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De novo transcriptome of the cosmopolitan dinoflagellate *Amphidinium carterae* to identify enzymes with biotechnological potential

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Dinoflagellates are phytoplanktonic organisms found in both freshwater and marine habitats. They are often studied because related to harmful algal blooms but they are also known to produce bioactive compounds for the treatment of human pathologies. The aim of this study was to sequence the full transcriptome of the dinoflagellate *Amphidinium carterae* in both nitrogen-starved and -replete culturing conditions (1) to evaluate the response to nitrogen starvation at the transcriptional level, (2) to look for possible polyketide synthases (PKSs) in the studied clone (genes that may be involved in the synthesis of bioactive compounds), (3) if present, to evaluate if nutrient starvation can influence PKS expression, (4) to look for other possible enzymes of biotechnological interest and (5) to test strain cytotoxicity on human cell lines. Results showed an increase in nitrogen metabolism and stress response in nitrogen-starved cells and confirmed the presence of a type I β-ketosynthase. In addition, L-asparaginase (used for the treatment of Leukemia and for acrylamide reduction in food industries) and cellulase (useful for biofuel production and other industrial applications) have been identified for the first time in this species, giving new insights into possible biotechnological applications of dinoflagellates.

Marine phytoplankton generates about half of the global primary productivity, regulating global biogeochemical cycles and supporting valuable fisheries[1,2]. A subset of these species produces a series of compounds/toxins involved in harmful algal blooms with serious economic consequences for the aquaculture and fishing industries and/or deleterious impacts on human health[3–5]. Microalgae are known to produce not only toxins, but also a series of compounds derived from primary or secondary metabolism with applications in several market sectors: cosmetics, nutrition, bioremediation, aquaculture and treatment of human pathologies[3,6–11]. Recently, new insights have been gained into both the ecology and biotechnology of these important marine species thanks to genome and transcriptome sequencing projects. Not many microalgal genomes have been sequenced to date. Genomes are available for the rhodophyte *Cyanidio schyzonmerolae*, the green-algae *Chlamydomonas reinhardtii*, the chlorophytes *Ostreococcus* and *Micromonas*, the diatoms *Thalassiosira pseudonana* and *Phaeodactylum tricornutum*, and the coccolithophore *Emiliania huxleyi* (as reviewed in ref.[12]). Other genomes are in progress, such as the diatoms *Skeletonema marinoi* (http://cemeb.science.gu.se/research/target-species-imago%20/skeletonema-marinoi) and *Pseudo-nitzschia multistriata*[13]. Dinoflagellates are known to produce a wide spectrum of bioactive molecules[6,10,11], but molecular resources are still poor because they have very large genomes, ranging from 1.85 to 112 Gbp[14,15]. However, several transcriptomes have been sequenced and many of these are included in the Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) (http://marinemicroeukaryotes.org/)[16].

In this study, we present the full-transcriptome of the dinoflagellate *Amphidinium carterae*. Considering that several studies have shown that different environmental conditions (e.g. nutrient starvation, UV radiation and

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