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## Genetics of Speciation (Ecological and Molecular)

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### 6B.1

#### SPECIATION IN DIATOMS: RECENT INSIGHTS, NEW PARADIGMS?

Koen Sabbe (Koen.Sabbe@ugent.be), Elie Verleyen (Elie.Verleyen@ugent.be), Pieter Vanormelingen (Pieter.Vanormelingen@ugent.be) and Wim Vyverman (Wim.Vyverman@ugent.be)

Laboratory of Protistology & Aquatic Ecology,  
Dept. Biology, Ghent University, Krijgslaan 281-S8,  
B-9000 Ghent, Belgium

Diatoms are one of the most species-rich and productive groups of micro-algae in the world's lakes and oceans. They are also characterized by a peculiar diplontic life cycle involving gradual size reduction during vegetative divisions and rapid size restitution, mostly as a result of sexual reproduction. Diversification is most pronounced in the raphid pennate diatom clade, a largely benthic group which despite its relatively young geological age (probably late Cretaceous) accounts for the majority of the over 200.000 diatom species estimated to exist.

This enormous diversity is puzzling, as current paradigm holds that since dispersal in microbes is ubiquitous, allopatric speciation must be strongly impeded due to global gene flow. Virtually nothing however is known about alternative speciation mechanisms. Here we present evidence, based on population-genetic and community-level studies on freshwater and marine raphid pennate diatoms, that allopatric processes may yet play an important role in diatom speciation. We show that gene flow between distant populations of marine and freshwater diatoms is restricted and displays a strong isolation by distance pattern. In addition, we show that communities of freshwater diatoms display the same regional and global biogeographical patterns as plants and animals, and that these have been shaped not only by contemporary environmental factors but also by climatic and geological events in the past. Finally, while little is known about the actual underlying molecular and genetic mechanisms driving speciation in diatoms, the recent discovery of a sophisticated density-dependent but environment-independent pheromone production-perception system in pennate diatoms suggests that pre-gametic reproductive isolation may play an important role in diatom speciation.

### 6B.2

#### THE PRIVATE LIFE OF *ECTOCARPUS*: GENETICS OF SEX AND ALTERNATION OF GENERATIONS

Susana Coelho (coelho@sb-roscoff.fr)

Station Biologique-Roscoff, Roscoff, France

The recent completion of the *Ectocarpus* genome is affording fundamental insights into brown algal reproductive biology. Currently, research in our group is focused on understanding two key phenomena during the *Ectocarpus* life cycle: the genetic control of sexuality and the regulation of the alternation between sporophyte and gametophyte generations. The genetic determination of sex requires either non-recombining chromosome regions or complete sex chromosomes, both of which have evolved independently and repeatedly across different species. Comparative analyses of sexual systems found in land plants and animals and other eukaryotes have played a key role in understanding how sexual systems evolve. In this context, the brown algae represent a highly interesting group not only because of their evolutionary distance from other eukaryotic lineages but also because they exhibit a broad range of levels of gamete dimorphism, ranging from isogamy to oogamy; furthermore, sex is expressed in the haploid phase, which should affect the evolution of sex chromosomes. We report on the mapping and genomic analysis of the male and female sex determining regions in *Ectocarpus*, elucidating its evolution and regulation. By exploiting resources generated as part of the *Ectocarpus* genome project we have identified a sex determining region of ~1 Mbp on the male genome, where recombination is totally suppressed. We are exploring the differences between male and female sequences in this region to retrace their evolutionary history. In parallel, deep transcriptome analysis is unraveling the transcriptional network involved in *Ectocarpus* sex determination and differentiation. We will discuss how the elucidation of sex determination in this third major eukaryotic lineage will help to test existing theories of the evolutionary dynamics of sex determining regions. Additionally, we will describe how genetic approaches, in particular the identification of life cycle mutants, is helping to