

Contributions

Evolution, biogeography and genetic diversity in *Veronica alpina* L. and related taxa Dirk C. Albach^{1,2} and Michael F. Fay²

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The *Veronica alpina* complex comprises about seven taxa of alpine to sub-alpine species typical of moist mountain meadows with a short growth period over a wide range of mountains in the Northern hemisphere. Their distribution has been highly influenced by glaciation history. As such, the complex has been chosen to investigate the effect of the ice age on distribution and genetic diversity in a circumpolar arctic-alpine group. The *V. alpina* complex offers the opportunity to compare genetic diversity in closely related species in North America, with mountains mainly running north-south, and Europe, with mountains mainly running east-west, thus blocking the north-south movement of species in front of the ice sheet. Therefore, it is hypothesised that the North American species retained more genetic diversity and depended less on refugia than their European counterparts.

Veronica alpina is widespread in Europe north and east to Greenland. The population in Pakistan is sometimes called *V. lasiocarpa* but no morphological differences could be found. From Greenland westwards across in North America, *V. wormskjoldii* replaces *V. alpina*. In addition, two narrowly endemic, closely related species occur in the western Rocky Mountains, *V. copelandii* in Northern California and *V. cusickii* between Oregon and British Columbia and eastwards barely reaching into Idaho. In Alaska, *V. wormskjoldii* hybridises with *V. stelleri* that occurs from Alaska to Japan (Hokkaido) and Korea. In central Japan, *V. stelleri* is replaced by *V. nipponica*.

Initial sequencing analysis using the *trnL-trnF* region of the chloroplast genome has indicated a close relationship of eastern North American *V. wormskjoldii* to European *V. alpina*, and of western North American *V. wormskjoldii* to Asian *V. stelleri*. The population in Pakistan is no more different from European populations than populations from different areas within Europe. Variation in DNA sequences, however, is not large enough to give conclusive results. Therefore, a more variable molecular marker system is needed to analyse the relationships in the species complex and the distribution of genetic diversity in these alpine species. AFLPs are a tool now frequently used to infer relationships between closely related species and within species. First results presented here support the conclusions from sequence data and allow to infer several clusters, maybe related to glacial refugia of the ice ages.

Circumpolar phylogeography of *Vaccinium uliginosum* inferred from cpDNA sequences Inger G. Alsos¹, Torstein Engelskjøn¹, Pierre Taberlet² and Christian Brochmann³

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The origin of the arctic flora and the localisation of glacial refugia and postglacial migration routes have been debated for more than 100 years. In this project, we use cpDNA data to infer the phylogeography of *Vaccinium uliginosum* L., of which three subspecies have been described: the circumpolar diploid ssp. *microphyllum*, the circumpolar/circumboreal-lowland tetraploid ssp. *uliginosum*, and ssp. *alpinum*, which has been recorded from southern mountains as well as subarctic areas. We have so far sequenced two non-coding cpDNA regions from 67 populations, which revealed 20 polymorphic sites combining into 12 haplotypes. The data were analysed using maximum parsimony. One arctic haplotype was extremely widespread, occurring from Alaska through arctic Canada, Greenland, Svalbard, and northernmost Norway to the Ural Mts. in Russia. This haplotype was closely related to other arctic haplotypes, as well as to haplotypes only found in the Alps and the Pyrenees. Another haplotype was found all over Scandinavia, Scotland, Iceland, and SE Greenland, with a closely related haplotype in Canada (Newfoundland). The latter two haplotypes correspond well with the distribution of the tetraploid ssp. *uliginosum*, which probably has evolved from arctic-alpine ancestors. Possible refugia areas and migration routes are discussed.