

DSV Seminars

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PhD Program in Environmental Life Sciences

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Seminar room, 1st floor, Q Building, Via Giorgieri n° 5, Trieste

Dr. Mariella Ferrante

Integrative Marine Ecology, Stazione
Zoologica Anton Dohrn
mariella.ferrante@szn.it

Host: Prof. Alberto Pallavicini

Love and death in planktonic diatoms

Diatoms, an important and very diverse group of microalgae, carry out 1/5 of the photosynthesis on Earth and are essential to aquatic ecosystems, being primary producers at the base of the ocean food web. They are phylogenetically close to brown algae, and share metabolic pathways with plants as well as animals. We study the molecular mechanisms underlying the response of diatom cells to different types of signals, including chemical signals derived from mating partners or from predators. For these studies, we use functional genomics approaches and genetic engineering, including the CRISPR/Cas9 technology, and different model diatoms. Among these, *Pseudo-nitzschia multistriata*, an ecologically relevant planktonic diatom with a controllable life cycle, is an excellent model system to explore the process of sexual reproduction. We sequenced the *P. multistriata* genome and elucidated the global gene expression changes occurring in cells of opposite mating type (MT+ and MT-) when they are exchanging signals during sexual reproduction. We also explored the mechanism of sex determination, unknown for diatoms. Using a transcriptomic-based approach we identified five MT-related genes that play a role in governing cell behaviour during sexual reproduction. By using genetic transformation, we are reconstructing the genetic network that connects them. Most importantly, we identified structural differences in the genomic region of one of the MT+ specific genes. We demonstrated that this gene acts as sex determinant in *P. multistriata* by overexpressing it in an MT- strain and observing sex reversal, confirming its role as master gene in the process. Finally, we are integrating the lab studies with in situ studies, exploiting a long-term series collection of ecological and biological data from the Gulf of Naples, to follow the species dynamics in natural samples through population genomics.

