

In search of the “population” - unorthodox sampling design to uncover large-scale eelgrass population structure

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Could our sampling design change the outcome?

Many marine populations are more or less **continually distributed** along coastlines, yet sampling regimes usually define haphazard locations as the unit of study, often dubbed ‘**population**’. This applies particularly to population genetic studies.

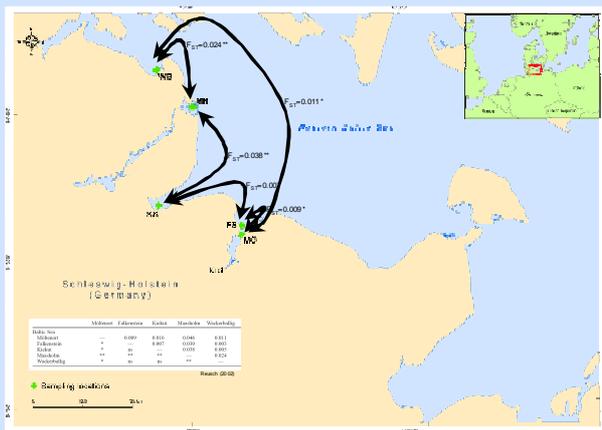
To assess the validity of current population definitions, we used **two eelgrass datasets**: an “old” dataset taken at predefined locations (Reusch, 2002) and a “new” monitoring dataset from 2010/11 taken in a continual approach.

The eelgrass samples were analysed following the same protocol for the **same 8 microsatellite loci**. Genetic data were explored by GENETIX, STRUCTURE and GENELAND.

"Old"

Sampling locations and design

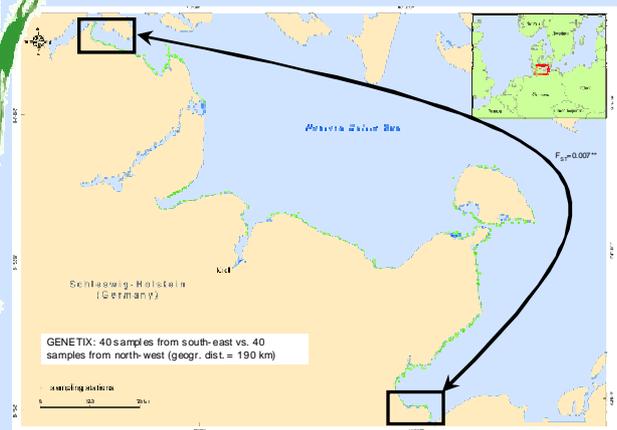
Eelgrass shoots were sampled at **5 predefined "populations"** (see map). In each population, defined as an area of 20 x 40 m parallel to the shore in 1-3 m depth, leaves of 40 to 50 plants were sampled at distances of ≥ 1 m resulting in a total of 210 samples. Populations were between 3 – 60 km distant from each other.



"New"

Sampling locations and design

Single eelgrass shoots were collected **continually every 500 m** in 3-4 m depth along the whole Baltic coast of Schleswig-Holstein (ca. 400 km). Additionally, at 110 vertical transects the deepest and shallowest shoots found were sampled resulting in 560 samples. *A priori* no populations were defined; only for analysis with GENETIX, the two most distant areas of the coastline were chosen for a pairwise calculation of the F_{ST} -value (see map).



Results

1. GENETIX: weak but significant substructure with 7 out of 10 pairwise comparisons showing at a scale of ≤ 60 km
2. STRUCTURE: most probable population number $k=4$, but no clear graphical pattern visible (Fig. 1)

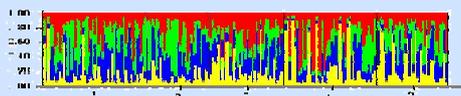


Fig. 1: Structure plot of all 210 samples, grouped by "populations", $k=4$

Results

1. GENETIX: artificially generated populations show similar significant substructure as "old" sampling design (map)
2. STRUCTURE: up to $k=50$ no population substructure and no graphical pattern was observed (Fig. 2)
3. GENELAND: Microsats combined with geographical coordinates also show no population substructure (not shown)

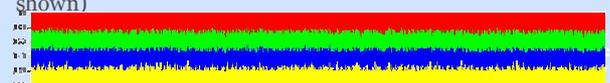


Fig. 2: Structure plot of all 560 samples, $k=4$

Conclusions

The two contrasting sampling designs could lead to different assumptions about population substructure of continually distributed species. To get a more accurate, unbiased picture of the reality, we propose a continual sampling design along natural gradients.



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