



GÖTEBORGS UNIVERSITET

Patterns of evolution in a young species, the Baltic seaweed *Fucus radicans*

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Akademisk avhandling för filosofie doktorexamen i naturvetenskap med inriktning mot biologi, som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras fredagen den 22 maj kl 10.00 i stora hörsalen, Institutionen för biologi och miljövetenskap – Tjärnö, Hättebacksvägen 7, 452 96 Strömstad

Abstract

To be able to interpret patterns of biodiversity it is important to understand the processes by which new species evolve and how closely related species remain reproductively isolated and ecologically differentiated. This thesis centers on the evolution of the two brown algae *Fucus radicans* and *Fucus vesiculosus* in the Baltic Sea, where *Fucus radicans* very recently diverged from *F. vesiculosus*, and where both species have acquired the unique character of asexual recruitment forming clones. Speciation is one of the most fundamental processes in biology, yet poorly understood. It is generally argued to build on a slow accumulation of differences between populations living in allopatry, but the formation of *F. radicans* most likely occurred without geographic separation and provides a unique opportunity to study the differentiation and evolution of a new species following a recent, rapid and sympatric speciation event. We investigated the spatial patterns of clonality in *F. radicans*, to understand how clones affect the potential for sexual reproduction, recombination and local adaptation. Results showed that rare sexual events, occasional long-distance migration and somatic mutations of large clones contribute new genotypic variation in populations of *F. radicans*. We further analysed the genetic structure of *Fucus* from areas not earlier investigated along the Finnish and Russian coasts of the Baltic Sea, comparing the results with previous data from Bothnian Sea and Estonia. The results indicated a genetic structure strongly affected by the geographic isolation of populations, but in most cases separating the two taxa at a local scale. In addition, we found some cases of strong genetic asymmetries with populations having fewer rare alleles than others, either as a consequence of directional gene flow or founder effects during colonization. Interestingly, in contrast to earlier findings from the Bothnian Sea, sexual reproduction remained important in the lowest salinities (<3‰) in eastern Gulf of Finland. Nevertheless, in *F. radicans* a few old clones have dominated much of the species' distribution over extensive periods of time suggesting that the distribution of genotypes cannot solely be ascribed to natural selection. Using a spatially explicit model, we tested a neutral scenario of colonization of a new environment by a species with the potential of both sexual and asexual reproduction. We found that a pattern with spatially and temporally dominant clones mixed with areas of sexual reproduction is quite unlikely during and thousands of generations after colonization of a new environment even so sexual reproduction eventually takes over. One hypothesis connected to the speciation process is that herbivores may have had different co-evolutionary effects on the two species. We assessed differences in inducible herbivory defense using an ecological experiment complemented by gene expression analysis. We found that *F. vesiculosus* produced deterrent chemicals faster than *F. radicans*, and that patterns of gene expression were different between the species under grazing by isopods. The evolutionary changes observed in transcriptional regulation of grazing resistance in these two macro algae has likely evolved under differential selection, with *F. vesiculosus* mainly distributed in areas of strong grazing pressure, while *F. radicans* is not found in such areas. My investigations have contributed with further understanding of the Baltic Sea *Fucus* system and its intriguingly rapid and recent speciation. In current times, climate change threatens Baltic Sea species and biodiversity, and increased knowledge of processes generating and maintaining biodiversity in this ecosystem seems particularly important and needed.

Key words: brown algae, *Fucus radicans*, sympatric speciation, clonality, somatic mutations, microsatellites, reproductive barriers, asymmetric migration, transcriptomic differences