

**CHINA SCHOLARSHIP COUNCIL / SORBONNE UNIVERSITE**

**Thesis proposal**

Title of the research project: **Exploring the role of LuxR transcriptional regulators in marine bacteria-phytoplankton interactions**

Joint supervision: **yes** Dr. LAMI Raphaël and Dr. JEANTHON Christian

Joint PhD (cotutelle): **no**

Thesis supervisor: Dr. LAMI Raphaël and Dr. JEANTHON Christian

Email address of the thesis supervisors: raphael.lami@obs-banyuls.fr ; jeanthon@sb-roscoff.fr

Institution: Sorbonne University

Doctoral school (N°+name): ED 227 – Sciences de la Nature et de l'Homme, Evolution et Ecologie

**Co-supervision Lab 1 :**

Research laboratory: Microbial Biodiversity and Biotechnology Lab (LBBM)

Name of the laboratory director: Pr. Marcelino SUZUKI

Email address of the laboratory director: suzuki@obs-banyuls.fr

**Co-supervision Lab 2 :**

Research laboratory : Adaptation & diversity in the marine environment (AD2M)

Name of the laboratory director: Dr. 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**

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**Exploring the role of LuxR transcriptional regulators in marine bacteria-phytoplankton interactions**

Keywords: Bacteria - phytoplankton - biofilm – virulence – marine environment

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#### **LAB 1**

Research laboratory: Microbial Biodiversity and Biotechnology Lab LBBM)

Address of the laboratory: Avenue P. Fabre 66650 BANYULS SUR MER, FRANCE

Name of the laboratory director: Pr. Marcelino SUZUKI

Email address of the laboratory director: suzuki@obs-banyuls.fr

#### **LAB 2**

Research laboratory: Adaptation and Diversity in the marine environment (AD2M)

Address of the laboratory: Place Georges Teissier CS 90074 29688 ROSCOFF

Name of the laboratory director: Dr. Fabrice NOT

Email address of the laboratory director: not@obs-banyuls.fr

## Subject description (2 pages max):

### 1) Study context

Marine phytoplankton is responsible for up to 50% of global primary production and at least half of this production is remineralized by marine heterotrophic bacteria. Interactions between these essential microbial groups are therefore widespread in marine environments, in particular within the phycosphere, which is the micro-environment surrounding each microalgal cell and immediately influenced by it. From an ecological perspective, microbial interactions are being increasingly recognized as a major force shaping microbial communities, with studies suggesting that biotic factors modulate community structure and function as much as abiotic factors, if not more. It is now well established that these bacteria-phytoplankton interactions strongly influence the biogeochemical cycle of carbon, the productivity and stability of marine trophic chains or even the release of atmospheric compounds playing a major climatic role. For these reasons, **improving our understanding of the mechanisms behind these interactions is a high-priority objective in the fields of marine microbiology and biogeochemistry.**

### 2) Details of the proposal

Bacteria-phytoplankton interactions in the phycosphere include numerous, complex and diversified examples of parasitic, mutualistic or commensal relationships. These inter-domain symbiotic relationships have led to remarkable coevolutions of metabolic pathways, signal receptors, and regulatory cascades in both prokaryotic and eukaryotic plankton. For example, some bacteria are able to stimulate the growth of phytoplankton through the production of vitamins and/or phytohormones such as auxin. Conversely, certain bacteria are able to kill microalgae by the secretion of a range of algicidal compounds.

Extensive research on plant-bacteria interactions has shown that the bacterial LuxR transcriptional regulators are involved in redox sensing, bacterial virulence, biofilm formation, quorum sensing interactions, and reception of ethanolamine signaling compounds. Overall, LuxR proteins appear to be involved in the sensing of the plant host environment. Similarly, evidence suggests that LuxR proteins could play a major role in bacteria-phytoplankton interactions. The *luxR* genes are found in the genomes of numerous Gram-negative marine bacteria, associated with a *luxI* gene when involved in quorum sensing interactions (*luxI* encodes a diffusible signal synthase). If the role of marine *luxR* genes has been well established in this case, the role of *luxR* solos (*i.e.*, without an associated *luxI* gene) remains enigmatic in marine prokaryotes, and has never been demonstrated formally.

