



INSTITUTIONEN FÖR MARINA VETENSKAPER

# **Genetic structuring in natural populations - the influence of life history strategies and asymmetric migration**

**Lisa Sundqvist**

Institutionen för marina vetenskaper  
Naturvetenskapliga fakulteten

Akademisk avhandling för filosofie doktorsexamen i naturvetenskap med inriktning biologi, som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras fredagen den 30:e september, 2016 kl. 10.00 i Hörsalen, Botanhuset, Institutionen för marina vetenskaper, Carl Skottsbergsgata 22B, Göteborg.

ISBN: 978-91-628-9899-1, tryckt version

ISBN: 978-91-628-9898-4, pdf nätet

Tillgänglig via <http://hdl.handle.net/2077/45832>

## Abstract

In this thesis I investigate aspects of genetic differentiation and factors influencing the structure of populations. This is done with a special focus on life histories and dispersal strategies common in the marine environment. Many marine organisms are planktonic or have a planktonic life stage and due to dispersal with ocean currents asymmetric migration between populations are thus a common occurrence. Here I present a method that makes it possible to calculate directional measures of genetic differentiation and relative migration. The method aims to advance measures of genetic differentiation and reveal more information in systems with asymmetric migration patterns. Knowledge about direction makes it easier to correlate gene flow to factors such as oceanographic connectivity. With the use of this method my coauthors and I have investigated the population genetic structure of the marine diatom *Skeletonema marinoi* and the two sibling species of macroalgae, *Fucus vesiculosus* and *F. radicans*, in the Baltic Sea area. We found that *S. marinoi* was genetically differentiated between all local populations along the salinity gradient from the Bothnian Sea to the North Sea entrance. The biggest difference was found between the two sides of the Danish Straits, thus this region indicates a major dispersal barrier. Local populations inside the Baltic Sea showed signs of adaptation to local salinities. Directional relative migration, calculated with our method, was found to be significantly correlated to oceanographic connectivity. Furthermore, asymmetric migration coming from the Baltic Sea coincided with the direction of the surface current. Many planktonic microalgae including *S. marinoi* form long-term resting stages that accumulates in the sediments. By constructing a simple genetic population model and also conducting a systematic literature review my coauthors and I have investigated if and how a life history strategy including resting stages can affect the genetic structure of a population. We found that resting stages can have an anchoring effect on local populations that can lead to genetic differentiation between adjacent populations despite ongoing gene flow. This anchoring effect may help explain how microalgae with huge dispersal potential can be found genetically differentiated on small geographical scales. When investigating the genetic population structure of *F. vesiculosus* and its newly evolved sister species *F. radicans* we found support for earlier conclusions of two reproductively isolated species. However, we conclude that the genetic pattern of these two species is very complex and that geographical differences are high.