

Phylogeography in the *Viola rupestris* and *V. riviniana* complexes – a preliminary study Thomas Marcussen¹, Inger Nordal¹ and Bengt Jonsell²

Viola subsection *Rostratae* Kupffer consists of several critical species complexes in Europe. These include e.g. *V. canina* L. and the two species investigated here, *V. rupestris* F.W. Smith and *V. riviniana* Reichenb.

Viola rupestris is a paleo-tetraploid species ($2n = 20$) with a very wide Eurasian distribution from the British Isles, Scandinavia, and the Pyrenees in the west and eastwards almost to the Beringian. In North America it is replaced by the closely related *V. adunca* Sm. ($2n = 20$), sometimes considered a subspecies of *V. rupestris*, and by *V. labradorica* Schrank. ($2n = 20$) in the north-eastern States and Greenland. *Viola rupestris* belongs mainly in the Boreal zone, although reaching the sub- to low-alpine belts in the mountains and the subarctic zone in Siberia and the extreme north of Scandinavia (North Cape). Allozyme electrophoresis (AAT, AMP and PGM) suggests four different postglacial migration routes within Europe: (1) One western route, today represented by the British and Dutch enclaves, (2) one Central European route, extending from the Alps and into the southern parts of Fennoscandia, (3) one north-eastern route represented by populations from northern Finland, and (4) one isolated North Scandinavian enclave, usually referred to as ssp. *relicta* Jalas. It is possible that ssp. *relicta* has a connection westwards and, thus, that it has been recruited from transatlantic populations of *V. adunca* or *V. labradorica* (this is being checked).

Viola riviniana is an allo-octoploid species ($2n = 40$) restricted to Europe. It is very closely related to *V. reichenbachiana* ($2n = 20$) which it shares one $2n = 20$ genome. In contrast to *V. rupestris*, it is mainly a woodland species, but occasionally growing up to more than 2000 m in the Alps. Allozyme electrophoresis identifies four different entities within the *V. riviniana* complex: One (1) includes British populations only, probably representing a western immigration route (like *V. rupestris*); (2) the second group includes Central European populations. These are, apparently, substantially influenced by (unidirectional?) introgression from *V. reichenbachiana* ($2n = 20$) and may not have differed much originally from the third group, (3) represented by Fennoscandian populations, where *V. reichenbachiana* is not present. (4) The fourth group consists of populations from the Alps. It is very distinct from the others, enzymatically as well as morphologically, and should be referred to a separate species (*V. "laricicola"* sp. nov.). If *V. "laricicola"* proves tetraploid ($2n = 20$), it may be the second parent of *V. riviniana* (this is being checked).

Molecular biogeography and genetic diversity of *Pulsatilla vernalis* (L.) Miller (Ranunculaceae) – a new project Michal Ronikier

Pulsatilla vernalis is a distinct, endemic to Europe species having a very special geographic distribution (Meusel, Jäger & Weinert 1965). This particular pattern was even defined as «*Pulsatilla vernalis* type» (Pawlowski 1929). It is a high mountain species living in isolated areas of European mountains' alpine and subnival zones (mainly Alps, Pyrenees, western Carpathians). On the other hand however, this plant appears also in very different ecological conditions, in the lowlands of Central Europe and Southern Scandinavia (entering the boreal zone but not expanding farther to its northern part). On the basis of a morphological study, four varieties were distinguished (Aichele & Schwegler 1957), differentiating the populations from various parts of geographic range. Three of these varieties allow to observe some spatial distributive sequence, repeated in two isolated areas: Central Europe and Southern Scandinavia. Var. *alpina* is present in the mountains of both areas, while var. *vernalis* and *bidgostiana* in the lowlands. The fourth variety, var. *pyrenaica*, occupies isolated areas of Pyrenean chain.

The genetic diversity of populations is being studied using PCR-based AFLP method (Vos et al. 1995) generating molecular markers from the whole genomic DNA. The representative population samples for this study are collected in all

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