IDENTIFICATION OF PROTEINS INVOLVED IN DIATOM BIO-SILICIFICATION PROCESS BASED ON THE COMPARATIVE PROTEOMIC APPROACH

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The ability of utilizing silica acid to bio-silicification is one of the most important life features of marine diatoms, as they can generate their highly ornamented silica cell walls (frustules). This ability is thought to be contributed to the diatom productivity in the oceans and the main procedure of the biogeochemical cycling of silicon. However molecular detail of this biological process is poorly understood. Therefore, unraveling the proteins involved in frustules biogenesis will facilitate our understanding of the molecular process involved in this important feature of diatom. In this study, a comparative proteomic approach was performed on the cells of a centric diatom *Thalassiosira pseudonana* and a pennate diatom *Pseudo-nitzschia multiseries*. The different expression patterns of proteins connected with silicon metabolism were determined during the silicified cell walls formation based on the 2-DE profiling compare. Furthermore, some proteins which are involved in silica uptake and bio-silicification were identified by mass spectrometry. The possible functions of the identified proteins were discussed. The results improve our understanding of the molecular mechanism of the silicon cell wall formation, and also enhance our understanding of the important role of diatom in silicon biogeochemical cycling.

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