



SERVICE DE LA RECHERCHE ET DE LA VALORISATION (SRV)

Ecole doctorale 305 « Energie Environnement »

AVIS DE PRESENTATION DE TRAVAUX EN VUE DE L'OBTENTION DU DOCTORAT

Monsieur Janan Khamo Gawra GAWRA soutiendra sa thèse le **23 mai 2022 à 14h00** à **Université de Perpignan Via Domitia 58 Avenue Paul Alduy F-66860 PERPIGNAN FRANCE**, salle **Amphithéâtre 5**, un doctorat de l'Université de Perpignan Via Domitia, spécialité **Biologie**.

TITRE DE LA THESE : Déterminants et poids relatif de la variation génétique et épigénétique dans la résistance de l'huître *Crassostrea gigas* au Pacific Oyster Mortality Syndrome

RESUME : Together with the increase of human population, there is a mathematical increase for food supply. Since 2008, mass mortality events of Pacific oysters (*Crassostrea gigas*) juveniles caused by the Pacific Oyster Mortality Syndrome (POMS) have threatened the oyster aquaculture industry. Studies on the resistance of *C. gigas* to POMS has demonstrated a genetic bases and more recently, it was shown to rely on early transcriptomic response to the viral infection. Although data about the involvement of epigenetics in POMS resistance are still scarce, the essential role of the transcriptome, from the basal level to the antiviral response, and the effect of environmental exposure on the resistance of oyster, collectively suggest that epigenetic can play an essential role. Here we propose a framework to study simultaneously the potential role of genetic and epigenetic in the expression of phenotype by using the *C.gigas*/POMS model at the natural population level. We developed an exome capture approach to obtain genetic (Single Nucleotide Polymorphisms; SNPs) and epigenetic (DNA methylation at CG context; CpGs) information. In the present thesis, the exome capture developed allowed us to capture the genetic and epigenetic variation on more than 65 % of the total exons. We showed that wild oyster populations differentially exposed to the POMS display signatures of selections both in their genome (SNPs) and in epigenome (CpGs). A high number of these SNPs and CpGs were located in genes involved in immune functions. These results confirmed that host population facing pathogen emergence could rely on genetic and epigenetic variation to rapidly adapt to emerging diseases. While our study confirms the essential role played by the DNA sequence it also shows that other mechanisms can interplay with this sequence to encode a resistant phenotype. However, they can also be independent from this DNA sequence and participate to the expression of resistance. These results confirm that holistic approaches of the resistance of host population must be envisioned to have access to most of the mechanisms at stake. In addition, it also demonstrates that epigenetic assisted selection would be a way to assist breeding industry without effects on the DNA sequence.

Directeur de thèse :

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Laboratoire où la thèse a été préparée : Interactions Hôtes-Pathogènes-Environnements

Le jury sera composé de :

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