Études (roughly equivalent to a Lead Research Technician position) to manage and implement the EvoGenArch ERC research project, especially aspects related to molecular ecology (molecular and bioinformatics aspects of the haplotagging approach, participating to field work, data management). The job provides the opportunity to explore a wide area of molecular ecology, from bench work to field work, with support from a lab technician and a bioinformatician for the most technical aspects of the job. The bench work (notably developing the new haplotagging approach in the lab) will compose most of the work load, followed by sequences analysis and data management, while field work will be the lightest part (two months each year). The candidate will work for the École Pratique des Hautes Études (PSL University), joining Pierre de Villemereuil's team, at the Institute for Systematics, Evolution, Biodiversity (ISYEB), located within the *Muséum National d'Histoire Naturelle* (MNHN) in Paris. This position is funded as part of the EvoGenArch ERC Starting Grant. The position starts on 2024-09-16.

Scientific context

A major challenge in evolutionary biology is to understand and predict the evolution of phenotypic traits influenced by many genes, a.k.a. quantitative traits, which represent the majority of adaptive traits. For this, we require an accurate knowledge of the statistical distribution of the effects of the genes (or QTL, for Quantitative Trait Loci) on the phenotype, or the "genetic architecture" of the trait. However, it has not been possible to firmly check theoretical predictions against empirical data, due to a lack of method to accurately infer genetic architecture.

The EvoGenArch project aims at developing a new method to study the distribution of the effects of QTL, and apply it to the team's species of interest (common lizard, *Zootoca vivipara*) on the one hand; and a wide set of species on the other hand. In order to obtain genomic data for the common lizard, and for some of the other species, we will use the new and innovating haplotagging approach, in order to obtain whole-genome sequences with linked-read providing information about molecular linkage and thus haplotypes. The Ingénieur·e d'Étude (IE) will be in charge of the management and implementation of the sequencing via the haplotagging approach, from the molecular work to the bioinformatics analysis, after some training at the GenSeq platform in Montpellier, in collaboration with Pierre-Alexandre Gagnaire. The IE will be seconded by the team lab technician, Pascaline Chifflet-Belle, and the team bioinformatician, Élise Gay, for this task. The IE will also be in charge of data management throughout the project, and participate in the field work on the common lizard system.

Job description

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- Design and refinement of the protocol for the haplotagging approach, in collaboration with the GenSeq platform in Montpellier, already experienced with this protocol, including on the common lizard, with the help of the team lab technician.
- Implementation of the haplotagging protocol for the common lizard system, as well as one or two other species pertaining to the last, comparative aspect of the project, with the help of the team lab technician.
- Analysis of the sequencing output of the haplotagging protocol, with the help of the team bioinformatician and a PhD candidate, to be hired, working on the common lizard.
- Data management of the project, including sequencing and field work data.
- Overall management of the logistical aspects of the research project, especially pertaining to the tasks described above.

The IE will have latitude to advise for overall refinement in the project, and will of course be associated to all aspects of the project, including dissemination, through authorship and feedback in the analysis and writing of scientific articles.

Hosting lab & team

Pierre de Villemereuil's research focuses on the genetics of adaptation, trying to understand how the levels of the genotype, phenotype and environment interacts to drive evolution in wild popu-

lations, notably in response to anthropic pressures. A combination of evolutionary ecology, quantitative genetics, population genomics and statistical modelling is necessary to unveil the patterns and processes of adaptation in the wild. The Institute for Systematics, Evolution, Biodiversity (ISYEB), located in the beautiful *Jardin des Plantes* of the *Muséum National d'Histoire Naturelle* in Paris, is one of the largest labs studying evolution in the city. ISYEB hosts worldwide leading science in evolution, systematics, phylogeny, genomics and ecology.

Requirements

- Master degree in fields related to molecular ecology (genetics, ecology, evolutionary biology)
- Demonstrated ability to successfully conduct a delimited research project
- Interest in working as part of a team to conduct a large and ambitious research project.
- Experience in bench work and molecular biology applicable to genotyping (e.g. DNA extraction, genotyping protocol, library preparation)
- Basic experience in bio-informatics and/or data management, e.g. familiarity with bash shell, R or Python.
- Interest for field work on the common lizard
- Basic (or higher) level in French will be appreciated

Selection process

Please send (1) a CV/résumé; (2) a short (max. 2 pages) letter of application highlighting past experience and accomplishment, your fit to the profile and your motivation for the position; and (3) a letter of recommendation or contact details of past supervisors to the address pierre.devillemereuil@ephe.psl.eu. Selected candidates will be auditioned by a committee of two to three persons, including the PI, starting from May 15th, for as long as the position is not filled. Candidates are not discriminated against based on their gender, ethnicity or sexual orientation, please all feel welcome to apply!