Implementing genetic diversity into marine restoration: A case study with Finnish charophytes

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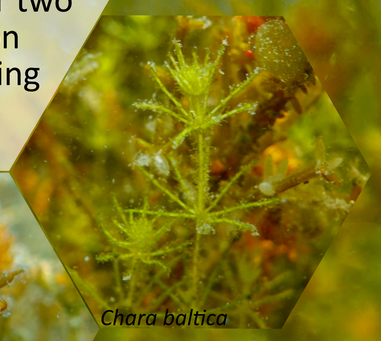
Genetic diversity is the most basic element of biodiversity, yet is still a largely neglected aspect of biodiversity. Sufficient genetic diversity provides the foundations to healthy and sustainable populations. It is important in defining a species adaptive potential, allowing species to adapt to changing environmental conditions. The ecological significance of intraspecific genetic variation is also often overlooked. For many species there is a lack of understanding of the intraspecific variation, leading to shortcomings in the management and protection of these species. For example, for charophytes (*Chara* spp.) information on genetic diversity, especially at an intraspecific level, is limited. This project aims to correct this for two species of charophytes common within the Baltic Sea by developing microsatellite genotyping protocols.

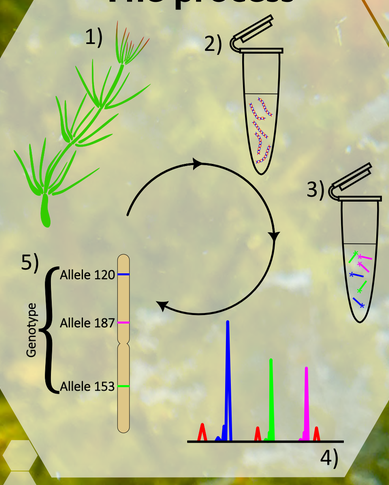


Chara baltica

Chara tomentosa

Microsatellites are powerful genetic markers capable of rapid genotyping. They are short sections of DNA consisting of repeated nucleotide motifs. The size of the DNA fragments (alleles) indicates the relatedness among individuals. After development they present a permanent resource for determining and monitoring genetic information.

The process

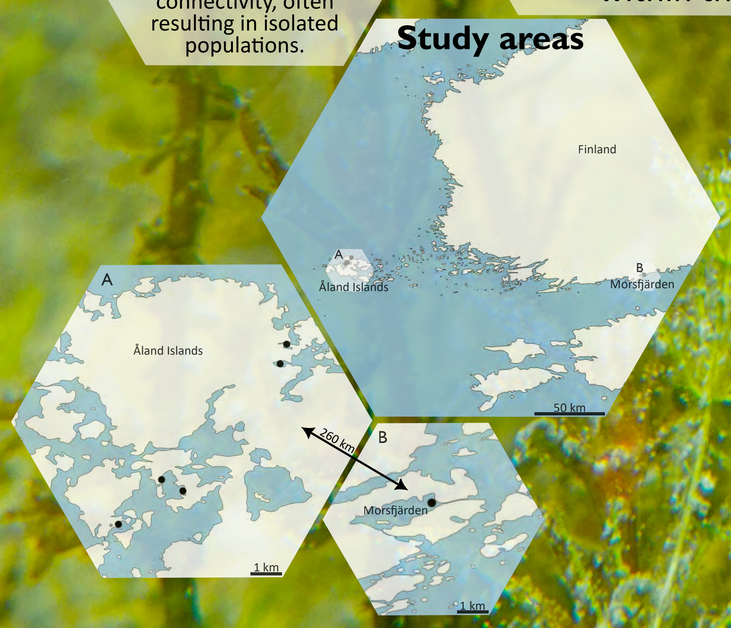


Process summary:
1) Thallus tissue is taken from the population. 2) DNA is extracted. 3) Microsatellites are targeted and labelled with fluorescent tags. 4) Alleles are determined on electropherograms. 5) The genotype is established.

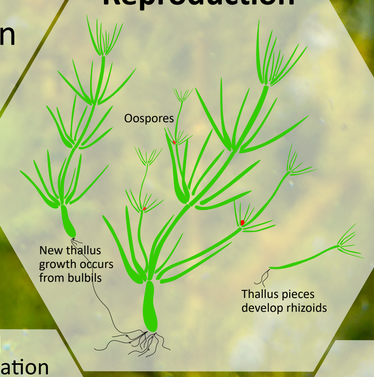
The Project aims to improve restoration success in charophytes by implementing knowledge on genetic diversity into restoration trials. Successful restoration restores a habitat to a healthy state with resilience to future changing conditions. To increase the chance of the long-term success, an understanding of how healthy, sustainable natural populations are structured and maintained is required. Central to this is knowledge on the genetic diversity, population structure, and reproductive mode. In species where both sexual and asexual reproduction is present, restored populations should represent the reproductive strategies of natural populations. This project, by genotyping individuals from many populations at various spatial scales, will establish baselines of both the intraspecific and interspecific variation alongside the reproductive mode among charophytes populations within the Baltic Sea.

Population structure is the organisation of genetic variation. It can infer the connectivity and geneflow between individuals and populations. Low population structure results in a homogenous population, whereby genetic material flows freely. High population structure construes reduced connectivity, often resulting in isolated populations.

Study areas

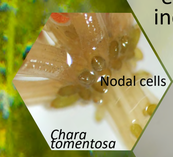


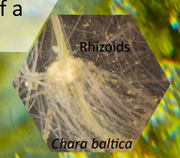
Reproduction



Sexual
1) Recombination present: genetic variation enhanced, adaptation promoted, favourable allele combinations separated; 2) Requires both male and female gametes, and has a higher energy expenditure associated with their production; 3) Often limited in unfavourable conditions

Asexual
1) No recombination: adaptation limited, favourable allele combinations maintained; 2) Rapid proliferation and/or colonisation in favourable conditions; 3) Frequent in unfavourable environments, often increases towards the range margin of a species





Restoration benefits from the inclusion of genetic information when obtaining source material or planning restoration techniques. This project will guide the selection of source material alongside the selection of effective restoration techniques of charophytes within the larger Biodiversea Life IP project. With the overall aim to improve the prospect of achieving sustainable and resilient restored charophyte habitats.

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