Post-doctoral position in population genomics (18-24 months).

Population and structural genomics underlying floral diversification in insect-mimicking orchids (genus Ophrys)

Overview of the project

Mediterranean Ophrys orchids mimic female insects through visual, tactile, and scent signals to attract males for pollination. The project focuses on *Ophrys aveyronensis*, a species composed of two geographically separated subspecies (*O. a. subsp. aveyronensis* in France and *O. a. subsp. vitorica* in Spain) that diverged less than 1,500 generations/5,000 years ago. Under the supervision of Yann Bourgeois (IRD Research Fellow) and Joris Bertrand (Senior Lecturer at Perpignan), you will contribute to the development of an ANR project (French National Research Agency), which aims to link genomics, phenotypes, and fitness through innovative approaches using an ambitious long-genome orchid model. Preliminary studies strongly suggest the involvement of structural variants in maintaining floral phenotypic diversity (Gibert et al. 2025). You will work to elucidate the proximal mechanisms and evolutionary pressures underlying this diversity.

You will focus on the genomic aspects of the project, developing new technologies (e.g., haplotagging, long-read Nanopore sequencing) to analyze, from an evolutionary biology perspective, the point and structural variations likely to shape floral traits in *Ophrys*. This involves bioinformatics processing of the generated data, as well as genotyping and quality control of variant calling.

You will contribute to the sampling plan and field missions (Northern Spain and Grands Causses).

You will develop population genetics modeling approaches to test various neutral and selective evolutionary scenarios regarding the origin and dynamics of variants.

You will collaborate with another postdoctoral researcher at the University of Perpignan Via Domitia to link genomic approaches with high-throughput phenotyping approaches.

Your Future Team

You will join the DIADE unit (Diversity, Adaptation, and Development of Plants, UMR232 UM/IRD/CIRAD) in Montpellier, a dynamic research environment at the forefront of plant evolutionary genomics. You will have access to regional and national high-performance computing infrastructures (Genotoul, French Institute of Bioinformatics) and collaborate with a local (CBGP, IRD) and international network of researchers working on the genomics of speciation and plant evolutionary biology. The project also involves field sessions in France and Spain.

Profile

You have developed the following skills:

1. Proven expertise in genome assembly, annotation, and comparative genomics; proficiency in command-line tools, scripting languages (Python, R, bash), and version control systems (Git); experience with job management systems and cluster computing environments.

2. Strong experience in whole-genome resequencing data analysis, including variant identification (SNPs, indels, transposable elements), selection scans, demographic inference, and experience with simulation tools (coalescent, msprime, SLIM, etc.).
3. Experience with challenging genomic datasets, particularly large genomes (>2 Gb) with high repetitive sequence content; familiarity with long-read sequencing technologies (PacBio, Oxford Nanopore) and associated analytical tools.
4. Knowledge of the identification, annotation, and population-level analysis of transposable elements; understanding of TE dynamics and their impact on genome evolution.

You demonstrate the following personal qualities:

1. **Autonomy and initiative:** Ability to independently manage complex analytical projects while knowing when to seek advice and collaborate.
2. **Rigor and attention to detail:** Commitment to producing high-quality, reproducible research with careful documentation and validation of results.
3. **Effective communication:** Strong scientific writing skills and the ability to present complex concepts clearly to diverse audiences; proficiency in English (French is a plus but not required).
4. **Adaptability and problem-solving:** Ability to tackle technical challenges, quickly learn new methods, and adjust approaches based on results.
5. **Collaborative spirit:** Enthusiasm for interdisciplinary teamwork, knowledge sharing, and contributing to a stimulating research environment.

Applications & information

People interested in applying or seeking further information should email both scientific leaders of the project, Joris Bertrand (joris.bertrand@univ-perp.fr) and Yann Bourgeois (yann.bourgeois@ird.fr). The application must include a CV (with a publication record) and contact details for two references who may be contacted during the selection process.

References

Baguette M., Bertrand J.A.M., Stevens V. & Schatz B. (2020) Why are there so many Bee-orchids? Adaptive radiation by intraspecific competition for mnemonic pollinators. Biological Reviews, 95, 1630-1663. DOI: 10.1111/brv12633

Gibert A., Buscail R., Baguette M., Fraïsse C., Roux C., Schatz B. & Bertrand J.A.M. (2024) Holocene climate change promoted allopatric divergence and disjunct geographic distribution in a bee orchid species. Journal of Biogeography, 51, 2424-2439. DOI:10.1111/jbi.14998

Gibert, A., Schatz, B., Buscail, R., Nguyen, D., Baguette, M., Barthes, N., and Bertrand, J.A.M. (2025), Floral phenotypic divergence and genomic insights in an *Ophrys* orchid: unraveling early speciation processes. *New Phytol*, 245: 849–868. https://doi.org/10.1111/nph.20190