

RESEARCH ARTICLE

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Diatom flagellar genes and their expression during sexual reproduction in *Leptocylindrus danicus*

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Abstract

Background: Flagella have been lost in the vegetative phase of the diatom life cycle, but they are still present in male gametes of centric species, thereby representing a hallmark of sexual reproduction. This process, besides maintaining and creating new genetic diversity, in diatoms is also fundamental to restore the maximum cell size following its reduction during vegetative division. Nevertheless, sexual reproduction has been demonstrated in a limited number of diatom species, while our understanding of its different phases and of their genetic control is scarce.

Results: In the transcriptome of *Leptocylindrus danicus*, a centric diatom widespread in the world's seas, we identified 22 transcripts related to the flagella development and confirmed synchronous overexpression of 6 flagellum-related genes during the male gamete formation process. These transcripts were mostly absent in the closely related species *L. aporus*, which does not have sexual reproduction. Among the 22 transcripts, *L. danicus* showed proteins that belong to the Intra Flagellar Transport (IFT) subcomplex B as well as IFT-A proteins, the latter previously thought to be absent in diatoms. The presence of flagellum-related proteins was also traced in the transcriptomes of several other centric species. Finally, phylogenetic reconstruction of the IFT172 and IFT88 proteins showed that their sequences are conserved across protist species and have evolved similarly to other phylogenetic marker genes.

Conclusion: Our analysis describes for the first time the diatom flagellar gene set, which appears to be more complete and functional than previously reported based on the genome sequence of the model centric diatom, *Thalassiosira pseudonana*. This first recognition of the whole set of diatom flagellar genes and of their activation pattern paves the way to a wider recognition of the relevance of sexual reproduction in individual species and in the natural environment.

Keywords: *Leptocylindrus*, Next generation sequencing, Transcriptome, Diatom, Sexual reproduction, Flagellar genes

Background

Diatoms are among the most important components of the marine pelagial, where they contribute ca 40% of the total production [1]. Diatom blooms fuel the whole trophic web and are responsible for a considerable part of the CO₂ drawdown in the world's oceans. In addition to the ecological role of diatom blooms in the oceanic biomass build-up, the enhanced asexual and sexual

reproduction rates during population outburst must have profound consequences for the genetic variability and fitness of the individual species, thus influencing evolutionary processes that are at the basis of the formidable success of diatoms [2, 3]. Sexual processes in diatoms are also crucial to the restoration of the cell size. Considerable miniaturization occurs during asexual division due to the peculiar structure of the rigid silica shell, composed of two unequal parts each inherited by daughter cells, which reconstruct new, smaller silica halves within the maternal ones. Therefore, following the high number of mitotic divisions during a bloom (1–2 per

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