Evolutionary lineages and species delimitation in the *Saxifraga rivularis* complex

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Marte Holten Jørgensen

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National Centre for
Biosystematics

National History Museums
and Botanical Garden
University of Oslo

Forord

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Marte Holten Jørgensen

Abstract

The delimitation of taxa in the *Saxifraga rivularis* complex is controversial. In the checklist for the *Pan-Arctic Flora*, the complex was tentatively divided into five species: the circumpolar *S. hyperborea*, the amphi-Atlantic *S. rivularis* and three amphi-Pacific taxa (*S. bracteata*, *S. flexuosa* and *S. arctolitoralis*). Two ploidal levels (2n = 26, 52) are known, indicating a possible history of reticulate evolution. In the present study, a combined approach using molecular (AFLP; 42 populations, 119 plants), ploidal (flow cytometry; 43 populations, 71 plants) and morphometric (81 populations, 216 plants) data were used to identify evolutionary lineages within the complex, and to delimit taxonomic species.

Three distinct evolutionary lineages were identified in all analyses of the AFLP data: the *Saxifraga bracteata* lineage, the *S. flexuosa*/*hyperborea* lineage and the *S. arctolitoralis*/*rivularis* lineage. The three lineages had different DNA ratios: 0.20-0.21, 0.16-0.17 and 0.36-0.38, respectively. The DNA ratios in combination with the intermediate position of the *S. arctolitoralis*/*rivularis* lineage between the two others in multivariate analysis of both genetic and morphological data, suggest an allopolyploid origin of this lineage, with the other two lineages as progenitors.

No single morphological character included in this study unambiguously separated among the lineages. They were, however, differentiated by combinations of characters, thus the lineages should be recognised at species level: *Saxifraga bracteata*, *S. hyperborea* (including *S. flexuosa*) and *S. rivularis* (including *S. arctolitoralis*).

Within the *Saxifraga flexuosa*/*hyperborea* lineage two genetical groups were identified, correlating with geography rather than the morphological pattern giving rise to the current taxonomic treatment. The groups may reflect genetical differentiation in glacial refugia through the last glaciation, but are not yet reflected in morphological differentiation, and a division into two taxa is therefore not supported. In the *S. arctolitoralis*/*rivularis* lineage, the separation of a Beringian population representing *S. arctolitoralis* from the Atlantic populations in AFLP data and morphology and the very distant geographical range suggest a subspecific ranking of *S. arctolitoralis*. Most of the variation within the *S. rivularis* complex is found in North Pacific areas. This, in combination with the proposed connection to *S. bracteata*, suggests a Beringian origin for the *S. arctolitoralis*/*rivularis* lineage with a later expansion to Atlantic areas.

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Et artskompleks består av arter en uerfaren taksonom ikke kan se forskjell på.
RE

Introduction

The arctic flora has been highly influenced by the climatic oscillations of the Quaternary (e.g., Andersen and Borns 1997). Glaciated and periglacial areas offer harsh conditions with very low temperatures, little precipitation in shade of glaciers (Frenzel *et al.* 1992), and naturally much disturbance, whereas glacial retreat leaves open soil to be colonised. Formation of glaciers causes previous sympatric populations to become allopatric, and divergent evolution will occur either by chance or by selection where populations are isolated in areas with, e.g., different climates, different bedrock or different biotic environments. Withdrawal of glaciers creates secondary contact zones where hybridisation between the divergent lineages can occur. These contact zones could be hotspots for evolution (Stebbins 1984). If two divergent lineages still can interbreed without reduction in offspring fertility, the genetic difference between the populations will decline. Low fertility in the hybrid offspring would allow the populations to remain distinct, whereas the offspring could survive through vegetative reproduction or become stabilised by chromosome doubling (Brochmann *et al.* in press).

Several hypotheses on the frequency and the evolutionary significance of polyploidy have been proposed throughout the years (reviewed by Brochmann *et al.* in press; Soltis *et al.* 2003). Grant (1963) estimated that 47% of all flowering plants are polyploid, whereas other authors have suggested a far larger percentage (Soltis *et al.* 2003). Otto and Whitton (2000) stated that polyploidisation may be the single most common mechanism of sympatric speciation in plants, and estimated that roughly 2-4% of all speciation events in angiosperms and about 7% in ferns involve polyploidy. Soltis *et al.* (2003) asked whether there are any true diploids. The often reduced fertility of early generations of new polyploids may increase rapidly in later generations (Ramsey and Schemske 2002), but new polyploids still meet a challenge of establishment among typically larger numbers of their progenitors. The different hypotheses proposed on how the polyploids establish include habitat differentiation due to an increased ecological amplitude or different ecological potential in the polyploid relative to its progenitors, and disturbance providing new habitats for the polyploids, not already occupied by the progenitors (Soltis *et al.* 2003).

As one of our most polyploid-rich areas and certainly one of the most recent ones, the Arctic has emerged as a model system for the study of the mode and frequency of polyploidisation and its evolutionary significance (Brochmann *et al.* in press). The arctic flora includes numerous polyploids that have originated at various scales in time and space. The majority of these appear to be of hybrid origin, stabilised by polyploidy (Brochmann and Steen 1999). Reconstruction of the evolutionary history of species complexes with several ploidal levels, and sorting of taxonomical difficulties within these, are important steps on the way to an understanding of these processes of reticulation and polyploidisation.

Saxifraga (Saxifragaceae) as currently defined includes about 440 species, mostly in the Arctic and the North Temperate regions (Webb and Gornall 1989). The genus shows considerable variation in morphology and chromosome number, the latter varying between $2n = 10$ and $2n = 198$ with several assumed basic numbers. The flowers are five-merous with 5 sepals, 5 petals, 2 x 5 stamens and a gynoecium consisting of 2 carpels united to a variable extent. They are usually pollinated by insects, although not adapted to any particular kind. Saxifrages reproduce by seed and/or vegetatively by bulbils (e.g., in *S. cernua*; Webb and Gornall 1989). Analyses based on *rbc*L and *mat*K sequences indicate that *Saxifraga* is polyphyletic (Soltis *et al.* 1996), and future disintegration of the genus is likely.

Gornall (1987) divided *Saxifraga* into 15 sections with a myriad of subsections and series. Section *Mesogyne* Sternb. is almost exclusively arctic-alpine, with a circumpolar distribution, and includes the following taxa: *S. sibirica* L., *S. carpatica* Sternb., *S. cernua* L. (including the North European endemics *S. svalbardensis* Øvstedal and *S. opdalensis* A.Blytt), *S. radiata* Small, *S. granulifera* Harry Sm., *S. yoshimurea* Miyabe & Tatew. and the *S. rivularis* L. complex (Webb and Gornall 1989; Zhmylev 1997; Jintang *et al.* 2001). The section comprises small perennials characterised by restricted vegetative growth, palmate, 5-11-lobed leaves usually with a semicircular to kidney-shaped outline, terminal flowers that are solitary or in a small cyme, white to pink petals and multicellular, uniseriate hairs on most plant parts (Webb and Gornall 1989). The species in this section have chromosome numbers between $2n = 16$ and $2n = 72$. The available phylogenetic analyses based on *mat*K, *rbc*L and ITS sequences suggest that the section is monophyletic (Soltis *et al.* 1996; Conti *et al.* 1999),

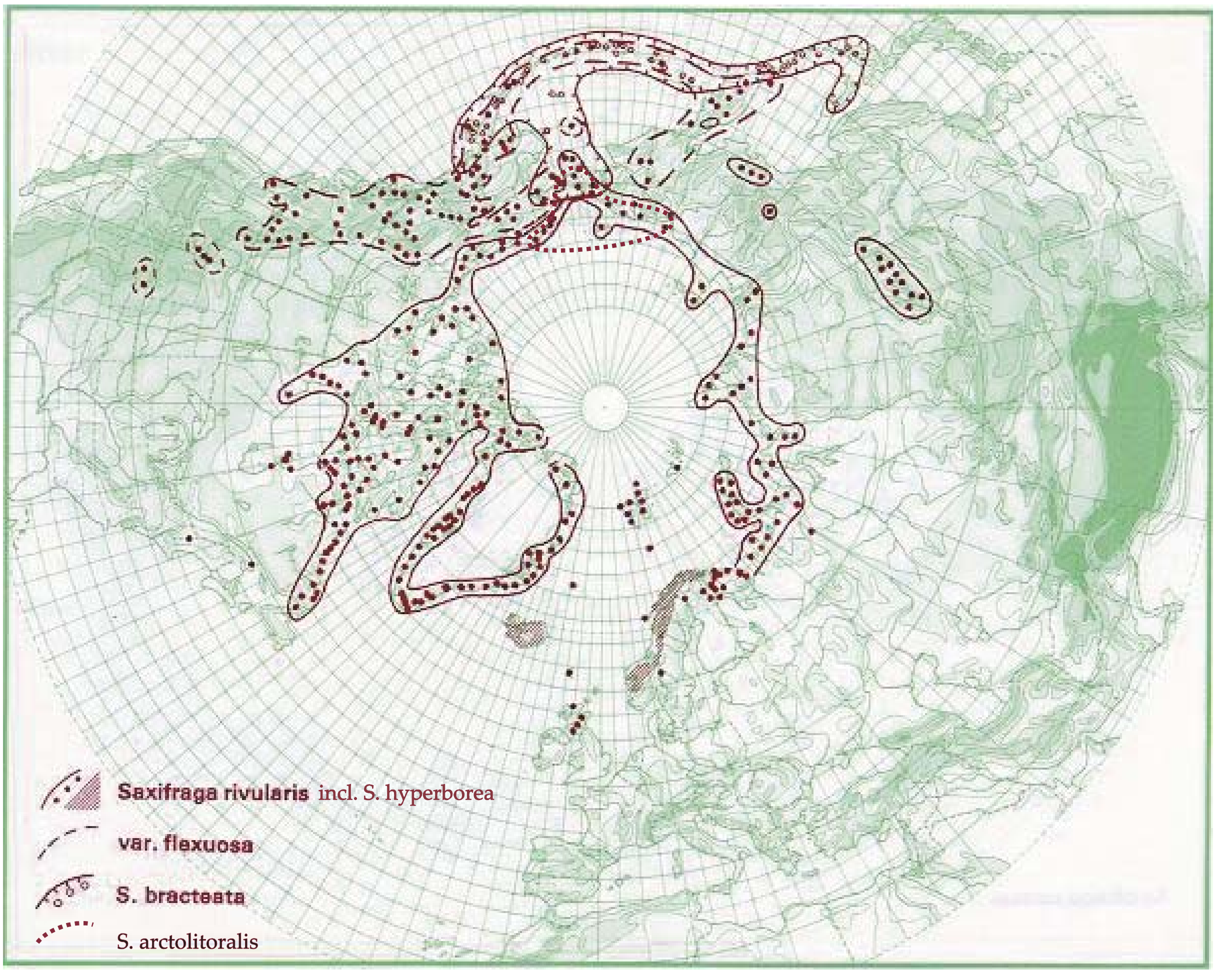


Figure 1: Distribution of the *Saxifraga rivularis* complex, modified after Hultén and Fries (1986), who included *S. hyperborea* in *S. rivularis*. The distribution of *S. arctolitoralis* is added according to Rebristaya and Yurtsev (1984) and revision by Reidar Elven of herbarium material in the University of Alaska Museum, Fairbanks (ALA; 2003).

although only four of the eight *Mesogyne* species were investigated. Preliminary phylogenetic analyses based on cpDNA sequences from an ongoing investigation of the phylogeny of *Mesogyne*, including almost all species in the section, support the monophyly of the section, and suggest that what here is defined as the *S. rivularis* complex represents a distinct lineage within the *Mesogyne* (Gabrielsen *et al.* in prep).

The *Saxifraga rivularis* complex is a circumpolar species group of small perennial herbs with palmate leaves, rounded leaf lobes, usually cymose inflorescences, ballistic seed dispersal, and small flowers with white to pink petals. The plants grow in snowbeds and along rivers and creeks in the Arctic and in northern Pacific and Atlantic alpine regions (Fig. 1; Hultén 1968; Yurtsev 1981). Two ploidal levels are recorded in this complex; $2n = 26$ and $2n = 52$, traditionally considered to represent diploids and tetraploids, respectively (e.g., Zhukova and Tikhonova 1971; Engelskjøn 1979; Löve and Löve 1982; Zhukova and Petrovsky 1987). The high basic number of 13 strongly indicates a hybrid origin from two different lineages with different primary basic numbers, but could also be the result of aneuploid decrease in a primary polyploid. Fixed heterozygosity at an isozyme locus indicates that the two ploidal levels represent tetra- and octoploids, respectively (Guldahl *et al.* in prep).

Figure 2: *Saxifraga rivularis* L. cultivated in the phytotron, University of Oslo, originally collected in southern Norway.

The Pan-Arctic Flora Project has tentatively accepted five species in the *Saxifraga rivularis* complex; the amphi-Atlantic *S. rivularis* L., the circumpolar *S. hyperborea* R.Br. and the three amphi-Pacific taxa *S. bracteata* D.Don, *S. flexuosa* Sternb. and *S. arctolitoralis* Jurtz. & V.V.Petrovsky (Elven *et al.* 2003). However, the species delimitation is controversial due to morphological similarity and lack of molecular data to support any hypothesis about evolutionary lineages. Still, in need of an initial framework I choose to follow Elven *et al*. (2003). Analyses of cpDNA sequences, ITS sequences and random amplified polymorphic DNA (RAPD) suggest that *S. opdalensis* and *S. svalbardensis* are of hybrid origin, both with *S. rivularis* and *S. cernua* as parental species (Brochmann *et al.* 1998; Steen *et al.* 2000). Although these taxa are descendants from *S. rivularis*, they were not included in the present study because they are well separated from the rest of the complex, in both morphology and genetics (Øvstedal 1975; Øvstedal 1998; Steen *et al.* 2000).

Linnaeus (1753) described *Saxifraga rivularis* as having 5-lobed, palmate basal and lower cauline leaves, ovate upper cauline leaves and bracts and unbranched stem beneath the cyme. Further characteristics of *S. rivularis* are stems up to 15 cm long, small, loose tufts or occasionally dense cushions as growth form, presence of runners, and white to pink, rarely red petals (Fig. 2; Rebristaya and Yurtsev 1984; Webb and Gornall 1989; Lid and Lid 1994). Linnaeus (1753) knew *S. rivularis* from river and creek margins in alpine parts of Lapland. Later authors have expanded the distribution to include circumpolar arctic and alpine areas when *S. rivularis* and *S. hyperborea* are treated as one taxon (Fig. 1; Polunin 1959; Hultén 1968; Rebristaya and Yurtsev 1984; Webb and Gornall 1989), or mostly amphi-Atlantic with extensions down to the Rocky Mountains (Weber 1966; Löve *et al.* 1971), whereas Elven *et al*. (2003) suggest that *S. rivularis* is strictly amphi-Atlantic. *Saxifraga rivularis* has the chromosome number 2*n* = 52 (e.g., Engelskjøn 1979; Löve and Löve 1982).

Figure 3: *Saxifraga hyperborea* R.Br. in Svalbard (Photo: H. H. Grundt).

Saxifraga hyperborea R.Br. (Fig. 3) was described by Robert Brown on material collected at Melville Island during an attempt to find the Northwest Passage in 1819-20 (Brown 1823). It was characterised as having glabrous, palmate leaves, woolly stems, oblong to linear sessile bracts and semi-inferior capsules (Brown 1823). The taxon is considered circumpolar by Elven *et al*. (2003; Fig. 1), and can be distinguished from *S. rivularis* by its smaller size, darker red colour, lack of runners and usually only 3-lobed leaves (Webb and Gornall 1989; Lid and Lid 1994). *Saxifraga hyperborea* has the chromosome number 2*n* = 26 (Engelskjøn 1979).

Saxifraga bracteata D.Don (Fig. 4) was described from East Sibiria (Don 1822) as a tuft-growing plant with large and numerous bracts in a near-capitate inflorescence, with flowers similar to those of *S. cernua*. The species has later been found on the Seward Peninsula and in the Aleutian Islands, Alaska, and along the Russian shores from Chukotka, through Kamchatka and the Kurile Islands, into the north of Japan (Fig. 1; Hultén and Fries 1986). *Saxifraga bracteata* has the chromosome number 2*n* = 26 (Zhukova 1982; Zhukova and Petrovsky 1987).

Figure 4: *Saxifraga bracteata* D.Don cultivated in the phytotrone, University of Oslo, collected on the Seward Peninsula, Alaska.

Saxifraga flexuosa Sternb. (Fig. 5), described by K. M. Sternberg in his *Revisio Saxifragarum* (1831), can be distinguished from *S. rivularis* by its strict inflorescence, long, erect pedicels with short, straight glandular hairs and clawed petals (Webb and Gornall 1989). The type is not traced (Webb and Gornall 1989), but was probably from Alaska (Elven *et al.* 2003). *Saxifraga flexuosa* is reported with the chromosome number $2n = 26$ (Mulligan and Porsild 1968; Löve *et al.* 1971; Zhukova and Tikhonova 1971) and is distributed from Colorado through the Rocky Mountains to Yukon and Alaska at the American side of the Pacific, and from Chukotka to Kamchatka at the Asian side (Fig 1; Hultén and Fries 1986).

Figure 5: *Saxifraga flexuosa* Sternb. in the Kigluaik Mts., Seward Peninsula, Alaska.

The type of *Saxifraga arctolitoralis* Jurtz. & V.V.Petrovsky (Fig. 6) was collected at the north-eastern part of the Chukotka Peninsula, and described as being very close to *S. hyperborea* R.Br., but differs in being lower of growth, with higher density of long, multicellular, non-coloured hairs, generally thicker stems and leaves, and having twice the chromosome number (i.e., $2n = 52$; Yurtsev 1981). *S. arctolitoralis* is distributed along the coast of Chukotka from the southern edge of the Chukotka Peninsula to Chaun Bay, on Wrangel Island and along the coast of western and northern Alaska (Fig 1; Rebristaya and Yurtsev 1984; Elven *et al.* 2003).

Looking at the number of synonyms recorded for the *Saxifraga rivularis* complex, the

Figure 6: *Saxifraga arctolitoralis* Jurtz. & V.V.Petrovsky; collection RE01-11 from Seward Peninsula, Alaska.

extensive confusion among authors becomes evident. *Saxifraga hyperborea* R.Br. has been recognised as both a subspecies and a variety of *S. rivularis*: *S. rivularis* ssp. *hyperborea* (R.Br.) Dorn and *S. rivularis* var. *hyperborea* (R.Br.) Hook, respectively (Elven *et al.* 2003). *Saxifraga flexuosa* Sternb. has also been recognised as a subspecies or a variety of *S. rivularis*: *S. rivularis* ssp. *flexuosa* (Sternb.) Gjærev., *S. rivularis* var. *flexuosa* (Sternb.) Engl. & Irmsch. and *S. rivularis* var. *stricta* Engl. (Elven *et al.* 2003). However, other authors have included this taxon as a subspecies of *S. hyperborea*: *S. hyperborea* ssp. *debilis* (Engelm.) Á.Löve, D.Löve & Kapoor (Löve *et al.* 1971). I will return to the latter in the discussion.

Besides the taxonomical confusion, several hypotheses about relationships have been proposed in this complex. Rebristaya and Yurtsev (1984) suggested that *Saxifraga arctolitoralis* is an autopolyploid descendant of *S. hyperborea*, and that *S. rivularis* has an ancestor in common with *S. hyperborea* and *S. bracteata*, predicted to be a diploid medium-sized plant growing on shady cliffs along the arctic coasts. Furthermore, they suggested that *S. flexuosa* is no more than *S. hyperborea* growing in the shadow of creek margins (Rebristaya and Yurtsev 1984). Brochmann *et al*. (1998) suggested that *S. rivularis* is of hybrid origin, *S. hyperborea* being the mother, based on *mat*K sequences and chromosome numbers.

Previous studies including plants from the *Saxifraga rivularis* complex have discovered little sequence variation between *S. rivularis* and *S. hyperborea*, and between these two and other *Mesogyne* species (e.g., Soltis *et al.* 1996; Brochmann *et al.* 1998; Conti *et al.* 1999). Hence, a search for other methods was appropriate. Amplified fragment length polymorphisms (AFLPs) are frequently used for resolving phylogenetic relationships at a low taxonomic level, when other methods fail to provide the necessary resolution (e.g., Hedrén *et al.* 2001; Koopman *et al.* 2001; Zhang *et al.* 2001; Buntjer *et al.* 2002; Marhold *et al.* 2002; Beardsley *et al.* 2003; Despres *et al.* 2003; Lihová *et al.* 2004), and have been used successfully at the intraspecific level in close relatives of the *S. rivularis* complex (i.e., *S. cernua* L. and *S. sibirica*; Kapralov, M. V., unpublished data; Bronken 2001; Kjølner *et al.* 2004).

The aims of this study were to identify evolutionary lineages in the *Saxifraga rivularis* complex based on AFLP data and flow cytometry and to investigate their phylogenetic relationships; i.e., to test the previous hypotheses by Rebristaya and Yurtsev (1984; *S. rivularis* has an ancestor in common with *S. hyperborea* and *S. bracteata*, *S. arctolitoralis* is an autopolyploid derived from *S. hyperborea*, and *S. flexuosa* and *S. hyperborea* are conspecific) and Brochmann *et al*. (1998; *S. rivularis* is an allopolyploid with *S. hyperborea* as one of the progenitors). I also aimed to find morphological characters delimiting taxonomic species in the complex, hence testing the taxonomic hypotheses in Elven *et al.* (2003; the *S. rivularis* complex comprises five taxa at species level).

Material and methods

Material

Material from most of the distribution area was collected during several seasons by several collectors, including my own fieldwork in Alaska and the southern part of Norway (Tab. 1). For the AFLP analysis, silica-dried material of usually three plants from each of 42 populations was included (Fig. 7). Fresh material of 71 plants from 43 populations cultivated in a phytotron was used for flow cytometry (Fig. 8). 216 herbarium specimens from 81 populations were included in the morphometric analysis (Fig. 9). These include plants from V. L. Komarov Botanical Institute, Russian Academy of Sciences (St. Petersburg; LE) examined during a study trip, the Swedish Museum of Natural History (Stockholm; S) and the Natural History Museums and Botanical Garden, University of Oslo (Oslo; O; Tab. 1). The same populations were chosen for all three analyses when possible.

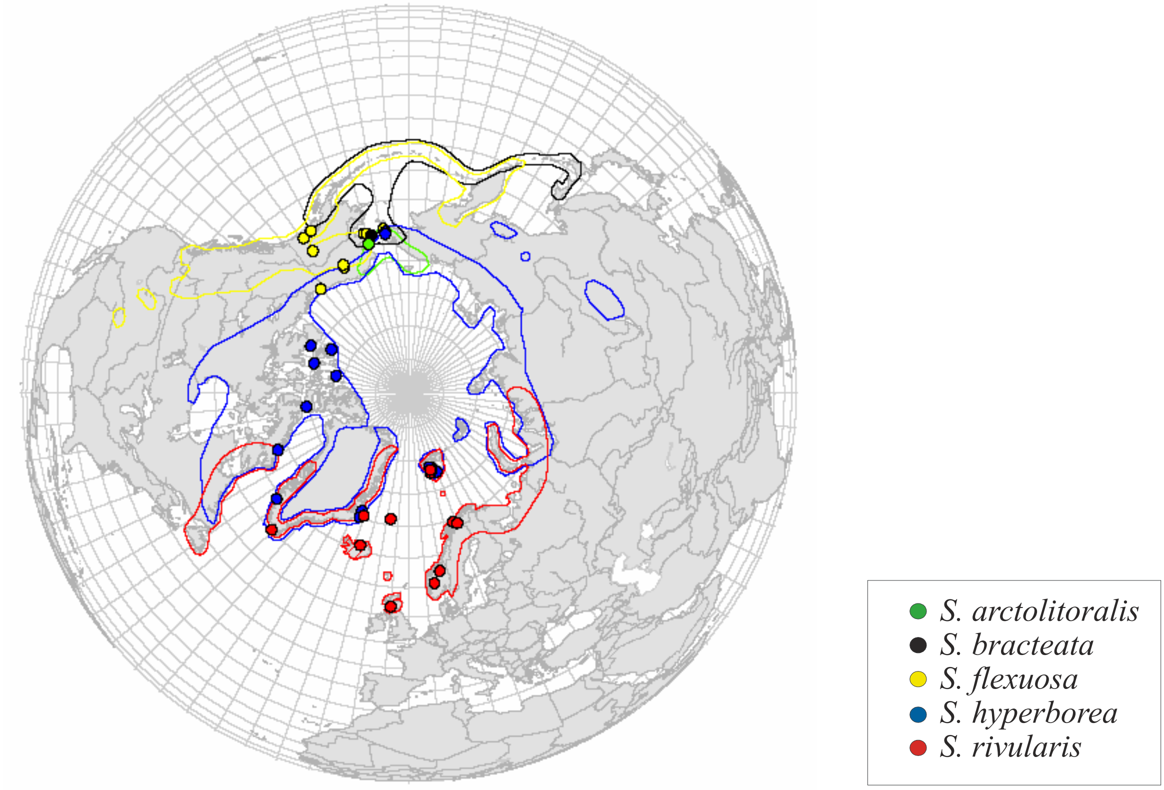


Figure 7: Silica-dried material used for AFLP analysis and approximate distributions of taxa after Hultén and Fries (1986) and Elven *et al*. (2003).

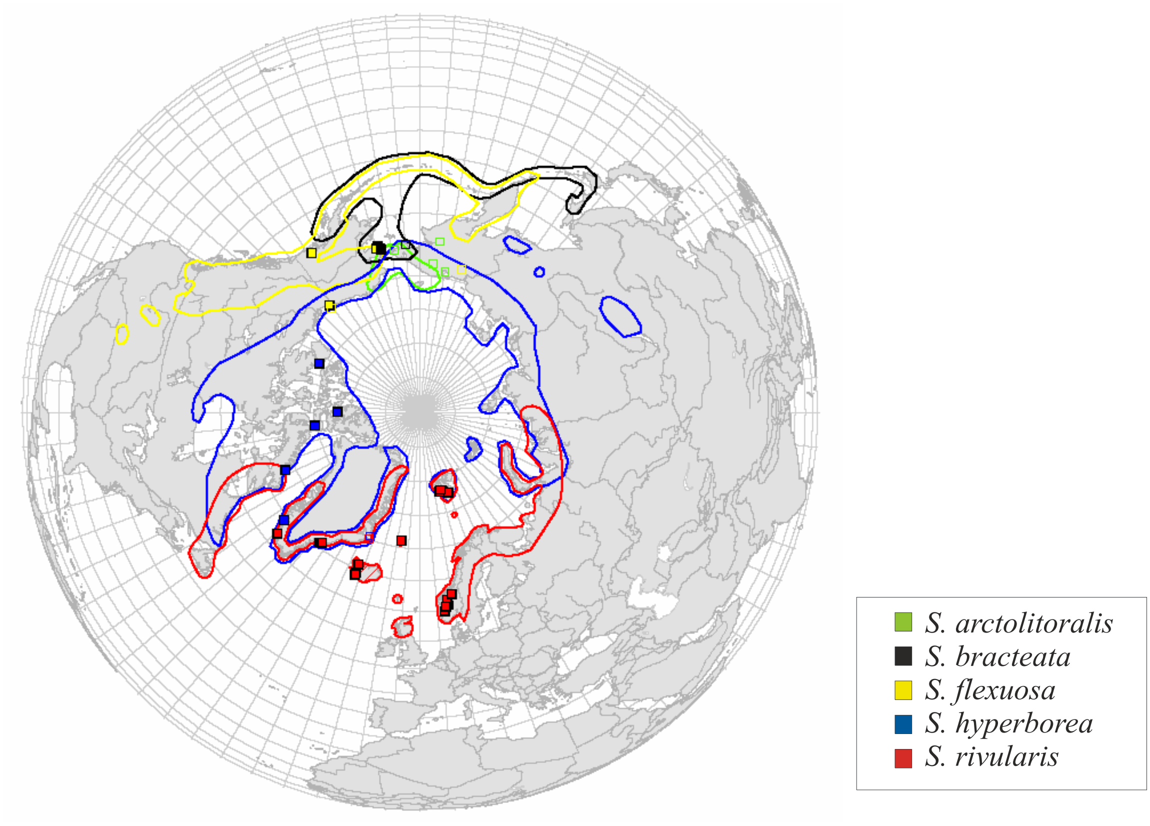


Figure 8: Origin of cultivated material used for flow cytometry in this study (filled squares) and previous chromosome counts or flow cytometry results (open squares; cf. Tab. 1). The approximate distributions of the taxa are after Hultén and Fries (1986) and Elven *et al.* (2003).

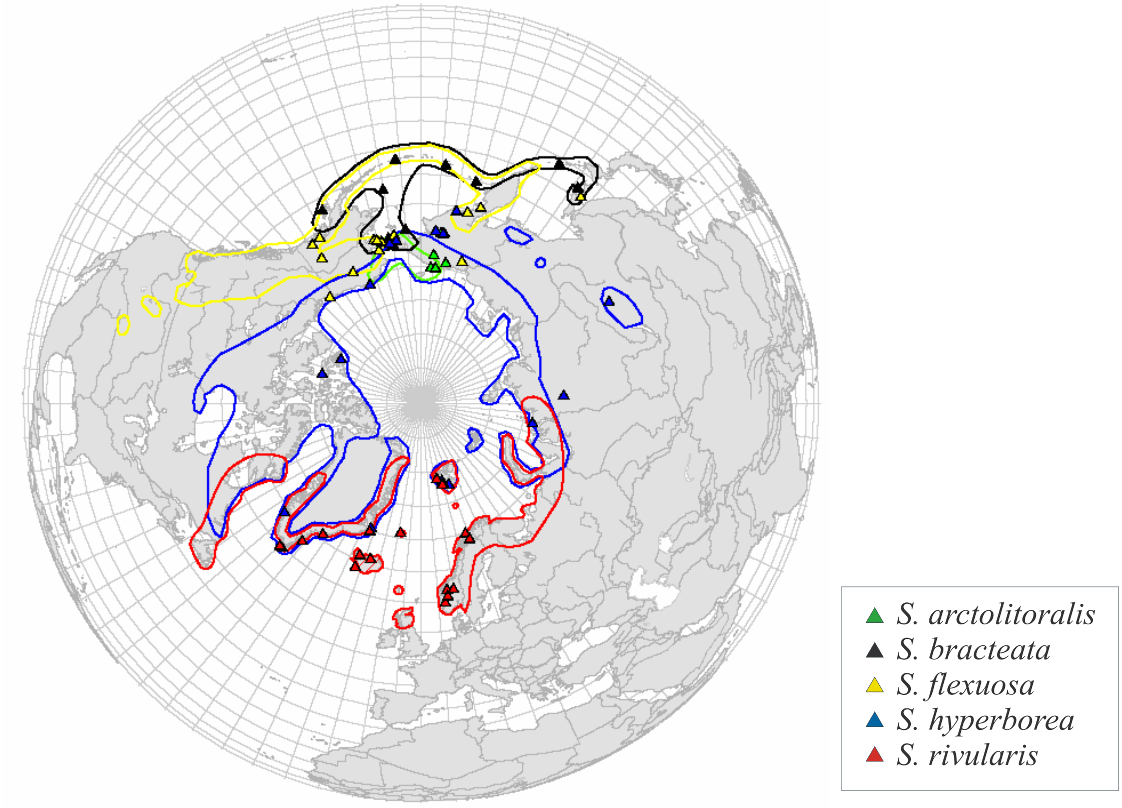


Figure 9: Origin of herbarium material used for morphometric analysis and approximate distributions of taxa after Hultén and Fries (1986) and Elven *et al.* (2003).

Table 1: Sampled material of the *Saxifraga rivularis* complex. The taxa are abbreviated as follows; arc = *Saxifraga arctolitoralis*, bra = *S. bracteata*, fle = *S. flexuosa*, hyp = *S. hyperborea* and riv = *S. rivularis*. Population ID gives the original collection code or herbarium registration number. Country/area is also given by abbreviation: CAN = Canada, GBR = Great Britain, GRL = Greenland, ISL = Iceland, NOR = Norway, RUS = Russia, SJM = Svalbard/Jan Mayen, USA = United States of America. Positive longitude and latitude means North and East, respectively, whereas negative means South and West. H gives herbarium of deposition of voucher specimens: LE = V. L. Komarov Botanical Institute, Russian Academy of Sciences, St. Petersburg, O = The National History Museums and Botanical Garden, University of Oslo, Oslo, and S = The Swedish Museum of Natural History, Stockholm. #H, #S and #C give the number of herbarium, silica-dried and cultivated plants included in this study, respectively. Previous chromosome counts and estimated ploidal levels from flow cytometry shown in the last column, are referred from (1) Zhukova and Petrovsky (1987), (2) Zhukova and Tikhonova (1971), (3) Zhukova *et al.* (1973), (4) Zhukova and Petrovsky (1980), (5) Guldahl *et al.* (in prep).