In this project, we will assess the role of *luxR* solos genes in the interactions between algicidal bacteria of the marine genus *Kordia* (family *Flavobacteriaceae*) and diatoms, the most abundant group of microalgae in temperate seas which produces about 25% of the total carbon fixed on the planet. Our preliminary results demonstrated that all known *Kordia* species (9 isolates) have the capacity to lyse diatoms. Analysis of all available *Kordia* genomes showed that they all contain numerous *luxR* genes (up to 16 in *K. algicida*). Our current hypothesis is that two *Kordia luxR* solos genes may be involved in phycosphere colonization and virulence against diatoms.

Indeed, successful colonization of the phycosphere can be enhanced by specific bacterial genetic traits, including chemotaxis, motility, and attachment to surfaces. Since it was

demonstrated that *luxR* genes are involved in host colonization through biofilm formation in phytopathogenic bacteria, we suspect that they could play a similar role in *Kordia* for phycosphere colonization. We also suspect a role of *luxR* genes in the virulence of *Kordia* against diatoms as we established the presence of (i) a gene encoding a caspase, an enzyme involved in diatom lysis, and (ii) a gene encoding a T9 secretion system, that plays roles in bacterial colonization and bacterial virulence in Flavobacteria. These genes are present in two different operons each carrying a *luxR* solo gene. Therefore, these LuxR proteins could act as transcriptional regulators of virulence or biofilm formation, eventually controlling the potential impact of *Kordia* on diatom blooms at the ecosystem scale.

**Task/Objective 1: Screening key physiological traits of *Kordia*: evaluation of biofilm production capacities of *Kordia* species and their specific host ranges within marine microalgae** : Our laboratories have already acquired preliminary data on the 9 *Kordia* species isolated so far that needs to be completed to decipher the ecological role of *Kordia* in the marine environment. The objective is to evaluate in all *Kordia* species key physiological traits (biofilm formation, virulence range) that may differentiate their interaction patterns and might be thereafter affected in *luxR* mutants. The work planned in Task 1 is based on well-established methodologies in the partners' laboratories.

**Task/objective 2: To investigate the role of *luxR* solo genes in *Kordia algicida*-diatom interactions.** Our hypothesis is that the two *luxR* solos genes play a role in biofilm formation and/or synthesis of algicidal compounds (such as caspase and T9SS in *K. algicida*). To test it, we will focus on the strain *K. algicida* OT-1, best studied *Kordia* species that demonstrates a generalist virulence pattern. According to our hypotheses, *luxR* deletion mutants ( $\Delta luxR$ ) should display (i) a decreased biofilm production and (ii) a lower virulence. Once mutants will be obtained, an overall analysis of the gene expression of the bacteria and the microalgae will be assessed through co-culture experiments. If our hypothesis on the role of the solo *luxR* genes is verified, this step will specify their modalities of action and their contribution to gene networks. If our hypothesis is not verified, our large-scale exploratory approach will allow to identify the potential other roles of the *luxR* genes.

The complementarity of these approaches that mainly involve microbial ecology and genetics promises a significant advance in the understanding of host-parasite interactions in the context of diatom blooms.

### 3) References

A few work conducted in our labs on the thesis topic :

Tourneroché A, Lami R, Hubas C, Blanchet E, Vallet M, Escoubeyrou K, Paris A, Prado S (2019) Bacterial-fungal interactions in the kelp endomicrobiota drive autoinducer-2 quorum sensing. *Frontiers in Microbiology* 10:1693 / hal-02277573

Rolland JL, Stien D, Sanchez-Ferandin S, Lami R (2016). Quorum sensing and quorum quenching in the phycosphere of phytoplankton: a case of chemical interactions in ecology. *Journal of Chemical Ecology*, 42(12), 1201-1211 / hal-01472696

Crenn K, Duffieux D, Jeanthon C (2018). Bacterial epibiotic communities of ubiquitous and abundant marine diatoms are distinct in short- and long-term associations. *Frontiers in Microbiology* 9:2879 / hal-02130560

Arsenieff L, Le Gall F, Rigaut-Jalabert F *et al.* (2020.) Diversity and dynamics of relevant nanoplanktonic diatoms in the Western English Channel. *The ISME Journal* 14:1966–1981.

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

The ideal candidate should:

- Present excellent skills in microbiology (culture of microbial strains, DNA manipulation). The successful candidate would ideally have skills in deletion mutant construction and/or computational analyses of large omics datasets.
- Have excellent English (speaking and writing, level C2 or equivalent). Rigor at bench work, intellectual honesty, autonomy, able to share and exchange data and results with colleagues.
- Be prepared to intense lab work in autonomy in an international environment, in between two different labs in France.

#### **Contacts:**

##### **Thesis supervisor**

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