

Evolution of the sex determination mechanisms in the diatom genus *Pseudo-nitzschia* (ELLIPOSE)

Director of Studies: Maria Immacolata Ferrante

Department of Integrative Marine Ecology

Seat: Naples, Italy

Project Summary

The evolution of sex in eukaryotes has long fascinated biologists. Sexual reproduction is costly but its benefits have made it almost ubiquitous in the tree of life, with asexuality arising in some branches as a secondary loss. Sex is therefore widely conserved. However, sex determination mechanisms are strikingly variable among different eukaryotes. The familiar X/Y chromosomes system is conserved in Mammals but other solutions are present in different animals, plants and fungi. In unicellular organisms, opposite sexes are called mating types (MTs), often determined by a mating type locus, a genomic region smaller than a chromosome. In 2018, we reported the first mating type locus for diatoms, an ecologically prominent group of unicellular microalgae in marine ecosystems.

The mating type plus (MT+) of the marine diatom *Pseudo-nitzschia multistriata* is determined by the monoallelic expression of the *MRP3* gene, which regulates four other MT Related (MR) genes. In this project, we plan to expand on this finding to identify the MT locus of other *Pseudo-nitzschia* species and explore the extent of conservation of the genes and of the mechanisms involved. The genus *Pseudo-nitzschia* comprises over 58 different species of which 28 are capable of producing a toxin harmful for humans and animals, justifying the interest in this specific group beyond the general relevance of questions related to sex determination.

To reach our goal, we will collect *Pseudo-nitzschia* strains in the Mediterranean and the Southeast Pacific, genotype them to assign the species and cross them to assign the MT. Comparative gene expression analyses on opposite MTs will identify MR genes in selected species. For two species, we will perform whole genome sequencing, producing new diatom genomes. The information collected will allow discovering the genes involved, and reveal the extent of conservation of the MT locus structure. Based on current understanding of the *P. multistriata* MT locus, apparently unique compared to other known systems, we predict that the study will unveil novelties, helping to understand genetic and epigenetic controls in diatoms. Additionally, by genotyping strains from several sites in the Southeast Pacific, the study will contribute to defining the biogeography of this important diatom genus; by producing new transcriptomes and genomes, the study will allow comparative analyses which will reveal patterns of evolution not only for the sex locus but also for other important traits; by comparing strains obtained from coastal vs oceanic provinces, it will be possible to reconstruct patterns of adaptation.