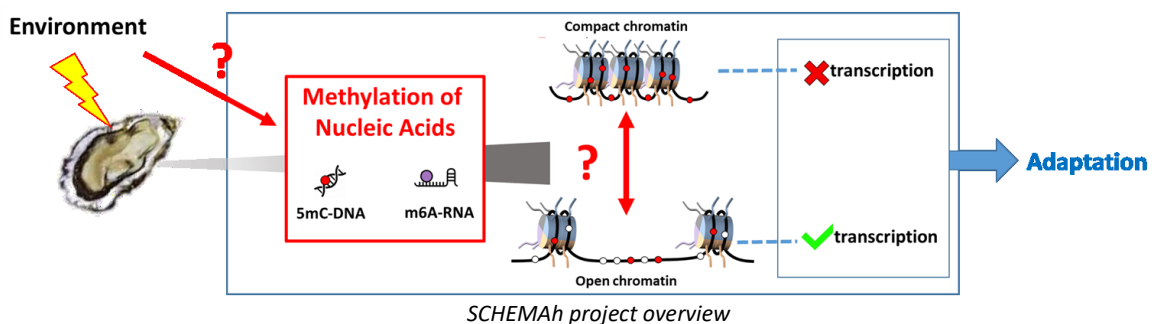


Post-Doctoral position: Chromatin Structure, Environment and Methylation of Nucleic Acids in the Oyster (SCHEMAh)

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Laboratory	UMR BOREA, MNHN, CNRS 8067, SU, IRD 207, UCN, UA ; Caen (FR) site
Position start	To be defined, not before Feb 1st 2022
Contract duration	12 months
Application deadline	December 17th, 2021
Salary	According to official guidelines, ca. 2600 euros brutto/month

Keywords :

Chromatin, Methylation, Environment, Epigenetics, Epitranscriptomics, Oyster, Ploidy, Conformation, Structure.



General context:

Organisms adapt to environmental changes thanks to modifying the expression of their genes leading to an appropriate physiological response. But which mechanism(s) guide(s) the orientation of this response? This question is crucial in the context of global change but remains largely elusive. Nevertheless, recent data suggest that gene expression would be determined by the environmental parameters through shaping the architecture of the genetic material, i.e. the structure of chromatin by the methylation of nucleic acids. Indeed, this prevalent epigenetic mechanism favours the condensation of chromatin (5mC-DNA methylation) and allows the locking of extra chromosomes (m6A-RNA methylation) in Mammals.

The cupped oyster *Crassostrea gigas* is the most important shellfish resource in Normandy, and its ecology makes it particularly exposed to changes in the environment (tides, seasons, global change). However, despite *C. gigas* present 5mC-DNA and m6A-RNA, and despite triploid oysters are fit can be fertile, the influence of environmental factors on nucleic acid methylation and chromatin structure in the oyster remains totally unknown to date.

The SCHEMAh project proposes for the first time to understand if and how the environment controls the structure of genetic material *via* nucleic acid methylation in the oyster model and thereby the expression of genes allowing its adaptation. Using innovative approaches on both the molecular (Chromatin Accessibility Assay, ATAC-seq, Nanopore sequencing) and the morphological (quantitative histology and 3D electron microscopy) levels, the SCHEMAh project will explore on the one hand, the link between DNA methylation (5mC) and chromatin structure, and on the other hand the existence of m6A-methylated non-coding RNAs (m6A-carRNAs) allowing triploid oysters to compensate for their aberrant chromosomal dosage. The pioneer fundamental knowledge brought by this project constitute a strong asset to understand the adaptation of the oyster *C. gigas*, a model of major

scientific interest and a key component of the Normandy coastal ecosystem, and more generally of species, towards the global change.

Missions :

The successful applicant will be mainly in charge of realizing the bioinformatic analyses of the data generated by the high-throughput sequencing methodologies undertaken within the project (RNA-seq, Methyl-seq, m6A-RNA-seq, ATAC-seq...). The recruited candidate, in addition, will more generally participate to the whole SCHEMAh project and therefore to generating the biological material (animal drug exposure and environmental challenges in the lab, dissections, nucleic acid extractions) and to constructing the DNA and RNA sequencing libraries, which may be partially outsourced. The successful applicant may also be involved in the development of the direct high-resolution mapping of nucleic acid modifications in the lab by Nanopore sequencing.

Expected skills and background :

The successful applicant will hold a PhD in Life Sciences dedicated to epigenomics, genomics, transcriptomics or molecular biology and bioinformatics. He/She will have a strong theoretical background in all these disciplines. He/She must have a solid experience in bioinformatic analysis of NGS data, as well as skills in molecular biology benchwork. An additional background or knowledge in marine models, ideally in an ecophysiological or environmental challenge context would be an asset but is not strictly required.

The recruited candidate will be integrated into a pluridisciplinary team and therefore should be curious and willing to work within a group comprising lecturers, researchers, engineers, PhDs and graduate students. Therefore, an appropriate English and/or French level is required that allows a fluent communication.

Working environment and means dedicated:

The present position will take place within the BOREA unit – Biology of Aquatic Organisms and Ecosystems - MNHN, CNRS 8067, SU, IRD 207, UCN, UA at the University of Caen Normandy (<https://borea.mnhn.fr>). The post doc will be hosted by the EMERGE team (EnvironMent, epi-gEnomes, deteRminisms and ontoGENy) (<https://borea.mnhn.fr/fr/equipe-recherche-axe-implantation/emerge-environnement-%C3%A9pi-g%C3%A9nomes-d%C3%A9terminismes-ontogen%C3%A8ses>), and will match the research axes ‘influence of environmental conditions on ontogenic processes’ and ‘epigenetics and ontogeny’ of the team.

The Caen University campus provides all the resources that are required within the frame of the project, notably regarding molecular biology. Most required equipments are available in the lab (Nanodrop, qPCR, Nanopore sequencer...). Some aspects will benefit from local university platforms such as the CMABio3 (center for biology-applied microscopy <https://www.unicaen.fr/laboratoire/plateau-technique-cmabio-centre-de-microscopie-appliquee-a-la-biologie-%C2%B7-cmabio/>), the CREC – Resource Center In Coastal Ecology (marine station in Luc-sur-Mer (<https://crec.unicaen.fr/>)) and the transcriptomic platform PROTEOGEN (<https://www.unicaen.fr/laboratoire/plateau-technique-proteogen-%C2%B7-proteogen/>). Heavy duty computing will be processed on the Ifremer supercalculator cluster (DATARMOR – <https://wwwz.ifremer.fr/pcdm/Equipement>).

Missions in marine station and off-site (congresses/collaborations) are to be expected. No specific risk beyond usual laboratory practices are to be especially considered.

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Application :
Resume + motivation letter + references
to guillaume.riviere@unicaen.fr
Subject : [SCHEMAh] postdoc

INDICATIVE BIBLIOGRAPHY (Coordinator, participants)

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