

Genetic and morphological diversity of closely related *Sphagnum angustifolium*, *S. fallax* and *S. flexuosum*

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Materials and Methods

Altogether 244 samples, from 22 European countries (Fig.1) were included to analyses, .



Fig. 1. Distribution of samples

Genetic and morphological analyses were performed on the very same genetic individual. All sample were identified on the basis of Daniels and Eddy 1984 (taxonomic groups).

Genetic data

- DNA extraction
- amplification of 11 microsatellite loci with standard PCR

- fragment length analyses (ABI 3130, GeneMarker 1.80)

Morphology

The morphological measurements were made on branches, branch and stem leaves.

(Nikon E 600, UTHSCSA ImageTools 3.00)

Data analyses

- separation of genetic groups (PCoA, AMOVA, GenAlEx 6.4.1., STRUCTURE 2.3.3.)
- separation of morphological groups (LDA, R 2.12.2)

Introduction

The *S. recurvum* group, a taxonomically difficult assemblage of the section *Cuspidata*, consists of morphologically highly similar species. The earlier studies examining genetic and morphological variability of the *S. recurvum* complex used only North European and North American specimens and morphological variability in other geographical regions were neglected. This is especially true for Central and Southern Europe where species grow under less favorable conditions and show ambiguous and mixed morphological features .

Results

1. Are the taxonomic and genetic groups are same or not?

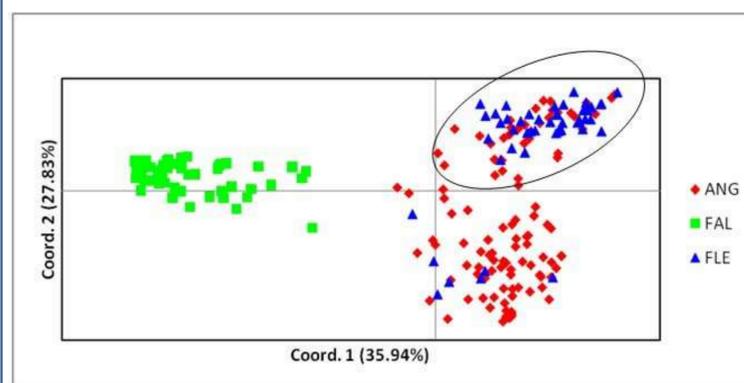


Fig. 2. Results of PCoA on the basis of 11 microsatellite loci

By contrast, plants representing the taxonomic groups *S. angustifolium* and *S. flexuosum* make up two weakly separated point clouds in which accessions of *S. angustifolium* and *S. flexuosum* are unresolved occurring in both sub clouds. *S. angustifolium* (ANG) accessions are found in both sub clouds.

The Principal Coordinates Analyses (PCoA) suggest that two major clusters can be distinguished based on the variability of microsatellite markers (Fig.2.). All samples identified as *S. fallax* (FAL) are clearly separated from the rest of the accessions.

2. Is there any sign of hybridization among taxa that might complicate their morphological delimitation?

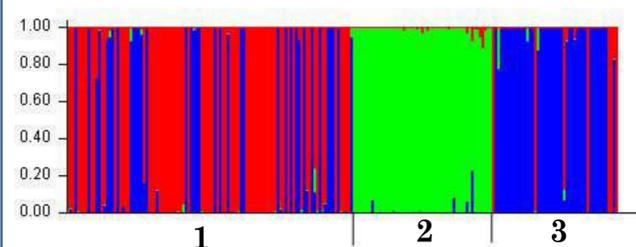


Fig.3 Results of STRUCTURE analyses (K=3) csoport esetében.

The numbers represents the taxonomic groups: 1-ANG, 2-FAL, 3-FLE. and the colors are reflected on genetic groups: red-ANG, green-FAL, blue-FLE

The STRUCTURE analyses supported three clusters which are well separated and only a low proportion of the specimens showed weak signs of admixture (Fig. 3). In line with results of the PCoA, the STRUCTURE analysis also suggests that taxonomic *S. fallax* belong to one species pool whereas taxonomic *S. angustifolium* and *S. flexuosum* samples do not correspond to one gene pool they are equally distributed in two gene pools and are thus not separated.

3. Are the genetic taxa separated on the base of morphological variables?

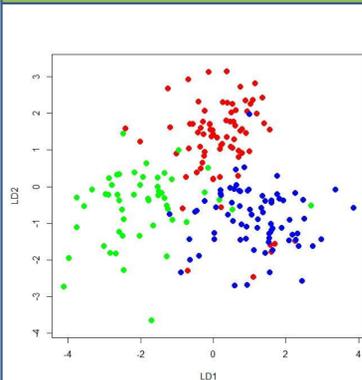


Fig.4.- Result of Linear Discriminant Analyses (LDA) with genetic groups on the base of eight independent morphological variables (red-ANG, green-FAL, blue-FLE)

Separation of the genetic groups based on their morphological characters was far from perfect. Although accessions of the three genetic groups were primarily restricted to the three edges of the point cloud they showed a considerable overlap (Fig 4.). The first discriminant function primarily separated *S. fallax* and *S. flexuosum* whereas the second function distinguished *S. angustifolium* from the rest of the species.

Discussion

Sphagnum recurvum group was divided up into three species on the base of taxonomy, however there were many ambiguous samples. There are also three species on the base of genetic diversity of 11 microsatellite loci, but these groups are not perfectly fitted to each other.

In the case of *S. fallax* the morphological and genetic groups are totally overlap, but the other two species are much more problematic, 28% of samples were misidentified, on the basis of emphasized features (see Table 1). The Linear Discriminant Function Analysis also misallocated about 8% of samples on the base of leaf morphology.

References

Daniels, R. E. és Eddy, A. 1984. *Handbook of European Sphagna*. Institute of Terrestrial Ecology, Huntingdon.

Acknowledgements

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