ÉCOLE NORMALE SUPÉRIEURE DE LYON

Offre de stage de Master / Master Internship offer

Date of the offer: 20/06/2024

Tuteur du stage et Laboratoire d'accueil / Internship supervisor and Host laboratory:

Equipe/Team: Developmental Epigenomics

Chef d'équipe / Team leader: Yad GHAVI-HELM (yad.ghavi-helm@ens-lyon.fr)

Adresse du stage / Address of the internship:
Institut de Génomique Fonctionnelle de Lyon (IGFL)
32-34 avenue Tony Garnier 69007 Lyon

Site internet de l'équipe / Team Website: https://www.ghavihelmlab.com

Langues parlées dans l'équipe / Languages spoken in the lab:
English and French

Anciens étudiants encadrés / Previous ENS student:
Esposito-Farese Anna anna.esposito-farese@ens-lyon.fr
Cressot Lucie lucie.cressot@ens-lyon.fr

Titre du projet de recherche / Research project title:

Mots clés / Keywords:
3D genome organization, transcription regulation, marine biology, plankton, spatial transcriptomics, genomics, imaging

Description du projet / Project description (subject and technics):

Chromatin organization within the eukaryotic nucleus plays a crucial role in the control of gene expression. This organization is apparent at different levels, ranging from the spatial positioning of genes within the nucleus to the formation of Topologically Associating Domains and transcription factories. Decades of research, primarily focused on cell lines and classical model organisms, have shed light on the basic principles governing chromosome higher-order architecture. However, the evolutionary conservation of these basic principles, especially outside the vertebrate subphylum and in species with unconventional genome structures, remains largely unexplored.

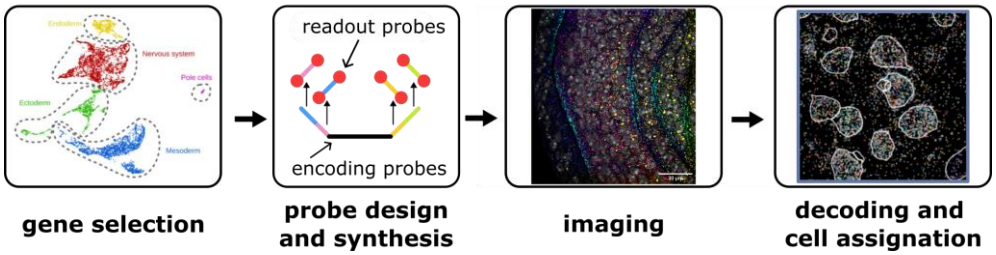
To address this gap, our team explores 3D genome organization and its function in transcriptional regulation in the plankton *Oikopleura dioica*, a species that offers a unique perspective on chromatin biology. *Oikopleura dioica* is a marine filter-feeder

found in oceans worldwide. One of the most striking features of *O. dioica* lies in its genome structure: (1) The genome of *O. dioica* has undergone extreme compaction, making it the smallest genome among non-parasitic animals with a size of ~65Mb across 3 chromosomes. (2) its genome is also characterized by an unprecedented level of genome scrambling compared to closely related species, with thousands of rearrangements affecting gene order. This extreme genome scrambling and compaction might have led *Oikopleura* to evolve unique ways of organizing chromatin in its nucleus. Our team leverages these unique features to unravel how radical deviations from a standard genome structure impact chromatin organization and, as a consequence, transcriptional regulation and cellular function.

For this purpose, we are combining state-of-the-art techniques in genomics and imaging, including single-cell sequencing and spatial transcriptomic (MERFISH) to establish how genome scrambling impacts chromatin organization and transcriptional regulation.

Different specific projects can be envisioned depending on the student's personal interest, ranging from purely experimental to purely computation or a mix of both.

This project will be performed in collaboration with the teams or Cristian Canestro in Barcelona and Nick Luscombe in Okinawa.



Principle of MERFISH

Publications du laboratoire ou revue recommandée sur le sujet / Lab publications or recommended review on the subject:

Extreme genome scrambling in marine planktonic Oikopleura dioica cryptic species. Plessy C. et al. Genome Res. 2024

Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. Denoeud F. et al. Science 2010

Enhancer-promoter interactions can form independently of genomic distance and be functional across TAD boundaries. Balasubramanian D. et al. NAR 2024

Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. Ghavi-Helm Y. et al. Nature Genetics 2019

Spatially resolved, highly multiplexed RNA profiling in single cells. Chen K. et al. Science 2015