

In order to test the persistence of plant communities over time, we decided to compare the intraspecific phylogeographies of five plants from the same community (*Cardamine* gr. *bellidifolia* L., *Cerastium cerastoides* (L.) Britton, *Omalotheca supina* (L.) DC., *Salix herbacea* L., *Sibbaldia procumbens* L., *Veronica alpina* L.). Ten individuals of these six plant species were sampled in three localities in Scandinavia, three localities in the Alps, and two localities in the Pyrenees. The intraspecific phylogeography will be assessed using the AFLP technique. We expect to find concordant phylogeographic patterns if plant communities are stable over time.

Patterns of populational differentiation in *Hypochaeris* (Asteraceae) of the southern Andes Karin Tremetsberger¹, Yan-Ping Guo², Alexandra Müllner¹, Rosabelle Samuel¹ and Tod Stuessy¹

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Less is known about effects of ice ages in southern South America than in Europe and North America. The Andes in southern Chile (south of Temuco) were completely glaciated, whereas only descent of local glaciers occurred throughout other Andean regions. Species of South American *Hypochaeris* sect. *Achyrophorus* are members of the high-Andean flora (Chile and Argentina) and serve to test hypotheses of biogeographic effects of ice ages in this region. We have analyzed three species that differ in ecology and reproductive modes: *H. tenuifolia*, a perennial allogamous pioneer on exposed lava slopes, and *H. acaulis* and *H. palustris*, both inbreeders localized in moist seeps along small arroyos.

Two hypotheses were tested: (1) regional patterns of genetic partitioning north of the glacial boundary do not correlate with isolation by distance and (2) genetic variation within glaciated southern regions is reduced in comparison to populations further north.

AFLP markers provide an estimate of genetic variation within and among populations. In *Hypochaeris tenuifolia*, three primer-combinations were analyzed yielding 206 fragments of which 186 (90%) were polymorphic. *Hypochaeris tenuifolia* has high dispersal and colonizing abilities. Genetic similarities exist between pioneer populations on ash slopes of Volcán Lonquimay (that erupted in 1988) and those more than 100 kilometers away. The distance class correlogram among populations throughout the species also indicates genetic correlations between populations up to 130 kilometers distant. This value is similar to those documented in other alpine species (Alps, Scandinavia). Absence of deep gaps in the intraspecific phylogeny also indicates lack of older historical separations. Isolation by distance may be the main factor responsible for these observed patterns, with past and present long distance gene flow via wind-dispersed seeds swamping effects of Pleistocene differentiation. The only suggestion of ice age isolation may be seen in characteristic fragments that show a slight regional geographic pattern of allelic differentiation characterizing northern, central, and southern parts of the range.

Hypochaeris acaulis and *H. palustris* are small herbs with limited dispersal capabilities and isolated to subalpine seeps. Genetic data reveal patterns of phylogeographic differentiation in these taxa, suggesting impacts from inbreeding as well as local Pleistocene glaciation. Reduction in genetic variation within and between populations is observed in the southern glaciated areas in contrast to northern parts of the range.

Several peripheral Pleistocene refugia for the alpine cushion plant *Saponaria pumila* (Caryophyllaceae) Andreas Tribsch and Peter Schönswetter

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Saponaria pumila (Caryophyllaceae) occurs in the Eastern Alps and in the southern parts of the Eastern Carpathians. Within the Alps its distribution shows strong affinities to presumptive Pleistocene refugial areas for the flora of the siliceous Alps (eastern-most Alps, Dolomites), but also extends to central parts (Hohe Tauern, Deferegger Alpen, Presanella, Sarntaler Alpen). Popu-

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 unambiguously 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 alleles, 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 alleles 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.

Genetic diversity and historical biogeography of two arctic-alpine ferns in Europe Johannes C. Vogel¹, Frederick J. Rumsey¹, Stephen J. Russell¹, John A. Barrett² and Mary Gibby³

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.) Desv. 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*.

Comparative phylogeography of *Arabis alpina* and *Arabidopsis lyrata* ssp. *petraea* in Europe Johannes C. Vogel¹, Steve Ansell² and John A. Barrett²

Distribution patterns of plants are influenced by ecological, genetic and historic factors. We have studied the genetic diversity of two closely related Brassicaceae 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.



Abb. 12: *Saponaria pumila*

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