

**CHINA SCHOLARSHIP COUNCIL / SORBONNE UNIVERSITE**

**Thesis proposal**

Title of the research project: Gametogenesis and development in the flat oyster *Ostrea edulis*: a genomic approach to improving reproduction. ....

Joint supervision: no

Joint PhD (cotutelle): no

Thesis supervisor: Arnaud TANGUY.....

Email address of the thesis supervisor: atanguy@sb-roscoff.fr.....

Institution: Sorbonne Université.....

Doctoral school (N°+name): ED 227 Sciences de la Nature et de l'Homme : écologie & évolution

Research laboratory: UMR 7144 ... Adaptation and Diversity in the Marine Environment (AD2M)  
.....

Name of the laboratory director: Fabrice NOT .....

Email address of the laboratory director: ...not@sb-roscoff.fr.....

**ECOLE DOCTORALE - NOTICE AND VALIDATION :**

**Avis très favorable. Sujet pleinement dans les thématiques de recherche de l'ED et structurant pour les établissements de tutelle.**



**Jérôme Sueur**

**Directeur Adjoint ED 227 Sciences de la nature et de l'homme : écologie et évolution**

## **Sorbonne Université/ China Scholarship Council program 2021**

### **Thesis proposal**

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Keywords: oyster, genomics, transcriptomics, reproduction, selection.....

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Email address of the thesis supervisor: [atanguy@sb-roscoff.fr](mailto:atanguy@sb-roscoff.fr) .....

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Research laboratory: ...UMR7144 Adaptation and Diversity in the Marine Environment (AD2M)  
.....

Address of the laboratory: ... Station Biologique de Roscoff, Place Georges Teissier, 29680  
ROSCOFF, FRANCE  
.....

Name of the laboratory director: ...Fabrice NOT.....

Email address of the laboratory director: [.....not@sb-roscoff.fr](mailto:.....not@sb-roscoff.fr).....

### **Subject description (2 pages max):**

## 1) Study context

Historically, French oyster farming has gone through a succession of development phases, stock exploitation or disease outbreaks. The latter have particularly disrupted production and are still today a major obstacle to oyster farming in many shellfish growing areas, particularly for the native European flat oyster *Ostrea edulis*. *O. edulis* presents an original reproductive cycle and, to date, much of our current knowledge is based on the work of Walne (1966, 1970) and has changed very little since then, particularly with regard to the molecular aspect of the different phases of gametogenesis. The lack of molecular data at the gene or protein level on the reproduction of *O. edulis* constitutes a real obstacle to the development of its production in hatcheries. However, the control of the reproductive cycle is the basis of the production system of any aquaculture species. Furthermore, the conditioning of brood stock is one of the key phases in the success of larval production, and therefore knowledge of the sexual cycle is essential. *O. edulis* does not have sex chromosomes but presents an asynchronous hermaphroditism, a rhythmic consecutive sexuality as well as the possibility that several sexual inversions may occur during the same breeding season. This behavior poses a major problem in the operation of hatcheries and particularly in the context of producing families on a bi-parental basis for application in genetic selection. Control of the reproduction cycle, the possibility of synchronizing gametogenesis and even orienting it are therefore necessary to optimize the production of these families and, more generally, the production of *Ostrea* larvae. In addition to the conditioning conventionally used playing on nutrition (selection of phytoplanktonic strains) and temperature, we are developing a new method of triggering gametogenesis using specific inducers. The identification of the latter is based on knowledge of the genome, sequenced at chromosomal level, and on the coupling of experimental and environmental approaches. Ultimately, the aim is to improve reproductive success and larval quality. The data obtained will also allow answering more fundamental questions concerning the molecular mechanisms of gamete alternation in a hermaphroditic species as well as the influence of environmental parameters on sex orientation.

## 2) Details of the proposal

The REPROSTREA project has two main objectives:

The first objective concerns the acquisition of fundamental data concerning the reproductive cycle and larval development of *O. edulis* by transcriptomic (RNAseq and quantitative PCR), proteomic (via the monitoring of concentration kinetics of selected proteins) and metabolic (gametogenesis quality indices, carbohydrate and lipid indices) approaches. All the data acquired will be integrated in a comparative approach with other mollusk models for which gametogenesis has already been described, the originality of *O. edulis* being based on the existence of a larval incubation phase. These data will contribute to better understand the molecular processes involved in the processes of hermaphroditism establishment. The influence of parameters such as diet composition and temperature will also be studied in order to better understand the physiology of reproduction. This axis will be mainly carried out through laboratory experiments. Gametogenesis monitoring will also be undertaken on oysters placed on natural sites whose environmental parameters are monitored in order to study the effect of environmental variations in the reproduction cycle.

The second objective concerns the research, production (recombinant proteins) and testing of the effects of molecules/effectors capable of triggering gonadal maturation in *O. edulis*. A first list of potential effectors (whose sequences have been identified in the genome) has already been drawn up and may be completed on the basis of the results obtained in the first objective. These effectors will be tested in order to

determine whether it is possible to influence the relative development of male or female gonads and/or to synchronize gametogenesis in order to limit the strong heterogeneity presently observed. In this project, several molecules (proteins and peptides) will be tested simultaneously in order to optimize the chances of obtaining the expected result. The addition of an induction test with a hormone, coupled or not with the selected inducers, will contribute to optimize our chances of success. An additional objective is to develop several inducers capable of differentially influencing both sexes.

The samples will be partly produced at the hatchery level in order to perfectly master the temporal kinetics of the development of the gonads but also of the larvae. Several successive cycles of gametogenesis are planned each year in order to have a large number of replicates but also to be able to test several experimental conditions in terms of nutrition and thermal diet. Sampling in natural populations will also be carried out to compare the data acquired in a controlled environment. In order to do so, an aid of the oyster farmers is planned. These samplings will also be based on the existing lots of genetically selected families produced within the framework of a previous project. The different stages of gametogenesis will be determined by histological analyses to which we will couple biochemical analyses. The combination of these parameters will allow us to obtain fine kinetics on the development of the gonads allowing also to make the best possible choice for transcriptomic analysis. The whole molecular description of the reproductive cycle, larval development, the effect of different conditions/effectors on gametogenesis will be carried out by coupling between a global RNAseq approach and quantitative PCR (on target genes). RNAseq libraries will be prepared in the laboratory and sequenced on external platforms. All bio-informatic analyses will be conducted in the laboratory. The transcriptomic data obtained will be compared with those obtained on other mollusk models in order to highlight similarities and/or differences between the modes of reproduction in these organisms. Immunochemical approaches will be also set up to better characterize the gametogenesis. Additional bio-informatics analysis for comparative genomics will be performed to identify specific genes or pathway related to hermaphroditism.

### **3) References**

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Yu, L. et al., 2018. *Mar Biotechnol (NY)*. 20(4):467-480. doi: 10.1007/s10126-018-9809-5.

Santerre et al., 2013. *Comp. Biochem. Physiol. A Mol. Integr. Physiol.* 165, 61–69. doi: 10.1016/j.cbpa.2013.02.007.

Walne, 1966. *Fishery investigation (Great Britain, Ministry of Agriculture, Fisheries and Food), Series II*, 25(4)

### **4°) Profile of the Applicant (skills/diploma...)**

Master degree with an interest for mollusk physiology, competences in bio-informatics for transcriptomic and genomic analyses, experience in molecular biology and laboratory work. Ability to work in team and competence in English writing.

**Contacts:****Thesis supervisor**

Arnaud TANGUY.....

Email address of the thesis supervisor: ...atanguy@sb-roscoff.fr.....