Acronyme du projet *(8 caractères maximum)* **: COMAlex**

Intitulé du projet en langue anglaise : Genetic linkage map of molecular phenotypes in the toxic dinoflagellate Alexandrium minutum: A multi-omic approach

Intitulé du projet *en langue française* : CartOgraphie génétique des phénotypes moléculaires par une approche Multi-omique chez le dinoflagellé toxique Alexandrium minutum.

Abstract:

Dinoflagellates are responsible for massive phytoplankton blooms with significant ecological, but also health and economic impacts, particularly when they involve toxin synthesizing species (Anderson et al 2012). Dinoflagellates have remarkable genomic characteristics, including gigantic genomes and gene expression regulation through the splicing of polycistronic pre-messenger RNAs (Wisecaver and Hackett 2011). Dinoflagellates of the genus *Alexandrium* are one of the main sources of harmful algal blooms (HAB) and are responsible for paralytic shellfish poisoning syndrome (PSP; Anderson et al. 2012). In France, the last major episodes occurred in the Bay of Brest (Rade de Brest) in the summer of 2012 (up to 40 million cells per liter), associated with PSP toxicities (more than 8000 µg eqSTX.kg^{-1} mussel meat), a new phenomenon at this location but repeated in 2013, 2014 and 2015. Despite mainly clonal growth during blooms, populations of *A. minutum* are composed of individuals that are extremely diverse genetically (Dia et al. 2014, Le Gac et al. 2016), from a toxicity point of view (Franco et al. 1994; Chou et al. 2004; Touzet et al. 2006), as well as in terms of morphology (Hansen et al, 2003) and production of extracellular compounds with cytotoxic, allelopathic, ichthyotoxic and hemolytic effects on marine organisms (Borcier et al. 2017; Castrec et al.; 2018; Long et al. 2018). One way to better understand the determinism of this intraspecific diversity with ecological, health and economic implications is to use a genetic approach that allows a genomic region to be associated with a phenotypic trait (discrete or quantitative). In this project, we propose to work on a family of *A. minutum* strains consisting of four genetically, morphologically and toxin-producing divergent parent strains and 79 descending clonal strains resulting from the sexual reproduction of the four parental strains. These strains will initially be genotyped using several tens of thousands of genetic markers in order to obtain a genetic lonkage map. In a second step, the molecular specificities of dinoflagellates will be better understood by analysing the transmission of molecular information from the genome to the transcriptome, then to the proteome and finally to the metabolome. In a third step, the analysis will focus on the segregation of the different molecular phenotypes, with a particular interest in toxins in the progeny.

The main objectives of this project can be considered at three levels.

1) The main objective is to develop functional genetic resources for *A. minutum*. These resources are totally non-existent in dinoflagellates and will allow to link genetics, gene expressions, proteins and metabolites. These resources will then be used to analyze different phenotypes of interest by integrating the different molecular levels. By combining the resources generated with complementary observations or experiments, it will be possible to use them for many future projects, particularly on local adaptation, divergence and population genomics.

2) The particular genomic characteristics of dinoflagellates suggest original cellular functioning, particularly with regard to the regulation of gene expression. The subject aims to better characterize this functioning and thus to characterize the transmission of molecular information between gene expression, protein and the presence of metabolites.

3) In this project, quantifications (genetics, RNA, proteins, metabolites) will be carried out at the global level, without any a priori, but we will focus more particularly on interpreting the results in terms of toxin production and thus making the link between toxin profiles, metabolites, proteins, gene expression and genetics. Indeed, the parent

strains used for crossbreeding have various toxic profiles (i.e. 2 non-toxic, the other 2 producing 3 and 6 toxins respectively). The subject therefore aims at a better understanding of the determinism and intermediates involved in the synthesis of PSP toxins.

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