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
arc	65-195	RUS	Magadan Oblast	Wrangel Island	Somnitelnaya Bay	72.500	180.000	26.07 1956	Zhukova, Petrovsky	LE	3			2*n* = 52 (1)
arc	68-09K	RUS	Magadan Oblast	W Chukotka	Chaunskaya Guba	69.000	170.000	04.07 1968	Levitsev, Korobkov, Yurtsev	LE	3			2*n* = 52 (1; 2)
arc	69-45K	RUS	Magadan Oblast	E Chukotka	Bukhta Provideniya, Ureliki settlement	64.500	173.191	04.07 1969	Korobkov	LE	1			2*n* = 52 (1)
arc	70-160y	RUS	Magadan Oblast	E Chukotka	Leymin Cape, Kitulinveem River	68.000	175.000	04.08 1970	Kozhevnikov, Nechaev, Yurtsev	LE	3			2*n* = 52 (1)
arc	71-17-1	RUS	Magadan Oblast	Wrangel Island	Somnitelnaya Bay	72.500	180.000	11.07 1971	Petrovsky, Taraskina,	LE	3			2*n* = 48 (1; 3)
arc	72-162	RUS	Magadan Oblast	W Chukotka	Lavrentiya settlement	65.614	-171.154	15.07 1972	Zhukova	LE	2			2*n* = 52 (1)
arc	MJ03.5[a]	RUS	Magadan Oblast	N Chukotka	Billingsa settlement	69.919	175.769	05.08 1981	Sergienko	LE	3			
arc	MJ03.6[a]	RUS	Magadan Oblast	N Chukotka	Pegtymel River Mouth	69.919	173.846	15.08 1981	Sergienko	LE	3			
arc	TG03/46[a]	RUS	Magadan Oblast	Zaliv Kresta	Komsomolskiy settlement	66.000	-179.200	22.06 1970	Dorogostayskaya	LE	3			
arc	W79-84	RUS	Magadan Oblast	Wrangel Island	Somnitelnaya Bay	72.500	180.000	07.07 1979	Petrovsky	LE	3			2*n* = 52 (1)
arc	RE-01-11	USA	Alaska	Seward Peninsula	Shishmaref Inlet S	66.530	-164.770	07.08 2001	Elven, Solstad	O	3	3		
bra	MJ03.3[a]	RUS	Sakhalin Oblast	Kuril'skiye Ostrova	Urup, Robune	46.000	150.000	03.08 1929	Bergman	S	3			
bra	3306	RUS	Sakhalin Oblast	Sakhalin	Zaliv Terpeniya (Patiens gulf)	48.000	144.000	02.10 1965	Egorova, Kolehanova	LE	1			
bra	70-58Pl	RUS	Magadan Oblast	E Chukotka	Nunligran settlement	64.818	-175.319	28.07 1970	Plieva	LE	3			2*n* = 26 (1)

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
bra	72	RUS	Kamchatskaya Oblast	Komandorskiye Ostrova	Toporkov Island	55.000	166.000	12.06 1929	Kardakova	LE	3			
bra	804	RUS	Kamchatskaya Oblast	Komandorskiye Ostrova	Toporkof Island, Sarannaja Bay	55.600	166.000	08.08 1920	Hultén	LE	3			
bra	MJ03.7[a]	RUS	Magadan Oblast	E Chukotka	Uelen Settlement	66.250	-170.500	23.07 1958	Derviz-Sokolova	LE	3			
bra	MJ03.8[a]	RUS	Magadan Oblast	Beringov Proliv	Ratmanov Island (Big Diomede Island)	65.818	-169.022	23.07 1958	Tikhomirov	LE	3			
bra	3189	RUS	Kamchatskaya Oblast	Komandorskiye Ostrova	Ostrov Beringa, S of Nikolskoje	55.185	166.000	02.07 1992	Svensson	S	3			
bra	1069	USA	Alaska	Aleutian islands	Atka	52.227	-174.296	04.07 1932	Eyerdam	S	3			
bra	8121	USA	Alaska	Aleutian islands	Shemya Island, Near Islands Group	52.727	174.111	21.06 1967	Shacklette	S	3			
bra	574a	USA	Alaska	Kodiak Island	Three Saints Bay	57.182	-153.489	07.08 1931	Eyerdam	S	3			
bra	1826	USA	Alaska	Pribilof Islands	St. Paul Island	57.182	-170.298	09.07 1899	Coville, Kearney	S	2			
bra	SUP02-188	USA	Alaska	Seward Peninsula	Teller, coast/cliffs W of Teller	65.247	-166.414	10.07 2002	Elven, Gabrielsen, Jørgensen	O	3	3	4	
bra	SUP02-199	USA	Alaska	Seward Peninsula	Teller, coast/cliffs W of Teller	65.249	-166.402	10.07 2002	Elven, Gabrielsen, Jørgensen			3	1	
fle	RE2260	CAN	Yukon Territory	Ivvavik National Park	British Mts., Buckland Hills NW	69.420	-139.642	03.08 1999	Elven	O	2		1	$2n = 2x$ (5)
fle	RE2263	CAN	Yukon Territory	Ivvavik National Park	British Mts., Buckland Hills NW	69.420	-139.642	03.08 1999	Elven			2		
fle	77-03Pl	RUS	Magadan Oblast	W Chukotka	Anjuiskoye Mts. Watershed of Machvavaam River and Pogynden River (confluences of Maly Anyuy), Razdelnays Mts.	68.182	163.929	28.06 1977	Petrovsky, Koroleva	LE	3			$2n = 26$ (1; 4)
fle	TG03/39[a]	RUS	Sakhalin Oblast	East Sakhalin Mts.	Nabilskiy Range, Lopatin Mt. (1609 m)	49.000	142.333	27.08 1988	Vyshin, Barkalov	LE	3			
fle	TG03/40[a]	RUS	Kamchatskaya Oblast	Koryakskiy National	Olyutorskiy county, Zaliv Korfa	60.333	166.333	14.07 1960	Gavriljuk	LE	3			

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
fle	TG03/42[a]	RUS	Kamchatskaya Oblast	Karaginskiy county	The shore of Penzhinskaya Guba, 2-3 km NE of Mys Kingi	59.000	163.000	21.08 1989	Dorotejev	LE	3			
fle	TG03/45[a]	RUS	Magadan Oblast	SE Chukotka	Mys Chaplina	64.400	172.200	20.07 1957	Gavriljuk, Talarich	LE	3			
fle	04-01	RUS	Magadan Oblast	Chutkotka Peninsula	the shore of Lavrentiya Bay 5 km SSW of Lavrentiya village	65.450	-171.033	26.08 1999	Razzhivin	O	3	3		
fle	RE-01-10	USA	Alaska	Seward Peninsula	Shishmaref Inlet S	66.500	-164.733	07.08 2001	Elven, Solstad	O	3	3		
fle	RE-C1	USA	Alaska	Kenai Peninsula	Kenai Mts., Portage Valley, S of Tangle Pond, Scree/Forefield	60.750	-148.750	11.08 2000	Elven, Solstad	O	3	3		
fle	SR1	USA	Alaska	Alaska Range NE	Delta drainage, Donelly Dome	63.767	-145.767	12.07 1998	Elven, Grundt	O	3	3		
fle	SUP02-150	USA	Alaska	Seward Peninsula	Teller Road, Mt W of Penny River	64.632	-165.679	11.07 2002	Elven, Gabrielsen, Jørgensen				2	
fle	SUP02-154	USA	Alaska	Valdez Area	Chugach Mts., Thompson Pass, N of summit, E side of valley	61.140	-145.733	06.07 2002	Elven, Gabrielsen, Jørgensen	O	1	3		
fle	SUP02-155	USA	Alaska	Valdez Area	Chugach Mts., Thompson Pass, N of summit, E side of valley	61.144	-145.712	06.07 2002	Elven, Gabrielsen, Jørgensen	O	3		1	
fle	SUP02-163	USA	Alaska	Seward Peninsula	Skookum Pass between Solomon River East Fork and Horton Creek	64.717	-164.050	08.07 2002	Elven, Gabrielsen, Jørgensen	O	3	3		
fle	SUP02-168	USA	Alaska	Seward Peninsula	Kigluaik Mts., Mt E of Shaw Creek	64.928	-164.983	09.07 2002	Elven, Gabrielsen, Jørgensen				1	
fle	SUP02-180	USA	Alaska	Seward Peninsula	Teller, coast/cliffs W of Teller	65.251	-166.391	10.07 2002	Elven, Gabrielsen, Jørgensen	O	3	3	2	
fle	SUP02-181	USA	Alaska	Seward Peninsula	Kigluaik Mts., Mt W of Shaw Creek	64.928	-164.994	09.07 2002	Elven, Gabrielsen, Jørgensen	O	3	3	2	
fle	SUP02-185	USA	Alaska	Seward Peninsula	Kigluaik Mts., Grand Singatook, S slope towards Teller Road	64.900	-166.183	12.07 2002	Elven, Gabrielsen, Jørgensen				2	
fle	SUP02-211	USA	Alaska	Seward Peninsula	Kigluaik Mts., Mt W of Shaw Creek	64.931	-164.988	09.07 2002	Elven, Gabrielsen, Jørgensen				2	
fle	SUP02-254	USA	Alaska	Arctic Slope	Castle Mt.	68.570	-152.577	30.07 2002	Elven			3		
fle	SUP02-265	USA	Alaska	Brooks Range	Endicott Mts., Chandler Lake, E shore vic. mouth of Kollutarak Creek	68.200	-152.683	22.07 2002	Elven	O	3	3		

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
hyp	G-6842	CAN	Northwest Territory	Queen Elizabeth Islands	Prince Patrick Island, Central plateau, Luzula barrens	76.750	-119.500	23.07 2000	Gillespie, Consaul	O	3	3		
hyp	RE2775	CAN	Northwest Territory	Queen Elizabeth Islands	Banks Island NE, Parker River valley, N side ca. 7 km from shore	73.626	-115.861	10.08 1999	Elven			3	1	$2n = 2x$ (5)
hyp	RE2957	CAN	Nunavut	Parry Islands	Melville Island SE, NE of head of Beverly Inlet, E of river, 0.5-2.5 km from sea	75.100	-107.380	14-15.08 1999	Elven	O	3			
hyp	RE2981	CAN	Nunavut	Parry Islands	Melville Island, Beverly Inlet, E of river, 0.5-2.5 km from sea	75.114	-107.645	14.08 1999	Elven			2		$2n = 2x$ (5)
hyp	RE3033	CAN	Nunavut	Ellesmere Island	Gabbro Peninsula, N of Isachsen, surroundings of the lake	78.825	-103.680	19.08 1999	Elven			3		$2n = 2x$ (5)
hyp	RE3425	CAN	Nunavut	Devon Island	Crocker Bay, E side near entrance	74.559	-82.790	25.08 1999	Elven			3	2	$2n = 2x$ (5)
hyp	RE3520	CAN	Nunavut	Baffin Island	Cape Hooper, Tanner Bay	68.438	-66.831	31.08 1999	Elven			3	3	$2n = 2x$ (5)
hyp	RE3525	CAN	Nunavut	Baffin Island	Cape Hooper. Iqualuit. Hills just NE of settlement.	68.417	-66.833	02.09 1999	Elven			1	1	$2n = 2x$ (5)
hyp	RE 3728	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3732	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3748	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3751	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3782	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3783	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 3898	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	RE 5713	CAN	Arctic Canada	*)				1999	Larsson, Lévesque				1	
hyp	AK-240	GRL	Kitaa	Kong Frederik IX Land	Nuuk, E of the airport, NW of the view-point (178 m)	64.194	-51.667	13.07 2002	Bronken	O	1	3	1	

Table 1: (cont.)

Taxon	Population ID	Country	Region	Subregion	Locality	Longitude	Latitude	Date	Collector(s)	H	# H	# S	# C	Chromosome numbers and ploidal levels
hyp	CB-99-027	GRL	Tunu	Jameson Land	SE of Scoresbysund, W of Mt. Inugsukajik	70.486	-21.948	31.07 1999	Brochmann	O	3	3		$2n = 2x$ (5)
hyp	CB-99-038	GRL	Tunu	Jameson Land	NE of Scoresbysund, close to town	70.486	-21.948	02.08 1999	Brochmann, Nyléhn, Bronken, Kjølner	O	3	3		$2n = 2x$ (5)
hyp	05-01	RUS	Magadan Oblast	Chutkotka Peninsula	4 km NW of Lorino hot springs	65.500	-171.506	28.08 1999	Razzhivin	O	3	3		
hyp	05-03	RUS	Magadan Oblast	Chutkotka Peninsula	4 km NW of Lorino hot springs	65.500	-171.506	28.08 1999	Razzhivin	O	3	3		
hyp	70-145	RUS	Magadan Oblast	Wrangel Island	Middle Neozhidannaya River, Krupny Creek	71.333	180.000	18.07 1970	Petrovsky, Zhukova	LE	3			$2n = 26$ (1)
hyp	71-06	RUS	Magadan Oblast	Wrangel Island	Rodzher Bay, Nasha River	71.333	180.000	01.07 1971	Petrovsky, Zhukova	LE	3			$2n = 26$ (1;3)
hyp	77-32	RUS	Magadan Oblast	Anadyrsky Raion	NW Rarytkin Range, right side of upper Lesnaye River	64.167	175.000	04.07 1977	Petrovsky, Zhukova	LE	3			$2n = 26$ (1)
hyp	TG03/28[a]	RUS	Krasnoyarskiy Kray	Taymyr Peninsula	Dikson Island, outside Dikson	73.500	80.233	06.08 1959	Dorogostaiskaya	LE	3			
hyp	TG03/31[a]	RUS	Krasnoyarskiy Kray	Putoran Mts.	Ayan Lake	69.000	93.500	13.07 1983	Kozhevnikov	LE	3			
hyp	TG03/34[a]	RUS	Buryato-Mongolskaya	Stanovoye Mts.	Burguya River (source), Kodar Ridge	57.500	118.500	11.07 1964	Malychev, Petrochenko	LE	3			
hyp	TG03/41[a]	RUS	Kamchatskaya Oblast	Korjaskij National District	Oljutorskij County	60.500	169.500	26.06 1960	Gavriljuk	LE	3			
hyp	TG03/43[a]	RUS	Magadan Oblast	Chukotka Peninsula	Zima Bay	64.500	172.500	09.07 1958	Tikhomirov	LE	2			
hyp	TG03/44[a]	RUS	Magadan Oblast	Beringov Proliv	Ratmanov Island (Big Diomide Island)	65.818	-169.022	01.08 1958	Tikhomirov	LE	3			
hyp	TMG-24SH	SJM	Svalbard	Nordenskiöld Land	NW of the mountain Breinosa, 150 m N of the oldest EISCAT antennae	78.156	16.048	14.07 1997	Brochmann, Gabrielsen, Steen	O	3	3		
hyp	TMG-26	SJM	Svalbard	Dickson Land	Idodalen, Kongressfjellet	78.550	15.367	26.07 1997	Elven	O	3	1		
hyp	TMG-27	SJM	Svalbard	Dickson Land	Idodalen, Kongressfjellet	78.550	15.367	26.07 1997	Elven	O	3	3		
hyp	TMG-34	SJM	Svalbard	Nordenskiöld Land	De Geer dalen, pass S of Skjørlokstupet	77.698	19.039	03.08 1997	Gabrielsen	O	3	2		

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
hyp	MJ03.2[a]	USA	Alaska	Point Barrow	Between coast and USC & GS Magnetic Station, ca 2 miles SW of Barrow Base	71.306	-156.750	05.07 1950	Thomas	O	3			
riv	TMG-43	GBR	Scotland	Argyll county	Glen Coe region, scree slope NW of the mountain Bidean nam Bian	56.667	-5.000	16.08 1997	Gabrielsen, Steen, Hansen, Tebbitt, Watson			3		
riv	3189	GRL	Tunu	Kong Frederik VI Kyst	Tôrnârssuk, Nûa	59.900	-44.350	31.07 1967	Kliim-Nielsen	O	3			
riv	MJ 03.1[a]	GRL	Tunu	Kong Frederik VI Kyst	Skjoldungen Area, Finnsbu	63.259	-41.386	10.08 1932	Devold, Scholander	O	3			
riv	MJ 03.4[a]	GRL	Tunu	Kong Frederik VI Kyst	Skjoldungen Area, Finnsbu	63.259	-41.386	10.08 1932	Devold, Scholander	O	3			
riv	AK-248	GRL	Kitaa	Kong Frederik IX Land	Paamiut. E of Paamiut city, ca. 1 km from the main city, in the crevice near the TV-tower	61.992	-49.647	07.07 2002	Bronken, Jacobsen				2	
riv	AK-281	GRL	Tunu	Kong Frederik VI Kyst	Nanortalik, NE slope of Storefjell	60.149	-45.289	22.07 2002	Bronken	O	1	3		
riv	CB-99-039	GRL	Tunu	Jameson Land	NE of Scoresbysund, close to town	70.486	-21.948	02.08 1999	Brochmann, Nyléhn, Bronken, Kjølner	O	3	3		$2n = 4x$ (5)
riv	CB-99-043	GRL	Tunu	Kong Christian IX Land	Tasiilaq E, Blomsterdalen, Upper lake	65.625	-37.733	22.07 1999	Alsos, Lund				2	$2n = 4x$ (5)
riv	CB-99-045	GRL	Tunu	Kong Christian IX Land	Tasiilaq distr., E of Kuummiut, Second river E	65.872	-36.959	24.07 1999	Alsos, Lund	O	3		1	$2n = 4x$ (5)
riv	CB-99-047	GRL	Tunu	Kong Christian IX Land	Tasiilaq distr., Betw. Kulusuk - airport	65.850	-36.980	26.07 1999	Alsos, Lund	O	3		1	$2n = 4x$ (5)
riv	AK-811	ISL	Vestfirðir	Hólmavík	by road 61, V of Hólmavík, In the mountains side of the mountain with the tower on 526m, before the exit to road 608	65.742	-22.109	05.07 2002	Skrede, Kjølner, Lund	O	1		2	
riv	AK-846	ISL	Vesturland	NE of Akranes	Akrafjall, SE of Akrafjall, in Berjadalur, walking up from Selbrekkja.	64.334	-21.928	02.07 2002	Skrede, Kjølner, Lund	O	1		2	
riv	AK-867	ISL	Norðurland eystra	Akureyri	Brook ~15 km E of Akureyri, by the sign Halshreppur, and a small weatherstation, on N of road 1	65.815	-17.993	08.07 2002	Skrede, Kjølner, Lund	O	1	3		

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
riv	CB-99-049	ISL	Vesturland	NE of Akranes	Akrafjall, Berjadalur	64.043	-21.900	28.07 1999	Alsos, Lund	O	3		3	$2n = 4x$ (5)
riv	AK-416a	NOR	Buskerud	Ål	Reineskarvet, N of Reinestølen	60.751	8.330	23.06 2002	Jørgensen	O	1			
riv	AK-416b	NOR	Buskerud	Ål	Reineskarvet, NE of Skardhovda	60.748	8.296	23.06 2002	Jørgensen				3	
riv	AK-441	NOR	Oppland	Lom	SE slope of Vardhø	61.671	8.045	25.06 2002	Bronken	O	1		2	
riv	AK-456	NOR	Hordaland	Odda	SW of Ulevåvatnet, E of Dyrskardnuten next to the tunnel-joint	59.845	7.059	15.08 2002	Bronken	O	1		2	
riv	AK-470	NOR	Sør-Trøndlag	Oppdal	Vinstradalen, SW slope of Leirtjønnkollen	62.437	9.731	27.06 2002	Bronken	O	1	3	1	
riv	AK-516	NOR	Hordaland	Finse	Along river between Jomfrunut and Kvannjolsnut	60.607	7.532	31.07 2002	Jørgensen, Skrede, Jacobsen	O	2	3	1	
riv	AK-745	NOR	Troms	Tromsø	Fløyfjellet	69.637	19.008	07.08 2002	Alsos, Westergård	O	2	3		
riv	AK-784	NOR	Troms	Storfjord	Lavkajavre	69.212	20.463	06.09 2002	Alsos, Westergård	O	1	3		
riv	TG03/30	RUS	Krasnoyarskiy Kray	Taymyria	Enisey. Sibizyanov E. coast	73.000	80.000	13.08 1980	Matreeva, Zanokha	LE	3			
riv	219876	SJM	Svalbard	Oscar II Land	Ny-Ålesund, harbour area	78.917	11.917	05.08 1975	Emanuelsson	O	3			
riv	AK-109	SJM	Jan Mayen		Blinddalen, close to southern part of Schertzegga	71.000	-8.500	29.07 2002	Wollan	O	1	3	1	
riv	AK-554	SJM	Svalbard	Nordenskiöld Land	Gruve7-fjellet	78.161	16.034	31.07 2002	Alsos, Westergård	O	1	3		
riv	AK-559	SJM	Svalbard	Nordenskiöld Land	Colesdalen	78.103	15.218	26.07 2002	Alsos, Westergård			3		
riv	TMG-21SR	SJM	Svalbard	Nordenskiöld Land	Bjørndalen, NW of the road, W-NW of discharge from Gruve 3	78.225	15.329	06.07 1997	Brochmann, Gabrielsen, Steen	O	3	2	1	$2n = 4x$ (5)

Table 1: (cont.)

Taxon	*Population ID*	*Country*	*Region*	*Subregion*	*Locality*	*Longitude*	*Latitude*	*Date*	*Collector(s)*	*H*	*# H*	*# S*	*# C*	*Chromosome numbers and ploidal levels*
riv	TMG-24SR	SJM	Svalbard	Nordenskiöld Land	NW of the mountain Breinosa, 150 m N of the oldest EISCAT antennae	78.156	16.048	14.07 1997	Brochmann, Gabrielsen, Steen				2	$2n = 4x$ (5)
riv	TMG-34	SJM	Svalbard	Nordenskiöld Land	De Geer dalen, pass S of Skjørlokstupet	77.698	19.039	03.08 1997	Gabrielsen				2	$2n = 4x$ (5)
riv	TMG-35	SJM	Svalbard	Nordenskiöld Land	Skjørlokstupet	77.698	19.081	03.08 1997	Fjellheim, Scheen				1	$2n = 4x$ (5)
riv	TMG-37	SJM	Svalbard	Oscar II Land	Alkhornet, just below it	78.217	13.833	04.08 1997	Gabrielsen				6	$2n = 4x$ (5), 2n= 43, 52, 85 (5)
riv	TMG-37B	SJM	Svalbard	Oscar II Land	Alkhornet, just below it	78.217	13.833	04.08 1997	Gabrielsen				1	$2n = 4x$ (5), 2n= 52 (5)
riv	TMG-39	SJM	Svalbard	Oskar II Land	Bohemanneset	78.383	14.667	04.08 1997	Gabrielsen				1	$2n = 4x$ (5), 2n= 26, 47, 52, 95 (5)

*) Cultivated material from seed bank. Samples collected during the Tundra Northwest 1999 expedition. Details about collection localities are not known.

[a] No official codes were registered for these populations.

AFLPs

Amplified fragment length polymorphisms (AFLPs; Vos *et al.* 1995) were obtained using GeneAmp PCR system 9700 (Applied Biosystems, Foster City, California, USA). The laboratory work was performed at the DNA laboratory at the Natural History Museums and Botanical Garden, University of Oslo.

DNA was isolated using the Qiagen DNeasy™ Kit in accordance with the DNeasy Plant Mini Handbook (Qiagen, Hilden, Germany), with the following exceptions. Approximately 1 cm^2 of silica dried leaves was used, whenever sufficient material was available. The material was crushed in 2 ml tubes with two tungsten carbide beads for 2 x 1 min in a mixer mill (MM301, Retsch GmbH & Co., Haan, Germany) at 20 Hz. 400 µl AP1 buffer was added, and the samples stored overnight at -80°C. After thawing in a 65°C heat block, 3.5 µl RNAse was added, and the mixtures incubated for 20 min at 65°C. The isolated DNA was eluted twice in 50 µl AE buffer and stored at -20°C.

5.5 µl of each DNA extraction was added 0.125 µl *Eco*RI (5 U) and 0.020 µl *Mse*I (1 U) restriction enzymes, 1.0 µl 10 µM *Eco*RI and 1.0 µl 10 µM *Mse*I adapters (Tab. 2), and 0.200 µl T4 DNA ligase (1 U) together with a reaction buffer containing 1.1 µl 10X T4 DNA buffer (with ATP), 1.1 µl 0.5 M NaCl, 0.55 µl BSA (1 mg/ml) and 0.405 µl autoclaved dH_2O, giving a reaction volume of 11 µl. The mixture was incubated for 2 – 3 h at 37°C and diluted 10 times with autoclaved dH_2O.

3 µl of the diluted restriction ligation product was added 2.5µl Taq buffer, 1.5 µl 1.5 mM $MgCl_2$, 2.0 µl 10 mM dNTP, 0.1 µl AmpliTaq, 14.9 µl autoclaved dH_2O and 0.5 µl 10 µM of

Table 2: Restriction sites, adapters and primer sequences used for AFLP analysis. Cutting sites are marked with $^{\downarrow}$ and $_{\uparrow}$, selective bases are shown in bold. * gives primers coloured with 6-FAM, ** primers coloured with JOE.

Restriction enzymes	*Eco*RI	*Mse*I
Restriction sites	5’-G$^{\downarrow}$AATT-3’	5’-T$^{\downarrow}$TA-3’
	3’-C TTAA$_{\uparrow}$G-5’	3’-A AT$_{\uparrow}$T-5’
Adapters	5’-CTCGTAGACTGCGTACC-3’	5’-GACGATGAGTCCTGAG-3’
	3’-CATCTGACGCATGGTTAA-5’	3’-TACTCAGGACTCAT-5’
Pre-selective primers	5’-GACTGCGTACCAATTC**A**-3’	5’-GATGAGTCCTGAGTAA**C**-3’
Selective primers	5’-GACTGCGTACCAATTC**AGA**-3’ *	5’-GATGAGTCCTGAGTAA**CAA**-3’
	5’-GACTGCGTACCAATTC**AGA**-3’ *	5’-GATGAGTCCTGAGTAA**CTG**-3’
	5’-GACTGCGTACCAATTC**ATC**-3’ **	5’-GATGAGTCCTGAGTAA**CAA**-3’

each of *Eco*RI-A and *Mse*I-C pre-selective primers (Tab. 2), giving a total reaction volume of 25 µl. The fragments were amplified according to the following PCR profile: 2 min at 72°C, 30 cycles of the three steps 30 sec at 94°C, 30 sec at 56°C and 1 min at 72°C, and one last hold of 10 min at 72°C. The products were diluted 10 times with autoclaved dH_2O.

After dilution, 5µl of the pre-selective products were added to a mixture of 2.5 µl Taq Gold buffer, 2.5 µl 1.5 mM $MgCl_2$, 2.0 µl 10 mM dNTP, 0.2 µl AmpliTaq Gold, 0.2 µl BSA, 11.6 µl autoclaved dH_2O and 0.5 µl 10 µM of each of the selective primers *Eco*RI-A§§ and *Mse*I-C§§ (Tab. 2). The PCR profile consisted of 10 min at 95°C, 13 cycles of the three steps 30 sec at 94°C, 1 min at 65-56°C (the temperature decreasing 0.7°C each cycle) and 1 min at 72°C, 23 cycles of the steps 30 sec at 94°C, 1 min at 56°C and 1 min at 72°C, and it finished off with a 10 min hold at 72°C.

1.5 µl of each selective PCR product was mixed in 11.5 µl HiDi (formamide) and 0.5 µl GeneScan Rox 500 size standard. The samples were denatured for 5 min at 95°C, and run at the ABI 3100 Sequencer (Applied Biosystems, Foster City, California, USA) with 40 sec injection time.

Eight pairs of AFLP selective primers were tested; E-AGA/M-CAA, E-AGA/M-CAG, E-AGA/M-CTG, E-AGA/M-CTT, E-ATC/M-CAA, E-ATC/M-CAG, E-ATC/M-CTG and E-ATC/M-CTT. Three of these (E-AGA/M-CAA, E-AGA/M-CTG and E-ATC/M-CAA) gave clear profiles with presumably the wanted amount of polymorphisms, and further testing was unnecessary.

The samples were visualised and aligned using GeneScan® Analysis Software version 3.7 (Applied Biosystems, Foster City, California, USA). Peaks in the range 50-500 base pairs were scored as present (1) or absent (0), the intensity threshold being 200, using Genographer version 1.6.0 (Benham 2001). Clear peaks beneath the threshold value were scored as indeterminate (as '?'), giving the opportunity to analyse them as present, absent or missing.

After the first round of scoring, it was evident that the samples were not fully reproducible. 18 samples were then run through restriction and ligation, pre-selective PCR, selective PCR and electrophoresis a second time, making it possible to compare the profiles of the same sample from two different runs. Only markers giving the same result twice were then scored, resulting in a total of 53 markers.

The molecular variation was visualised using principal coordinate analysis (PCO) in NTSYSpc version 2.02 (Rohlf 1999) with simple matching as a similarity measure based on equality in both presence and absence of AFLP fragments.

The AFLP data were analysed by both hierarchical and non-hierarchical clustering. Neighbour joining analyses were performed in PAUP* version 4.0b10 (Swafford 2001), with Nei-Li distance measure (Nei and Li 1979) and 1000 jackknife and bootstrap replicates. A Bayesian approach using Structure version 2 (Pritchard *et al.* 2000) calculated a logarithmic probability for the data given a number of clusters, and assigned the specimens to this clusters probabilistically. The method may be applied to dominant markers under a no admixture model, assuming no linkage between the loci. 10 replicates of each value of K (= the number of groups) were run for different selections of samples with a burn-in period of 100 000 and 1000 000 iterations.

Parsimony analysis was performed using heuristic search with 1000 replicates, tree bisection-reconnection as branch-swapping algorithm and 10 addition sequence replicates in PAUP* version 4.0b10 (Swafford 2001), as were 1000 jackknife and bootstrap replicates with nearest-neighbour interchange algorithm. Tree scores were calculated. An analysis with the same settings was also performed on the dataset excluding *Saxifraga rivularis* due to its polyploidy and hypothesised hybrid origin.

Molecular variances (AMOVA) were calculated using the software Arlequin version 2.000 (Schneider *et al.* 1997). AMOVA can be used for AFLP markers as haplotypic data (Schneider *et al.* 1997).

Flow cytometry

DNA ratios were obtained from Plant Cytometry Services, The Netherlands, based on fresh plant material using DAPI staining and *Lactuca sativa* L. as internal standard. A few cm^2 (20-50 mg) leaf material was chopped with a razor blade and a DNA buffer (at pH 8) containing 5.0 mM Hepes, 10.0 mM $MgSO_4 \times 7H_2O$, 50.0 mM KCl, 0.2% Triton X-100, 2% DTT (dithiothreitol) and 4 mg/l DAPI, was added. The solution was filtered through a nylon filter of 40 µm mesh size. The flow cytometer PAS II (Partec GmbH, Münster, Germany) was used with a high pressure mercury lamp (OSRAM HBO 100 Long Life; OSRAM GmbH, München, Germany), heat protection filter KG-1, excitation filters UG-1 and BG-38, dichroic mirrors TK 420 and TK 560 and emission filter GG 435. DNA histograms were obtained using the Flows 2.00 Software Package (Partec GmbH, Münster, Germany).

Morphometrics

45 primary and eight derived morphological characters (Tab. 3, Fig. 10, 11) where chosen based on characters used in floras (i.e., Polunin 1959; Hultén 1968; Rebristaya and Yurtsev 1984; Lid and Lid 1994) and own observations. The morphological characters were scored using a stereo magnifier and is further explained in Table 3. Only one replicate were made for each plant due to the small size of most specimens.

Descriptive statistics for the five tentative taxa and all morphological characters were calculated using SPSS 11.0 (SPSS Inc., Chicago, Illinois, USA). A Mann-Whitney *U* test for equality of medians was performed by the same program for all morphological characters and all combinations of taxa, as well as the combination of the groups 1a and 1b inferred from the Structure analysis.

Multivariate analyses were run on 16 continuous and nine discrete morphological characters (Tab. 3). The characters were chosen with the intention of separating the taxa, and only characters giving significant differences between most taxa in the Mann-Whitney *U* test were included. However, if a derived index character was included, at least one of the primary characters from which it was calculated, was excluded from the analyses. The 16 continuous morphological characters were analysed for all plants with PCO in NTSYSpc version 2.02 (Rohlf 1999), after standardising by ranging (scaling all characters between 0 and 1), and using Euclidean distance measure. Kendall's τ correlations between the PCO axes and the continuous morphological characters included in the multivariate analysis were calculated in SPSS 11.0 (SPSS Inc., Chicago, Illinois, USA).

Table 3: Morphological characters examined in the *Saxifraga rivularis* complex. P/D indicates if the character is primary (P) or derived (D). Character types are given by Q - qualitative, D - quantitative discrete and C - quantitative continuous. Characters included in multivariate analyses are given in column P1 (continuous characters) and P2 (discrete characters). All measurements are in mm.

