

## Identification of the mating type locus in pennate diatoms

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Diatoms form one of the most diverse and productive groups of algae, with an estimated 200,000 species responsible for more than 1/5 of the world's primary production. They are also very interesting from a biotechnological point of view, with huge potential for the production of high-value bioproducts such as lipids, pigments and biofuels. Diatoms have a unique diplontic life cycle characterized by gradual size reduction which ultimately leads to programmed cell death. The latter, which can lead to loss of strains and cultures, can only be avoided by sexual reproduction, which enables cell size restitution via a specialized type of zygote, called the auxospore. Sex is cell-size activated, i.e. it can only be induced below a species-specific size threshold. Despite these unique features, not much is known about the molecular base of sexual reproduction and sex determination in diatoms. We are currently identifying the sex determination system of the pennate diatom *Seminavis robusta*. Crossing two strains resulted in a F1 mapping population containing 116 offspring. The segregants were analyzed with 54 *EcoRI*+2/*MseI*+3 AFLP primer combination resulting in 500 AFLP markers. Overall, we identified 15 MT- and 13 MT+ linkage groups from the analysis of 500 AFLP markers, covering 1549 and 1418 cM, respectively. Five putatively homologous linkage groups, including the sex-linkage group, were identified between MT- and MT+ linkage groups. Currently, we are identifying the MT locus by complementing the AFLP linkage mapping by a Bulk Segregant Analysis (BSA), in combination with high throughput sequencing.

We will identify sequence alterations between plus and minus mating types and map them on the genome sequence of *Seminavis robusta* which will be available soon (Bones A., Norwegian University of Science and Technology).

In the near future, we will perform a functional characterization of the MT genes by RT-PCR and genetic transformation. The evolution of the selected MT locus genes will be studied in related diatom species. This will allow us to further investigate species formation in diatoms.