

# **Bloom dynamics and population genetics of marine phytoplankton — Community, species and population aspects**

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## Abstract

Phytoplankton are the most important primary producers in the world's oceans and coastal waters, accounting for nearly half of the global net primary production. Although they are such important organisms, little is known about the ecology and dynamics of phytoplankton. The importance of phytoplankton resting stages, the coupling between cells in the sediment and watermass and how environmental changes affect the population structure is uncertain. The record of a specific species in a given area is foregone by either advection of the species from adjacent areas, or by growth of a few cells present in the water. Many groups of phytoplankton have the ability to form resting stages to provide short- or long-term survival, and these stages can be resuspended and subsequently germinate and thereby be re-established in the water mass.

Diatoms constitute the single largest group of microalgae and they are mainly marine but found in all aquatic environments. Diatom blooms can develop fast, and they can grow at low levels of light, which gives the cells an advantage during spring blooms in temperate areas where light is a limiting factor. To successfully meet selective pressure in a variety of ecological niches, it is hypothesized that diatoms display high phenotypic and genetic diversity. *Skeletonema marinoi* (Sarno et Zingone) is a marine diatom, often dominating temperate coastal waters during spring bloom. The mechanisms for dispersal and expansion of populations of this species are, as for most diatoms, complex and difficult to predict. Possibly the presence of different populations at different seasons is caused by strong directional selection in a continuously growing population, or by a complete replacement of one population by another.

The general aim of this thesis was to study marine phytoplankton dynamics at community, species and population level, and we used *S. marinoi* as model organism for the population studies. In order to perform some investigations, appropriate methods have been developed. I have focused on the interaction between water mass and sediment, both in temperate waters and in a tropical area, investigated the importance of resting stages and small-scale hydrographical changes for the phytoplankton community structure as well as population genetics and microevolutional processes of population dynamics.

The results from a tropical area show that benthic resting stages contribute to blooms by resuspension, germination, and proliferation as planktonic cells in the water column, and thus, the cells can influence the phytoplankton community in the water column. There can be an alternation of the species composition if a plankton community is seeded by resting stages or by planktonic cells, and geographically the strategies of seeding can differ within the same species. The composition of the phytoplankton community is exceedingly affected by small-scale hydrographic changes and several of these factors are potentially tightly coupled. These changes have implications on the sampling, and therefore frequent sampling is important.

When clones of *S. marinoi* were examined, the morphological character defining another species of the same genus—*Skeletonema dohrnii* (Sarno et Kooistra)—was found in most of the clones. The phylogenetic variation in LSU rDNA in the *S. marinoi* clade were of the same magnitude or greater than differences between *S. dohrnii* and *S. marinoi*. The two species are not suggested to be merged since there may be a separation in the biogeographical distribution of the two species.

A series of molecular methods were used to study various aspects of phytoplankton ecology. For estimating the proportion of dinoflagellate versus diatom biovolume or biomass and the absolute diatom biovolume or biomass, real-time PCR technique constitutes a quick and accurate method. Another useful tool is microsatellite markers, and the characterisation and development of primers enabled the study of population genetics of *S. marinoi*. Resting stages from undisturbed and dated sediment cores from a fjord with anoxic bottom conditions, were germinated and cultures established. The fjord has during a few decades been hypereutrophicated and populations found during this time were significantly different from populations found before and after. The post- and pre-eutrophication populations showed no significant genetic difference. Environmental changes may favour only some populations from a pool of several different populations at a specific location, and maybe other changes would favour different populations.

**Keywords:** Phytoplankton, dynamics, *Skeletonema marinoi*, population genetics, resting stages