No	*P/D*	*Type*	*Short name*	*Character*	*P1*	*P2*	*Note*
1	P	Q	Runners	Presence of runners		X	0 - absent, 1 - present
2	P	Q	Dev_stage	Developmental stage of plant			0 - early flowering stage, 1 - late flowering stage, 2 - fruit stage
3	P	C	L_fl_stem	Length of flowering stem	X		
4	P	C	L_fl_ped	Length of lowest flower pedicel			In late flowering and fruit stage only
5	D		L_ped_l_fl	Length of lowest flower pedicel / length of flowering stem	X		
6	P	D	No_flowers	No of buds/flowers/fruits per flowering stem			
7	P	D	No_cauline	No of cauline leaves per flowering stem			
8	D		No_caul_l_fl	No of cauline leaves per flowering stem / length of flowering stem	X		
9	P	Q	Pigments	Pigments		X	0 - green, 1 - anthocyanin-coloured hypanthium and petals, 2 - anthocyanin-coloured hypanthium, petals and upper part of stem, 3 - the whole plant anthocyanin-coloured
10	P	Q	Dens_stem	Hair density at the lower 1/3 of stem		X	0 - glabrous, 1 - sparsely haired, 2 - densely haired
11	P	Q	Sh_hyp_e	Shape of hypanthium, early stage			0 - bowl-shaped, 1 - v-shaped
12	P	Q	Sh_hyp_l	Shape of hypanthium, late stage			0 - bowl-shaped, 1 - v-shaped
13	P	C	L_hyp_e	Length of hypanthium, early stage			
14	P	C	L_hyp_l	Length of hypanthium, late stage	X		
15	P	Q	Hyp_gland	Presence of hypanthium glandular hairs			0 - absent, 1 - present
16	P	Q	Dens_hyp	Density of hypanthium glandular hairs		X	1 - sparse, 2 - dense
17	P	C	L_gland	Length of hypanthium glandular hairs	X		
18	P	D	No_cells_gland	No. of cells, hypanthium glandular hairs			
19	P	Q	Colour_gland	Colour of hair partition walls, upper pedicel		X	0 - not coloured, 1 - weakly purple coloured, 2 - purple coloured
20	P	C	L_sepal	Length of sepal			Maximum length
21	P	C	W_sepal	Width of sepal			Maximum width
22	D		L_sep_l_hyp	Length of sepal / length of hypanthium, late stage	X		
23	D		W_sep_l_hyp	Width of sepal / length of hypanthium, late stage	X		
24	D		W_l_sepal	Width of sepal / length of sepal	X		

Table 3: (cont.)

No	*P/D*	*Type*	*Short name*	*Character*	*P1*	*P2*	*Note*
25	P	Q	Sh_sep_apex	Sepal apex shape			0 - acute, 1 - intermediate, 2 - obtuse
26	P	C	L_petal	Length of petal			Maximum length
27	P	C	W_petal	Width of petal	X		Maximum width
28	D		W_l_petal	Width of petal / length of petal	X		
29	P	Q	Sh_petal	Shape of petal		X	0 - oblong, 1 - intermediate, 2 - elliptic, broadly rounded
30	P	C	L_gynoec	Length of gynoecium			Fruit stage only
31	P	Q	Dist_ubract	Distinction of uppermost bract			0 - not distinct, 1 - distinct
32	P	Q	Dist_ubr_pet	Distinction of uppermost bract petiole			0 - not distinct, 1 - distinct
33	P	C	L_ubract	Length of uppermost bract lamina			Maximum length
34	P	C	W_ubract	Width of uppermost bract lamina	X		Maximum width
35	D		W_L_ubract	Width of uppermost bract lamina / length of uppermost bract lamina	X		
36	P	D	No_lobes_ubr	No of lobes, uppermost bract		X	
37	P	Q	Dist_lbract	Distinction of lowest bract			0 - not distinct, 1 - distinct
38	P	Q	Dist_lbr_pet	Distinction of lowest bract petiole			0 - not distinct, 1 - distinct
39	P	C	L_lbr_pet	Length of lowest bract petiole	X		
40	P	C	L_lbract	Length of lowest bract lamina			Maximum length
41	P	C	W_lbract	Width of lowest bract lamina			Maximum width
42	P	D	No_lobes_lbr	No of lobes, lowest bract			
43	P	Q	Sh_lbr_apex	Shape of middle lobe apex, lowest bract			0 - rounded, 1 - intermediate, 2 - angled
44	P	C	L_leaf	Length of basal leaf lamina	X		Maximum length
45	P	C	W_leaf	Width of basal leaf lamina			Maximum width
46	D		W_L_leaf	Width of basal leaf lamina / length of basal leaf lamina	X		
47	P	C	Dist_inc	Distance from basal leaf incision to basal leaf lamina base	X		
48	P	Q	Sh_inc	Shape of basal leaf incision			0 - v-shaped, 1 - intermediate, 2 - u-shaped
49	P	D	No_lobes_leaf	No of lobes, basal leaf		X	
50	P	Q	Sh_leaf_apex	Shape of middle lobe apex, basal leaf		X	0 - rounded, 1 - intermediate, 2 - angled
51	P	Q	Str_sheath	Structure of basal leaf petiole sheath			0 - thin/pale, 1 - intermediate, 2 - firm/brown
52	P	Q	Sh_sheath	Shape of basal leaf petiole sheath shoulder			0 - rounded, 1 - intermediate, 2 - angled
53	P	Q	Fri_sheath	Density of basal leaf petiole sheath fringes			0 - absent, 1 - sparse, 2 - dense

The nine discrete morphological characters were also standardised by ranging and analysed with PCO using the similarity measure of Rogers and Tanimoto (1960) that makes special allowance for multistate characters (Sokal and Sneath 1963). Kendall's τ correlations between all PCO axes and the discrete morphological characters included in the analyses were calculated using SPSS 11.0 (SPSS Inc., Chicago, Illinois, USA).

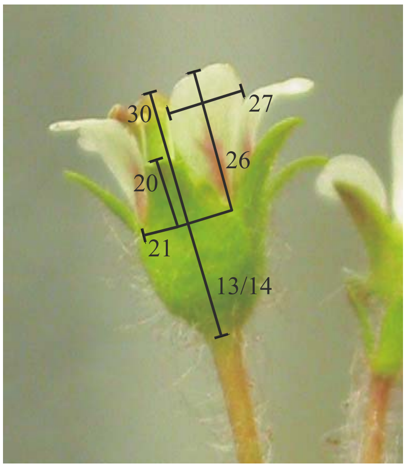


Figure 10: Flower characters measured: Length of hypanthium (characters 13 and 14; cf. Tab. 3), length of sepal (character 20), width of sepal (character 21), length of petal (character 26), width of petal (character 27) and length of gynoecium (character 30).

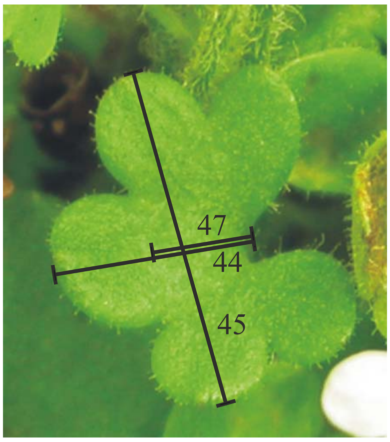


Figure 11: Basal leaf characters measured: Length of basal leaf lamina (character 44; cf. Tab. 3), width of basal leaf lamina (character 45) and distance from incision to basal leaf lamina base (character 47).

Results

AFLP variation

The use of AFLP was appropriate in this study. More variable markers were obtained than in previous studies in *Saxifraga* section *Mesogyne* based on cpDNA sequencing and RAPDs (e.g., Guldahl *et al.* in prep; Brochmann *et al.* 1998). Although the number of AFLP markers was low due to reproducibility problems, 53 markers were obtained (41 parsimony informative; Appendix 1) seem to be sufficient to conclude about relationships at the interspecific level. Furthermore, the final dataset only contained markers with unambiguous peaks which were reproduced twice.

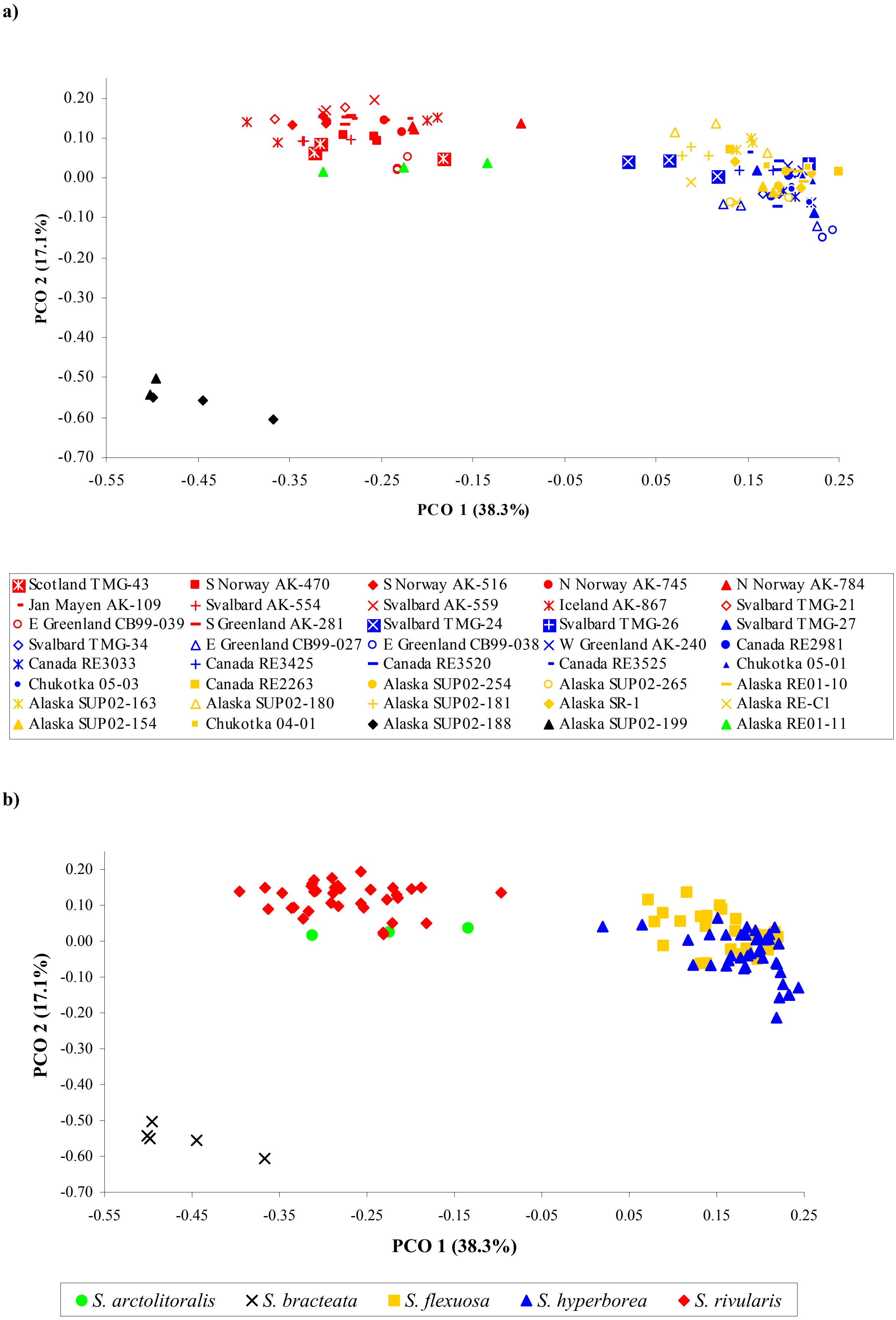
Seven markers were present in *Saxifraga arctolitoralis*, *S. flexuosa*, *S. hyperborea* and *S. rivularis*, but not in *S. bracteata* (121.5a, 171.1a, 196.5a, 60.3b, 157.1b, 167.1b and 168.4b; cf. Appendix 1), one marker was only present in *S. bracteata* (353.7a), one was exclusively shared by *S. arctolitoralis* and *S. bracteata* (167c), and three were exclusively shared among *S. arctolitoralis*, *S. bracteata* and *S. rivularis* (190.8b, 253.8b and 196.6c). Exception for *S. bracteata*, no taxa had fixed species-specific markers.

In all analyses the results were more or less the same, independent of whether uncertain peaks were included as present or missing. Since the former gave a clearer picture, the latter is not shown for any of the analyses.

PCO analyses

The PCO analyses of the total material grouped the plants into three distinct groups along axes 1 and 2 (Fig. 12 a and b): one *Saxifraga arctolitoralis*/*rivularis* group, one *S. flexuosa*/*hyperborea* group and one *S. bracteata* group. PCO axis 3 gave little new information although it spanned 8.2 % of the variation, mostly the variation within the *S. flexuosa*/*hyperborea* group (Fig. 12 c).

PCO analyses of the two largest groups were also performed separately. The *Saxifraga arctolitoralis*/*rivularis* group showed some separation according to latitude along the first


a)
PCO 2 (17.1%)
0.20
0.10
0.00
-0.10
-0.20
-0.30
-0.40
-0.50
-0.60
-0.70
-0.55
-0.45
-0.35
-0.25
-0.15
-0.05
0.05
0.15
0.25
PCO 1 (38.3%)
Scotland TMG-43
S Norway AK-470
S Norway AK-516
N Norway AK-745
N Norway AK-784
Jan Mayen AK-109
Svalbard AK-554
Svalbard AK-559
Iceland AK-867
Svalbard TMG-21
E Greenland CB99-039
S Greenland AK-281
Svalbard TMG-24
Svalbard TMG-26
Svalbard TMG-27
Svalbard TMG-34
E Greenland CB99-027
E Greenland CB99-038
W Greenland AK-240
Canada RE2981
Canada RE3033
Canada RE3425
Canada RE3520
Canada RE3525
Chukotka 05-01
Chukotka 05-03
Canada RE2263
Alaska SUP02-254
Alaska SUP02-265
Alaska RE01-10
Alaska SUP02-163
Alaska SUP02-180
Alaska SUP02-181
Alaska SR-1
Alaska RE-C1
Alaska SUP02-154
Chukotka 04-01
Alaska SUP02-188
Alaska SUP02-199
Alaska RE01-11
b)
PCO 2 (17.1%)
0.20
0.10
0.00
-0.10
-0.20
-0.30
-0.40
-0.50
-0.60
-0.70
-0.55
-0.45
-0.35
-0.25
-0.15
-0.05
0.05
0.15
0.25
PCO 1 (38.3%)
S. arctolitoralis
S. bracteata
S. flexuosa
S. hyperborea
S. rivularis

c)

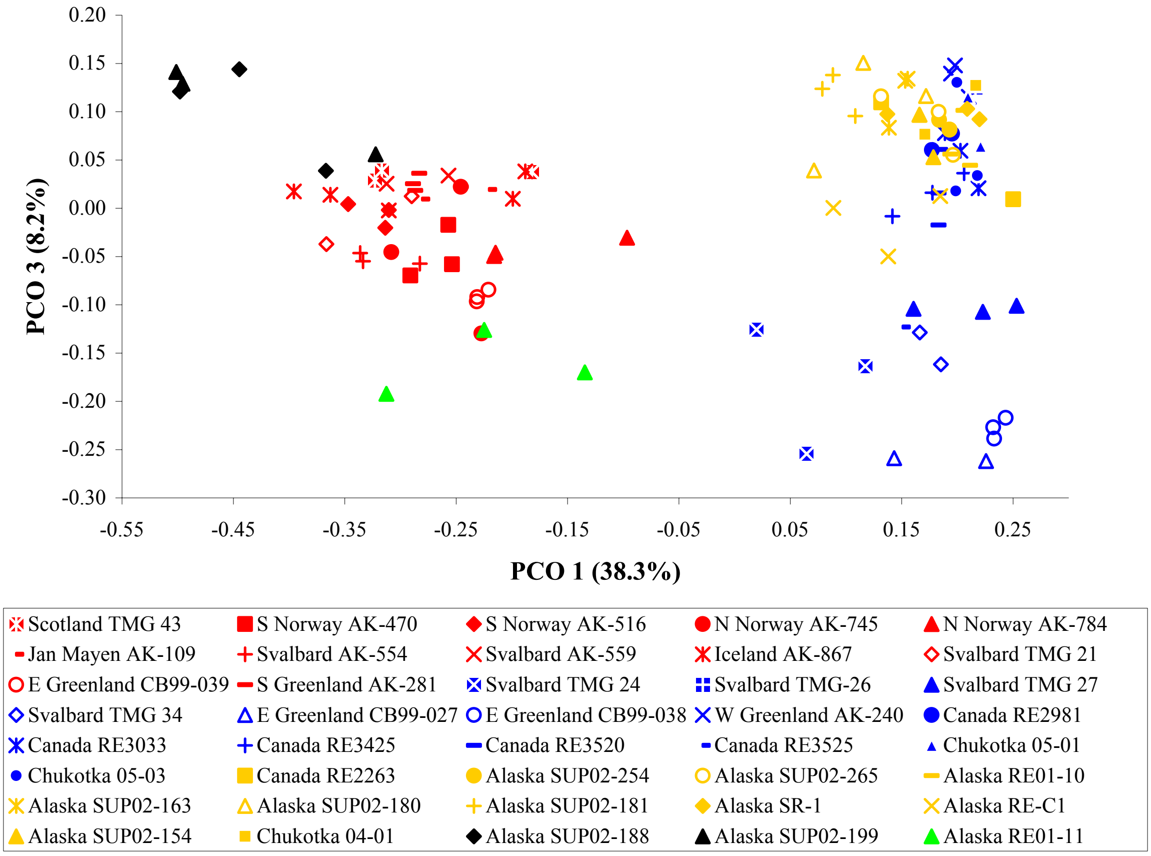


Figure 12: PCO analysis of the total material of the *Saxifraga rivularis* complex based on SM-similarity and 53 AFLP markers. **a)** Plants sorted by population along PCO axes 1 and 2. **b)** Plants tentatively sorted by taxon along PCO axes 1 and 2. **c)** Plants sorted by population along PCO axes 1 and 3.

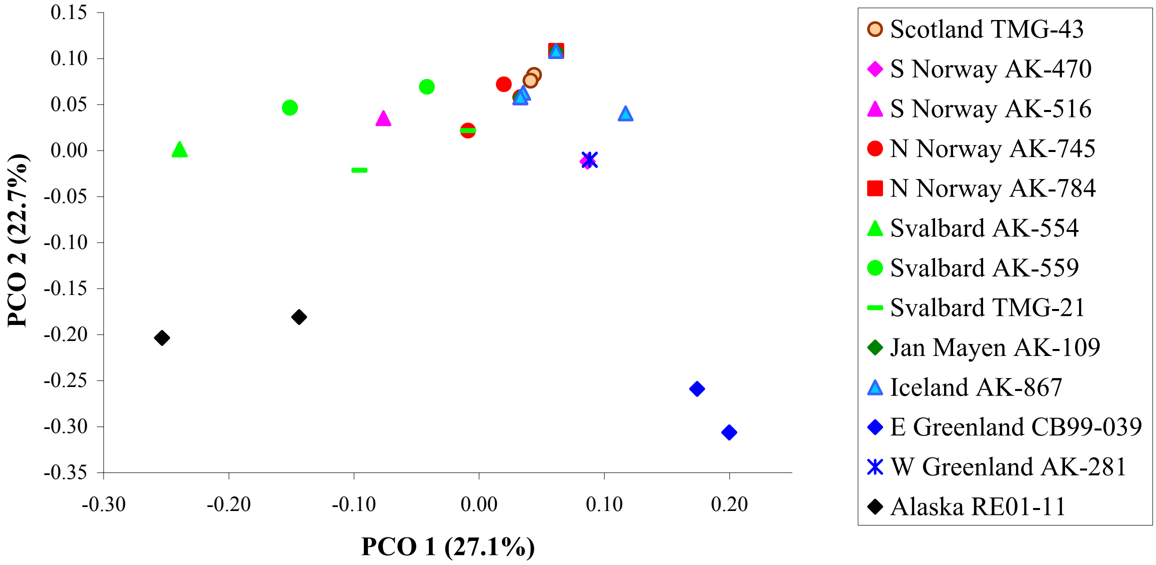


Figure 13: PCO analysis of 12 populations of *Saxifraga rivularis* and one population of *S. arctolitoralis* (RE01-11) based on SM-similarity and 53 AFLP markers.

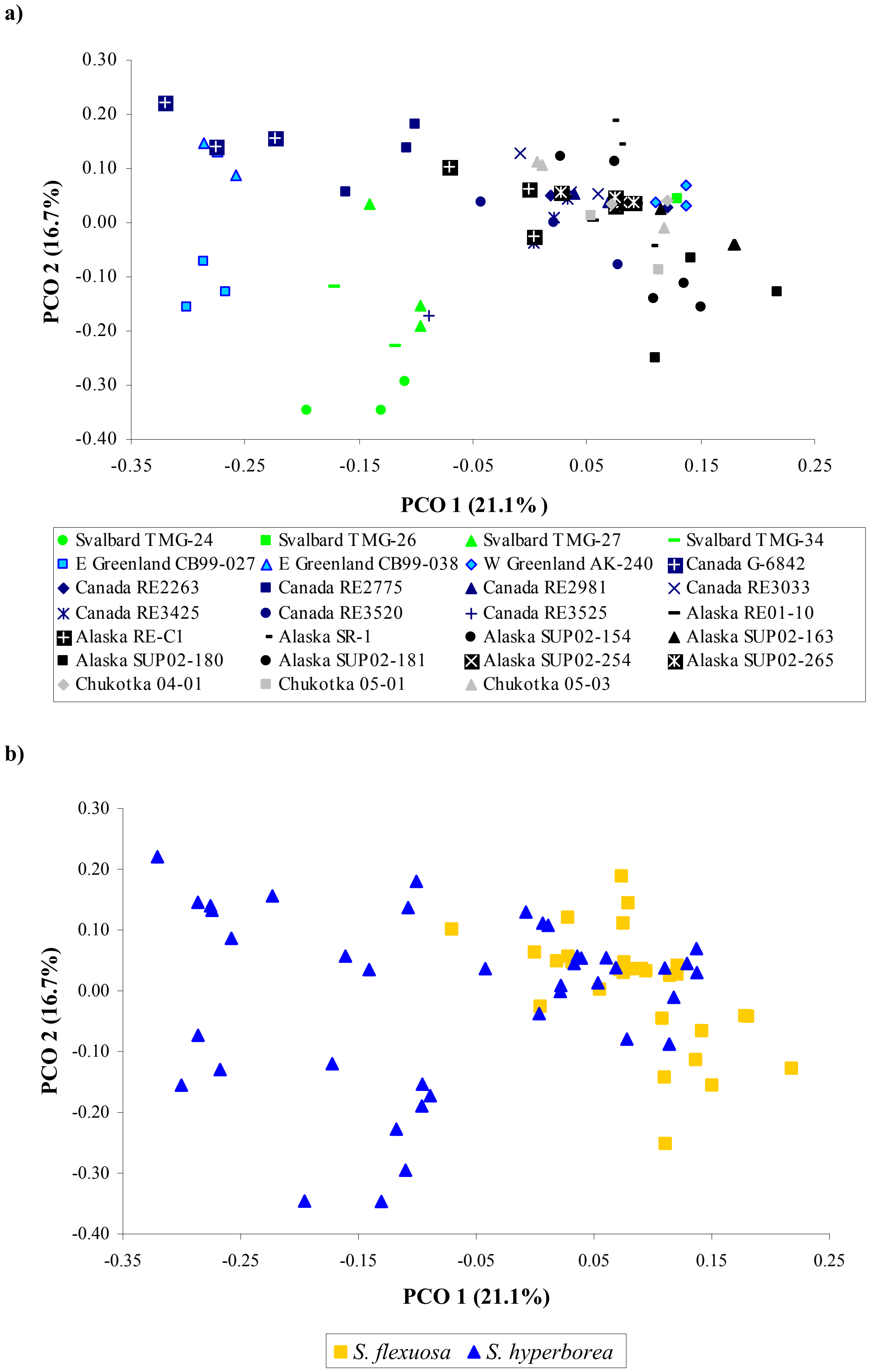


Figure 14: PCO analysis of 11 populations of *Saxifraga flexuosa* and 16 populations of *S. hyperborea* based on SM-similarity and 53 AFLP markers. **a)** Plants sorted by population. **b)** Plants tentatively sorted by taxon.

axis, and the second axis separated the two populations from Beringia and East Greenland from the other populations (Fig. 13). Otherwise little geographical structure was identified within the lineage. The *S. flexuosa*/*hyperborea* group showed little structure corresponding to the tentative species (Fig. 14). However, the Atlantic populations were mainly found at low values for PCO axis 1, whereas the Beringian populations mainly were found at high values for PCO axis 1.

Cluster analyses

In the Structure analyses, the highest probability of data given a number of groups (Ln P(D); Fig. 15) were obtained at K = 7 and K = 8. However, the program was not able to assign all the specimens to specific groups given these values of K, hence a lower number of groups was appropriate. K = 4 gave stability in distribution of plants between the groups and in the probability of the data (Fig. 15, 16), thus four was the highest reliable number of groups obtained. One cluster comprised two Beringian populations (Group 3; the *Saxifraga bracteata* cluster). One included populations mostly from the Atlantic coastlines, Norway and the *S. arctolitoralis* population from Alaska (Group 2; the *S. rivularis* cluster). The third and fourth clusters corresponded to the geographical pattern observed in the PCO analysis of the *S. flexuosa*/*hyperborea* group (Fig. 14); group 1b included mainly Pacific populations (from Chukotka, Alaska, Canada and West Greenland) and group 1a included mostly Atlantic populations (from Svalbard, East Greenland and Canada, but also some specimens from Alaska; Fig. 17). Analysing the three large groups separately gave no further information about geographical structure within the taxa (not shown).

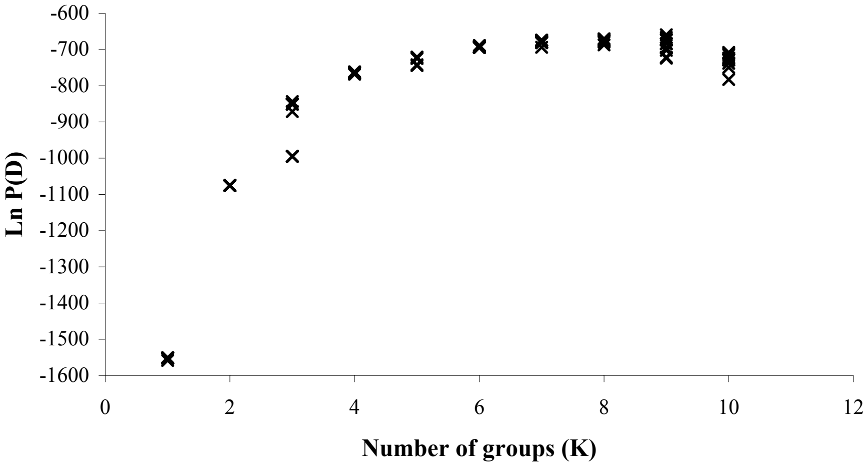


Figure 15: Logarithmic probability of data given a number of groups inferred from Structure analyses of 53 AFLP markers and 119 plants. 10 replicates are shown for each number of groups.

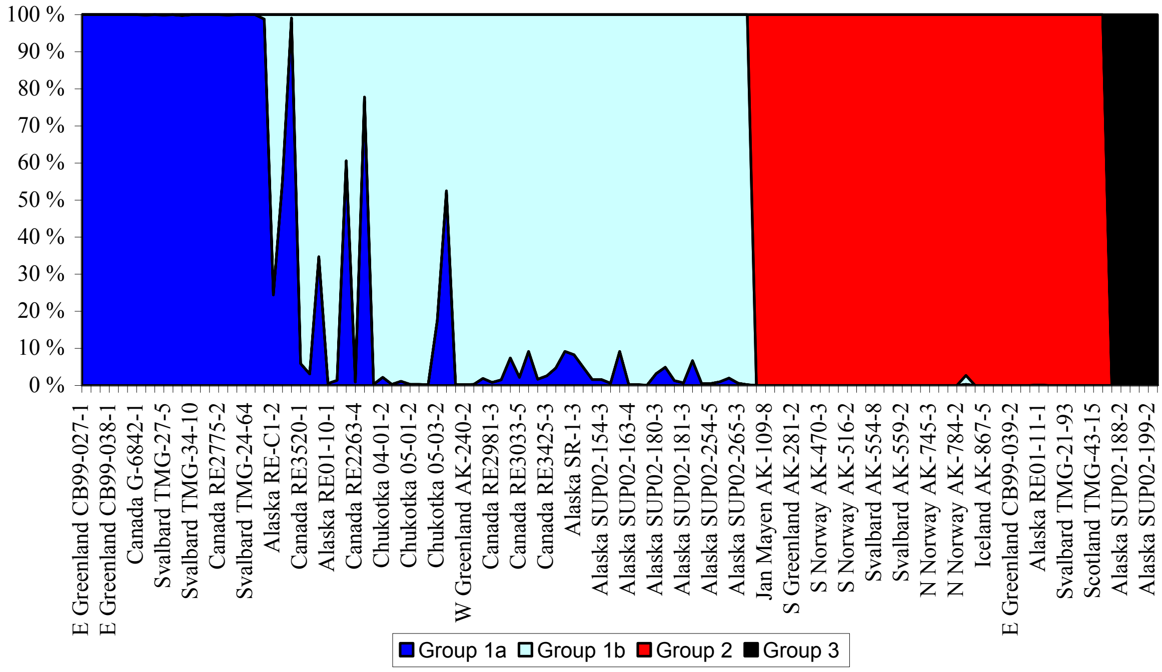


Figure 16: Clustering of the total material of the *Saxifraga rivularis* complex into 4 groups inferred from Structure analysis. Ln P(D) = -761.8. *Saxifraga flexuosa* and *S. hyperborea* are divided into groups 1a and 1b, although not corresponding to the tentative taxa, *S. rivularis* and *S. arctolitoralis* are joined in group 2, whereas only *S. bracteata* plants were allocated to group 3.

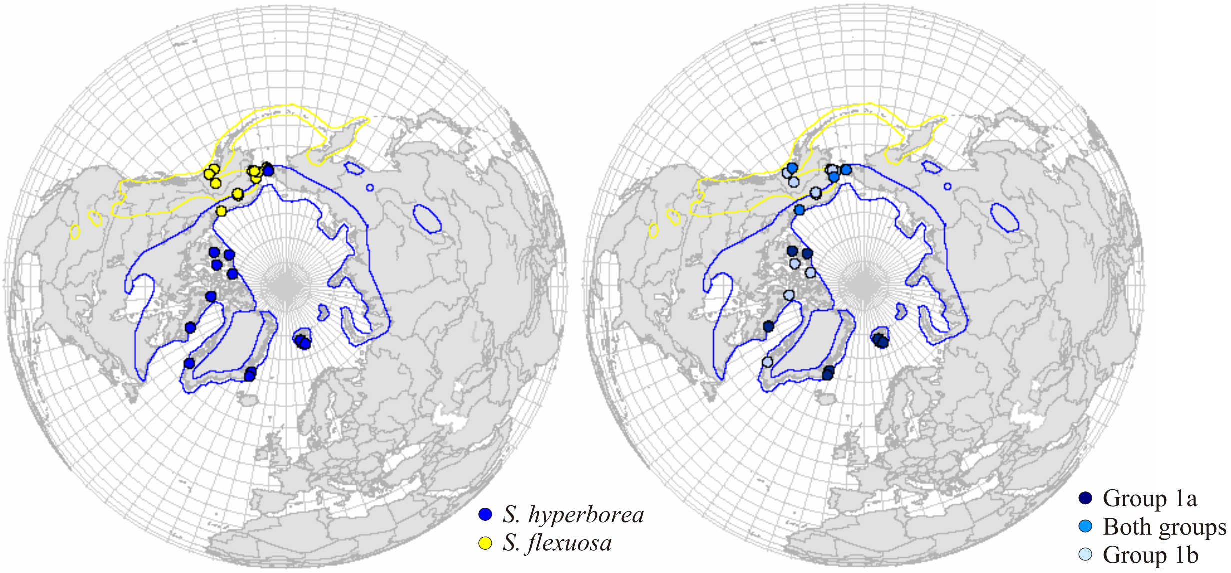


Figure 17: The populations of *Saxifraga flexuosa* and *S. hyperborea* marked by taxon (left) and to which group the population was assigned in the Structure analyses (right).

Neighbour joining analyses of the AFLP data split the plants into two well-defined clusters separating *Saxifraga bracteata* from the rest, with 100 in both bootstrap and jackknife support (Fig. 18). Treating the indeterminate values in the dataset as 'presence' gave some support to a subcluster comprising *S. hyperborea* and *S. flexuosa*. The subcluster was not supported when indeterminate values were treated as missing, but the tree topology was still more or less the same (not shown). The group of populations of *S. rivularis* and *S. arctolitoralis* was paraphyletic in the midpoint rooted neighbour joining tree. However, when *S. bracteata* was excluded from the analysis, *S. rivularis* and *S. arctolitoralis* made a closely packed cluster separated from *S. flexuosa*/*hyperborea* with 83 in bootstrap value and 68 in jackknife support (not shown).

