Molecular insights into the mating system of the marine diatom *Pseudo-nitzschia multistriata* using genetic and genomic approaches

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Thesis submitted for the degree of

Doctor of Philosophy (PhD)

in Life and Biomolecular Sciences

December 2015

Open University, London

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Abstract

Sexual reproduction is a fundamental phase in the life cycle of diatoms, linked to the production of genotypic diversity and the formation of large-sized initial cells that ensure population persistence. It occurs only within cells below a certain threshold size and, in heterothallic diatoms, only between strains of opposite mating types.

We aim at identifying genes involved in mating type determination in the marine planktonic diatom *Pseudo-nitzschia multistriata*. This species is recorded in coastal waters worldwide and produces the neurotoxin domoic acid. A reference genome has been generated and transcriptomes have been produced for strains of opposite mating type (MT+ and MT-).

Differential expression analysis provided a list of candidate MT-biased genes validated with qPCR. Four MT-biased genes were identified, two in MT+ and two in MT-. The expression pattern of the candidate genes was followed in a 24 hours' time course experiment to verify whether they were regulated in dependence of light or cell cycle phases. Experimental evidences demonstrated their involvement during mating recognition in early stages of sexual reproduction while preliminary genetic analyses excluded that they could be the master gene responsible for mating type determination. The description of the four genes was improved through computational characterization to understand their role in the chemical communication occurring between opposite mating types. A further step towards the identification of the MT locus will include a Bulked Segregant Analysis applied to a library of 30 MT+ and 30 MT- F1 strains obtained through DNA deep sequencing.

Elucidating the molecular and genetic basis of MT determination and sexual reproduction in diatoms will contribute to a better understanding of the regulation and evolution of their life cycles and reproductive strategies. Results from this study could also provide

molecular markers to trace the distribution of MT+ and MT- cells in environmental samples.