UNIVERSITY OF NAPLES "FEDERICO II"



DOCTORATE SCHOOL IN BIOLOGY

Cycle XXXIV

Omic approaches for the identification of biosynthetic pathways for bioactive compounds in the diatom *Thalassiosira rotula*

Coordinator Prof. Sergio Esposito **Ph.D. student** Federica Di Costanzo

Tutor Dr. Giovanna Romano

Co-tutor Dr. Valeria Di Dato

2018 - 2021

ABSTRACT

Diatoms are eukaryotic unicellular microorganisms widespread in all environments and responsible for about 20 % of the primary productivity on Earth. The evolutionary success of these organisms is greatly due to their metabolic plasticity that allows them to survive in different and, sometimes, challenging conditions of life through the production of a variety of bioactive molecules for defense, communication and adaptation to environmental changes.

In the last years, diatoms have gained increasing attention for their bioactive molecules that may find applications in pharmaceutical, cosmeceutical, nutraceutical and other biotechnological sectors and for their potential to become "biofactories" for a sustainable and eco-friendly production of several valuable metabolites.

My PhD thesis work was aimed at the exploitation of the biotechnological potential of the diatom *Thalassiosira rotula*, with a particular focus on lipid-derived bioactive compounds. Indeed, *T. rotula* was selected for its previously reported ability to produce unsaturated aldehydes as defence mechanism against copepods grazing that furthermore demonstrated to possess anti-proliferative and pro-apoptotic activities against different human carcinoma cell lines. Through the analysis of its transcriptome, several pathways involved in the production of bioactive molecules, i.e. secologanin, polyketides, prostaglandins and phytosterols, have been identified. Their existence has been confirmed by evaluating the gene expression of the key enzymes involved in each of the pathways listed. Moreover, their expression level was assessed along the growth or under different nutritional stresses, to evaluate their regulation and possible involvement in the response to stress conditions. For some of these pathways, the end products have been qualitatively and/or quantitatively analysed.

In addition to the transcriptome mining, the interaction of *T. rotula* with associated bacteria was studied, revealing the existence of three novel bacterial species. The analysis of their genomes revealed the presence of different biosynthetic gene clusters, among which a mixed non-ribosomal peptide synthetase/type 1 polyketide synthase (NRPS/T1PKS) pathway, potentially responsible for the production of interesting bioactive compounds. A qPCR-based approach helped in the characterization of their requirements for growing through the test of different culture media, both in presence or

absence of the diatom, and of their tolerance to different antibiotic mix and concentrations.

Altogether, the results here reported provide new stimuli in the field of marine biotechnology, as they show the presence of functionally active interesting biosynthetic pathways in the cosmopolitan species *T. rotula* and its associated bacterial community, paving the way for the utilization of these microorganisms for future biotechnological developments.