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Genetic variation among different populations of *Aster tripolium* L. grown on naturally and anthropogenic salt-influenced habitats: implications for conservation strategies

Introduction

The sea aster, *Aster tripolium* L. subsp. *tripolium* is a common halophyte of the salt meadows in the temperate regions (Fig. 1) [1]. It is also found in naturally and anthropogenic salt-influenced inland habitats, such as potash mine dumps [2].

Fig. 1 Photography of the Baltrum habitat with the pasture (right) and the fallow (left) along the dividing fence (Baltrum 22/5/2002). The higher parts were situated in the front and the lower parts at the level of the fence in the background.

The genetic relationships among populations in different habitats were investigated, and the genotype related to vegetational parameters and abiotic soil factors as possible indicators of natural selection. On the island Baltrum a salt meadow was divided into shore, higher and lower pasture and fallow (Fig. 1). Near Hannover habitats from the foot of four potash mine dumps or in another case from a close sink were selected. As an outgroup plants from Japan were included.

Investigations

DNA was extracted from five plants from each *Aster tripolium* population and analyzed for random amplified polymorphic DNA (RAPD) (Fig. 2).

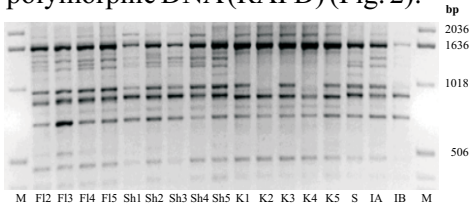

Fig. 2 Representative RAPD band pattern of 17 *Aster tripolium* individuals using Primer K20 (Roth, Germany). Abbreviations: Fl2 to Fl5, lower fallow; Sh1 to Sh5, shore; K1 to K5, Kobe (Japan); S, Sehnde; IA and IB, Ilten; M, marker; bp, basepairs.

By the use of seven primers 35 (50%) polymorphic bands in 51 individuals and 45 different detectable genotypes could be identified (Fig. 3).
The genetic variation was determined by the neighbor-joining method, the principal coordinate analysis and the analysis of molecular variance. Three genetic groups could be found reflecting the geographic site (Fig. 3). Even by excluding the Japanese group, a Baltrum and a deposit dumps group could be distinguished with a genetic variation of 33.3%. A high variation of 57.6% was found within populations and only 9.1% among populations.

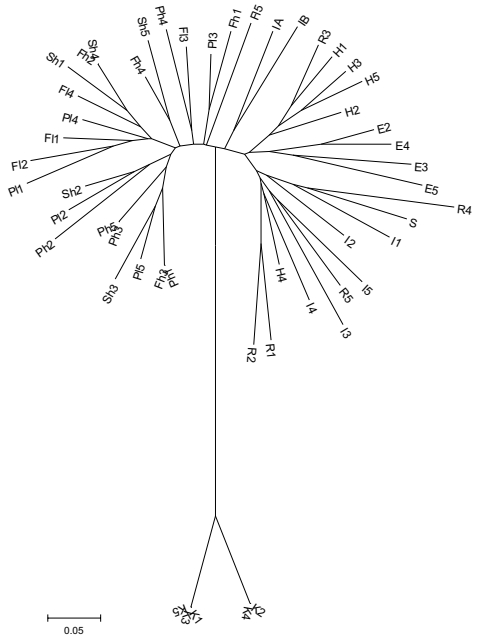

Fig. 3 Dendrogram of genetic relationships among 51 different individuals of *Aster tripolium*. The neighbor-joining method (Mega2.1) was applied to an average "taxonomic" distance matrix among the individuals (NTSYSPc 2.11L) which is indicated by the scale bar.

A genetic diversity of 3.25 +/- 0.55 for plants from the different ecological habitats on Baltrum indicates a closer relation than for plants growing at the different deposit dumps (3.99 +/- 1.23).
Salt concentration and salt composition of the soil determined by flame emission spectrometry and by energy dispersive X-ray-microanalysis were very heterogeneous. Additionally pH values were measured.

There was no correlation with the genotype found. Also no influence of phytosociological factors, such as coverage or height of vegetation, and land use systems like grazing or pasture could be detected, although they showed a clear effect on the frequency of *Aster tripolium* (Fig. 4). At the inland habitats the inter specific competition is low. Grazing promotes a perennial life-style and the growth as vegetative clone.

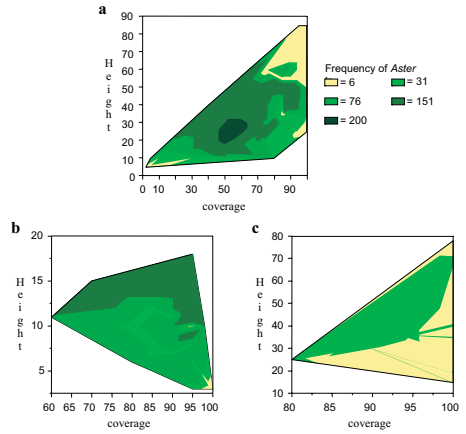

Fig. 4 Multivariate analysis of the frequency of *Aster tripolium* related to the coverage (x-axis) and height (y-axis) of the vegetation. (A) Empelde, (b) lower pasture, and (c) lower fallow. The results from one out of two transects are shown.

Conclusion

The results argue for a conservation of anthropogenic salt-contaminated habitats to maintain and further increase genetic variability not only on the species level but also within a species.
To clarify the origin of newly colonized inland habitats by *Aster tripolium* further investigations are necessary. Co-dominant marker systems like microsatellites might be suitable to detect more variations after short periods of evolutionary separation.

References

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