Parsimony analyses

Parsimony analysis of the data gave strong jackknife and bootstrap support to a clade of *Saxifraga bracteata*, and some support to a clade comprising *S. hyperborea* and *S. flexuosa*, whereas the combined *S. rivularis* and *S. arctolitoralis*, although closely connected, was paraphyletic (Fig. 19). Excluding *S. rivularis* and *S. arctolitoralis* from the analysis reduced the homoplasy index (Tab. 4).

AMOVA analyses

61.93% of the variation was explained among the groups when the plants were divided into three groups, whereas the within populations variation decreased from 20.42% to 14.30% compared to keeping them all in one group (Tab. 5). Further division of one of the groups (*Saxifraga flexuosa*/*hyperborea*, corresponding to group 1a and b in the Structure analysis; Fig. 16), gave a small decrease in the among groups variation to 59.37% (Tab. 5). However, when the *S. flexuosa*/*hyperborea* populations were analysed separately, the division reduced the within populations variation and the among groups variation was 21.02%, almost twice as much as if divided by tentative taxa (12.18%; Tab. 6).

Variation in ploidal levels

Three levels of DNA contents were found by flow cytometry; *Saxifraga rivularis* had DNA ratios of approximately 0.38, *S. hyperborea* and *S. flexuosa* had DNA ratios of 0.16-0.18 and the ratios of *S. bracteata* were 0.20-0.21 (Fig. 20; Appendix 2). The first corresponded to chromosome number $2n = 52$, whereas the last two corresponded to the chromosome number $2n = 26$. Thus, *S. bracteata* had larger chromosomes than *S. flexuosa*/*hyperborea*, while *S. rivularis* had the same amount of DNA as the sum of the other two.

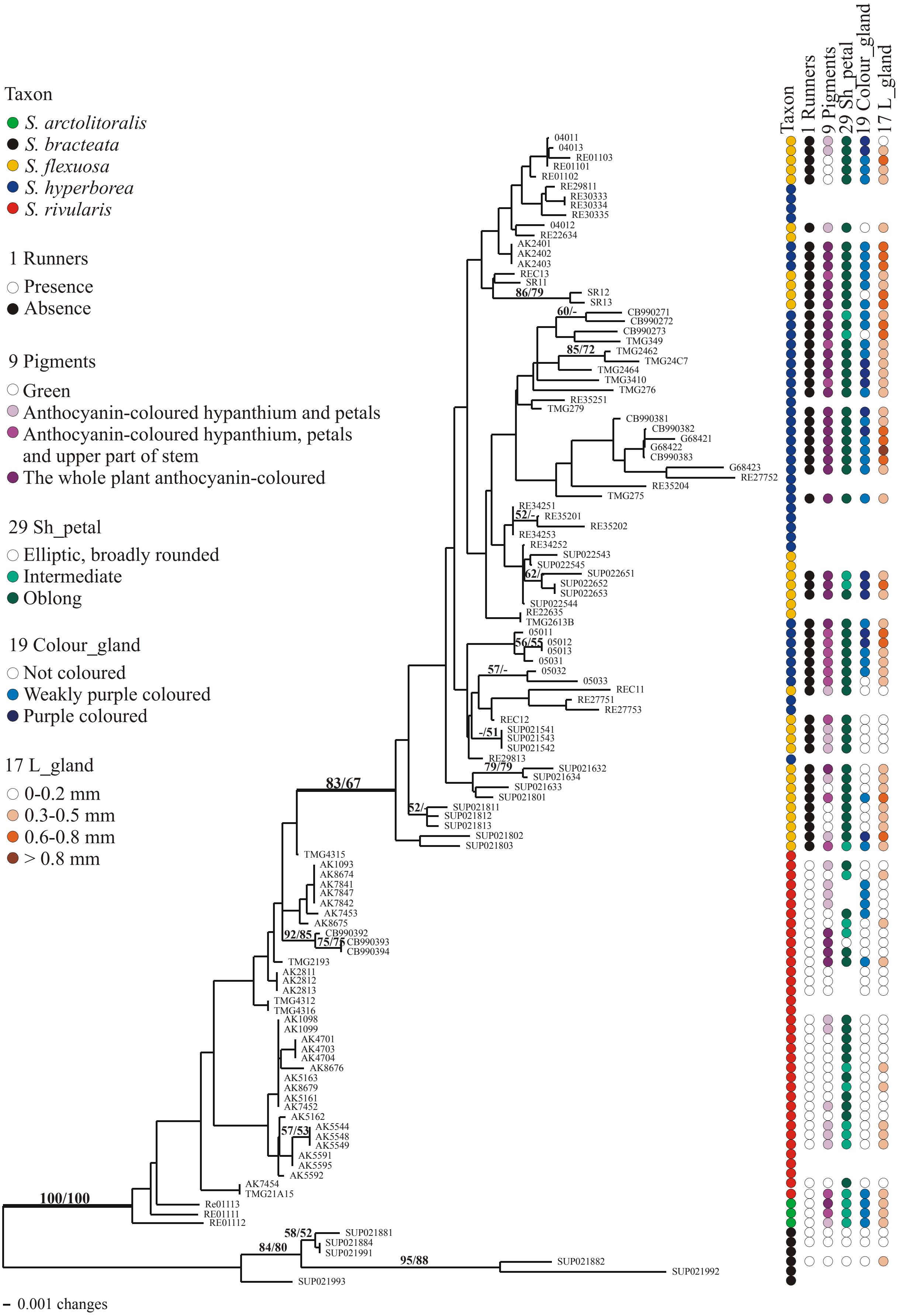


Figure 18: Midpoint rooted neighbour joining tree of the total material of the *Saxifraga rivularis* complex from Nei-Li distance based on 53 AFLP markers. Jackknife/bootstrap values higher than 50 are indicated above supported branches. Distribution of five morphological characters among plants from populations included in the analysis, but not necessarily the same specimens, are given to the right. Character codes are given in Table 3.

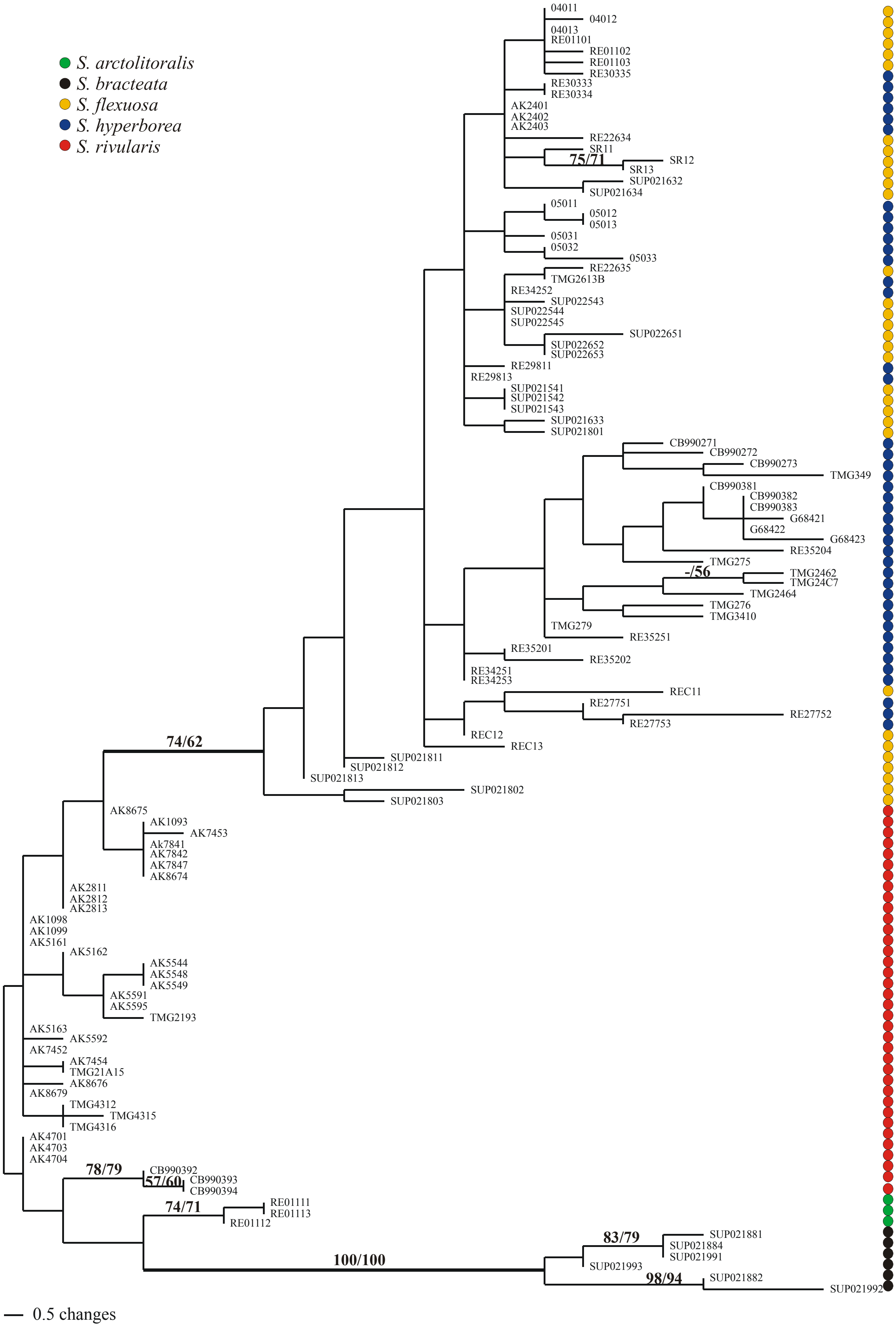


Figure 19: One of the most parsimonious trees of the *Saxifraga rivularis* complex inferred from 53 AFLP characters. Jackknife/bootstrap support higher than 50 is given above the branches. Midpoint rooted.

Table 4: Tree scores from parsimony analysis of the total material of the *Saxifraga rivularis* complex and the dataset without the *S. rivularis* and *S. arctolitoralis* plants.

	All samples	*Excluding* S. rivularis *and* S. arctolitoralis
Tree length	196	135
Consistency index, CI	0.282	0.326
Retention index, RI	0.845	0.756
Rescaled consistency index, RC	0.238	0.246
Homoplasy index, HI	0.718	0.674

Table 5: AMOVA analysis of the total material of the *Saxifraga rivularis* complex divided into one, three and four groups, obtained from the Structure analyses. P ≤ 0.00001 for all the variance components.

	Source of variation	*Degrees of freedom*	*Sum of squares*	*Variance components*	*Percentage of variation*
One group	Among populations	41	472.973	3.73628	79.58
	Within populations	77	73.833	0.95887	20.42
	Total	118	546.807	4.69515	
Three groups	Among groups	2	260.184	4.15253	61.93
	Among populations within groups	39	212.789	1.59327	23.76
	Within populations	77	73.833	0.95887	14.30
	Total	118	546.807	6.70468	
Four groups	Among groups	3	289.956	3.39965	59.37
	Among populations within groups	38	183.018	1.36745	23.88
	Within populations	77	73.833	0.95887	16.75
	Total	118	546.807	5.72598	

Table 6: AMOVA analysis of 74 plants from 27 populations of *Saxifraga hyperborea* and *S. flexuosa* as one group, and divided into two groups: one according to taxa and one following the results from the Structure analysis. P ≤ 0.00001 for all the variance components.

	Source of variation	*Degrees of freedom*	*Sum of squares*	*Variance components*	*Percentage of variation*
One group	Among populations	26	164.725	1.90610	62.98
	Within populations	47	52.667	1.12057	37.02
	Total	73	217.392	3.02666	
Two groups by Structure	Among groups	1	29.722	0.71510	21.02
	Among populations within groups	25	134.954	1.56702	46.05
	Within populations	47	52.667	1.12057	32.93
	Total	73	217.392	3.40269	
Two groups by taxa	Among groups	1	20.469	0.39161	12.18
	Among populations within groups	25	144.256	1.70255	52.96
	Within populations	47	52.667	1.12057	34.86
	Total	73	217.392	3.21473	

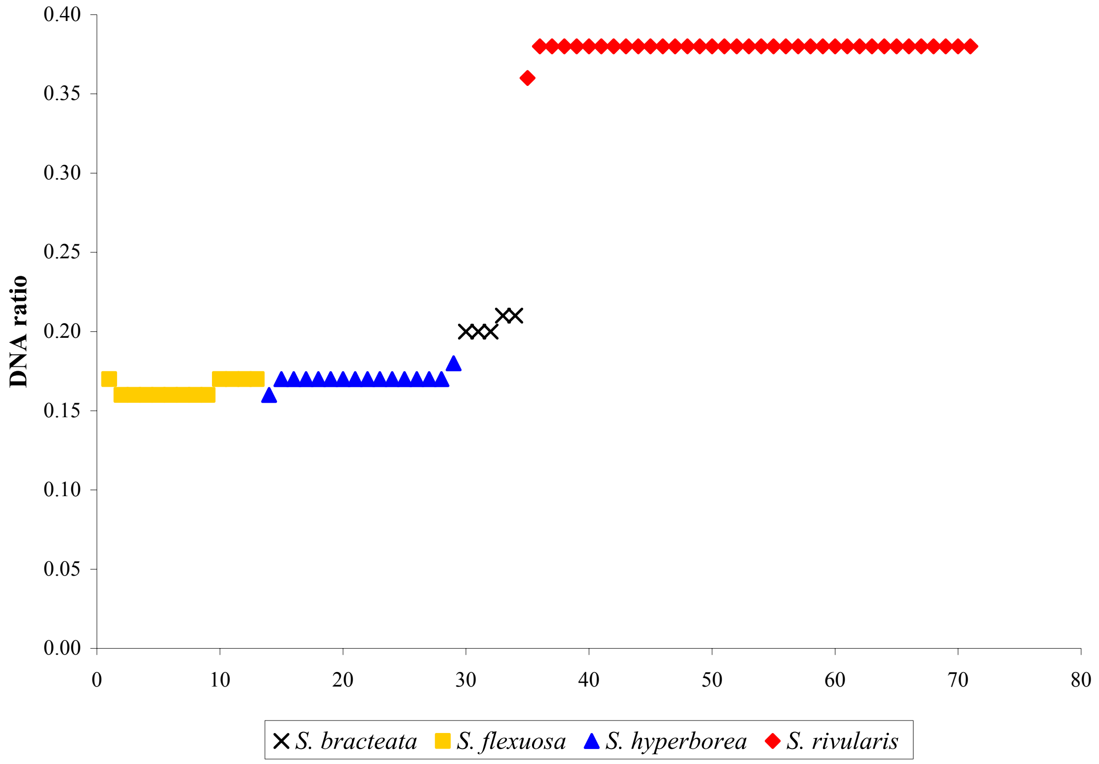


Figure 20: DNA ratio for 71 plants determined by flow cytometry using DAPI staining and *Lactuca sativa* L. as internal standard. *Saxifraga arctolitoralis* was not included due to lack of material.

Morphological variation

The morphological data are given in Appendix 3, and descriptive statistics for all the characters are given in Table 7. The Mann-Whitney *U* test showed significant differences among the taxa in more than half of the characters when comparing *Saxifraga bracteata* to the rest (i.e., 30 or more) whereas only 12 characters showed significant differences between *S. hyperborea* and *S. flexuosa* (Tab. 8, 9). The other combinations of taxa showed significant differences in 20-30 characters. When comparing the groups 1a and 1b obtained from the Structure analysis (Fig. 16), including only plants that were allocated unambiguously, only four characters showed significant differences between the groups (Tab. 8). Boxplots for selected characters are shown in Figure 21.

Saxifraga bracteata had broadly elliptic petals and had runners. It was typically larger than the other taxa, with longer flowering stems, longer and broader bracts and leaves, and larger flowers, as well as more numerous flowers, bracts and lobes (Tab. 7, 8; Fig. 21).

Table 7: Descriptive statistics for all measured and derived morphological characters. Character code is according to Table 3. N is number of plants.

		S. arctolitoralis					*S. bracteata*					*S. flexuosa*					*S. hyperborea*					*S. rivularis*				
No	*Character*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*
1	Runners	23	1	1	1.0	0.00	27	0	1	0.93	0.27	42	0	0	0.0	0.00	58	0	0	0.0	0.00	36	0	1	0.94	0.23
2	Dev_stage	33	0	2	1.27	0.80	35	0	2	0.86	0.94	45	0	2	1.13	0.81	60	0	2	0.92	0.81	42	0	2	1.24	0.82
3	L_fl_stem	33	10	79	27.14	16.34	34	34	177	90.9	40.22	45	14.5	125	63.88	24.58	60	11	97	43.45	21.7	42	8	121	48.12	28.06
4	L_fl_ped	23	0.5	28	8.08	6.81	17	1.3	19.5	7.19	6.27	29	0	42	14.76	10.47	34	0.7	33	9.7	8.00	28	0.5	34	9.21	7.47
5	L_ped_l_fl	23	0.02	1	0.3	0.24	16	0.01	0.18	0.06	0.05	29	0	0.41	0.19	0.11	34	0.04	0.53	0.18	0.12	28	0.01	0.55	0.17	0.12
6	No_flowers	33	1	5	2.17	0.75	35	1	29	5	4.65	45	1	6	2.49	1.08	60	1	4	2.33	0.82	42	1	5	2.12	0.74
7	No_cauline	33	0	8	2.52	1.50	34	0	35	8.1	5.98	45	1	7	2.71	1.39	59	1	5	2.37	1.11	42	0	7	2.31	1.28
8	No_caul_l_fl	33	0	0.29	0.11	0.07	34	0	0.31	0.1	0.05	45	0.01	0.17	0.05	0.03	59	0.01	0.22	0.07	0.05	42	0	0.15	0.06	0.04
9	Pigments	19	0	3	2.32	0.95	36	0	1	0.08	0.28	45	0	3	1.53	1.31	60	2	3	2.68	0.47	42	0	3	1.0	1.23
10	Sh_hyp_e	7	1	1	1.0	0.00	17	0	1	0.53	0.51	12	0	1	0.67	0.49	21	0	1	0.86	0.36	10	0	1	0.1	0.32
11	Sh_hyp_l	26	0	1	0.92	0.27	16	0	1	0.75	0.45	33	0	1	0.82	0.39	38	0	1	0.79	0.41	32	0	1	0.28	0.46
12	L_hyp_e	7	1.2	2.3	1.67	0.40	15	0.9	2.5	1.74	0.47	12	0.7	1.9	1.36	0.40	21	1.1	2	1.52	0.24	10	1.1	2.5	1.67	0.47
13	L_hyp_l	26	1.2	5	2.59	0.93	16	1.3	5.2	2.82	1.05	33	0.9	3.6	2.01	0.61	38	1	3	1.83	0.55	32	1.2	3.8	2.23	0.59
14	L_sep_l_hyp	26	0.6	1.86	1.07	0.30	16	0.53	3.21	1.32	0.63	33	0.58	1.8	1.07	0.35	38	0.6	2	1.17	0.31	31	0.61	1.8	1.03	0.28
15	W_sep_l_hyp	26	0.24	1.08	0.61	0.20	16	0.38	1.86	0.85	0.41	33	0.38	1.5	0.68	0.25	38	0.37	1.3	0.7	0.20	31	0.4	1.42	0.70	0.20
16	Hyp_gland	32	1	1	1.0	0.00	34	1	1	1.0	0.00	45	1	1	1.0	0.00	60	1	1	1.0	0.00	42	1	1	1.0	0.00
17	Dens_hyp	32	1	2	1.42	0.48	34	1	2	1.21	0.41	45	1	2	1.27	0.45	60	1	2	1.3	0.46	42	1	2	1.12	0.33
18	L_gland	32	0.2	1.1	0.51	0.24	34	0.1	1.3	0.39	0.33	45	0.2	1.1	0.49	0.22	60	0.1	1.5	0.54	0.28	42	0.1	0.4	0.21	0.08
19	No_cells_gland	32	3	8	3.98	1.35	34	2	8	4.4	1.75	45	3	10	4.91	1.44	60	2	10	4.95	1.73	42	3	5	3.46	0.70
20	Colour_gland	33	1	2	1.64	0.49	35	0	2	1.19	0.82	45	0	2	1.07	0.86	60	0	2	1.55	0.57	42	0	2	0.5	0.67
21	Dens_stem	33	1	2	1.53	0.50	35	0	2	1.06	0.48	45	1	2	1.11	0.32	60	0	2	1.1	0.35	42	0	1	0.76	0.43
22	W_sepal	33	1.5	3.95	2.5	0.53	35	1.8	5.3	3.06	0.76	45	1.2	2.9	1.89	0.37	60	1.5	3	2.01	0.27	41	1	3.6	2.18	0.47
23	L_sepal	33	0.9	2.1	1.41	0.28	35	1.2	4.9	2.03	0.69	45	0.7	2.2	1.21	0.32	60	0.9	2	1.22	0.26	41	1	2	1.44	0.27
24	Sh_sep_apex	33	0	1	0.5	0.50	35	0	2	0.86	0.65	45	0	2	0.89	0.65	60	0	2	0.93	0.63	41	0	2	1.09	0.77
25	W_l_sepal	33	0.38	1	0.58	0.13	35	0.36	1.06	0.68	0.19	45	0.39	1.21	0.65	0.16	60	0.41	1	0.61	0.13	41	0.48	1.18	0.68	0.14
26	W_l_petal	23	0.25	0.49	0.38	0.07	27	0.34	1.03	0.54	0.15	38	0.18	0.55	0.34	0.08	57	0.25	0.75	0.39	0.09	31	0.24	0.79	0.44	0.13
27	L_petal	23	2.3	5.5	3.68	0.84	28	2.3	6.5	4.42	1.10	39	2	3.8	3.01	0.45	57	1.7	4.3	3.15	0.60	31	1.4	5.4	3.35	0.86
28	W_petal	23	1	2.3	1.38	0.39	27	1.2	3.9	2.36	0.81	38	0.5	1.9	1.03	0.3	57	0.8	2.4	1.19	0.31	31	0.6	2.7	1.46	0.51
29	Sh_petal	23	0	1	0.83	0.39	29	1	2	1.93	0.26	39	0	2	0.21	0.47	57	0	1	0.05	0.23	31	0	2	0.42	0.62
30	L_gynoec	16	2.3	6	3.89	0.76	12	2.1	4.5	3.62	0.74	17	2.1	4.1	2.88	0.53	18	2.7	5.2	3.4	0.66	22	2.3	5	3.68	0.76
31	Dist_ubract	29	1	1	1.0	0.00	32	1	1	1.0	0.00	38	1	1	1.0	0.00	53	0	1	0.98	0.14	37	1	1	1.0	0.00
32	Dist_ubr_pet	29	0	1	0.41	0.48	31	0	1	0.74	0.44	38	0	1	0.13	0.34	52	0	0	0.0	0.00	37	0	1	0.46	0.51
33	W_ubract	29	0.8	5.8	2.76	1.45	31	1	16	6.78	3.77	37	0.4	6.7	1.88	1.37	48	0.5	5.2	1.7	0.92	37	0.6	9.4	3.17	2.06
34	L_ubract	29	2.6	10.5	5.31	2.19	31	2.3	14.7	6.7	3.10	38	1.4	9.5	4.92	2.17	51	1.2	7.4	4.72	1.53	37	2.5	8.9	5.05	1.79
35	W_L_ubract	29	0.19	1.58	0.59	0.38	31	0.39	2.03	1.06	0.45	38	0.16	1.76	0.39	0.27	47	0.17	0.95	0.37	0.18	37	0.2	2	0.65	0.42
36	No_lobes_ubr	29	1	5	1.74	1.31	31	1	7	2.71	1.42	38	1	5	1.39	0.86	51	1	5	1.2	0.66	37	1	5	1.54	1.02
37	Dist_lbract	9	1	1	1.0	0.00	32	1	1	1.0	0.00	18	0	1	0.89	0.32	24	0	1	0.96	0.20	12	0	1	0.75	0.45

Table 7: (cont.)

		S. arctolitoralis					*S. bracteata*					*S. flexuosa*					*S. hyperborea*					*S. rivularis*				
No	*Character*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*	*N*	*Min*	*Max*	*Mean*	*SD*
38	Dist_lbr_pet	9	0	1	0.67	0.5	31	0	1	0.94	0.25	15	0	1	0.53	0.52	23	0	1	0.48	0.51	9	0	1	0.89	0.33
39	L_lbr_pet	6	6	19	10.67	4.79	27	0.8	29	5.06	5.74	8	2.3	14.2	5.63	4.77	11	1.8	505	49.69	151	8	1.6	17.2	8.86	4.51
40	L_lbract	8	3.5	13	5.68	3.08	30	4.8	15.9	9.24	3.11	15	3	12.5	6.5	2.25	23	3.9	8	5.48	1.27	8	3.1	10.2	6.14	2.56
41	W_lbract	7	1.2	7.5	4.17	2.5	28	3.8	33.6	13.21	6.91	15	1.4	9.2	5.57	2.51	23	0.5	8	3.71	2.07	7	1.5	8.3	5.69	2.25
42	No_lobes_lbr	8	1	3	2.25	1.04	30	1	9	5	1.98	15	1	5	2.73	1.16	23	1	3	2.09	1	8	1	5	2.75	1.28
43	Sh_lbr_apex	4	1	1	1	0	26	1	2	1.42	0.5	13	0	1	0.46	0.52	16	0	1	0.69	0.48	7	0	2	1.29	0.76
44	L_leaf	33	2.8	6.4	4.37	0.88	33	4.8	13.9	9.24	2.45	43	2.8	9	4.4	1.28	58	2.3	6.1	4.07	0.92	42	2.6	7.4	4.41	1.09
45	W_leaf	33	3.2	11.2	6.84	1.53	33	9.5	32	16.67	4.81	42	3.4	14.4	6.86	2.14	58	3.2	10.4	6.38	1.68	41	3	12.6	8.13	2.07
46	W_L_leaf	33	0.91	2.21	1.59	0.32	33	1.36	2.67	1.82	0.27	42	1.06	1.89	1.55	0.17	58	0.95	2.12	1.57	0.25	41	1.11	2.5	1.84	0.26
47	Dist_inc	33	1.1	3.6	2.2	0.57	33	2.1	7.5	5.04	1.68	42	1.1	5.5	2.27	1.03	58	0.8	3	1.96	0.57	42	0.9	4.2	1.91	0.69
48	Sh_inc	33	0	2	0.77	0.53	33	0	2	1.41	0.61	42	0	1	0.33	0.48	58	0	1	0.34	0.48	42	0	2	1.38	0.73
49	No_lobes_leaf	33	2	5	4.42	0.94	33	5	11	6.79	1.54	43	3	5	4.51	0.86	58	3	5	4.17	0.99	42	3	5	4.83	0.54
50	Sh_leaf_apex	32	0	2	1.05	0.41	33	1	2	1.67	0.48	43	0	1	0.47	0.5	58	0	2	0.62	0.52	42	0	2	0.79	0.61
51	Str_sheath	33	0	1	0.92	0.25	32	0	2	1.47	0.72	41	0	2	0.78	0.72	60	0	2	0.57	0.59	42	0	2	1.26	0.73
52	Sh_sheath	32	0	2	1.28	0.61	31	0	2	1.13	0.88	41	0	2	0.76	0.8	60	0	3	0.77	0.85	42	0	2	1.55	0.74
53	Fri_sheath	33	1	2	1.12	0.33	31	1	2	1.03	0.18	41	1	2	1.02	0.16	60	1	1	1	0	42	0	1	0.9	0.3

Saxifraga flexuosa and *S. hyperborea* could be separated from *S. rivularis* and *S. arctolitoralis* by their lack of runners, and by their typically darker colour of hair partition walls (Tab. 7, 8; Fig. 21). *Saxifraga flexuosa* and *S. hyperborea* showed significant differences in the amount of pigmentation and the colour of the hair partition walls, *S. hyperborea* being typically more purple than *S. flexuosa* (Tab. 7, 8; Fig. 21). *Saxifraga flexuosa* had also typically longer flowering stems and flowering pedicels than *S. hyperborea* (Tab. 7, 8; Fig. 21).

Saxifraga arctolitoralis was typically more small-grown than *S. rivularis*, and had more pigmentation, was more densely covered by hairs, and its hairs were typically longer and had more colour (Tab. 7, 8; Fig. 21).

Neither continuous nor discrete morphological characters gave distinct groups in the multivariate analyses. Even though the taxa had separated centres of distribution, overlap was always present. Multivariate analysis of the continuous morphological characters gave no clear groups, but indicated the separation of two clusters along PCO axis 1 (Fig. 22). Most of the *Saxifraga bracteata* specimens were found in the left part of the plot, whereas *S. arctolitoralis*, *S. flexuosa*, *S. hyperborea* and *S. rivularis* were found to the right.

Table 8: Mann-Whitney *U* test for equality of medians in measured and derived characters. Character code is according to Table 3. *) gives the characters included in the multivariate analyses. Taxa are abbreviated: arc - *Saxifraga arctolitoralis*, bra - *S. bracteata*, fle - *S. flexousa*, hyp - *S. hyperborea* and riv - *S. rivularis*. 1a and 1b refer to the Structure groups, of which only plants with unambiguous allocation have been included here. ss means difference significant at p < 0.01, s means difference significant at p < 0.05, and blank means no significant difference in medians.

		arc *bra*	*arc* *fle*	*arc* *hyp*	*arc* *riv*	*bra* *fle*	*bra* *hyp*	*bra* *riv*	*fle* *hyp*	*fle* *riv*	*hyp* *riv*	*la* *lb*
1	Runners*)		ss	ss		ss	ss			ss	ss	
3	L_fl_stem*)	ss	ss	ss	ss	ss	ss	ss	ss	ss		
4	L_fl_ped		ss			ss			s	s		
5	L_ped_l_fl*)	ss				ss	ss	ss				
6	No_flowers	ss				ss	ss	ss				
7	No_cauline	ss				ss	ss	ss				
8	No_caul_l_fl*)		ss	ss	ss	ss	ss	ss	s			
9	Pigments*)	ss	s		ss	ss	ss	ss	ss		ss	ss
10	Dens_stem*)	ss	ss	ss	ss			ss		ss	ss	
11	Sh_hyp_e	s			ss		s	s		ss	ss	
12	Sh_hyp_l				ss			ss		ss	ss	
13	L_hyp_e					s						
14	L_hyp_l*)		s	ss		ss	ss	s			ss	
15	Hyp_gland											
16	Dens_hyp*)	s			ss						s	
17	L_gland*)	ss			ss	ss	ss	s		ss	ss	
18	No_cells_gland		ss	ss				s		ss	ss	
19	Colour_gland*)	s	ss		ss		s	ss	ss	ss	ss	
20	L_sepal	ss	ss	ss		ss	ss	ss		ss	ss	
21	W_sepal	ss	ss	ss	ss	ss	ss	ss	s	ss		
22	L_sep_l_hyp*)										s	
23	W_sep_l_hyp*)											
24	W_l_sepal*)	s	s		ss						s	
25	Sh_sep_apex	s	ss	ss	ss							
26	L_petal	s	ss	s		ss	ss	ss				
27	W_petal*)	ss	ss	s		ss	ss	ss	s	ss	ss	s
28	W_l_petal*)	ss			s	ss	ss	s	s	ss	s	
29	Sh_petal*)	ss	ss	ss	ss	ss	ss	ss	s		ss	
30	L_gynoec		ss	s		ss			s	ss		
31	Dist_ubract											
32	Dist_ubr_pet	ss	ss	ss		ss	ss	s	ss	ss	ss	
33	L_ubract					s	ss	s				
34	W_ubract*)	ss	ss	ss		ss	ss	ss		ss	ss	
35	W_L_ubract*)	ss	s	ss		ss	ss	ss		ss	ss	
36	No_lobes_ubr*)	ss		s		ss	ss	ss			s	
37	Dist_lbract							ss				
38	Dist_lbr_pet	s				ss	ss				s	
39	L_lbr_pet*)	s		s				s				
40	L_lbract	ss				ss	ss	s				
41	W_lbract	ss				ss	ss	ss	s		s	
42	No_lobes_lbr	ss				ss	ss	ss				
43	Sh_lbr_apex					ss	ss			s	s	
44	L_leaf*)	ss				ss	ss	ss				
45	W_leaf	ss			ss	ss	ss	ss		ss	ss	
46	W_L_leaf*)	ss			ss	ss	ss			ss	ss	
47	Dist_inc*)	ss			s	ss	ss	ss				
48	Sh_inc	ss	ss	ss	ss	ss	ss			ss	ss	
49	No_lobes_leaf*)	ss			s	ss	ss	ss		s	ss	s
50	Sh_leaf_apex*)	ss	ss	ss	s	ss	ss	ss		s		
51	Str_sheath	ss		ss	ss	ss	ss			ss	ss	
52	Sh_sheath		ss	ss	s			s		ss	ss	s
53	Fri_sheath			ss	ss			s		s	s	

Saxifraga arctolitoralis and *S. rivularis* were mostly found at high values for PCO axis 2, whereas *S. flexuosa* and *S. hyperborea* were found at low values for PCO axis 2 (Fig. 22). The third and fourth PCO axes revealed no new information (not shown). PCO axis 1 correlated strongly with characters in which *S. bracteata* was typically larger than the other taxa, i.e., length of flowering stem (character 3), width of petal (character 27), length of leaf (character 44) and distance from basal leaf incision to basal leaf lamina base (character 47; Tab. 10). PCO axis 2 was strongly correlated to length of hypanthium glandular hairs (character 17; Tab. 10).

