lations of this cushion plant are found on wind exposed slopes and ridges on silicates between 1700 and 2700 m.

To test whether *S. pumila* survived the last ice age in only one or in several refugia, 162 individuals from 34 populations covering the whole alpic distribution area were analysed using AFLP-fingerprinting.

Three selective primer combinations resulted in 230 unambigously scoreable fragments of which 151 were polymorphic. Both a PCoA (Principal Coordinate Analysis) and a Neighbour Joining Tree show a division into two groups of populations: (1) Niedere Tauern and easternmost parts of the Central Alps; (2) from Nockberge and Hohe Tauern to the west. Within the second group some western populations are characterised by a low genetic variation within the population, most probably due to recent (postglacial) establishment via long distance dispersal (Sarntaler Alpen, Presanella, Deferegger Alpen, northern Dolomites). Private allels, which might indicate a longterm isolation are mainly found in the presumptive refugial areas in the east but also in some populations from the Dolomites. This is a hint that *S. pumila* survived the last ice age in situ also there. There is some indication that also the eastern parts of Hohe Tauern might have been inhabited even within the ice sheet (but not far from its edge) because the genetic variation of the populations in this region is quite high and some private allels can be found.

The results are in congruence with the hypothesis of peripheral Pleistocene refugial areas and remigration into central parts of the Alps. There is no evidence for a survival of disjunct populations in formerly heavily glaciated areas. The high level of genetic variation and also the existence of many private alleles in the easternmost populations (e.g. Koralpe, Gleinalpe, Saualpe, Ameringkogel) is in correspondence with the occurrence of some endemic or relic taxa in this region and is an interesting fact regarding conservation priorities.

Abb. 12: *Saponaria pumila*

Genetic diversity and historical biogeographyof two arctic-alpine ferns in Europe

Johannes C. Vogel [1], Frederick J. Rumsey [1], Stephen J. Russell [1], John A. Barrett [2] and Mary Gibby [3]

Several fern species have genuine arctic-alpine distributions in the northern Hemisphere. Five diploid species, i.e. *Asplenium viride* Huds., *Athyrium distentifolium* Tausch ex Opiz, *Dryopteris expansa* (C.B. Presl) Fraser-Jenkins & Jermy, *Polystichum lonchitis* (L.) Roth., *Woodsia ilvensis* (L.) R. Br. and three tetraploid species, *Cryptogramma crispa* (L.) R. Br., *Cystopteris montana* (Lam.) Desvaux and *Woodsia alpina* (Bolton) S.F. Gray are distributed widely in Europe. By exploring discontinuities of ploidy-levels, breeding systems and genetic variation we have developed ferns as model organisms to address questions such as (1) postglacial colonisation versus in situ survival during the ice-age, (2) biogeographic links and relationships between different regions (3) assessing conservation priorities and needs. We will compare data from two large data sets on *Asplenium viride* and *Athyrium distentifolium*.

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Comparative phylogeography of *Arabis alpina* and *Arabidopsis lyrata* ssp. *petraea* in Europe

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Distribution patterns of plants are influenced by ecological, genetic and historic factors. We have studied the genetic diversity of two closely related Brassicacae in Europe, *Arabis alpina* and *Arabidopsis lyrata* ssp. *petraea*, in order to determine (1) their ploidy levels and prevailing breeding systems, (2) to reconstruct their postglacial colonisation routes and (3) to determine areas in Europe where populations might have survived during and after the Weichselian glaciation.

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