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Identification of the meiotic toolkit in diatoms and exploration of meiosis-specific *SPO11* and *RAD51* homologs in the sexual species *Pseudo-nitzschia multistriata* and *Seminavis robusta*

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Abstract

Background: Sexual reproduction is an obligate phase in the life cycle of most eukaryotes. Meiosis varies among organisms, which is reflected by the variability of the gene set associated to the process. Diatoms are unicellular organisms that belong to the stramenopile clade and have unique life cycles that can include a sexual phase.

Results: The exploration of five diatom genomes and one diatom transcriptome led to the identification of 42 genes potentially involved in meiosis. While these include the majority of known meiosis-related genes, several meiosis-specific genes, including *DMC1,* could not be identified. Furthermore, phylogenetic analyses supported gene identification and revealed ancestral loss and recent expansion in the *RAD51* family in diatoms. The two sexual species *Pseudo-nitzschia multistriata* and *Seminavis robusta* were used to explore the expression of meiosis-related genes: *RAD21, SPO11-2, RAD51-A, RAD51-B* and *RAD51-C* were upregulated during meiosis, whereas other paralogs in these families showed no differential expression patterns, suggesting that they may play a role during vegetative divisions. An almost identical toolkit is shared among *Pseudo-nitzschia multiseries* and *Fragilariopsis cylindrus*, as well as two species for which sex has not been observed, *Phaeodactylum tricornutum* and *Thalassiosira pseudonana*, suggesting that these two may retain a facultative sexual phase.

Conclusions: Our results reveal the conserved meiotic toolkit in six diatom species and indicate that Stramenopiles share major modifications of canonical meiosis processes ancestral to eukaryotes, with important divergences in each Kingdom.

Keywords: Meiosis, Diatoms, Sexual reproduction, *SPO11*, *RAD51*

Background

The process of sexual reproduction is a hallmark for all the major eukaryotic groups [1–3]. It is believed that all asexual eukaryotes have evolved from sexual ancestors [1, 4], and it has been proposed that the last eukaryotic common ancestor (LECA) possessed the full set of genes known to be involved in meiosis [5–8]. Meiosis is not performed exactly in the same way in different groups: differences can be found for instance in the mechanisms of crossover formation and in the structure of the synaptonemal complex, and these differences are reflected in a variable set of meiosis-related genes [9].

Our understanding of the meiotic process, and consequently our knowledge of the gene repertoire required, is relatively strong for Opisthokonta and plants. However, despite the fact that a number of publications have recently appeared on a variety of unicellular organisms [5, 6, 9–11], information on most groups that contribute to the greater part of eukaryotic diversity are still scarce.

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