None of the continuous morphological characters separated any of the taxa completely from the rest. Although many size characters separated *Saxifraga bracteata* from the other taxa, there was always some degree of overlap (Fig. 21, 23, 24).

Even though multivariate analysis of the discrete morphological characters showed some trends, there was still a great extent of overlapping (Fig. 25). *Saxifraga flexuosa*/*hyperborea*, and *S. bracteata* were found at the left and right part of the plot, respectively, with *S. arctolitoralis* and *S. rivularis* in between along PCO axis 1. This axis was strongly correlated with runners (character 1), pigments (character 9) and shape of petal (character 29; Tab. 11). PCO axis 2 gave no additional information.

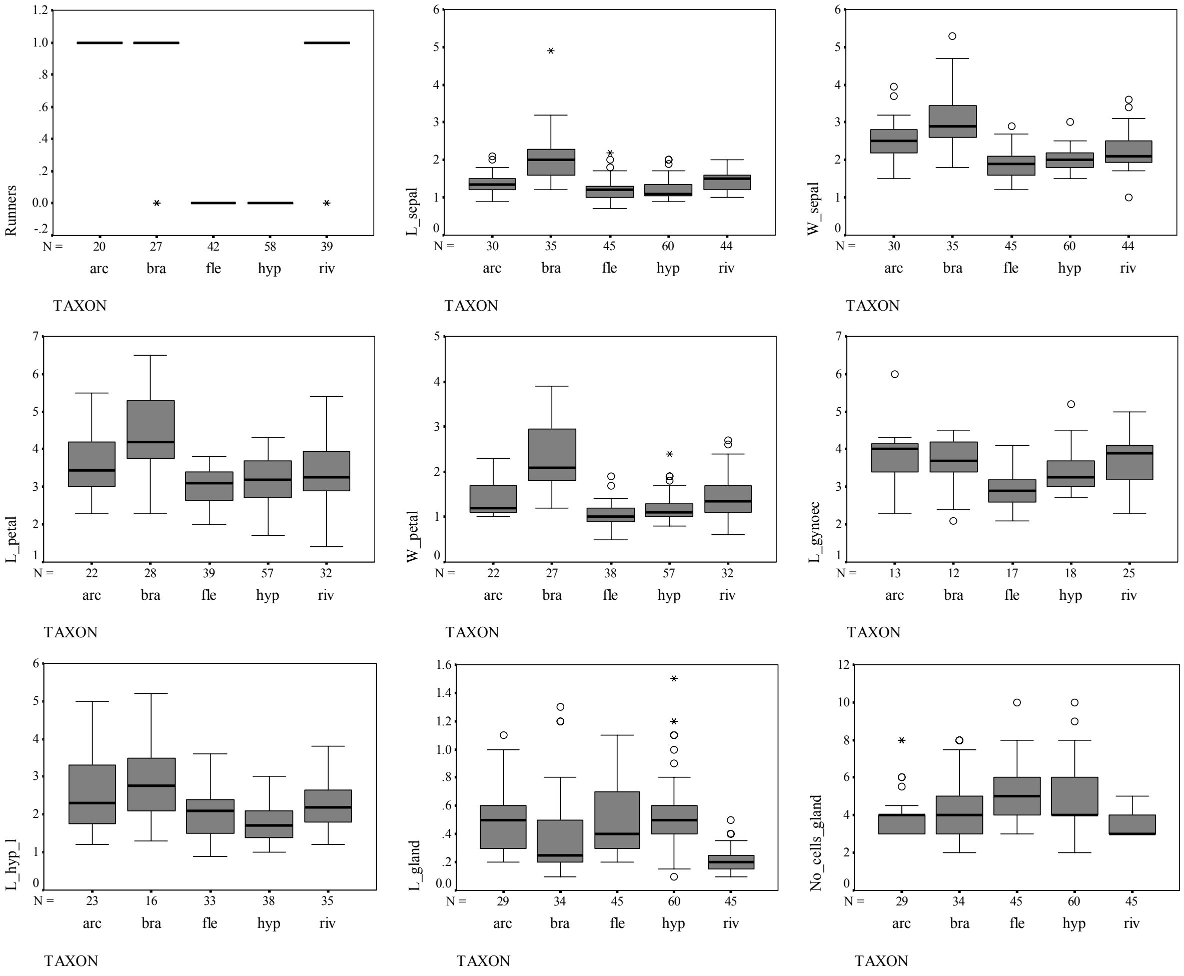
Multivariate analysis of the nine discrete morphological characters for *Saxifraga hyperborea* and *S. flexuosa* alone gave no separation, neither between the taxa nor between the Structure groups (Fig. 26, 27), whereas a similar analysis for *S. rivularis* and *S. arctolitoralis* gave a fairly good separation of the two (Fig. 28). PCO axis 1 of the latter was strongly correlated with hair density at the lower 1/3 of stem (character 10), colour of hair partition walls (character 19) and shape of petal (character 29; Tab. 11).

The only two qualitative morphological characters dividing the taxa into distinct groups were shape of petal (character 29) and runners (character 1). *Saxifraga bracteata* had broadly elliptic petals while the rest had more or less oblong. Runners were almost uniformly present in the investigated material of *S. arctolitoralis*, *S. bracteata* and *S. rivularis*, whereas they were absent in *S. hyperborea* and *S. flexuosa* (Fig. 18, 21; Tab. 7, 8). Also pigments (character 9) and colour of hair partition walls (character 19) showed rather clear tendencies: *S. hyperborea* and *S. arctolitoralis* had much pigmentation, *S. bracteata* and *S. rivularis* had little or no pigmentation, and *S. flexuosa* were somewhere in between (Fig. 18, 21; Tab. 7, 8).

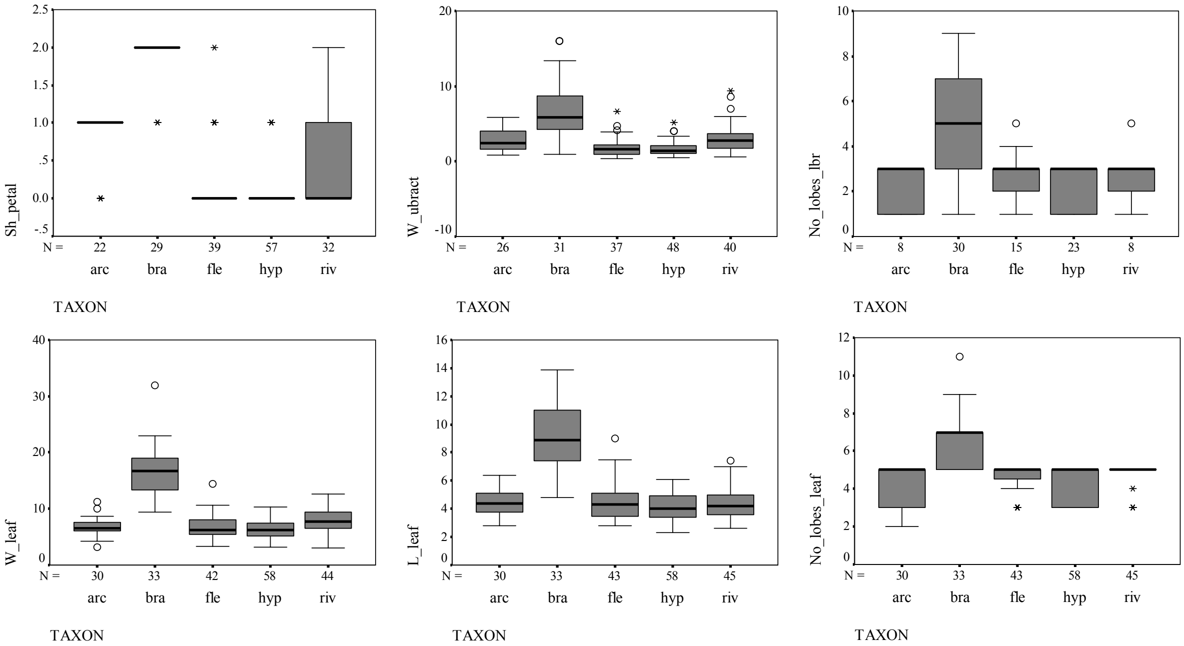
Table 9: The Mann-Whitney *U* test in Table 8 summarised by number of characters with difference in medians between the taxa, significant at P < 0.05.

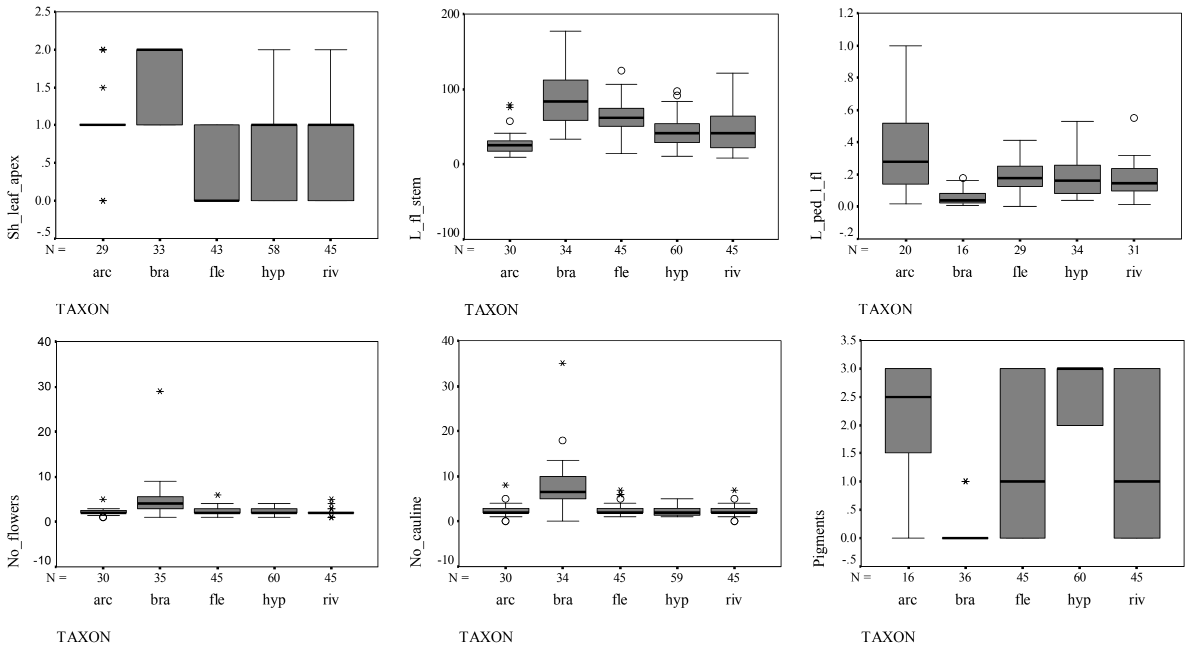
	S. arctolitoralis	*S. bracteata*	*S. flexuosa*	*S. hyperborea*	*S. rivularis*
S. arctolitoralis	-	35	23	23	23
S. bracteata		-	36	35	36
S. flexuosa			-	12	26
S. hyperborea				-	30
S. rivularis					-

a)


Runners
1.2
1.0
.8
.6
.4
.2
0.0
-.2
N = 20 27 42 58 39
arc bra fle hyp riv
TAXON
L_sepal
N = 30 35 45 60 44
arc bra fle hyp riv
TAXON
W_sepal
N = 30 35 45 60 44
arc bra fle hyp riv
TAXON
L_petal
N = 22 28 39 57 32
arc bra fle hyp riv
TAXON
W_petal
N = 22 27 38 57 32
arc bra fle hyp riv
TAXON
L_gynoec
N = 13 12 17 18 25
arc bra fle hyp riv
TAXON
L_hyp_l
N = 23 16 33 38 35
arc bra fle hyp riv
TAXON
L_gland
1.6
1.4
1.2
1.0
.8
.6
.4
.2
0.0
N = 29 34 45 60 45
arc bra fle hyp riv
TAXON
No_cells_gland
N = 29 34 45 60 45
arc bra fle hyp riv
TAXON

b)


Sh_petal
2.5
2.0
1.5
1.0
.5
0.0
-.5
N = 22 29 39 57 32
arc bra fle hyp riv
TAXON
W_ubract
20
10
0
-10
N = 26 31 37 48 40
arc bra fle hyp riv
TAXON
No_lobes_lbr
N = 8 30 15 23 8
arc bra fle hyp riv
TAXON
W_leaf
N = 30 33 42 58 44
arc bra fle hyp riv
TAXON
L_leaf
N = 30 33 43 58 45
arc bra fle hyp riv
TAXON
No_lobes_leaf
N = 30 33 43 58 45
arc bra fle hyp riv
TAXON



c)

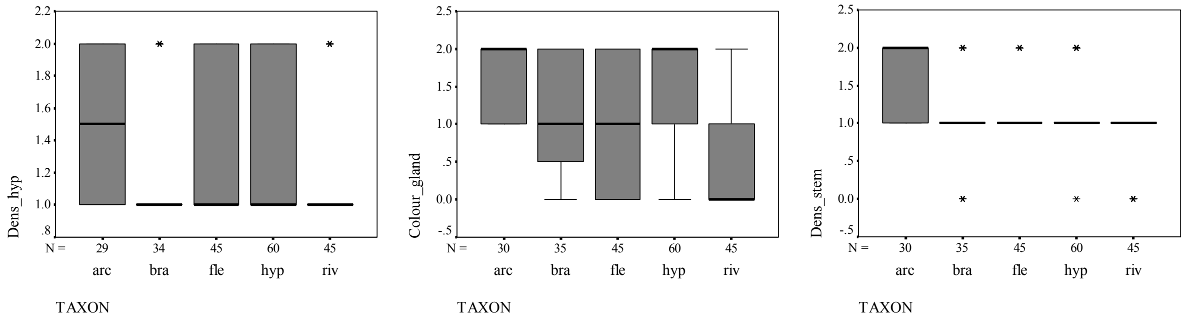


Figure 21: Box plots of 24 morphological characters. Taxa are given by abbreviations: arc = *Saxifraga arctolitoralis*, bra = *S. bracteata*, fle = *S. flexuosa*, hyp = *S. hyperborea* and riv = *S. rivularis*. The character codes are explained in Table 3. **a)** Characters differentiating between the *S. flexuosa*/*hyperborea* lineage and the other lineages. **b)** Characters differentiating between the *S. bracteata* lineage and the *S. arctolitoralis*/*rivularis* lineage. **c)** Characters differentiating between *S. arctolitoralis* and *S. rivularis*.

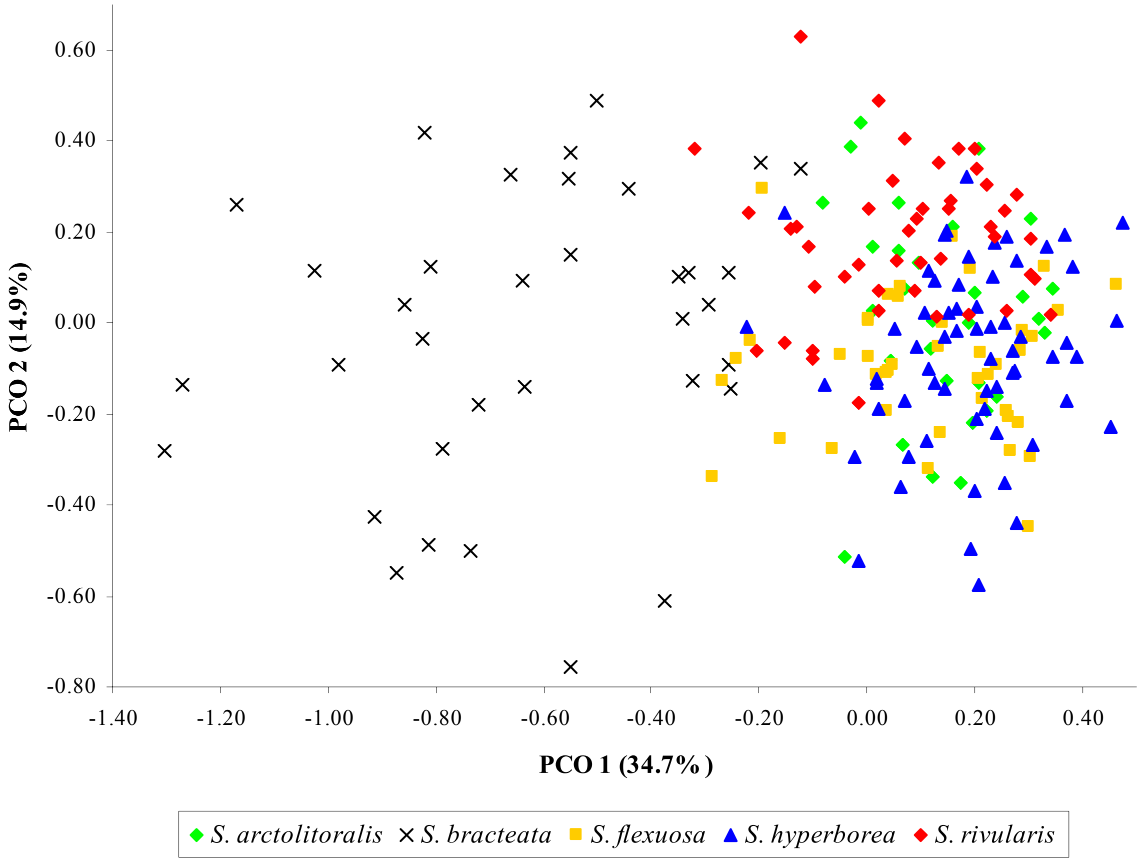


Figure 22: PCO analysis of the total material of the *Saxifraga rivularis* complex based on 16 continuous morphological characters (Tab. 3) standardised by ranging and using Euclidean distance.

Table 10: Kendall's τ correlation coefficients for the 16 continuous morphological characters and the PCO axes 1, 2 and 3 calculated from these for the total material. * gives correlations with $P < 0.05$, ** gives correlations with $P < 0.01$.

		PCO1	*PCO2*	*PCO3*
3	L_fl_stem	-0.41**	-0.28**	-0.34**
5	L_ped_l_fl	0.10	-0.07	0.25**
8	No_caul_l_fl	0.04	0.17**	0.48**
14	L_hyp_l	-0.14*	-0.21**	0.50**
17	L_gland	0.15**	-0.59**	0.03
22	L_sep_l_hyp	-0.07	0.10	-0.35**
23	W_sep_l_hyp	-0.16**	0.22**	-0.53**
24	W_l_sepal	-0.16**	0.20**	-0.24**
27	W_petal	-0.46**	0.18**	0.16**
28	W_l_petal	-0.35**	0.29**	0.09
34	W_ubract	-0.35**	0.14**	0.10*
35	W_l_ubract	-0.28**	0.30**	0.15**
39	L_lbr_pet	0.01	-0.19*	-0.06
44	L_leaf	-0.62**	-0.16**	0.01
46	W_l_leaf	-0.15**	0.24**	0.05
47	Dist_inc	-0.60**	-0.16**	0.02

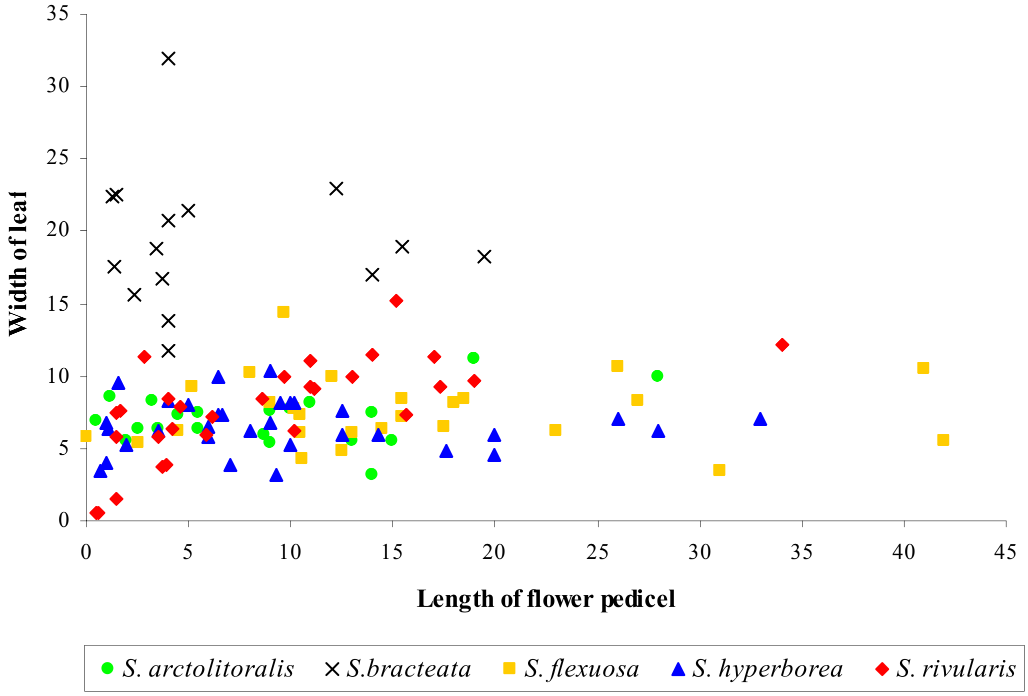


Figure 23: Scatter plot of the total material of the *Saxifraga rivularis* complex: the *x* values are lengths of flower pedicel (character 4), whereas the *y* values are widths of basal leaf (character 45).

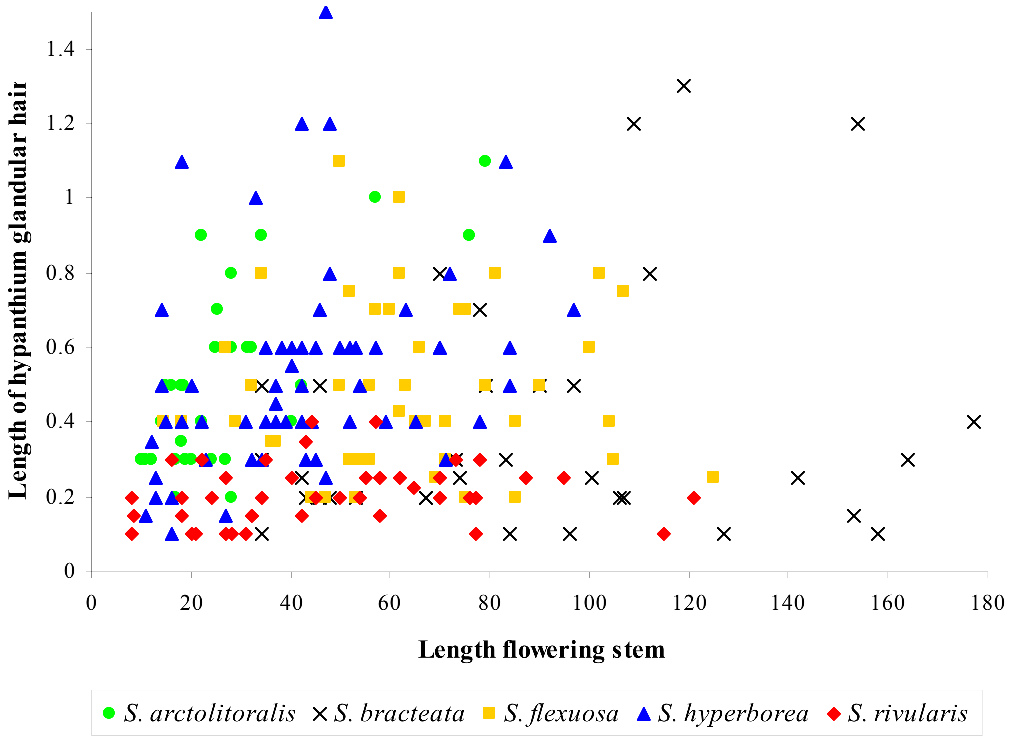


Figure 24: Scatter plot of the total material of the *Saxifraga rivularis* complex: the *x* values are lengths of flowering stem (character 3), whereas the *y* values are lengths of hypanthium glandular hairs (character 17).

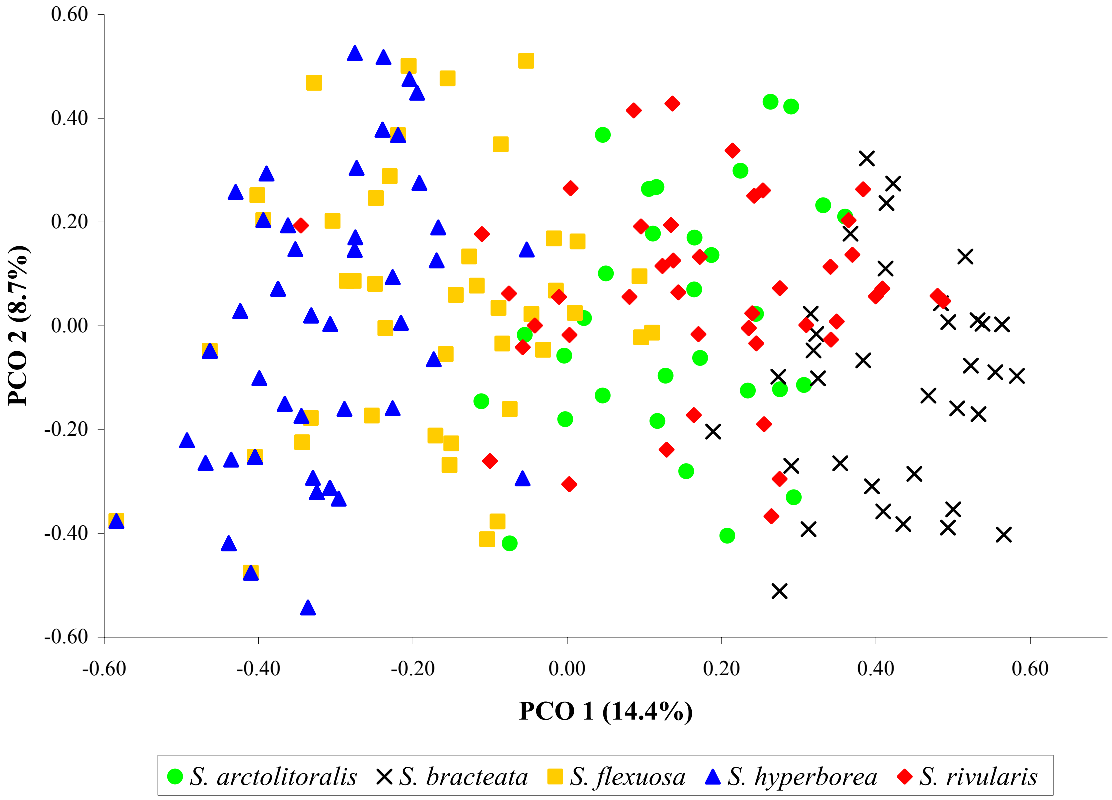


Figure 25: PCO analysis of the total material of the *Saxifraga rivularis* complex from nine discrete morphological characters (Tab. 3) standardised by ranging and using RT similarity measure.

Table 11: Kendall's τ correlation coefficients for nine discrete morphological characters and PCO axes calculated from these for the total material of the *Saxifraga rivularis* complex (disc), for the *S. arctolitoralis* and *S. rivularis* plants alone (arcriv) and for the *S. hyperborea* and *S. flexuosa* plants alone (flehyp). * gives correlations with P < 0.05, ** gives corralations with P < 0.01.

	1 Runners	*9 Pigments*	*10 Dens_stem*	*16 Dens_hyp*	*19 Colour_gland*	*29 Sh_petal*	*36 No_lobes_ubr*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*
PCO1_disc	0.68**	-0.60**	0.00	-0.03	-0.24**	0.64**	0.43**	0.43**	0.45**
PCO2_disc	-0.04	0.00	0.07	0.53**	-0.43**	-0.07	-0.05	0.12*	-0.22**
PCO3_disc	0.15*	0.14**	0.04	-0.10	0.01	-0.10	-0.18*	0.02	0.19**
PCO1_arcriv	0.04	0.25**	0.49**	0.39**	0.54**	0.45**	0.03	-0.25**	0.21*
PCO2_arcriv	-0.08	-0.19	-0.01	0.35**	-0.38*	0.14	0.33**	0.17	-0.12
PCO3_arcriv	0.16	0.13	0.06	0.34**	0.28**	0.21	0.27**	0.23*	-0.02
PCO1_flehyp		0.34**	-0.10	-0.56**	0.49**	-0.02	0.03	-0.45**	0.20*
PCO2_flehyp		-0.20*	-0.10	-0.21**	0.00	-0.03	0.09	0.35**	0.69**
PCO3_flehyp		0.17**	-0.18*	0.32**	0.46**	0.10	-0.31**	0.39**	0.05

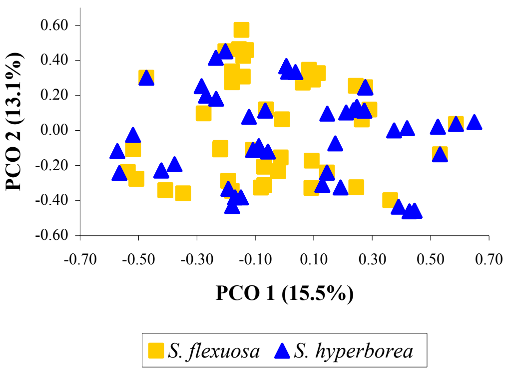


Figure 26: PCO analysis of *Saxifraga hyperborea* and *S. flexuosa* from nine discrete morphological characters (Tab. 3) standardised by ranging and using RT similarity measure.

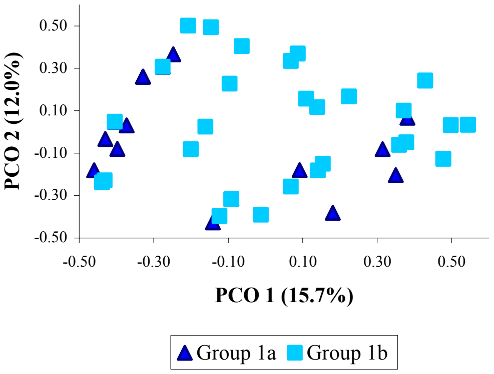


Figure 27: PCO analysis of 52 plants classified as group 1a and 1b according to the Structure analysis from nine discrete morphological characters (Tab. 3), standardised by ranging and using RT similarity measure.

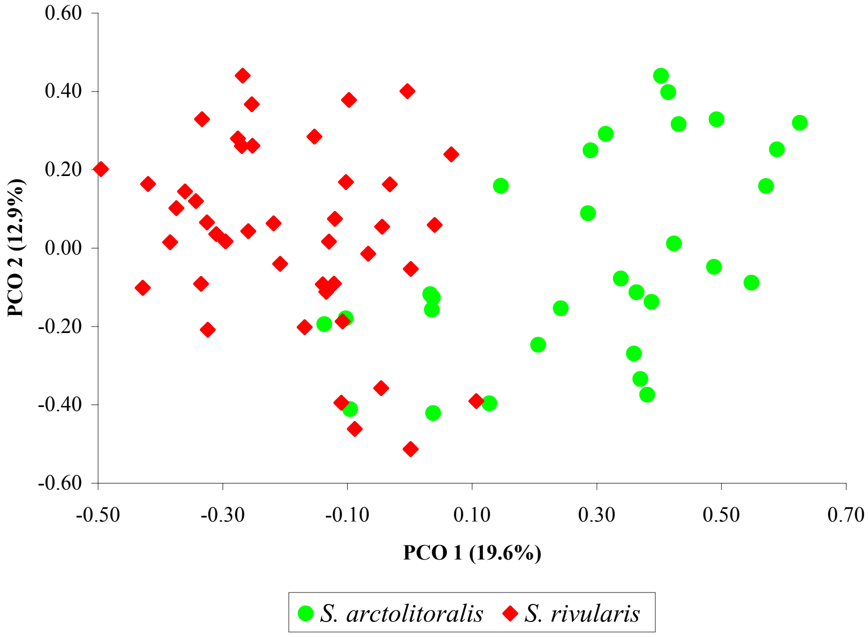


Figure 28: PCO analysis of *Saxifraga arctolitoralis* and *S.rivularis* from nine discrete morphological characters (Tab. 3) standardised by ranging and using RT similarity measure.

