

middle Alps (6), Silvretta to Kitzsteinhorn, is intermediate between (3) and (4). Mantel tests were used to assess the goodness-of-fit between our grouping and the genetic distance matrix and gave congruent results.

Our results suggest, that *A. alpina* survived the last glaciations in at least four regions (1–4). There is no evidence for nunatak survival in the western part of the main chain of the Eastern Alps (6). In fact, it was colonised from refugia to the south (3) and to the east (4). Within regions (1)–(4) no contributions to the nunatak-debate can be derived from our data: due to the overall weak structuring within regions, it is not possible to decide, whether plant populations within the well-defined regions survived on nunataks or outside the ice-shield.

**Immigration AND in situ glacial survival in the lowalpine *Erinus alpinus*?** Ivana Stehlík<sup>1</sup>, J. Jakob Schneller<sup>1</sup> and Konrad Bachmann<sup>2</sup>

It was hypothesised that *Erinus alpinus* survived in south-west peripheral refugia during glaciation. Its present-day, mainly sub-alpine distribution is nearly continuous in a south-west to north-eastern direction along the Alps. Nevertheless, *E. alpinus* is also known from proposed glacial refugia in the northern Prealps. Twelve plants each from 22 populations covering the proposed postglacial immigration route from possible southern French refugia along the north-western edge of the Alps were collected, including several populations from northern alpine refugia. High genetic variation was detected by AFLP, but no variation was found in PCR-RFLP of cpDNA. Hence, interpretations were mainly based on AFLP data. Using cluster analyses, several Mantel tests and AMOVAs, three basic groups could be discriminated. One contained all populations from Central Switzerland, one all individuals from the Rigi mountain and one all other populations (west-eastern group). While the two south-western most populations, sampled as potential refugial sources, were not genetically distinct of the west-eastern group, there was a clear genetic isolation between Rigi and Central Switzerland. Over all, west-eastern individuals showed slightly higher numbers of fragments than individuals from Central Switzerland and Rigi, while there was a decline in the number of fragments within the west-eastern group from West to East (lowest number at the eastern distribution edge of *E. alpinus*). No individual was genetically intermediate between the west-eastern, the Central Swiss and Rigi individuals, pointing to a lack of gene flow.

The present investigation demonstrates how two genetically contrasting processes acted at distant timespans. The genetic pattern in Central Switzerland and Rigi pointed to an in situ survival on nunataks in the northern Prealps (possibly dating back to 60–28 ky AD), whereas the west-eastern gene-pool immigrated postglacially from southern France through the prealpine lowlands (after the retreat of glaciers, 14.6 ky AD), leaving out the colonisation of Central Switzerland. In many cases, potentially different historical genetic patterns have possibly been swamped by immigrating genotypes. Nearly lacking gene flow among central Swiss and west-eastern populations and the geographic remoteness of the Rigi mountain (lakes on three sides) enable that this old genetic pattern is still detectable in *E. alpinus*.

**Comparative phylogeography of alpine plants** Pierre Taberlet, Ludovic Gielly and Philippe Choler

In a previous comparative study, we compared the intraspecific phylogeographic structure of ten taxa across Europe, including mammals, amphibians, insects, and plants. The most striking result was the considerable dissimilarity among European-wide phylogeographic patterns. It seems that each taxon has responded independently to Quaternary cold periods. As a consequence, assemblages of plants comprising particular communities might be not stable over time, an observation consistent with previous findings based mainly on fossil pollen data.

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