



UNIVERSITÉ DE
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PROGRAMME D'EXCELLENCE I-SITE

UMR 5244 Université de Montpellier-CNRS-IFREMER- Université de Perpignan via Domitia
Interactions Hôtes-Pathogènes-Environnements (IHPE)
Université de Perpignan via Domitia
58, avenue Paul Alduy, Bât R, F-66860 Perpignan Cedex, France
Tel : 33 (0)4 68 66 20 50
<https://ihpe.fr>

Job Title: Post-Doctoral Researcher – Haplotype-Resolved Assembly and Structural Variation of Polyploid Genomes in Transmissible Cancers of the Blue Mussel (M/F)

Affiliated Unit: Host-Pathogen-Environment Interactions (IHPE)

Contract Type: Fixed-term contract (CDD)

Duration: 18 months

Project Title: “Mechanisms and evolutionary significance of hyperploidy variations in a long-lived parasitic cancer”

Project Acronym: HYPERCAN

Overall Project Duration: 2023–2028

Project Summary:

The goal of the HYPERCAN project is to decipher how transmissible cancer lineages in bivalves, which have been evolving over hundreds of years, cope with clonal degeneration and succeed in generating sufficient genetic diversity to persist in host populations despite the absence of sexual reproduction. The main hypothesis is that hyperploidy—a hallmark of these cancers—contributes to increased clonal heterogeneity and temporarily masks the genetic load.

To test this hypothesis, we will investigate the evolutionary processes underlying *Mytilus trossulus* Transmissible Neoplasia (MtrBTNs), a form of transmissible cancer affecting marine mussels.

HYPERCAN is structured around three main research questions:

1. **Ploidy and fitness** – What is the fitness of MtrBTN cells depending on their ploidy level?
2. **Evolutionary dynamics** – How does evolution proceed in MtrBTN cancers?
3. **Hyperploidization and its effects** – How is hyperploidy generated, and what is the fate of newly emerged hyperploidy lineages?

Answering these questions will provide several major insights:

- Understanding the genetic mechanisms driving the evolution of these long-lived transmissible cancers.
- Evaluating the evolutionary and phenotypic effects associated with hyperploidy in both transmissible and conventional cancers.
- Providing the scientific community with reference genomes and biobanks of MtrBTN lineages.

Main Mission:

The primary mission of the postdoctoral researcher will be to produce high-quality reference genomes of MtrBTN transmissible cancers in blue mussels. The researcher will process and assemble long-read sequencing data (PacBio, ONT, and Hi-C) to generate haplotype-resolved assemblies of these polyploid genomes, as planned in the HYPERCAN project. Obtaining such reference genomes is a critical step for the continuation of the project and for the broader scientific community working on this topic. The researcher will also analyze nucleotide and structural variants identified in these genomes.



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Tasks and Responsibilities:

- Develop and validate a pipeline for assembling polyploid MtrBTN genomes
- Publish the genome assembly pipeline and reference genomes in a peer-reviewed scientific journal
- Participate in routine lab activities

Job Constraints:

- Occasional weekend work may be required (maximum one Saturday per month)

Ideal Candidate Profile:

Required Qualifications / Field of Training:

- PhD in Biology
- Experience in complex genome assembly

Required Qualities:

- Strong organizational skills
- Perseverance
- Scientific curiosity
- Ability to work as part of a team