> *A species is a community, or a number of related communities, whose distinctive morphological characters are, in the opinion of a competent systematist, sufficiently definite to entitle it, or them, to a specific name.*
>
> C. T. Regan (1925)

Discussion

Three main evolutionary lineages

The three distinct groups obtained in all analyses of the AFLP data, that also contained different DNA amounts, probably represent three evolutionary lineages within the *Saxifraga rivularis* complex: the *S. bracteata* lineage, the *S. flexuosa*/*hyperborea* lineage and the *S. arctolitoralis*/*rivularis* lineage. The *Saxifraga arctolitoralis*/*rivularis* lineage is probably an allopolyploid lineage derived from the two others (Fig. 29). The intermediacy of the *S. arctolitoralis*/*rivularis* lineage between the *S. bracteata* and the *S. flexuosa*/*hyperborea* lineage both genetically and morphologically supports a hybrid origin of the *S. arctolitoralis*/*rivularis* lineage. It is tempting to suggest that the DNA ratios found in the *S. arctolitoralis*/*rivularis* lineage (0.36-0.38) which equal the sum of the ratios in the *S. bracteata* lineage (0.21-0.21) and the *S. flexuosa*/*hyperborea* lineage (0.16-0.17) is a clear indication of the same. However, the evolution of genome size in polyploids is complex, making such a direct interpretation problematic (Levin 2002). The hypothesis on the allopolyploid origin of the *S. arctolitoralis*/*rivularis* lineage is supported by previous analyses of allozyme data (Guldahl *et al.* in prep). Preliminary analyses of nuclear DNA sequences of *Mesogyne* species also suggest a close relationship between the *S. bracteata* lineage and the *S. arctolitoralis*/*rivularis* lineage (Gabrielsen *et al.* in prep). Chloroplast DNA sequences from section *Mesogyne* indicate that the *S. flexuosa*/*hyperborea* lineage is the maternal progenitor (Brochmann *et al.* 1998). Thus, the *S. bracteata* lineage probably represents the paternal parent. Hence the results agrees with the hypothesis of Rebristaya and Yurtsev (1984) in that *S. rivularis* has an ancestor in common with *S. hyperborea* and *S. bracteata*, and the hypothesis of Brochmann *et al*. (1998) in that the *S. flexuosa*/*hyperborea* lineage is one

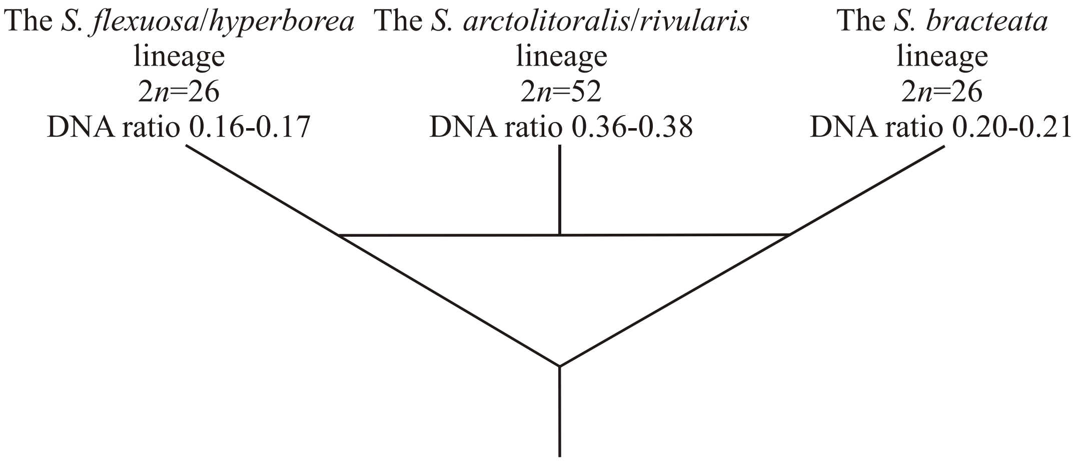


Figure 29: Evolutionary lineages in the *Saxifraga rivularis* complex proposed by the results of this study.

of the progenitors of *S. rivularis*. However, the hypothesis of Rebristaya and Yurtsev (1984) that *S. arctolitoralis* has originated as an autopolyploid from *S. hyperborea* can be rejected.

Fixed heterozygosity at one isozyme locus was found in both *Saxifraga rivularis* and *S. hyperborea* (Guldahl *et al.* in prep), indicating that the *S. flexuosa*/*hyperborea* lineage is tetraploid and that the *S. arctolitoralis*/*rivularis* lineage is octoploid. Although the ploidal level of the *S. bracteata* lineage has not yet been estimated directly, the same chromosome number as the *S. flexuosa*/*hyperborea* lineage indicates that also this lineage is polyploid. Putative parents of the two supposed tetraploids are not known. However, presence of fixed heterozygosity does not necessarily mean allopolyploid origin from two different species. Grundt *et al.* (in press) found that *Draba lactea* Adams probably originated from a single diploid lineage, *D. palanderiana* Kjellm., and suggested that its fixed heterozygosity was caused by origin from cross-incompatible populations of the same taxonomic species. Thus, the three lineages in the *S. rivularis* complex may have originated independently from one or more diploid progenitors.

It is not possible to exclude other potential ancestors of the *Saxifraga arctolitoralis*/*rivularis* lineage before the full phylogeny of section *Mesogyne* is resolved. However, assuming that the *S. rivularis* complex is monophyletic, which is supported by the preliminary results by Gabrielsen *et al*. (in prep), the only alternative hypothesis is that the parental lineages were immediate progenitors, now extinct, of the present-day species.

Divergence within the main lineages

The two groups within the *Saxifraga flexuosa*/*hyperborea* lineage observed in the Structure analysis (one mainly Atlantic and one mainly Pacific), did not correspond to the tentative taxonomic units suggested by Elven *et al*. (2003). The groups may reflect differentiation in glacial refugia through the glaciations, but are not yet reflected in morphological differentiation. Similar patterns with divergence among Atlantic and Beringian populations have been found for *S. oppositifolia* and several arctic small mammals, the divergence representing 5-10 full glacial cycles (Hewitt 2004). A Beringian refugium as proposed by many authors, reviewed by Abbott and Brochmann (2003), seems probable for the Pacific sublineage. However, the *S. flexuosa*/*hyperborea* lineage is also present further south in the Rocky Mountains (Weber 1967; Löve *et al.* 1971; Hultén and Fries 1986), and survival south of the Cordilleran ice sheet is also a possibility. The Atlantic sublineage could have survived in a refugium in Middle Europe or further east (South Ural or Sibiria). All these areas have previously been suggested as refugia for arctic-alpine plants such as *S. cernua* (Bronken 2001), *Dryas octopetala* L. (Skrede 2004), *Vaccinium uliginosum* L. (Alsos 2003) and *Beckwithia glacialis* (L.) Á.Löve & D.Löve (Schönswetter *et al.* 2003). However, the *S. flexuosa*/*hyperborea* lineage is absent from Middle Europe and the Ural Mountains today, making these areas less probable as refugia. As plants of the lineage easily survives the mild climate in the southern Rocky Mountains, previous presence in Middle Europe or the Urals should be reflected in presence of the lineage in these areas today. Thus, survival in western Atlantic areas included in the contemporary distribution area, is more probable. Several ice-free uplands and nunataks occured along the East and West coast of Greenland and on Baffin Island and Ellesmere Island in Canada (Brochmann *et al.* 2003), and local glacial survival in these areas has previously been suggested for the equally hardy *S. oppositifolia* (Abbott *et al.* 2000; Brochmann *et al.* 2003).

With the exception of three Beringian populations of the *S. flexuosa*/*hyperborea* lineage, no material from the Russian arctic coast was included in the analyses of the molecular data. Thus, it is not possible to conclude on where the Atlantic sublineage survived the last glaciations. It is also possible that more sublineages can be identified when material from this area is analysed.

No subdivision of the *Saxifraga arctolitoralis*/*rivularis* lineage was observed in the Structure analysis. However, the Beringian population referred to as *S. arctolitoralis* and one population from East Greenland were separated from the other populations in the separate PCO analysis of this lineage, and in the parsimony analysis of the total material. The separation may indicate isolation and possibly glacial survival in different areas during late Pleistocene. Beringia is a possible refugium for the amphi-Beringian part of this lineage, whereas the amphi-Atlantic part may have survived on the European tundra. The distinction of the population from East Greenland may be an indication of local glacial survival in Greenland or further west.

Geographical origin of the *Saxifraga arctolitoralis*/*rivularis* lineage

The *Saxifraga arctolitoralis*/*rivularis* lineage has an extremely disjunct distribution; *S. rivularis* is amphi-Atlantic and *S. arctolitoralis* is amphi-Beringian. Their ranges are separated by approximately 100 degrees in Russia (70ºE to 170ºE, between Northwest Sibiria and North Chukotka) and by approximately 70 degrees in North America (80ºW to 150ºW, between Baffin Land/Hudson Bay and North Alaska). The distribution of the *S. arctolitoralis*/*rivularis* lineage can be explained by a single origin followed by vicariance or long-distance dispersal, or by multiple origins and dispersal of one or more of them. In both cases a Beringian origin is probable because the Beringian *S. bracteata* lineage probably was one of the parental lineages.

Distribution patterns with such large gaps are rare, and only two other arctic-alpine examples are found: *Beckwithia glacialis* and *Luzula arcuata* (Wahlenb.) Sw. (Lipkin and Murray 1997; Elven *et al.* 2003). *Beckwithia glacialis* has probably colonized the northern amphi-Atlantic areas from source populations in the Eastern Alps (Schönswetter *et al.* 2003). However, nothing further have been published on the place of origin for this taxon, and American populations were not included in that study. In the *L. arcuata* group, most variation is found in North Pacific areas, with several proposed taxa, perhaps indicating an origin in this area (Elven *et al.* 2003). In the *Saxifraga rivularis* complex the variation pattern is similar. This fact, in combination with the above proposed connection with the strictly amphi-Pacific *S. bracteata* lineage, indicates a Beringian origin of the *S. arctolitoralis*/*rivularis* lineage.

The disjunct distribution pattern of the *Saxifraga arctolitoralis*/*rivularis* lineage could be explained by long-distance dispersal events. Both this study and other research based on AFLPs from populations of *S. rivularis* in the amphi-Atlantic areas show little geographical structure, thus gene flow between the areas seems likely (Westergaard 2004). Since *S. rivularis* is predominantly self-pollinating (Brochmann and Håpnes 2001), gene flow is most likely caused by seed dispersal. *Saxifraga cernua* shows a pattern with one cpDNA haplotype being disjunctly distributed in amphi-Atlantic and Beringian areas (Bronken 2001). Even though *S. cernua* has no adaptation for long-distance dispersal, Bronken suggested that dispersal could still have taken place, for instance in bird feathers or droppings. When studying the circumpolar phylogeography of *S. oppositifolia* L., Holderegger and Abbott (2003) found that both ITS sequences and cpDNA-RFLP haplotypes divided the plants into two main lineages: one American/Beringian and one European. The pattern was mainly explained by vicariance. However, the exception, a population from Nordkapp, Norway, with an American/Beringian cpDNA haplotype, was explained by long-distance dispersal from North Greenland or Taymyr Peninsula, Russia.

If the distribution pattern results from one or a few long-distance dispersal events, less variation could be expected among the amphi-Atlantic populations than the amphi-Beringian due to a bottleneck effect. However, with only one Beringian population included in the study, comparison of levels of variation were not possible.

As long-distance dispersal between Beringian and amphi-Atlantic areas has been suggested for close relatives of and similar dispersal modes as the *Saxifraga arctolitoralis*/*rivularis* lineage, this possibility cannot be ruled out. However, the wide range of the two disjunct distribution areas, the distinction of the Beringian population compared to the others, and the fact that *S. rivularis* was common in several places in Norway and Scotland already during the deglaciation phase and Allerød, respectively (Birks 1993; Huntley 1994), suggests that if the disjunction is caused by long-distance dispersal, such a dispersal event between the two main distribution areas must have taken place either before or during Weichselian.

An alternative and perhaps more probable explanation for the distribution patterns observed in the *Saxifraga rivularis* lineage, *Beckwithia glacialis* and *Luzula arcuata* is vicariance. The three groups all grow in habitats with comparatively oceanic conditions and good snow protection in winter (Lid and Lid 1994), whereas the gaps are found in areas with very dry, continental conditions (100-300 mm precipitation p.a.; Moen 1998). The climatic conditions along the coasts of Arctic Canada and Northern Russia are strongly influenced by the frozen Polar Sea. In warmer interglacial periods with an open Polar Sea, more oceanic conditions probably prevailed in these areas (e.g., 120 000 BP; Frenzel *et al.* 1992). Ice-core evidence from Vavilov, North Russia, Svalbard, Greenland, Canada and Antarctic suggests a widespread Arctic glacier retreat in Eem and early Holocene, including the complete melting of Canadian ice caps (Koerner and Fisher 2002). Investigation of stratified interglacial lacustrine sediments from Baffin Island, Arctic Canada, showed that the last interglacial had warmer, more oceanic conditions for at least 10 ka (Miller *et al.* 1999), making a connection between the now disjunct distribution areas possible in North America.

The morphological differences between *Saxifraga arctolitoralis* and *S. rivularis* could indicate multiple origins from the same progenitors, and thus reflect the amount of variation within the parental lineages. Also the limited material available of *S. arctolitoralis* makes it impossible to fully exclude that *S. rivularis* and *S. arctolitoralis* may be two separate lineages or at least be the result of two separate hybridization events. However, even though further investigation is needed, the genetic similarities shown here suggest that they represent two diverging population groups, descendants from the same allopolyploid.

Delimitation of taxonomic species

Due to the relatively recent formation of the arctic flora, much variation between the closely related taxa in the *Saxifraga rivularis* complex is not to be expected. No single morphological character included in this study unambiguously separated among the lineages in the complex. The three evolutionary lineages identified by all analyses of the AFLP data and by the flow cytometry results, could however be differentiated by a combination of characters. Thus, the lineages are most appropriately recognised at the species level: *S. bracteata*, *S. hyperborea* (including *S. flexuosa*) and *S. rivularis* (including *S. arctolitoralis*). The morphological differentiation between the *S. arctolitoralis*/*rivularis* lineage and the *S. flexuosa*/*hyperborea* lineage is supported by an investigation of the two lineages in Svalbard (Guldahl *et al.* in prep).

Saxifraga bracteata D.Don

The *Saxifraga bracteata* lineage was well separated from the other lineages in all analyses, morphologically as well as genetically and in DNA ratios. Morphologically *S. bracteata* can be separated from the other two lineages by its typically large size and its many large leaf-like bracts. Thus, there is no reason not to retain *S. bracteata* as a species. However, only two populations from geographically very close localities have been included in both AFLP and flow cytometry analysis, and these might not give a correct picture of the variation within the taxon.

Saxifraga hyperborea R.Br. and *S. flexuosa* Sternb.

The *Saxifraga flexuosa*/*hyperborea* lineage was fairly well supported, whereas little supported structure was identified within the group in the phylogenetic analyses. This lineage can be separated from the *S. arctolitoralis*/*rivularis* lineage by its lack of runners, its longer hairs and its smaller flowers. There is ,however, little morphological differences supporting the two taxa *S. flexuosa* and *S. hyperborea* as traditionally defined. Thus, the results in this study suggest that only one taxon is appropriate at the species level.

The morphological characters differing between the proposed taxa were mainly characters easily explained by habitat differences, as pigmentation and size. For the proposed *Saxifraga hyperborea* in the cold arctic tundra light-absorbing pigmentation is an advantage, while the exposure in the open area makes height a disadvantage. The proposed *S. flexuosa* growing in the shadow on cliffs or creek ravines in milder areas further south, have little need for pigmentation, but height might be useful in stretching for some light. Hence the results support the hypothesis of Rebristaya and Yurtsev (1984); that *S. flexuosa* is only a shadow-growing *S. hyperborea*. Or, at least, a correlation between habitat and morphology is supported.

The two groups identified by the Structure analysis do not correspond to the distribution areas of the two proposed taxa *Saxifraga hyperborea* and *S. flexuosa*, and only four of the 53 morphological characters examined showed significant differences among the two Structure groups. Thus, the genetic differentiation is not reflected in morphology, and the two Structure groups can not (yet) be recognised taxonomically.

No material from the southern Rocky Mountains was included in this study. Thus, it is not possible to reject the taxon *Saxifraga hyperborea* ssp. *debilis* used by Löve *et al.* (1971) as synonymuous with *S. flexuosa*. Löve *et al.* (1971) recognised a cline from the north to the south of the mountain range with *S. hyperborea* s.str. and *S. hyperborea* ssp. *debilis* at the respective extremes. They suggested to keep *S. hyperborea* ssp. *debilis* for practical reasons, rather than regarding it as only a nameless ecotype (Löve *et al.* 1971). Whether this observed cline is of taxonomic significance can not be determined until material from this area has been analysed.

Saxifraga rivularis **L. and** ***S. arctolitoralis*** **Jurtz. & V.V.Petrovsky**

The high genetic similarity observed between *Saxifraga arctolitoralis* and *S. rivularis* indicates that separation of the two at the species level is artificial. Even though *S. arctolitoralis* was rather well supported in the parsimony analysis, only one Beringian population was included, and the support was lower than for the *S. rivularis* population from East Greenland. Because the *S. rivularis* lineage is predominantly self-pollinating (Brochmann and Håpnes 2001) and a ballist with no adaptation to long-distance dispersal (Webb and Gornall 1989), some correlation between geographic and genetic distance is to be expected. However, with only one population of *S. arctolitoralis* included in the analyses, the variation observed within this taxa will not be representative.

Saxifraga rivularis and *S. arctolitoralis* both have chromosome number 2*n* = 52 (Guldahl *et al.* in prep; Zhukova and Tikhonova 1971; Engelskjøn 1979; Yurtsev 1981; Löve and Löve 1982; Zhukova and Petrovsky 1987), but the DNA ratio of *S. arctolitoralis* is not yet known due to lack of material. Hence, material of *S. arctolitoralis* should be collected and cultivated for further investigation. Final conclusions about the taxonomic rank of the two groups here called *S. arctolitoralis* and *S. rivularis*, are premature at the present stage. Nevertheless, the morphological differences found between the two indicate that the taxa at least deserve subspecific ranking.

Weber (1966; 1967) claimed populations co-occurring with *Saxifraga hyperborea* ssp. *debilis* in the southern Rocky Mountains to be *S. rivularis* s.str. His claim was based on, amongst other traits, large pollen grains and long stomata compared to *S. hyperborea* ssp. *debilis*, morphological characters typically distinguishing a polyploid from a diploid. Löve *et al*. (1971) recorded the chromosome number $2n = 52$ from populations in the same area, and recorded the plants as *S. rivularis* s.str. Even though the morphological differences between what Weber call *S. rivularis* s.str. and *S. hyperborea* ssp. *debilis* correspond to the results in this study, diagnostic characters such as the presence of runners have not yet been examined (Weber 1966). If the hypothesis of Weber (1966) and Löve *et al*. (1971) is supported when material from the southern Rocky Mountains is investigated, *S. rivularis* has an even stranger geographical distribution pattern with three disjunct and widely separated ranges. However, there is also a possibility that the plants identified as *S. rivularis* s.str. by Weber and Löve *et al*. represents an additional polyploid taxon of the *S. rivularis* complex in the southern Rocky Mountains. If so, the taxon is probably close to the *S. flexuosa*/*hyperborea* lineage, the only lineage represented south of the Cordilleran glaciation.

Key to the taxa - a proposal

The sizes and numbers correspond to the 25% and 75% percentiles for the measured characters (see Fig. 21).

1. Runners absent. Flowers small: sepals 1.8-2.1 mm long and 1.0-1.3 mm wide, petals oblong, 2.7-3.4 mm long and 0.9-1.3 mm wide. In fruit: gynoecium 2.8-3.5 mm long, hypanthium 1.5-2.2 mm long. Hypanthium hairs 0.3-0.7 mm with 4-6 cells. ....*Saxifraga flexuosa*/*hyperborea*

1. Runners present. Flowers large: sepals 2.0-3.5 mm long and 1.3-2.3 mm wide, petals oblong to broadly elliptic, 3.0-5.4 mm long and 1.1-3.0 mm wide. In fruit: gynoecium 3.2-4.2 mm long, hypanthium 1.8-3.5 mm long. Hypanthium hairs 0.2-0.6 mm with 3-5 cells..2

    2. Petals broadly elliptic, 1.8-3.0 mm wide. Bracts similar to basal leaves with 3-7 lobes. Basal leaves large, 14-20 mm wide and 7-11 mm long with 5 or more angled lobes. Flowering stem 70-120 mm with 4-8 near-sessile flowers and 5-10 cauline leaves in each inflorescence. Plant green............*Saxifraga bracteata*

2. Petals oblong, 1.1-1.8 mm wide. Bracts smaller and simpler than basal leaves, with 1-3 lobes. Basal leaves small, 6-9 mm wide and 3.8-5.0 mm long with 3-5 rounded lobes. Flowering stem 15-70 mm with 2-3 pedunculate flowers and 2-3 cauline leaves in each inflorescence. Plant green to purple............................3

3. Hypanthium densely covered by long glandular hairs (0.3-0.6 mm) with purple partition walls. The whole plant pigmented or at least the inflorescence. Flowering stem short, 15-30 mm, sparsely to densely covered by hairs..*Saxifraga arctolitoralis*

3. Hypanthium sparsely covered by short glandular hairs (0.2 mm) with uncoloured or weakly coloured partition walls. The whole plant green or some pigmentation in the inflorescence. Flowering stem long, 20-70 mm, glabrous or sparsely covered by hairs................*Saxifraga rivularis*

Concluding remarks

The *Saxifraga rivularis* complex is divided into three lineages supported by molecular data, cytology, and morphology: the *S. bracteata* lineage, the *S. flexuosa/hyperborea* lineage, and the *S. arctolitoralis/rivularis* lineage. The last two were further divided into Beringian and Atlantic sublineages, indicating glacial survival in at least two different refugia. Both molecular, morphological and cytological analysis suggest that the *S. arctolitoralis/rivularis* lineage is allopolyploid with the *S. flexuosa/hyperborea* lineage and the *S. bracteata* lineage as progenitors. However, this assumes that the *S. rivularis* complex is monophyletic, and includes all potential parental taxa still extant. Thus, the full phylogeny of section *Mesogyne* is needed before final conclusions can be drawn.

The three evolutionary lineages in the *Saxifraga rivularis* complex can be differentiated morphologically, and are most appropriately recognised at species level. Consequently, *S. flexuosa* and *S. arctolitoralis* should be included in *S. hyperborea* and *S. rivularis* respectively. It was not possible to distinguish between *S. flexuosa* and *S. hyperborea*, neither morphologically nor by DNA contents or AFLPs. Thus, the dataset did not even support keeping *S. flexuosa* as a taxon at a subspecific level. Nevertheless, material from Rocky Mountains should be included before concluding about *S. hyperborea* ssp. *debilis* (Engelm.) A. Löve, D. Löve & Kapoor. *Saxifraga arctolitoralis* is morphologically distinguishable from *S. rivularis*, but they are genetically close, and have the same ploidal level. The results shown here suggests that *S. arctolitoralis* should be included in *S. rivularis*, but further investigation of molecular variation and DNA content in *S. arctolitoralis* is needed before conclusions about the rank of the taxon are finally drawn. Also material from the southern Rocky Mountains should be investigated to decide whether *S. rivularis* s.lat. is present in this area, or whether the polyploid recorded here by Weber (1966) and Löve *et al.* (1971) is a different, but closely related taxon.

References

Abbott, R. J. and Brochmann, C. 2003. History and evolution of the arctic flora: in the footsteps of Eric Hultén. *Molecular Ecology* 12: 299-313.

Abbott, R. J., Smith, L. C., Milne, R. I., Crawford, R. M. M., Wolff, K. and Balfour, J. 2000. Molecular analysis of plant migration and refugia in the Arctic. *Science* 289: 1343-1346.

Alsos, I. G. 2003. *Conservation biology of the most thermophilous plant species in the Arctic. Genetic variation, recruitment and phylogeography in a changing climate*. Dr. scient. thesis. University of Tromsø. Tromsø.

Andersen, B. G. and Borns, H. W. 1997. *The ice age world*. Scandinavian University Press, Oslo.

Beardsley, P. M., Yen, A. and Olmstead, R. G. 2003. AFLP phylogeny of *Mimulus* section *Erythranthe* and the evolution of hummingbird pollination. *Evolution* 57: 1397-1410.

Benham, J. J. 2001. *Genographer*. 1.6.0. Montana State University, Montana.

Birks, H. H. 1993. The importance of plant macrofossils in late-glacial climatic reconstructions: an example from Western Norway. *Quaternary Science Reviews* 12: 719-726.

Brochmann, C. and Steen, S. W. 1999. Sex and genes in the flora of Svalbard - implications for conservation biology and climate change. The species concept in the high North - a Panarctic flora initiative, Oslo 38: 33-72.

Brochmann, C. and Håpnes, A. 2001. Reproductive strategies in some arctic *Saxifraga* (Saxifragaceae), with emphasis on the narrow endemic *S. svalbardensis* and its parental species. *Botanical Journal of the Linnean Society* 137: 31-49.

Brochmann, C., Xiang, Q.-Y., Brunsfeld, S. J., Soltis, D. E. and Soltis, P. S. 1998. Molecular evidence for polyploid origins in *Saxifraga* (Saxifragaceae): the narrow arctic endemic *S. svalbardensis* and its widespread allies. *American Journal of Botany* 85: 135-143.

Brochmann, C., Gabrielsen, T. M., Nordal, I., Landvik, J. Y. and Elven, R. 2003. Glacial survival or tabula rasa? The history of North Atlantic biota revisited. *Taxon* 52: 417-450.

Brochmann, C., Brysting, A. K., Alsos, I. G., Borgen, L., Grundt, H. H., Scheen, A.-C. and Elven, R. Polyploidy in arctic plants. *Botanical Journal of the Linnean Society*: in press.

Bronken, P. 2001. *Circumpolar chloroplast and nuclear DNA variation in* Saxifraga cernua. Cand. scient. thesis. University of Oslo. Oslo.

Brown, R. 1823. *Chloris Melvilliana. A list of plants collected in Melville Island in the year 1820 by the officers of the voyage of discovery under the orders of Captain Parry*. John Murray, London.

Buntjer, J. B., Otsen, M., Nijman, I. J., Kuiper, M. T. R. and Lenstra, J. A. 2002. Phylogeny of bovine species based on AFLP fingerprinting. *Heredity* 88: 46-51.

Conti, E., Soltis, D. E., Hardig, T. M. and Schneider, J. 1999. Phylogenetic relationships of the silver saxifrages (*Saxifraga*, sect. *Ligulatae* Haworth): implications for the evolution of substrate specificity, life histories, and biogeography. *Molecular Phylogenetics and Evolution* 13: 536-555.

Despres, L., Gielly, L., Redoutet, W. and Taberlet, P. 2003. Using AFLP to resolve phylogenetic relationships in a morphologically diversified plant species complex when nuclear and chloroplast sequences fail to reveal variability. *Molecular Phylogenetics and Evolution* 27: 185-196.

Don, D. 1822. A monograph of the genus *Saxifraga*. *The Transactions of the Linnean Society of London* 13: 341-452.

Elven, R., Murray, D. F., Razzhivin, V. Y. and Yurtsev, B. A. 2003. *Checklist of the Pan-Arctic Flora (PAF). Vascular plants. Draft version.* University of Oslo, Oslo.

Engelskjøn, T. 1979. Chromosome number in vascular plants from Norway, including Svalbard. *Opera Botanica* 52: 1-38.

Frenzel, B., Pécsi, M. and Velichko, A. A. 1992. *Atlas of paleoclimates and paleoenvironments of the northern hemisphere. Late Pleistocene - Holocene*. Geographical Research Institute, Hungarian Academy of Sciences; Gustav Fischer Verlag, Budapest.

Gabrielsen, T. M., Elven, R. and Brochmann, C. Phylogeny and evolution in *Saxifraga* section *Mesogyne*. in prep.

Gornall, R. J. 1987. An outline of a revised classification of *Saxifraga* L. *Botanical Journal of the Linnean Society* 95: 273-292.

Grant, V. 1963. *The origin of adaptation*. Colombia University Press, New York.

Grundt, H. H., Popp, M., Brochmann, C. and Oxelman, B. Polyploid origins in a circumpolar complex in *Draba* (Brassicaceae) inferred from cloned nuclear DNA sequences and fingerprints. *Molecular Phylogenetics and Evolution*: in press.

Guldahl, A. S., Gabrielsen, T. M., Scheen, A.-C., Borgen, L., Spjelkavik, S., Steen, S. W. and Brochmann, C. The *Saxifraga rivularis/hyperborea* species complex in Svalbard: a molecular-morphological approach. in prep.

Hedrén, M., Fay, M. F. and Chase, M. W. 2001. Amplified fragment length polymorphisms (AFLP) reveal details of polyploid evolution in *Dactylorhiza* (Orchidaceae). *American Journal of Botany* 88: 1868-1880.

Hewitt, G. M. 2004. Genetic consequences of climatic oscillations in the Quarternary. *Philosophical Transactions of the Royal Society of London* 359: 183-195.

Holderegger, R. and Abbott, R. J. 2003. Phylogeography of the Arctic-Alpine *Saxifraga oppositifolia* (Saxifragaceae) and some related taxa based on cpDNA and its sequence variation. *American Journal of Botany* 90: 931-936.

Hultén, E. 1968. *Flora of Alaska and neighboring territories. A manual of the vascular plants.* Stanford University Press, Stanford.

Hultén, E. and Fries, M. 1986. *Atlas of North European vascular plants north of the Tropic of Cancer I-III.* Koeltz Scientific Books, Königstein.

Huntley, B. 1994. Late Devensian and Holocene paleoecology and paleoenvironments of the Morrone Birkwoods, Aberdeenshire, Scotland. *Journal of Quaternary Science* 9: 311-336.

Jintang, P., Gornall, R. J. and Ohba, H. 2001. *Saxifraga* L. *in* Zhengyi Wu and Peter H. Raven. *Flora of China. Vol. 8 (Brassicaceae through Saxifragaceae).* Science Press & Missouri Botanical Garden Press, Beijing & St. Louis.

Kjølner, S., Såstad, S. M., Taberlet, P. and Brochmann, C. 2004. Amplified fragment length polymorphism versus random amplified polymorphic DNA markers: clonal diversity in *Saxifraga cernua*. *Molecular Ecology* 13: 81-86.

Koerner, R. M. and Fisher, D. A. 2002. Ice-core evidence for widespread Arctic glacier retreat in the Last Interglacial and the early Holocene. *Annals of Glaciology* 35: 19-24.

Koopman, W. J. M., Zevenbergen, M. J. and Van den Berg, R. G. 2001. Species relationships in *Lactuca* SL (Lactuceae, Asteraceae) inferred from AFLP fingerprints. *American Journal of Botany* 88: 1881-1887.

Levin, D. A. 2002. *The role of chromosomal change in plant evolution*. Oxford University Press, Inc., New York.

Lid, J. and Lid, D. T. 1994. *Norsk flora*. 6th ed. by R. Elven. Det Norske Samlaget, Oslo.

Lihová, J., Marhold, K., Tribsch, A. and Stuessy, T. F. 2004. Morphometric and AFLP re-evaluation of tetraploid *Cardamine amara* (Brassicaceae) in the Mediterranean. *Systematic Botany* 29: 134-146.

Linnaeus, C. 1753. *Species plantarum: exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas.* Impensis Laurentii Salvii, Holmiae.

Lipkin, R. and Murray, D. F. 1997. *Alaska rare plant field guide*. U. S. Department of the Interior, Office of Equal Opportunity, Washington, D. C.

Löve, Á. and Löve, D. 1982. IOPB Chromosome number reports LXXV. *Taxon* 31: 334-360.

Löve, Á., Löve, D. and Kapoor, B. M. 1971. Cytotaxonomy of a century of Rocky Mountain orophytes. *Arctic and Alpine Research* 3: 139-165.

Marhold, K., Lihová, J., Perný, M., Grupe, R. and Neuffer, B. 2002. Natural hybridization in *Cardamine* (Brassicaceae) in the Pyrenees: evidence from morphological and molecular data. *Botanical Journal of the Linnean Society* 139: 275-294.

Miller, G. H., Mode, W. N., Wolfe, A. P., Sauer, P. E., Bennike, O., Forman, S. L., Short, S. K. and Stafford, T. W. 1999. Stratified interglacial lacustrine sediments from Baffin Island, Arctic Canada: chronology and palaeoenvironmental implications. *Quaternary Science Reviews* 18: 789-810.

Moen, A. 1998. *Nasjonalatlas for Norge: Vegetasjon.* Statens kartverk, Hønefoss.

Mulligan, G. A. and Porsild, A. E. 1968. Chromosome numbers of some plants from the unglaciated central Yukon plateau, Canada. *Canadian Journal of Botany* 47: 655-662.

Nei, M. and Li, W. H. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences of the United States of America* 76: 5269-5273.

Otto, S. P. and Whitton, J. 2000. Polyploid incidence and evolution. *Annual Review of Genetics* 34: 401-437.

Polunin, N. 1959. *Circumpolar arctic flora*. Oxford University Press, London.

Pritchard, J. K., Stephens, M. and Donnelly, P. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155: 945-959.

Ramsey, J. and Schemske, D. W. 2002. Neopolyploidy in flowering plants. *Annual Review of Ecology, Evolution and Systematics* 33: 589-639.

