

Avis de Soutenance

Monsieur Ajithkumar MUNUSAMY

Spécialité : Biologie de l'environnement, des populations, écologie

Soutiendra publiquement ses travaux de thèse intitulés

« Les bases génétique des mortalités massives de moules en France . »

dirigés par Monsieur Lionel DEGREMONT

Soutenance prévue le *mardi 25 février 2025* à 14h00

Lieu :

La Rochelle Université

Amphithéâtre Michel Crépeau

44 avenue Albert Einstein,
Pôle Communication, Multimédia et Réseau
17000, La Rochelle

Composition du jury proposé

M. Lionel DEGREMONT	Institut Français de Recherche pour l'Exploitation de la Mer	Directeur de thèse
M. Pierre BOUDRY	Institut Français de Recherche pour l'Exploitation de la Mer	Examinateur
Mme Jildou SCHOTANUS	Wageningen University	Examinatrice
Mme Lillehammer MARIE	NOFIMA	Examinatrice
Mme Phocas FLORENCE	INRAE	Rapporteuse
M. Vandeputte MARC	INRAE	Rapporteur
M. Pierrick HAFFRAY	Syndicat des Sélectionneurs Avicoles et Aquacoles Français	Invité
M. Tim REGAN	Roslin Institute, University of Edinburgh	Invité

Résumé :

France is one of the main contributors to mussel production in Europe. Since 2014, abnormal mussel mortalities (AMM) have been frequent in France, the causative agent being still unknown. This project investigates the genetic basis of resistance to MA outbreaks in two mussel species (*Mytilus edulis* and *Mytilus galloprovincialis*) and their natural hybrids grown in France. Mussel families tested at two sites from October 2017 to June 2018 revealed low to moderate heritability values for survival and significant genotype-environment interaction. In addition, mussel families were evaluated in the context of an experimental infection in July 2018, using a pathogenic strain of *Vibrio splendidus* isolated during episodes of MA in 2014. The weak genetic correlation between the field infection and the experimental infection suggests that this strain of *Vibrio* was not the primary cause of the mortality epidemic observed at the two sites in 2018. No response to selection for MAiD has been observed in co-residential experiments using donors from MAiD sites, while epidemics of high mortality have occurred for both species, indicating that without access to field conditions, it is impossible to mimic a MA in the laboratory. Microbiota analysis revealed that *Vibrio* was the predominant genus in moribund mussels, followed by *Colwellia*, *Tropicibacter*, *Malaciobacter* and *Fusibacter*. In addition, the genomic architecture of resistance to a pathogenic strain of *V. splendidus* has shown that this trait is polygenic, suggesting that genomic selection is likely more efficient than marker-assisted selection. In addition, genomic selection can improve accuracy by up to 19% compared to pedigree-based selection. Finally, the response to selection to increase or decrease cytogenetic quality after a generation of selection was 1.44% for *M. edulis* and no response to selection for *M. galloprovincialis*. More importantly, this trait was not correlated with survival, using a cohabitation experiment with donors sampled at a site where a massive epidemic of mortality occurs each year. The mussel industry could use all the results of this work to counter future outbreaks of MAiD, which could be more frequent and intense in the future in the context of global warming.