**Postdoctoral position**

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**Investigating the epigenetic origin of the fast-renewed inbreeding depression**

**Where :**

* Laboratoire Interactions Hôtes-Pathogènes-Environnements (IHPE), UMR5244 Université de Perpignan Via Domitia (<http://ihpe.univ-perp.fr/>)
* In collaboration with the Centre d’Ecologie Fonctionnelle et Evolutive (CEFE) of Montpellier

**Key words** : Genetic and epigenetic, DNA methylation, inbreeding depression, Physa acuta

**Period : 3 years from** February 1st of 2025 to January 31st of 2028

**Context**:

The post-doctoral fellow will participate in the ANR FRIDA project (Fast-Renewed Inbreeding Depression in Animals, Project No. ANR-23-CE02-0033-01). The goal of the FRIDA project is to investigate new ideas regarding the speed at which inbreeding depression (ID) can arise and its potential persistence in the absence of genetic variation due to epigenetic inheritance. Two characteristics suggest that the epigenetic component may play a role as a source of fast-renewed inbreeding depression (FRID): (i) the ability to generate heritable variation rapidly and (ii) a tendency to revert to ancestral states over generations. This research will focus on *Physa acuta*, a simultaneous hermaphrodite snail known for its high level of ID in natural populations. *P. acuta* can also self-fertilize when no partner is available.

In a previous task, we created highly inbred lines through 28 generations of self-fertilization and crossed two of these lines to produce an F1 “outbred clone.” Since all F1 progeny should be genetically identical, both self-fertilized and cross-fertilized F2 individuals should exhibit the same level of heterozygosity, except for any new mutations that may have occurred in the recent generations. However, significant ID was observed, indicating that ID can develop much more quickly than expected based on typical rates of deleterious mutations. The project aims to investigate the genomic and epigenomic compositions of inbred versus outbred offspring to test genetic versus epigenetic component for FRID.

**Task description :**

The postdoctoral fellow will focus on deciphering the following:

1. The inheritance patterns of specific epigenetic marks (DNA methylations) and their co-inheritance with sequence variants. Oxford Nanopore Technology (ONT) will be employed to track the inheritance of both DNA sequences and methylation in F0-F1-F2 families. This technique enables haplotype-specific characterization of epigenetic marks. The DNA methylation analysis will aim to identify differentially methylated regions (DMRs) in the parental inbred lines and subsequently track these regions through the F1 and F2 generations to investigate parent-offspring resemblance in methylation and the principles of epigenetic transmission (i.e., the methylation equivalent of heterozygosity).
2. Whether inbreeding depression (ID) can occur with extremely low heterozygosity and how much epigenomic correlates of ID are observed under these conditions. MBD-seq analysis will be utilized to epi-genotype 150 F2 individuals to (i) assess whether genetic heterozygosity varies among self-fertilized, sibling-crossed, and cousin-crossed individuals and (ii) determine if these groups differ in terms of the overall amount and distribution of methylation.

Biological samples will be available for all tasks. Phenotypic data will be generated in a parallel work package. The postdoctoral fellow will be involved in basic molecular biology experiments, including DNA extraction and library construction, as well as in the bioinformatics data processing of the sequenced samples.

**Desired skills :**

A conceptual background in ecology, and evolutionary biology and/or population genetics is necessary and an interest toward epigenetic will be appreciated.

An experience in new generation sequencing and in bioinformatics is required.

Basic competence in molecular biology will be welcome

Expérience in writing scientfic papers ans scientific oral presentations is necessary

**Framework :**

The postdoctoral fellow will participate in the ANR FRIDA project, led by Dr. Patrice David (CEFE). He will be involved in Work Package 4, titled "Genomics and Epigenomics of Inbred Individuals." The generation and processing of ONT data will be conducted under the supervision of Dr. Aline Muyle (CEFE), while the generation and processing of MBD-seq data will be overseen by Christoph Grunau (Dr at UPVD) and Céline Cosseau (Dr. at UPVD). Both partner laboratories, CEFE and IHPE, will provide the most suitable conditions for bench experiments and data processing.

The postdoctoral fellow will be primarily based in Perpignan (IHPE). He/She will need to regularly travel and spend time in Montpellier (CEFE) for training on ONT analyses and to exchange with the ANR partners.

**Contact:**

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⏵Scientific leader of the project -> Patrice David : patrice.david@cefe.cnrs.fr

⏵Scientific responsible for the WP4 -> Céline Cosseau : [celine.cosseau@univ-perp.fr](mailto:celine.cosseau@univ-perp.fr)

**How to apply :**

Appplication link will be open really soon.

Please, contact the people in charge with the project before applying.