Rebristaya, O. V. and Yurtsev, B. A. 1984. *Saxifraga* L. Pp. 25-88 *in* B. A. Yurtsev. *Arkticheskaya flora SSSR. IX. Droseraceae-Leguminosae. 1. Droseraceae-Rosaceae*. Izdatelstvo "Nauka", Leningrad.

Regan, C. T. 1925. *Organic evolution*. Report of the British Association for the Advancement of Science. London.

Rogers, D. J. and Tanimoto, T. T. 1960. Computer program for classifying plants. *Science* 132: 1115-1118.

Rohlf, F. 1999. *NTSYS-pc. Numerical taxonomy and multivariate analysis system.* 2.02. Exeter Software, New York.

Schneider, S., Kueffer, J., Roessli, D. and Excoffier, L. 1997. *Arlequin 2.000: a software for population genetic analysis*. Genetics and Biometry Laboratory, University of Geneva, Geneva.

Schönswetter, P., Paun, O., Tribsch, A. and Niklfeld, H. 2003. Out of the Alps: colonization of Northern Europe by East Alpine populations of the glacier buttercup *Ranunculus glacialis* L. (Ranunculaceae). *Molecular Ecology* 12: 3373-3381.

Skrede, I. 2004. *Immigration of the wind-dispersed* Dryas octopetala *L. (mountain avens; 'reinrose') to the isolated arctic archipelago of Svalbard*. Cand. scient. thesis. University of Oslo. Oslo.

Sokal, R. R. and Sneath, P. H. A. 1963. *Principles of numerical taxonomy*. W. H. Freeman and Company, San Fransisco.

Soltis, D. E., Soltis, P. S. and Tate, J. A. 2003. Advances in the study of polyploidy since *Plant speciation*. *New Phytologist* 161: 173-191.

Soltis, D. E., Kuzoff, R. K., Conti, E., Gornall, R. and Ferguson, K. 1996. matK and rbcL gene sequence data indicate that *Saxifraga* (Saxifragaceae) is polyphyletic. *American Journal of Botany* 83: 371-382.

Stebbins, G. L. 1984. Polyploidy and the distribution of the arctic-alpine flora: new evidence and a new approach. *Botanica Helvetica* 94: 1-13.

Steen, S. W., Gielly, L., Taberlet, P. and Brochmann, C. 2000. Same parental species, but different taxa: molecular evidence for hybrid origins of the rare endemics *Saxifraga opdalensis* and *S. svalbardensis* (Saxifragaceae). *Botanical Journal of the Linnean Society* 132: 153-164.

Sternberg, K. M. 1831. *Revisio Saxifragarum, Supplementum II*, Prague.

Swafford, D. L. 2001. *PAUP. Phylogenetic analysis using parsimony.* 4.0b10. Sinauer Associates, Sunderland.

Vos, P., Hogers, R., Bleeker, M., Reijans, M., Vandelee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J., Kuiper, M. and Zabeau, M. 1995. Aflp - a new technique for DNA-fingerprinting. *Nucleic Acids Research* 23: 4407-4414.

Webb, D. A. and Gornall, R. J. 1989. *A manual of saxifrages and their cultivation*. Timber Press, Portland.

Weber, W. A. 1966. *Additions to the flora of Colorado - IV*. University of Colorado Press, Boulder.

Weber, W. A. 1967. *Rocky Mountain flora*. University of Colorado Press, Boulder.

Westergaard, K. 2004. *Phylogeography of the high arctic* Saxifraga rivularis *L. inferred by amplified fragment length polymorphisms (AFLPs)*. Cand. scient. thesis. University of Tromsø. Tromsø.

Yurtsev, B. A. 1981. Seven new taxa of flowering plants from the northeastern Asia and adjacent territories. *Botanicheskiy Zhurnal* 66: 1041-1046. [In Russian].

Zhang, L. B., Comes, H. P. and Kadereit, J. W. 2001. Phylogeny and quaternary history of the European montane/alpine endemic *Soldanella* (Primulaceae) based on ITS and AFLP variation. *American Journal of Botany* 88: 2331-2345.

Zhmylev, P. Y. 1997. Systematical review of rockfoils (*Saxifraga* L.) of Russia and contiguous territories: subgenera *Porphyrion* and *Saxifraga*. *Bulletin Moskovskogo obscestva ispytateley prirody, Otdel biologiceskiy* 102: 42-48. [In Russian].

Zhukova, P. 1982. Chromosome numbers of some plant species of north-eastern Asia. *Botanicheskiy Zhurnal* 67: 360-365. [In Russian].

Zhukova, P. and Tikhonova, V. 1971. Chromosome numbers of certain plant species indigenous to the Chukotsky province. *Botanicheskiy Zhurnal* 56: 868-875. [In Russian].

Zhukova, P. and Petrovsky, V. V. 1980. Chromosome numbers and taxonomy of some species of the Anyui Mts. *Botanicheskiy Zhurnal* 65: 651-659. [In Russian]

Zhukova, P. and Petrovsky, V. V. 1987. Karyotaxonomic study of some species of the genus *Saxifraga* (Saxifragaceae) from northern Asia. *Botanicheskiy Zhurnal* 72: 632-640. [In Russian]

Zhukova, P., Petrovsky, V. V. and Plieva, T. V. 1973. The chromosome numbers and taxonomy of some plant species from Siberia and Far East. *Botanicheskiy Zhurnal* 58: 1331-1342. [In Russian]

Øvstedal, D. O. 1975. A new *Saxifraga* from Svalbard. *Astarte* 8: 23-27.

Øvstedal, D. O. 1998. Variation within some Nordic *Saxifraga* species (Saxifragaceae). *Nordic Journal of Botany* 18: 171-181.

Appendices

Appendix 1 AFLP data

Scoring of AFLPs. Taxa are given by abbreviations: arc = *Saxifraga arctolitoralis*, bra = *S. bracteata*, fle = *S. flexuosa*, hyp = *S. hyperborea* and riv = *S. rivularis*. Specimen ID gives population ID (cf. Table 1) and specimen number. Each marker (columns) is named by length and primer combination (a is E-AGA/M-CAA, b is E-AGA/M-CTG and c is E-ATC/M-CAA; cf. Tab. 2). Presence/absence is denoted by '1'/'0' and undetermined by '?'.

Taxon	***Specimen ID***	*76.9 a*	*80.6 a*	*87.7 a*	*101 a*	*107.3 a*	*116.3 a*	*121.5 a*	*137.5 a*	*139.5 a*	*150.5 a*	*154.5 a*	*170.1 a*	*172.5 a*	*195.3 a*	*196.5 a*	*211.6 a*	*213.5 a*	*215.5 a*	*220.2 a*
arc	RE01-11-1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	?	1	1	1
arc	RE01-11-2	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	?	1	1	1
arc	RE01-11-3	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
bra	SUP02-188-1	0	1	1	1	0	1	0	0	1	0	1	0	1	1	0	1	0	1	1
bra	SUP02-188-2	0	1	1	1	1	1	0	0	0	0	1	0	1	0	0	1	0	1	1
bra	SUP02-188-4	0	1	1	1	0	1	0	0	1	0	1	0	1	1	0	1	0	1	1
bra	SUP02-199-1	0	1	1	1	0	1	0	0	1	0	1	0	1	1	0	1	0	1	1
bra	SUP02-199-2	0	1	1	1	0	1	0	0	0	0	1	0	1	0	0	0	0	?	?
bra	SUP02-199-3	0	1	1	1	?	1	0	0	1	0	1	0	1	1	0	1	0	1	1
fle	04-01-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	04-01-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	0	1	1
fle	04-01-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	RE01-10-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	RE01-10-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	RE01-10-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	RE2263-4	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	0	1	1
fle	RE2263-5	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	?	1
fle	RE-C1-1	1	1	1	1	1	1	1	0	1	?	1	1	0	1	1	0	0	1	0
fle	RE-C1-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	RE-C1-3	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	0	?	1
fle	SR-1-1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	0	1	1
fle	SR-1-2	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	?	0	?	1
fle	SR-1-3	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	0	1	1
fle	SUP02-154-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1

Taxon	***Specimen ID***	*76.9 a*	*80.6 a*	*87.7 a*	*101 a*	*107.3 a*	*116.3 a*	*121.5 a*	*137.5 a*	*139.5 a*	*150.5 a*	*154.5 a*	*170.1 a*	*172.5 a*	*195.3 a*	*196.5 a*	*211.6 a*	*213.5 a*	*215.5 a*	*220.2 a*
fle	SUP02-154-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-154-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-163-2	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1
fle	SUP02-163-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	0	1
fle	SUP02-163-4	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1
fle	SUP02-180-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	?	1	1
fle	SUP02-180-2	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1
fle	SUP02-180-3	1	0	1	1	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1
fle	SUP02-181-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-181-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-181-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-254-3	1	1	1	1	0	1	1	?	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-254-4	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-254-5	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-265-1	0	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-265-2	0	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
fle	SUP02-265-3	0	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	05-01-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	05-01-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	05-01-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	05-03-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	05-03-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	?	1
hyp	05-03-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	?	?	1
hyp	AK-240-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	AK-240-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	AK-240-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	CB99-027-1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1
hyp	CB99-027-2	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	0	1	1	1
hyp	CB99-027-3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
hyp	CB99-038-1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1
hyp	CB99-038-2	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	?
hyp	CB99-038-3	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1
hyp	G-6842-1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1
hyp	G-6842-2	?	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1

Taxon	***Specimen ID***	*76.9 a*	*80.6 a*	*87.7 a*	*101 a*	*107.3 a*	*116.3 a*	*121.5 a*	*137.5 a*	*139.5 a*	*150.5 a*	*154.5 a*	*170.1 a*	*172.5 a*	*195.3 a*	*196.5 a*	*211.6 a*	*213.5 a*	*215.5 a*	*220.2 a*
hyp	G-6842-3	1	1	1	1	1	1	1	1	1	0	1	1	?	1	1	0	0	0	0
hyp	RE2775-1	1	1	1	1	1	1	1	0	1	0	?	1	1	0	1	0	0	1	1
hyp	RE2775-2	1	1	1	1	1	1	1	0	1	0	0	1	1	0	1	0	1	0	0
hyp	RE2775-3	1	1	1	1	1	1	1	0	1	0	1	1	1	0	1	0	0	1	0
hyp	RE2981-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	RE2981-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3033-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3033-4	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	?	1
hyp	RE3033-5	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3425-1	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3425-2	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3425-3	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3520-1	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3520-2	1	0	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	RE3520-4	1	1	1	1	1	1	1	?	0	0	1	1	1	1	1	0	0	1	1
hyp	RE3525-1	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	?	1	1
hyp	TMG-24-62	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	?	1	1	1
hyp	TMG-24-64	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-24C-7	1	0	1	1	1	1	1	?	1	0	1	1	1	1	1	?	0	1	1
hyp	TMG-26-13B	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-27-5	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-27-6	1	0	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-27-9	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-34-10	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	0	0	1	1
hyp	TMG-34-9	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	?	0	1	1
riv	AK-109-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-109-8	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-109-9	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-281-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-281-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-281-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1

Taxon	*Specimen ID*	*76.9a*	*80.6a*	*87.7a*	*101a*	*107.3a*	*116.3a*	*121.5a*	*137.5a*	*139.5a*	*150.5a*	*154.5a*	*170.1a*	*172.5a*	*195.3a*	*196.5a*	*211.6a*	*213.5a*	*215.5a*	*220.2a*
riv	AK-470-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-470-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-470-4	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-516-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-516-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-516-3	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-554-4	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-554-8	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-554-9	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-559-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-559-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-559-5	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-745-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-745-3	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	?	1	1	1
riv	AK-745-4	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	1	1	1	1
riv	AK-784-1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-784-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	AK-784-7	1	1	1	1	1	1	1	0	1	0	1	1	1	?	1	?	1	1	1
riv	AK-867-4	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-867-5	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-867-6	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	AK-867-9	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	CB99-039-2	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	?	1	1	1
riv	CB99-039-3	1	1	1	1	1	1	1	0	1	0	1	?	1	1	1	?	1	1	0
riv	CB99-039-4	1	1	1	1	1	1	1	0	1	0	1	?	1	1	1	?	1	1	0
riv	TMG-21-93	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
riv	TMG-21A-15	1	1	1	1	1	1	1	?	1	0	1	1	1	1	1	1	1	1	1
riv	TMG-43-12	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	0	1	1
riv	TMG-43-15	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	0	1	1
riv	TMG-43-16	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	0	1	1

Appendix 1

Taxon	***Specimen ID***	*241.7 a*	*289.1 a*	*353.7 a*	*439.9 a*	*50.5 b*	*53.6 b*	*60.3 b*	*157.1 b*	*158.8 b*	*160.4 b*	*167.1 b*	*168.4 b*	*173.9 b*	*190.8 b*	*223.5 b*	*250 b*	*253.8 b*	*63.8 c*
arc	RE01-11-3	1	1	0	?	1	1	1	1	1	0	1	1	1	1	1	1	1	1
arc	RE01-11-2	1	?	0	1	1	1	1	1	1	0	?	1	?	1	1	1	1	1
arc	RE01-11-1	?	1	0	?	1	1	1	1	1	0	1	1	1	1	1	1	?	?
bra	SUP02-199-3	1	1	1	0	1	1	0	0	1	0	0	0	1	1	1	1	1	1
bra	SUP02-199-2	1	1	1	0	1	1	0	0	1	0	0	0	1	1	0	?	?	1
bra	SUP02-199-1	1	1	1	0	0	1	0	0	1	0	0	0	1	1	1	1	1	1
bra	SUP02-188-4	1	1	1	0	0	1	0	0	1	0	0	0	1	1	1	1	?	1
bra	SUP02-188-2	1	1	1	0	1	1	0	0	1	0	0	0	1	1	0	1	?	1
bra	SUP02-188-1	1	1	1	0	0	1	0	0	1	0	0	0	1	1	1	1	1	1
fle	SUP02-265-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-265-2	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-265-1	0	1	0	1	1	1	1	1	1	1	1	1	0	0	0	1	0	1
fle	SUP02-254-5	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-254-4	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-254-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-181-3	?	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-180-3	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-181-2	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-180-2	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	?	1
fle	SUP02-181-1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-180-1	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-163-4	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-163-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-163-2	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-154-3	0	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-154-2	0	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	SUP02-154-1	0	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE01-10-3	0	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE01-10-2	?	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE01-10-1	0	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1

Taxon	*Specimen ID*	*241.7 a*	*289.1 a*	*353.7 a*	*439.9 a*	*50.5 b*	*53.6 b*	*60.3 b*	*157.1 b*	*158.8 b*	*160.4 b*	*167.1 b*	*168.4 b*	*173.9 b*	*190.8 b*	*223.5 b*	*250 b*	*253.8 b*	*63.8 c*
fle	RE2263-5	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE2263-4	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	?	?
fle	SR-1-3	0	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE-C1-3	1	1	0	?	1	1	1	1	1	1	1	1	1	0	1	1	0	1
fle	SR-1-2	0	?	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	?
fle	RE-C1-2	?	1	0	?	1	1	1	1	1	1	1	1	0	0	?	1	0	1
fle	SR-1-1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	RE-C1-1	1	1	0	0	1	1	1	1	1	1	1	1	0	0	1	0	0	1
fle	04-01-3	0	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	04-01-2	0	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1
fle	04-01-1	0	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	G-6842-3	0	1	0	0	?	?	?	1	1	0	1	1	0	0	1	1	0	1
hyp	G-6842-2	0	1	0	0	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	G-6842-1	0	1	0	0	1	1	1	1	1	0	1	1	0	0	?	1	0	1
hyp	AK-240-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	AK-240-2	0	1	0	?	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	AK-240-1	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	TMG-24-64	?	1	0	?	1	1	1	1	1	1	1	1	1	0	1	1	1	1
hyp	TMG-24-62	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1
hyp	TMG-34-10	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	TMG-34-9	1	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	CB99-038-3	0	1	0	0	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	CB99-038-2	0	1	0	0	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	CB99-038-1	0	1	0	?	1	1	1	1	1	0	1	1	0	0	1	1	0	?
hyp	TMG-26-13B	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	TMG-27-9	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	TMG-27-6	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	TMG-27-5	0	1	0	0	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	TMG-24C-7	1	1	0	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1
hyp	CB99-027-3	1	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	CB99-027-2	1	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1

Taxon	***Specimen ID***	*241.7 a*	*289.1 a*	*353.7 a*	*439.9 a*	*50.5 b*	*53.6 b*	*60.3 b*	*157.1 b*	*158.8 b*	*160.4 b*	*167.1 b*	*168.4 b*	*173.9 b*	*190.8 b*	*223.5 b*	*250 b*	*253.8 b*	*63.8 c*
hyp	CB99-027-1	?	1	0	1	1	1	1	1	1	0	1	1	0	0	0	1	0	1
hyp	RE3033-5	0	1	0	?	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	RE3033-4	0	1	0	?	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	RE3520-4	0	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	RE2775-3	?	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE2981-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE3033-3	0	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	RE3425-3	?	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE2775-2	0	1	0	0	1	1	?	1	1	1	1	1	0	0	1	1	0	1
hyp	RE3425-2	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE3520-2	?	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	05-03-3	0	1	0	?	1	1	1	1	1	1	1	1	0	0	0	0	0	1
hyp	RE2775-1	1	1	0	0	1	1	1	1	1	1	1	1	0	0	1	1	0	?
hyp	RE2981-1	0	1	0	1	1	1	1	1	1	0	1	1	0	0	1	1	0	1
hyp	RE3425-1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE3520-1	?	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	RE3525-1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
hyp	05-03-2	0	1	0	?	1	1	1	1	1	1	1	1	0	0	0	1	0	1
hyp	05-01-3	0	1	0	1	1	1	1	1	1	1	1	1	0	0	0	1	0	1
hyp	05-03-1	0	1	0	?	1	1	1	1	1	1	1	1	0	0	0	1	0	1
hyp	05-01-2	0	1	0	1	1	1	1	1	1	1	1	1	0	0	0	1	0	1
hyp	05-01-1	0	1	0	1	1	1	1	1	1	1	1	1	0	0	0	1	0	1
riv	AK-867-9	1	1	0	1	?	?	?	1	1	1	1	1	1	1	1	1	1	1
riv	AK-867-6	1	1	0	?	1	1	1	1	1	1	0	1	1	1	1	1	1	1
riv	AK-867-5	1	1	0	?	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	AK-867-4	?	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	?	1
riv	AK-784-7	1	1	0	?	1	1	1	1	1	1	1	1	?	?	1	1	?	1
riv	AK-784-2	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-784-1	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-745-4	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-745-3	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Taxon	***Specimen ID***	*241.7 a*	*289.1 a*	*353.7 a*	*439.9 a*	*50.5 b*	*53.6 b*	*60.3 b*	*157.1 b*	*158.8 b*	*160.4 b*	*167.1 b*	*168.4 b*	*173.9 b*	*190.8 b*	*223.5 b*	*250 b*	*253.8 b*	*63.8 c*
riv	AK-745-2	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-559-5	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-554-9	1	1	0	?	1	1	1	1	1	0	1	1	?	1	1	1	1	1
riv	AK-554-8	1	1	0	?	1	1	1	1	1	0	1	1	1	1	1	1	1	1
riv	AK-559-2	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-559-1	1	1	0	1	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-554-4	1	1	0	?	1	1	1	1	1	0	1	1	?	1	1	1	1	1
riv	AK-516-3	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-516-2	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-516-1	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-470-4	1	?	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-470-3	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	AK-470-1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	?	1
riv	AK-281-3	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	AK-281-2	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	AK-281-1	1	1	0	?	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	AK-109-9	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	AK-109-8	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	TMG-21-93	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	AK-109-3	1	1	0	?	1	1	1	1	1	1	1	1	?	1	1	1	1	1
riv	TMG-43-16	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	TMG-43-15	1	1	0	?	1	1	1	1	1	1	1	1	1	0	1	1	1	1
riv	TMG-43-12	1	1	0	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1
riv	CB99-039-4	1	1	0	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	CB99-039-3	1	1	0	0	1	1	1	1	1	1	1	1	0	1	?	1	1	1
riv	CB99-039-2	1	1	0	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1
riv	TMG-21A-15	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Taxon	*Specimen ID*	*76.5 c*	*79.6 c*	*82.2 c*	*85.5 c*	*93.7 c*	*117.1 c*	*120.3 c*	*133.6 c*	*142.2 c*	*157.6 c*	*159.6 c*	*167 c*	*178 c*	*196.6 c*	*237.2 c*	*271.8 c*
arc	RE01-11-3	1	1	1	0	0	1	0	0	1	1	1	?	0	1	0	?
arc	RE01-11-2	1	1	1	0	0	1	0	0	1	1	?	?	0	1	0	0
arc	RE01-11-1	1	1	?	0	0	1	0	0	?	1	?	?	0	?	0	?
bra	SUP02-199-3	1	1	1	0	0	1	0	1	1	1	1	1	0	1	0	0
bra	SUP02-199-2	1	0	1	0	0	1	0	0	1	0	1	1	0	1	0	0
bra	SUP02-199-1	1	1	1	0	0	1	0	1	1	1	1	1	0	1	0	0
bra	SUP02-188-4	1	1	1	0	0	1	0	?	1	1	1	?	0	1	0	0
bra	SUP02-188-2	1	1	1	0	0	1	0	0	1	0	1	?	0	1	0	0
bra	SUP02-188-1	1	1	1	0	0	1	1	1	1	1	1	1	0	1	0	0
fle	SUP02-265-3	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-265-2	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
fle	SUP02-265-1	1	?	1	0	0	1	0	0	1	1	1	0	0	0	0	0
fle	SUP02-254-5	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-254-4	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-254-3	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-181-3	1	1	1	0	1	1	0	?	1	1	1	0	0	0	0	0
fle	SUP02-180-3	1	1	1	0	1	1	0	0	1	1	?	0	0	0	0	?
fle	SUP02-181-2	1	1	1	0	1	1	0	?	1	1	0	0	0	0	0	0
fle	SUP02-180-2	1	1	?	1	1	1	0	0	1	1	?	0	0	0	0	0
fle	SUP02-181-1	1	1	1	1	1	1	0	1	1	1	0	0	0	0	0	0
fle	SUP02-180-1	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-163-4	1	1	1	1	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-163-3	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-163-2	1	0	1	1	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-154-3	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-154-2	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
fle	SUP02-154-1	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
fle	RE01-10-3	1	1	?	1	0	1	0	0	1	?	0	0	0	0	0	1
fle	RE01-10-2	1	1	1	1	0	1	0	0	1	?	0	0	0	0	0	?
fle	RE01-10-1	1	1	1	?	0	1	0	0	1	1	0	0	0	0	0	?

Taxon	*Specimen ID*	*76.5 c*	*79.6 c*	*82.2 c*	*85.5 c*	*93.7 c*	*117.1 c*	*120.3 c*	*133.6 c*	*142.2 c*	*157.6 c*	*159.6 c*	*167 c*	*178 c*	*196.6 c*	*237.2 c*	*271.8 c*
fle	RE2263-5	1	?	1	?	0	?	0	0	1	?	0	0	0	0	0	0
fle	RE2263-4	1	?	1	1	0	1	0	0	?	?	0	0	0	0	0	0
fle	SR-1-3	1	1	0	1	0	1	0	0	1	?	0	0	0	0	0	0
fle	RE-C1-3	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
fle	SR-1-2	1	1	0	?	0	?	0	0	?	?	0	0	0	0	0	0
fle	RE-C1-2	1	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0
fle	SR-1-1	1	1	1	?	0	1	0	0	1	1	0	0	0	0	0	0
fle	RE-C1-1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0
fle	04-01-3	1	1	?	1	0	1	0	0	1	1	0	0	0	0	0	?
fle	04-01-2	1	?	?	1	0	1	0	0	1	?	0	0	0	0	0	?
fle	04-01-1	1	1	?	1	0	1	0	0	1	1	0	0	0	0	0	?
hyp	G-6842-3	1	1	?	0	0	1	0	0	?	0	0	0	0	0	1	0
hyp	G-6842-2	1	1	1	0	0	1	0	0	?	0	0	0	0	0	?	0
hyp	G-6842-1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	1	0
hyp	AK-240-3	1	1	1	1	0	1	0	0	1	?	0	0	0	0	0	0
hyp	AK-240-2	1	1	1	1	0	1	0	0	1	1	0	0	0	0	0	0
hyp	AK-240-1	1	1	1	?	0	1	0	0	1	1	0	0	0	0	0	0
hyp	TMG-24-64	1	1	1	0	1	1	1	1	1	1	0	0	0	0	1	1
hyp	TMG-24-62	1	1	1	0	1	1	1	0	1	0	0	0	0	0	1	1
hyp	TMG-34-10	1	1	1	0	0	1	1	0	1	0	1	0	0	0	1	1
hyp	TMG-34-9	1	?	1	1	1	1	1	0	1	0	0	0	0	0	0	1
hyp	CB99-038-3	1	?	1	0	0	1	0	0	?	0	0	0	0	0	1	0
hyp	CB99-038-2	1	1	1	0	0	1	0	0	?	0	0	0	0	0	1	0
hyp	CB99-038-1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	1	0
hyp	TMG-26-13B	1	1	?	1	0	1	0	0	1	1	0	0	0	0	0	0
hyp	TMG-27-9	1	1	1	0	0	1	0	0	1	1	0	0	0	0	1	1
hyp	TMG-27-6	1	1	1	?	0	1	1	0	1	1	0	0	0	0	1	1
hyp	TMG-27-5	1	?	1	1	0	1	0	0	1	1	0	0	0	0	1	1
hyp	TMG-24C-7	1	1	1	0	1	1	1	0	1	0	0	0	0	0	?	1
hyp	CB99-027-3	1	1	1	1	0	1	0	0	1	0	0	0	0	0	1	1

Taxon	*Specimen ID*	*76.5 c*	*79.6 c*	*82.2 c*	*85.5 c*	*93.7 c*	*117.1 c*	*120.3 c*	*133.6 c*	*142.2 c*	*157.6 c*	*159.6 c*	*167 c*	*178 c*	*196.6 c*	*237.2 c*	*271.8 c*
hyp	CB99-027-2	1	1	1	0	0	1	0	0	1	0	0	0	0	0	1	1
hyp	CB99-027-1	1	1	1	0	0	1	0	0	1	0	0	0	0	0	1	1
hyp	RE3033-5	1	1	1	1	0	1	0	0	1	1	0	0	0	0	0	?
hyp	RE3033-4	1	1	?	?	0	1	0	0	1	?	0	0	0	0	0	0
hyp	RE3520-4	1	1	1	0	0	1	0	0	1	1	?	0	1	0	?	0
hyp	RE2775-3	1	1	1	0	0	1	0	0	?	0	0	0	0	0	?	0
hyp	RE2981-3	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
hyp	RE3033-3	1	1	1	?	0	1	0	0	1	1	0	0	0	0	0	0
hyp	RE3425-3	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
hyp	RE2775-2	1	1	1	0	0	1	0	0	?	0	0	0	0	0	?	0
hyp	RE3425-2	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
hyp	RE3520-2	1	1	1	0	0	1	?	0	1	1	0	0	1	0	0	0
hyp	05-03-3	1	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0
hyp	RE2775-1	1	1	1	0	0	1	0	0	?	0	0	0	0	0	1	0
hyp	RE2981-1	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0
hyp	RE3425-1	1	1	1	0	0	1	0	0	1	?	0	0	0	0	0	0
hyp	RE3520-1	1	1	1	0	0	1	0	0	1	?	0	0	1	0	0	0
hyp	RE3525-1	1	1	?	0	0	1	0	0	1	1	0	0	1	0	1	1
hyp	05-03-2	1	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0
hyp	05-01-3	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	?
hyp	05-03-1	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	0
hyp	05-01-2	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	?
hyp	05-01-1	1	1	?	0	0	1	0	0	1	?	0	0	0	0	0	?
riv	AK-867-9	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	AK-867-6	1	1	1	0	0	1	0	1	1	1	1	0	0	?	0	0
riv	AK-867-5	1	1	1	0	0	1	0	?	1	1	?	0	0	0	0	0
riv	AK-867-4	1	1	1	0	0	1	0	1	1	1	?	0	0	0	0	0
riv	AK-784-7	1	1	1	0	0	1	0	?	?	?	?	0	0	0	0	0
riv	AK-784-2	1	1	1	0	0	1	0	?	?	?	?	0	0	0	0	0
riv	AK-784-1	1	1	1	0	0	1	0	?	1	?	?	0	0	0	0	0

Taxon	*Specimen ID*	*76.5 c*	*79.6 c*	*82.2 c*	*85.5 c*	*93.7 c*	*117.1 c*	*120.3 c*	*133.6 c*	*142.2 c*	*157.6 c*	*159.6 c*	*167 c*	*178 c*	*196.6 c*	*237.2 c*	*271.8 c*
riv	AK-745-4	1	1	1	0	0	1	0	1	1	1	?	0	0	?	0	0
riv	AK-745-3	1	1	1	0	0	1	0	1	1	?	?	0	0	0	0	0
riv	AK-745-2	1	1	1	0	0	1	0	1	1	1	?	0	0	?	0	0
riv	AK-559-5	1	1	1	?	0	1	0	1	1	1	1	0	0	?	0	?
riv	AK-554-9	1	1	1	?	0	1	0	1	1	1	1	0	0	?	0	?
riv	AK-554-8	1	1	1	1	0	1	0	1	1	1	1	0	0	?	0	?
riv	AK-559-2	1	1	1	?	0	1	0	1	1	1	1	0	0	?	0	0
riv	AK-559-1	1	1	1	1	0	1	0	1	1	1	?	0	0	?	0	?
riv	AK-554-4	1	1	1	1	0	1	0	1	1	1	1	0	0	1	0	?
riv	AK-516-3	1	1	1	0	0	1	0	1	1	1	?	0	0	?	0	0
riv	AK-516-2	1	1	1	0	0	1	0	1	1	1	1	0	0	?	0	?
riv	AK-516-1	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	AK-470-4	1	1	1	0	0	1	0	?	1	?	?	0	0	?	0	0
riv	AK-470-3	1	1	1	0	0	1	0	?	1	?	?	0	0	?	0	0
riv	AK-470-1	1	1	1	0	0	1	0	?	1	1	?	0	0	?	0	0
riv	AK-281-3	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	AK-281-2	1	1	1	0	0	1	0	?	1	1	1	0	0	1	0	0
riv	AK-281-1	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	AK-109-9	1	1	1	0	0	1	0	1	1	1	?	0	0	?	0	0
riv	AK-109-8	1	1	1	0	0	1	0	1	1	1	?	0	0	?	0	0
riv	TMG-21-93	1	1	1	1	0	1	0	1	1	1	1	0	0	1	0	1
riv	AK-109-3	1	1	1	0	0	1	0	1	1	1	?	0	0	0	0	0
riv	TMG-43-16	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	TMG-43-15	1	1	1	0	0	1	0	?	1	1	1	0	0	?	0	0
riv	TMG-43-12	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0
riv	CB99-039-4	1	?	1	0	0	1	0	0	1	0	1	0	0	1	0	0
riv	CB99-039-3	1	?	1	0	0	1	0	0	1	0	1	0	0	1	0	0
riv	CB99-039-2	1	1	1	0	0	1	0	0	1	0	1	0	0	1	0	0
riv	TMG-21A-15	1	1	1	0	0	1	0	1	1	1	1	0	0	1	0	0

Appendix 2 Flow cytometry data

DNA ratio in 71 plants determined by flow cytometry using DAPI staining and *Lactuca sativa* L. as internal standard. Specimen ID gives population ID (cf. Table 1) and specimen number. Taxa are given as abbreviations: riv = *Saxifraga rivularis*, hyp = *S. hyperborea*, fle = *S. flexuosa* and bra = *S. bracteata*. *Saxifraga arctolitoralis* was not included due to lack of material.

