Comments and Suggestions for Authors

This study explores genes that are expressed in a diatom during growth conditions that support formation of gametes and sexual reproduction. Genes associated with the meiotic toolkit were found to be expressed, whereas flagellar genes were not found to be expressed. The first result is consistent with sexual reproduction, whereas the later result is somewhat unexpected given results from previous studies of other species. This study is fine as far as it goes and may be what is possible in this system/organism. What would make this of greater impact is if the introduction and discussion covered advances in what is known about other stremenopiles such as oomycetes, or other organisms such as fungi and algae. The authors could consider for example citing a recent chapter by Goodenough and Heitman that covers an evolutionary perspective on sexual reproduction:

Origins of eukaryotic sexual reproduction.

Goodenough U, Heitman J.


Thank you for the positive comments.

We have added a new paragraph at the beginning of the introduction and a sentence in the discussion with reference to the suggested review.

Specific questions.

Has a mating type locus or sex chromosome been identified in this or any other diatom?

So far, there are two reports only that address this issue, both in pennate diatoms which are generally heterothallic (they have two separated sexes).

In Vranstechelman et al, 2013, the authors generated mating type-specific linkage maps for the benthic pennate diatom Seminavis robusta. The mating type phenotype was mapped as a monogenic trait, and the work represented the first evidence for a genetic sex determining mechanism in a diatom, although the boundaries of the specific region and the specific gene/s involved have not been found. The second paper is our own publication, Russo et al., 2018, in which we used a transcriptomics approach to identify mating type related genes in the pennate planktonic diatom Pseudo-nitzschia multistriata, and demonstrated that one of these genes, MRP3, acts as a sex determinant. MRP3 is able to specify the mating type plus (MT+) and unfortunately has no homology with known genes, therefore we do not know its specific function in the cell. There is no conservation between P. multistriata and S. robusta in terms of the genes contained in the mating type locus, and our personal belief is that mating type systems in diatoms have evolved multiple times. Moreover, the P. multistriata mating type related genes are not conserved in centric diatoms (Russo et al., 2018).

Nothing is known for centric diatoms which are generally homothallic, like S. marinoi.
Are the genes that are involved in pheromone production or sensing known, or might these be among the genes that are induced here?

Again, the only available studies for diatoms have been carried out in *S. robusta* and *P. multistriata*, in which some genes potentially involved in pheromone production and sensing have been identified (see Moeys et al., 2016 and Basu et al., 2017). The most important ones in these two species do not have a wide conservation and many lack any annotation.

It is very likely that some of the genes induced in *S. marinoi* are required for pheromone production or sensing, and more work is required to provide support. We highlighted the conserved induced genes between *P. multistriata* and *S. marinoi* (the SIG genes in Table 3) because these could be some of the candidates to follow. Pheromones are supposed to be species-specific to avoid breeding between cells of different species, however processes downstream of the response to the very first signals might be more conserved across species.

We added a comment in the discussion (lines 457-460).


