

**ABSTRACT:** Knowledge of within-species genetic diversity is essential to understanding many ecological and evolutionary processes. Factors affecting genetic diversity in the marine snail *Littorina saxatilis* were studied on different spatial scales and with different genetic markers. This species does not have a pelagic larval dispersal stage, and even close-by populations usually have great morphological and genetic differences.

If a species normally disperses only short distances and therefore is at risk of inbreeding, behavioural mechanisms may evolve to compensate the loss of genetic diversity. One possible mechanism in the study species is multiple paternity, the incidence of which was studied by collecting females from natural populations and allowing them to produce offspring from stored sperm. The offspring and females were then genotyped using microsatellite DNA markers. Female snails were found to carry offspring sired by high numbers of males per female. This may have great consequences in retaining genetic diversity through dispersal events or population fluctuations.

In other chapters of the thesis, genetic structure was studied with the help of microsatellite, allozyme and mitochondrial DNA markers. Populations were highly structured on small spatial scales (<1 km) as a result of partial reproductive isolation and strong selection on two allozyme loci. On larger scales - if the selected loci were excluded - most populations were highly differentiated from each other, but the population structure was essentially random due to a large effect of genetic drift. Microsatellite and allozyme estimates of differentiation were concordant except for lower levels of differentiation at the microsatellite loci. At even larger spatial scales (>500 km), mitochondrial DNA sequencing was used to detect signals of past population differentiation. Some areas had haplogroups showing ancient divergence from other populations, but in Northern Europe there were extremely widespread haplotypes, likely due to recent population expansion.

Some causes and consequences of genotyping errors in microsatellites were examined using both experimental data and simulation studies. Null alleles were found to be present at many populations in several of the loci commonly used for population genetic studies in *Littorina saxatilis*, but we found that correction methods can compensate for the bias, and that null alleles are unlikely to be a critical problem for estimating genetic structure in model systems similar to ours.

**Keywords:** *Littorina saxatilis*, genetic diversity, genetic structure, multiple paternity, microsatellites, allozymes, mitochondrial DNA, null alleles.