



Ecology of marine diatoms through omics:
from community structure to single species investigation

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Abstract

Diatoms are a major component of marine phytoplankton and play a key role in global elemental cycles and marine food webs. Their ecological success relies to their underlying genetic and functional diversity, both at community and single species levels; despite their importance, diatoms' biology and ecology is far from being completely understood, given the scarcity of global-scale observations and the large number of uncultured species. The general aim of my thesis was to explore diatom global-scale diversity from community to species level by applying and developing different methodological frameworks. This study was mainly based on metabarcoding, metagenomic and metatranscriptomic data sets provided by *Tara* Oceans and *Tara* Oceans Polar Circle expeditions. I first described diatom communities from a statistical perspective to provide a general overview of the macroecological structure of different types of High Throughput Sequencing data. I further investigated diatom diversity across the currents that bring waters from the North Atlantic to the Arctic Ocean; I here characterized taxonomic composition of communities, along with the description of the main environmental features that shape diatom assemblages. Moreover, I described how the expression of functional genes involved in iron uptake, transport and varied across the sampling sites. I then moved to a lower taxonomic rank and focused on a single genus, i.e., *Pseudo-nitzschia*, one of the most abundant and ubiquitous diatom genera that includes toxigenic species responsible of harmful blooms. I described *Pseudo-nitzschia* biogeography at global scale at high taxonomical resolution and explored its ecology through links to abiotic and biotic factors, with a particular focus on the interactions with bacteria. Finally, I performed a functional analysis of a set of genes whose expression in diatoms is strongly up-regulated during sexual reproduction; by integrating a phylogeny-based approach, I tested the role of these genes as potential molecular markers to detect sexual reproduction events in diatom natural populations.