MicroRNAs-mediated environmental adaptation in marine microalgae: from physiological responses to biotechnology applications

Director of Studies: Sabrina Carrella

Department of Ecosustainable Marine Biotechnology

Seat: Naples, Italy

Project Summary

Marine microalgae are rich in bioactive compounds and exhibit the potential for manufacturing a wide range of bioproducts. Advances in algal genomics, genetic engineering and synthetic biology is facilitating the development of industrial strains suitable to specific production purposes. However, a serious limitation to strain improvement is our incomplete understanding of gene and metabolic network regulation in most microalgal species. Microalgae have a well-developed metabolism to survive even under extreme stress conditions in which gene silencing mechanisms have been reported to be involved in modulating metabolic responses to stress in microalgae. In particular, microRNAs (miRNAs) are a class of endogenous non-coding RNAs that play an essential role in post-transcriptional gene regulation in plants and animals. They are key factors in stress response molecular pathways triggering cellular responses and metabolic adjustments to stress conditions. The project proposes to identify and characterize marine Chlamydomonas miRNAs-mediated response to different stress conditions. The final goals are the identification of miRNA bio-indicators of environmental health, and the functional characterization of those miRNAs involved in the production of bioactive molecules to create novel strategies for biotechnological applications. We will proceed by the miRNOme analysis of marine *Chlamydomonas* in different stress conditions (AIM1), whose results will be used to functionally characterize the commonly altered miRNAs with the identification and validation of direct mRNA targets (AIM2). Finally, the project will lead to the creation of the "ChlamyRNA" database (AIM3), a publicly available, user–friendly, web-accessible database. The availability of this bioinformatic source will represent a new instrument for researchers for the implementation of marine biotechnological resources, techniques and products.

One of the main outcomes of this work will be a significant step towards for a better comprehension of the general architecture of the miRNOme and genetic network of *Chlamydomonas*, which are still largely unexplored. The sequencing and bioinformatic approaches developed during this project will shed light on new characteristic of specific marine microalgae giving new ecological and biotechnological information for this important renewable marine resource. This thesis is expected to combine marine biology, molecular biology and bioinformatics. This interdisciplinary approach will provide new insights into the biotechnological exploitation of marine genetic resources.