

Population genetics of the red alga *Furcellaria lumbricalis* along a salinity gradient based on microsatellite and SNP markers



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Geographical range of *Furcellaria lumbricalis* (Hudson)



- The perennial red alga *Furcellaria lumbricalis* occurs in cold waters of the North Atlantic and Arctic Oceans.
- The environments differ in their salinity, some being clearly marginal.

Our aims are:

- To develop **new genetic markers** for red algae (putatively neutral microsatellites, EST-derived microsatellites, EST-derived SNPs)
- To examine **genetic diversity and differentiation** of red algal populations in Northern Europe
- To compare **neutral vs. adaptive genetic variation** on a population level in nature.

Neutral vs. adaptive variation

• Selection is considered to act on adaptive loci only, whereas genetic drift, gene flow and reproductive patterns affect genetic variation at all loci to the same extent.

• Genetic variation in expressed genes indicates adaptive capability of algae in a changing environment.

• Data analyzed with ARLEQUIN 3.01

• Putatively neutral microsatellites, mean $F_{ST} = 0.095$

- among Atlantic Ocean populations 0.081
- among Baltic Sea populations 0.109

• EST-derived microsatellites, mean $F_{ST} = 0.398$

- among Atlantic Ocean populations 0.253
- among Baltic Sea populations 0.095

• EST-derived SNPs, mean $F_{ST} = 0.522$

- among Atlantic Ocean populations 0.160
- among Baltic Sea populations 0.171

→ **clear differentiation based on EST-derived markers (selection?)**

• Differences in variation pattern between marker types

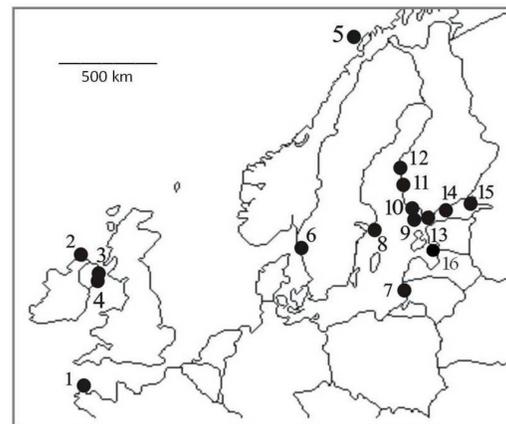
• Less variation at EST-derived marker loci

References

- [1] Kostamo K, Olsson S & Korpelainen H. Identification of salinity stress-responsive genes in the red alga *Furcellaria lumbricalis* (Rhodophyta) by expressed sequence tag analysis. *Journal of Experimental Marine Biology and Ecology* 404: 21–25.
- [2] Kostamo K, Korpelainen H & Olsson S. Comparative study on the population genetics of the red algae *Furcellaria lumbricalis* occupying different salinity conditions. *Marine Biology* 159(3): 561–571.
- [3] Excoffier, L., Guillaume, L. & Schneider, S. 2005. Arlequin (version 3.0): An integrated software package for population genetics data analysis. *Evol. Bioinf. Online* 1:47–50.
- [4] Pritchard, J.K., Stephens, M. & Donnelly, P. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155:945–959.

Genetic markers for geographically distinct populations

Transcriptomic libraries were generated from two populations from different geographical locations and salinity conditions (the Atlantic Ocean and the brackish Baltic Sea) [1].



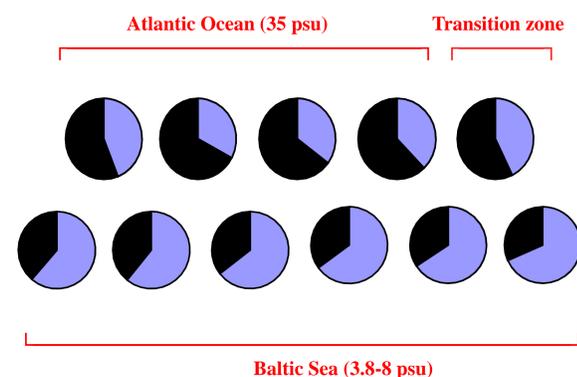
Genetic markers developed:

- Microsatellites (coding and non-coding) [2]
- SNP markers (coding)
- 16 populations investigated from salinity conditions ranging from 3.6 psu to 35 psu

Differentiation between marine and brackish populations

• Bayesian Structure analysis STRUCTURE 2.2 [4] was used to determine the number and distribution of genetic clusters.

• A view of great differentiation between marine and brackish population was supported ($K=2$, the Atlantic Ocean and Baltic Sea).



• Polymorphisms of *F. lumbricalis* within coding regions showed considerable differentiation, and the SNPs possessed even greater differentiation than did EST-derived microsatellites while no major differentiation can be seen based on putatively neutral markers..

• Even if no evidence of selection was detected, the level of differentiation detected in SNP markers indicates the presence of other evolutionary factors than genetic drift.

Outlook

- The results obtained will aid to understand the molecular basis of adaptation in natural populations subjected to adverse environmental conditions (low salinity).
- Further characterization by primer walking will be performed for the most promising microsatellite markers.