Specimen ID	*Taxon*	*DNA ratio*
AK-109-13	riv	0.38
AK-248-12	riv	0.38
AK-248-13	riv	0.38
AK-416-11	riv	0.38
AK-416-12	riv	0.38
AK-416-13	riv	0.38
AK-441-12	riv	0.38
AK-441-13	riv	0.38
AK-456-13	riv	0.38
AK-456-14	riv	0.38
AK-470-13	riv	0.38
AK-516-10	riv	0.38
AK-811-13	riv	0.38
AK-811-14	riv	0.38
AK-846-12	riv	0.38
AK-846-13	riv	0.38
CB99-043-1	riv	0.38
CB99-043-4	riv	0.38
CB99-045-2	riv	0.38
CB99-047-5	riv	0.38
CB99-049-3	riv	0.38
CB99-049-4	riv	0.38
CB99-049-5	riv	0.38
TMG-21-77	riv	0.38
TMG-24-57	riv	0.38
TMG-24-60	riv	0.38
TMG-34-17	riv	0.38
TMG-34-27	riv	0.38
TMG-35-9	riv	0.38
TMG-37-3	riv	0.38
TMG-37-4	riv	0.38
TMG-37-8	riv	0.38
TMG-37B-5	riv	0.36
TMG-37-10 IIB	riv	0.38
TMG-37-12	riv	0.38
TMG-37-15	riv	0.38
TMG-39-10	riv	0.38
AK-240-14	hyp	0.17
RE2775-1	hyp	0.17
RE3425-2	hyp	0.18
RE3425-3	hyp	0.17
RE3520-1	hyp	0.17
RE3520-2	hyp	0.17
RE3520-3	hyp	0.17
RE3525-1	hyp	0.16
RE3728	hyp	0.17
RE3732	hyp	0.17
RE3748	hyp	0.17
RE3751	hyp	0.17
RE3782	hyp	0.17
RE3783	hyp	0.17
RE3898	hyp	0.17
RE5713	hyp	0.17
SUP02-150-1	fle	0.17
SUP02-150-2	fle	0.16
SUP02-155-4	fle	0.16
SUP02-168-2	fle	0.16
SUP02-180-1	fle	0.16
SUP02-180-6	fle	0.16
SUP02-181-1	fle	0.16
SUP02-181-2	fle	0.17
SUP02-185-6	fle	0.17
SUP02-185-7	fle	0.16
SUP02-211-6	fle	0.17
SUP02-211-8	fle	0.16
RE2260-3	fle	0.17
SUP02-188-6	bra	0.20
SUP02-188-7	bra	0.20
SUP02-188-8	bra	0.21
SUP02-188-9	bra	0.20
SUP02-199-2	bra	0.21

Appendix 3 Morphological data

Morphological data. Taxa are given by abbreviations: arc = *Saxifraga arctolitoralis*, bra = *S. bracteata*, fle = *S. flexuosa*, hyp = *S. hyperborea* and riv = *S. rivularis*. Specimen ID gives population ID (cf. Table 1) and specimen number. Character codes are according to Table 3. Measurements are in mm. Missing values are denoted '?'.

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
arc	65-195-1	1	0	20	?	?	2	5	0.25	3	1	1	?	1.3	?	1	2	0.30	3	1	1.4	2.9	?	?
arc	65-195-2	?	0	17	?	?	2	2	0.12	3	2	1	?	1.4	?	1	2	0.20	3	1	1.2	1.8	?	?
arc	65-195-3	1	0	12	?	?	2	3	0.25	3	2	1	?	1.2	?	1	2	0.30	3	1	1.3	3.0	?	?
arc	68-09K-1	?	1	24	9.0	0.38	3	4	0.17	?	2	?	1	?	2.7	1	2	0.30	4	2	1.7	2.8	1.04	0.63
arc	68-09K-2	1	1	29	?	?	1	2	0.07	?	1	?	1	?	1.3	1	1	0.40	4	2	1.4	2.3	1.77	1.08
arc	68-09K-3	1	1	16	3.5	0.22	2	3	0.19	?	2	?	1	?	2.3	1	2	0.50	4	2	1.3	2.5	1.09	0.57
arc	69-45K-1	1	0	32	?	?	3	4	0.13	?	2	1	?	2.0	?	1	1	0.60	4	2	1.2	2.2	?	?
arc	70-160y-1	1	2	28	14.0	0.50	5	8	0.29	?	1	?	1	?	3.4	1	1	0.80	4	1	1.5	2.9	0.85	0.44
arc	70-160y-2	1	2	18	9.0	0.50	2	2	0.11	?	2	?	1	?	3.4	1	1	0.50	3	1	1.8	2.3	0.68	0.53
arc	70-160y-3	1	2	12	?	?	1	0	0.00	?	2	?	1	?	3.2	1	1	0.30	3	2	2.1	2.7	0.84	0.66
arc	71-17-1	1	0	19	?	?	2	3	0.16	3	1	1	?	2.3	?	1	2	0.30	3	2	2.0	2.0	?	?
arc	71-17-2	1	0	27	?	?	3	3	0.11	3	1	1	?	1.7	?	1	1	0.30	3	2	1.1	2.2	?	?
arc	71-17-3	1	0	28	?	?	2	2	0.07	2	1	1	?	1.8	?	1	1	0.20	3	2	1.1	1.8	?	?
arc	72-162-1	1	2	10	5.5	0.55	2	2	0.20	?	2	?	1	?	2.5	1	1	0.30	4	2	1.3	2.2	0.88	0.52
arc	72-162-2	?	2	17	2.5	0.15	2	2	0.12	3	2	?	1	?	2.0	1	1	0.30	3	1	1.2	2.2	1.10	0.60
arc	MJ03.5.1	?	1	34	19.0	0.56	2	2	0.06	1	2	?	1	?	3.0	1	2	0.90	4	1	1.7	4.0	1.32	0.55
arc	MJ03.5.2	?	2	28	15.0	0.54	2	1	0.04	3	2	?	1	?	3.5	1	1	0.60	4	1	1.8	3.7	1.06	0.51
arc	MJ03.5.3	?	2	28	28.0	1	3	4	0.14	0	2	?	1	?	4.2	?	?	?	?	1	1.2	2.5	0.60	0.29
arc	MJ03.6.1	?	2	42	14.0	0.33	3	2	0.05	?	2	?	1	?	5.0	1	1	0.50	3	2	1.2	3.2	0.64	0.24
arc	MJ03.6.2	?	2	26	10.0	0.39	3	3	0.10	?	2	?	1	?	3.1	1	2	0.70	5	2	1.5	2.5	0.81	0.48
arc	MJ03.6.3	?	2	22	13.0	0.59	2	2	0.09	?	2	?	1	?	3.7	1	2	0.90	6	2	1.6	2.8	0.77	0.44

Taxon	Specimen ID	1 Runners	2 Dev_stage	3 L_fl_stem	4 L_fl_ped	5 L_ped_l_fl	6 No_flowers	7 No_cauline	8 No_caul_l_fl	9 Pigments	10 Dens_stem	11 Sh_hyp_e	12 Sh_hyp_l	13 L_hyp_e	14 L_hyp_l	15 Hyp_gland	16 Dens_hyp	17 L_gland	18 No_cells_gland	19 Colour_gland	20 L_sepal	21 W_sepal	22 L_sep_l_hyp	23 W_sep_l_hyp
arc	TG03-46-1	1	1	57	8.7	0.15	2	3	0.05	2	1	?	1	?	1.2	1	1	1.00	8	2	1.2	1.5	1.25	1.00
arc	TG03-46-2	1	1	76	1.2	0.02	3	4	0.05	2	1	?	1	?	1.8	1	1	0.90	6	2	1.5	2.3	1.28	0.83
arc	TG03-46-3	1	1	79	11.0	0.14	2	2	0.03	1	1	?	1	?	1.4	1	1	1.10	8	2	1.2	2.6	1.86	0.86
arc	W79-84-1	1	2	25	5.5	0.22	2	3	0.12	?	1	?	1	?	1.7	1	2	0.60	4	2	1.2	1.8	1.06	0.71
arc	W79-84-2	1	2	32	4.5	0.14	2	3	0.08	?	1	?	1	?	2.3	1	2	0.60	4	2	1.3	2.5	1.09	0.54
arc	W79-84-3	1	2	19	2.0	0.11	2	2	0.11	?	1	?	1	?	2.1	1	2	0.50	4	2	1.4	2.8	1.31	0.67
arc	RE-01-11-1	1	1	40	3.2	0.08	2	1	0.03	2	2	?	0	?	2.1	1	2	0.40	6	1	1.4	2.6	1.24	0.67
arc	RE-01-11-2	1	1	18	0.5	0.03	2	1	0.06	1	2	?	1	?	1.7	1	2	0.35	4	1	0.9	2.0	1.18	0.53
arc	RE-01-11-3	?	1	11	?	?	1	0	0.00	3	2	?	0	?	1.7	1	2	0.30	3	1	1.4	2.1	1.24	0.82
bra	70-58_Pl_1	1	1	154	14.0	0.09	5	8	0.05	0	1	?	1	?	3.8	1	1	1.20	8	2	4.9	5.3	1.39	1.29
bra	70-58_Pl_2	1	2	119	19.0	0.16	9	18	0.15	0	1	?	1	?	2.8	1	1	1.30	8	2	1.3	3.5	1.25	0.46
bra	70-58_Pl_3	1	2	109	19.5	0.18	6	12	0.11	0	1	?	1	?	3.0	1	1	1.20	8	2	1.3	3.4	1.13	0.43
bra	72.1	?	0	48	?	?	3	7	0.15	0	1	1	?	?	?	1	1	0.20	3	2	1.4	2.8	?	?
bra	72.2	1	0	43	?	?	1	4	0.09	0	2	1	?	2.5	?	1	2	0.20	3	2	1.9	1.8	?	?
bra	72.3	?	0	46	?	?	1	5	0.11	0	1	1	?	2.1	?	1	1	0.50	4	2	2.3	2.5	?	?
bra	804.1	1	2	112	4.0	0.04	29	35	0.31	0	1	?	1	?	5.2	1	1	0.80	5	2	2.0	3.8	0.73	0.38
bra	804.2	1	?	?	?	?	?	?	?	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?
bra	804.3	?	2	?	7.5	?	5	?	?	0	1	?	1	?	1.8	1	1	0.20	3	2	1.9	2.8	1.56	1.06
bra	3306	?	2	67	5.0	0.07	7	8	0.12	0	1	?	1	?	2.3	1	1	0.30	3	2	1.2	3.3	1.43	0.52
bra	MJ03.3.1	0	0	83	?	?	2	11	0.13	0	1	1	?	2.0	?	1	1	0.25	5	2	2.1	3.5	?	?
bra	MJ03.3.2	0	0	101	?	?	3	14	0.13	0	1	1	?	2.1	?	1	1	0.30	8	2	2.3	3.6	?	?
bra	MJ03.3.3	1	0	164	?	?	4	10	0.06	0	1	1	?	?	?	1	1	0.25	5	2	2.4	3.8	?	?
bra	MJ03.7.1	1	2	74	2.3	0.03	4	7	0.09	0	1	?	1	?	3.8	1	1	0.50	4	1	2.1	2.0	0.53	0.55
bra	MJ03.7.2	?	2	90	4.0	0.04	6	12	0.13	0	1	?	1	?	2.7	1	1	0.50	5	2	2.3	2.7	1.00	0.85
bra	MJ03.7.3	?	2	79	4.0	0.05	5	10	0.13	0	1	?	1	?	3.0	1	1	0.50	4	1	1.8	2.0	0.67	0.60
bra	MJ03.8.1	1	1	97	3.4	0.04	4	7	0.07	0	1	?	1	?	2.4	1	1	0.70	5	1	2.1	3.4	1.42	0.88
bra	MJ03.8.2	?	2	78	1.3	0.02	6	10	0.13	0	2	?	1	?	4.2	1	1	0.80	8	1	2.1	2.9	0.69	0.50
bra	MJ03.8.3	1	1	58	?	?	3	6	0.10	0	1	?	?	?	?	?	?	?	?	2	1.3	2.7	?	?

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
bra	SUP02-188-E1	1	0	70	?	?	4	6	0.09	0	1	1	?	1.8	?	1	2	0.20	3	0	1.5	2.6	?	?
bra	SUP02-188-E2	1	0	67	?	?	3	4	0.06	0	1	1	?	1.7	?	1	2	0.50	5	0	1.7	2.9	?	?
bra	SUP02-188-E3	1	0	34	?	?	3	4	0.12	0	1	1	?	2.1	?	1	1	0.10	3	0	1.8	2.5	?	?
bra	3189-1	1	2	127	15.5	0.12	4	7	0.06	0	1	?	0	?	2.0	1	1	0.25	4	1	2.7	3.6	1.80	1.35
bra	3189-2	1	2	142	3.7	0.03	3	4	0.03	0	0	?	0	?	2.2	1	1	0.10	3	0	2.2	2.6	1.18	1.00
bra	3189-3	1	2	96	1.4	0.01	3	3	0.03	0	1	?	0	?	1.3	1	1	0.15	3	0	1.2	2.1	1.62	0.92
bra	1826-1	?	1	153	1.5	0.01	8	12	0.08	0	0	?	1	?	1.4	1	1	0.40	6	1	2.6	4.5	3.21	1.86
bra	1826-2	1	2	177	12.2	0.07	9	11	0.06	0	1	?	0	?	3.2	1	1	0.20	3	1	3.2	4.7	1.47	1.00
bra	1069-1	1	0	106	?	?	3	6	0.06	0	1	0	?	1.3	?	1	1	0.10	2	1	1.9	3.0	?	?
bra	1069-2	?	0	158	4.0	0.03	8	0	0.00	0	1	0	?	2.4	?	1	1	0.20	4	1	2.8	3.4	?	?
bra	1069-3	1	0	107	?	?	2	6	0.06	0	1	0	?	1.3	?	1	1	0.10	2	0	2.3	2.3	?	?
bra	574a-1	1	0	84	?	?	5	5	0.06	0	0	0	?	1.5	?	1	1	0.30	5	0	1.4	3.0	?	?
bra	574a-2	1	0	73	?	?	3	4	0.05	0	1	0	?	1.4	?	1	1	0.20	4	0	1.7	2.9	?	?
bra	574a-3	1	0	53	?	?	4	4	0.08	0	1	0	?	1.8	?	1	2	0.20	4	0	1.5	3.1	?	?
bra	8121-1	1	0	46	?	?	4	6	0.13	1	2	0	?	1.2	?	1	2	0.25	3	2	1.9	2.6	?	?
bra	8121-2	1	0	42	?	?	3	5	0.12	1	2	0	?	0.9	?	1	2	0.10	3	1	2.1	2.7	?	?
bra	8121-3	1	0	34	?	?	3	5	0.15	1	2	?	?	?	?	1	2	0.30	4	2	2.0	2.7	?	?
fle	77-03_Pl_1	0	1	79	13.0	0.16	2	2	0.03	3	1	?	1	?	1.2	1	1	0.50	4	2	1.1	1.7	1.42	0.92
fle	77-03_Pl_2	?	1	62	0.0	0.00	2	3	0.05	3	1	?	1	?	2.0	1	1	0.80	5	2	1.2	1.9	0.95	0.60
fle	77-03_Pl_3	0	1	90	9.0	0.10	2	2	0.02	3	1	?	1	?	2.1	1	1	0.50	4	2	1.1	1.5	0.71	0.52
fle	04-01-1	0	2	85	10.5	0.12	4	5	0.06	1	1	?	1	?	2.2	1	1	0.20	4	2	1.4	1.9	0.86	0.64
fle	04-01-2	0	1	67	8.0	0.12	4	3	0.04	1	1	?	1	?	2.2	1	2	0.40	5	0	2.2	2.3	1.05	1.00
fle	04-01-3	0	1	56	10.5	0.19	2	1	0.02	1	1	?	1	?	2.2	1	1	0.30	4	2	1.0	1.8	0.82	0.45
fle	RE01-10-1	0	2	125	18.5	0.15	6	7	0.06	0	1	?	0	?	2.4	1	2	0.25	4	1	0.9	1.4	0.58	0.38
fle	RE01-10-2	0	2	71	10.2	0.14	4	4	0.06	0	2	?	0	?	1.5	1	2	0.40	5	0	1.3	2.1	1.40	0.87
fle	RE01-10-3	0	1	52	2.5	0.05	2	1	0.02	0	2	?	0	?	1.9	1	2	0.75	6	0	1.2	2.0	1.05	0.63
fle	RE2260-1	0	2	81	31.0	0.38	4	4	0.05	3	1	?	1	?	2.4	1	1	0.80	6	2	1.2	1.7	0.71	0.50
fle	RE2260-2	0	2	75	18.0	0.24	2	1	0.01	3	1	?	1	?	3.6	1	1	0.70	6	2	1.5	2.3	0.64	0.42

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
fle	RE-C1-1	0	0	47	10.6	0.23	3	3	0.06	2	1	?	1	?	1.6	1	1	0.20	4	0	1.0	2.2	1.38	0.63
fle	RE-C1-2	0	0	75	15.5	0.21	2	1	0.01	2	1	?	0	?	2.2	1	1	0.20	4	1	1.4	1.8	0.82	0.64
fle	RE-C1-3	0	0	105	5.2	0.05	2	3	0.03	1	1	?	0	?	2.2	1	1	0.30	4	1	1.3	1.6	0.73	0.59
fle	SUP02-154-E	0	0	44	?	?	2	3	0.07	1	1	1	?	1.2	?	1	2	0.20	4	0	1.0	1.4	?	?
fle	SUP02-155-8	0	1	29	?	?	2	3	0.10	3	1	1	?	1.8	?	1	2	0.40	5	0	1.2	1.7	?	?
fle	SUP02-155-9	0	0	36	?	?	3	6	0.17	3	1	1	?	1.6	?	1	1	0.35	3	0	1.2	1.7	?	?
fle	SUP02-155-10	0	1	34	?	?	3	3	0.09	2	1	0	?	1.4	?	1	1	0.80	4	0	1.2	1.4	?	?
fle	SUP02-163-E1	0	1	18	?	?	1	1	0.06	3	1	?	1	?	1.3	1	2	0.40	6	0	0.7	1.6	1.23	0.54
fle	SUP02-163-E2	0	1	15	?	?	1	2	0.14	1	2	1	?	0.9	?	1	1	0.40	6	0	0.7	1.8	?	?
fle	SUP02-163-E3	0	1	37	6.5	0.18	2	2	0.05	0	2	?	1	?	1.4	1	1	0.35	4	0	0.9	1.6	1.14	0.64
fle	SUP02-180-8	0	0	100	41.0	0.41	4	6	0.06	2	1	?	1	?	2.7	1	2	0.60	5	1	2.0	2.3	0.85	0.74
fle	SUP02-180-9	0	0	107	42.0	0.39	4	2	0.02	1	1	?	1	?	1.7	1	1	0.75	6	2	1.7	2.7	1.59	1.00
fle	SUP02-180-10	?	0	104	26.0	0.25	4	4	0.04	2	1	?	1	?	2.2	1	1	0.40	5	1	1.7	1.4	0.64	0.77
fle	SUP02-181-8	0	0	62	?	?	4	4	0.06	0	1	1	?	1.7	?	1	1	0.43	4	0	1.2	1.9	?	?
fle	SUP02-181-9	0	0	71	?	?	3	3	0.04	0	1	1	?	1.1	?	1	1	0.40	5	0	0.9	1.2	?	?
fle	SUP02-181-10	0	1	69	?	?	3	2	0.03	0	1	0	?	1.9	?	1	1	0.25	3	0	1.6	2.0	?	?
fle	SUP02-265-E1	0	2	32	?	?	2	2	0.06	3	1	0	?	1.8	?	1	2	0.50	6	2	1.0	2.1	?	?
fle	SUP02-265-E2	0	2	27	?	?	1	2	0.07	3	1	0	?	0.7	?	1	2	0.60	8	2	0.7	1.6	?	?
fle	SUP02-265-E3	0	2	52	?	?	1	2	0.04	3	1	?	1	?	1.8	1	2	0.30	6	2	1.2	1.6	0.89	0.67
fle	TG03-39-1	0	2	62	14.5	0.23	2	2	0.03	0	1	?	1	?	2.2	1	1	1.00	6	1	1.1	2.2	1.00	0.50
fle	TG03-39-2	0	0	50	15.5	0.31	2	4	0.08	0	1	?	1	?	3.0	1	1	1.10	7	1	1.2	2.1	0.70	0.40
fle	TG03-39-3	0	0	60	23.0	0.38	2	2	0.03	0	1	?	1	?	2.7	1	1	0.70	5	1	1.3	2.1	0.78	0.48
fle	TG03-40-1	0	2	71	11.7	0.16	2	2	0.03	0	1	?	1	?	1.5	1	1	0.30	4	2	1.5	2.7	1.80	1.00
fle	TG03-40-2	0	2	56	?	?	2	2	0.04	0	1	1	?	1.0	?	1	1	0.50	5	2	0.8	1.4	?	?
fle	TG03-40-3	0	1	54	?	?	2	1	0.02	0	1	1	?	1.2	?	1	1	0.30	3	2	1.1	2.0	?	?
fle	TG03-42-1	0	1	65	?	?	1	1	0.02	0	1	?	1	?	1.2	1	1	0.40	4	1	1.8	1.8	1.50	1.50
fle	TG03-42-2	0	1	53	9.7	0.18	2	2	0.04	0	2	?	1	?	2.1	1	1	0.20	3	1	1.2	2.1	1.00	0.57
fle	TG03-42-3	0	2	57	4.5	0.08	2	2	0.04	1	1	?	1	?	0.9	1	1	0.70	7	2	0.8	1.5	1.67	0.89

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
fle	TG03-45-1	0	2	63	17.5	0.28	2	3	0.05	3	1	?	1	?	1.2	1	1	0.50	4	2	1.2	1.9	1.58	1.00
fle	TG03-45-2	0	2	50	2.0	0.04	2	3	0.06	3	1	?	1	?	1.2	1	1	0.50	3	2	1.1	2.0	1.67	0.92
fle	TG03-45-3	0	2	66	?	?	1	2	0.03	3	1	?	1	?	2.8	1	1	0.60	4	2	1.1	2.2	0.79	0.39
fle	SR-1-1	0	2	85	12.5	0.15	3	4	0.05	3	1	?	1	?	1.6	1	1	0.40	4	1	0.9	1.8	1.13	0.56
fle	SR-1-2	0	2	102	27.0	0.26	3	3	0.03	3	1	?	0	?	2.4	1	2	0.80	10	0	1.3	2.9	1.21	0.54
fle	SR-1-3	?	2	74	12.0	0.16	3	2	0.03	3	1	?	1	?	2.6	1	1	0.70	7	1	1.2	2.3	0.88	0.46
hyp	70-145.1	0	0	52	20.0	0.38	2	3	0.06	3	1	?	1	?	3.0	1	1	0.60	4	2	1.1	1.9	0.63	0.37
hyp	70-145.2	0	0	59	14.3	0.24	2	3	0.05	3	1	?	1	?	1.8	1	1	0.40	4	2	0.9	1.8	1.00	0.50
hyp	70-145.3	0	0	53	28.0	0.53	2	2	0.04	3	1	?	1	?	2.2	1	1	0.60	4	2	1.1	2.5	1.14	0.50
hyp	71-06.1	0	0	37	?	?	2	3	0.08	2	1	1	?	1.7	?	1	1	0.50	4	2	1.2	2.3	?	?
hyp	71-06.2	0	0	33	?	?	4	4	0.12	2	1	1	?	1.5	?	1	2	1.00	6	2	0.9	1.6	?	?
hyp	71-06.3	0	0	31	?	?	2	2	0.06	2	1	1	?	1.6	?	1	1	0.40	3	1	1.2	1.6	?	?
hyp	77-32.1	0	0	42	?	?	2	2	0.05	2	1	1	?	1.5	?	1	2	1.20	9	2	1.1	2.0	?	?
hyp	77-32.2	0	0	39	?	?	2	1	0.03	2	1	1	?	1.3	?	1	1	0.40	3	2	1.1	2.0	?	?
hyp	77-32.3	0	0	40	?	?	3	3	0.08	2	1	1	?	1.4	?	1	1	0.60	5	2	1.0	2.0	?	?
hyp	MJ03.2.1	0	2	13	0.7	0.05	2	2	0.16	3	1	1	?	1.6	?	1	1	0.20	3	2	1.4	2.0	?	?
hyp	MJ03.2.2	0	2	16	?	?	1	3	0.19	3	1	1	?	1.2	?	1	2	0.20	3	1	1.0	2.0	?	?
hyp	MJ03.2.3	0	2	11	?	?	2	?	?	3	1	?	?	?	?	1	1	0.15	3	1	1.0	1.6	?	?
hyp	RE2957-1	0	2	47	8.0	0.17	2	1	0.02	3	1	?	1	?	2.5	1	2	1.50	8	2	1.9	2.2	0.88	0.76
hyp	RE2957-2	0	2	48	9.0	0.19	2	1	0.02	3	1	?	1	?	3.0	1	1	1.20	7	2	1.3	2.1	0.70	0.43
hyp	RE2957-3	0	2	44	12.5	0.28	2	1	0.02	3	1	?	1	?	3.0	1	1	0.40	4	2	1.2	1.8	0.60	0.40
hyp	TG03-28-1	0	2	84	6.5	0.08	3	4	0.05	3	1	?	1	?	1.4	1	1	0.50	4	2	1.1	1.8	1.29	0.79
hyp	TG03-28-2	0	2	83	6.7	0.08	2	1	0.01	2	1	?	1	?	1.6	1	2	1.10	7	2	1.1	2.0	1.25	0.69
hyp	TG03-28-3	0	2	97	20.0	0.21	2	2	0.02	3	1	?	1	?	1.4	1	1	0.70	5	2	1.1	2.0	1.43	0.79
hyp	TG03-31-1	0	1	84	33.0	0.39	3	5	0.06	3	1	?	1	?	2.0	1	1	0.60	4	2	1.2	2.0	1.00	0.60
hyp	TG03-31-2	0	1	71	26.0	0.37	2	3	0.04	3	1	?	1	?	1.3	1	1	0.30	3	2	1.1	1.7	1.31	0.85
hyp	TG03-31-3	0	1	92	5.0	0.05	2	2	0.02	3	1	?	1	?	1.9	1	2	0.90	6	2	1.2	2.3	1.21	0.63
hyp	TG03-34-1	0	0	48	12.5	0.26	3	3	0.06	2	1	?	1	?	1.5	1	2	0.80	6	2	1.3	2.0	1.33	0.87

Taxon	Specimen ID	1 Runners	2 Dev_stage	3 L_fl_stem	4 L_fl_ped	5 L_ped_l_fl	6 No_flowers	7 No_cauline	8 No_caul_l_fl	9 Pigments	10 Dens_stem	11 Sh_hyp_e	12 Sh_hyp_l	13 L_hyp_e	14 L_hyp_l	15 Hyp_gland	16 Dens_hyp	17 L_gland	18 No_cells_gland	19 Colour_gland	20 L_sepal	21 W_sepal	22 L_sep_l_hyp	23 W_sep_l_hyp
hyp	TG03-34-2	0	0	50	?	?	1	1	0.02	2	1	?	1	?	1.8	1	1	0.60	3	2	1.2	2.0	1.11	0.67
hyp	TG03-34-3	0	0	35	?	?	1	2	0.06	2	1	?	1	?	1.6	1	1	0.60	4	2	1.3	2.4	1.50	0.81
hyp	TG03-41-1	0	1	23	?	?	2	1	0.04	3	1	1	?	1.6	?	1	1	0.30	4	1	1.1	2.4	?	?
hyp	TG03-41-2	0	1	16	?	?	1	1	0.06	3	1	1	?	1.1	?	1	1	0.10	2	2	1.1	2.0	?	?
hyp	TG03-41-3	0	0	20	?	?	3	2	0.10	2	1	1	?	1.5	?	1	1	0.50	5	2	1.1	2.4	?	?
hyp	TG03-43-1	0	1	78	6.5	0.08	4	5	0.06	3	1	?	1	?	1.9	1	2	0.40	4	2	1.1	2.3	1.21	0.58
hyp	TG03-43-2	0	1	70	9.0	0.13	3	4	0.06	3	1	?	1	?	2.1	1	2	0.60	5	2	1.3	2.3	1.10	0.62
hyp	TG03-44-1	0	1	42	?	?	1	3	0.07	3	1	1	?	2.0	?	1	1	0.60	4	2	1.1	2.2	?	?
hyp	TG03-44-2	0	0	54	2.0	0.04	3	4	0.07	3	1	?	1	?	2.0	1	1	0.50	4	2	1.1	2.0	1.00	0.55
hyp	TG03-44-3	0	0	57	10.0	0.18	3	5	0.09	3	1	?	1	?	1.7	1	1	0.60	4	2	1.0	2.1	1.24	0.59
hyp	TMG-24A-35	0	1	47	7.0	0.15	3	3	0.06	3	2	?	0	?	2.0	1	1	0.25	4	2	1.7	2.0	1.00	0.85
hyp	TMG-24C-35	?	1	35	?	?	3	3	0.09	3	1	1	?	1.7	?	1	1	0.40	4	2	1.4	1.7	?	?
hyp	TMG-24C-36	0	1	42	?	?	3	3	0.07	3	1	1	?	1.4	?	1	1	0.40	5	1	1.0	2.0	?	?
hyp	TMG-26-11B	0	0	13	1.1	0.08	2	1	0.08	3	1	?	1	?	1.1	1	1	0.25	3	1	0.9	1.8	1.64	0.82
hyp	TMG-26-11C	0	0	12	?	?	2	2	0.17	3	2	?	0	?	1.2	1	1	0.35	4	1	0.9	2.1	1.75	0.75
hyp	TMG-26-13C	0	0	27	1.0	0.04	2	2	0.07	3	2	?	0	?	1.5	1	1	0.15	3	1	0.9	2.2	1.47	0.60
hyp	TMG-27-E1	0	1	37	?	?	4	3	0.08	2	1	1	?	1.8	?	1	1	0.45	6	1	2.0	2.3	?	?
hyp	TMG-27-E2	0	2	34	?	?	3	2	0.06	3	1	0	?	2.0	?	1	1	0.30	4	1	2.0	2.1	?	?
hyp	TMG-27-E3	0	2	42	?	?	3	3	0.07	3	1	0	?	1.3	?	1	1	0.50	5	2	1.0	2.0	?	?
hyp	TMG-34-E1	0	2	45	3.5	0.08	2	2	0.04	2	1	?	0	?	1.6	1	2	0.30	4	1	1.3	1.9	1.19	0.81
hyp	TMG-34-E2	0	2	65	?	?	1	3	0.05	3	2	?	1	?	2.2	1	1	0.40	5	2	1.6	2.0	0.91	0.73
hyp	TMG-34-E3	0	1	32	1.6	0.05	2	3	0.09	2	0	?	0	?	1.7	1	1	0.30	4	1	0.9	1.5	0.88	0.53
hyp	AK-240-2	0	2	70	10.0	0.14	2	1	0.01	3	1	?	0	?	2.9	1	1	0.60	5	1	1.4	3.0	1.03	0.48
hyp	05-01-1	0	1	38	6.0	0.16	3	2	0.05	2	2	?	1	?	1.3	1	2	0.60	6	2	1.5	1.9	1.46	1.15
hyp	05-01-2	0	2	45	9.5	0.21	2	2	0.04	2	2	?	1	?	1.2	1	2	0.60	6	2	1.2	1.8	1.50	1.00
hyp	05-01-3	0	2	37	10.5	0.28	2	3	0.08	2	2	?	0	?	1.7	1	2	0.40	5	1	1.4	2.2	1.29	0.82
hyp	05-03-1	0	0	15	?	?	4	3	0.20	3	1	1	?	1.4	?	1	1	0.40	4	1	1.5	1.5	?	?
hyp	05-03-2	0	1	22	4.0	0.18	4	3	0.14	2	1	?	1	?	1.2	1	2	0.40	4	1	1.0	1.5	1.25	0.83

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
hyp	05-03-3	0	1	18	6.0	0.33	4	4	0.22	2	1	?	1	?	1.9	1	2	0.40	4	0	0.9	1.8	0.95	0.47
hyp	CB99-038-1	0	1	52	10.2	0.20	2	2	0.04	3	1	?	1	?	2.2	1	2	0.40	6	1	1.3	1.7	0.77	0.59
hyp	CB99-038-2	?	1	63	17.6	0.28	2	2	0.03	3	1	?	1	?	1.0	1	1	0.70	6	2	1.3	2.0	2.00	1.30
hyp	CB99-038-3	0	2	72	9.3	0.13	2	1	0.01	3	1	?	0	?	2.6	1	1	0.80	8	1	1.4	2.0	0.77	0.54
hyp	CB99-027-1	0	0	43	?	?	2	1	0.02	3	1	0	?	1.7	?	1	2	0.30	7	1	1.4	2.2	?	?
hyp	CB99-027-2	0	0	40	?	?	2	1	0.03	3	1	1	?	1.4	?	1	1	0.55	7	1	1.6	2.1	?	?
hyp	CB99-027-3	0	0	46	?	?	3	2	0.04	3	1	1	?	1.3	?	1	2	0.70	8	0	1.0	2.2	?	?
hyp	G-6842-1	0	1	14	1.0	0.07	2	1	0.07	3	1	?	1	?	1.7	1	1	0.70	8	1	1.1	1.8	1.06	0.65
hyp	G-6842-2	0	1	18	1.7	0.09	2	1	0.06	3	1	?	1	?	1.6	1	1	1.10	10	1	1.6	2.1	1.31	1.00
hyp	G-6842-3	0	1	14	?	?	1	2	0.14	3	1	?	1	?	1.3	1	1	0.50	8	1	1.1	1.8	1.38	0.85
riv	3189.1	?	2	43	10.2	0.24	2	2	0.05	0	1	?	0	?	3.3	1	2	0.35	4	2	1.6	2.8	0.85	0.48
riv	3189.2	1	2	78	13.0	0.17	2	1	0.01	0	1	?	1	?	3.8	1	1	0.30	3	2	1.7	3.4	0.89	0.45
riv	3189.3	1	2	50	14.0	0.28	2	1	0.02	0	1	?	1	?	2.7	1	1	0.20	4	2	1.7	2.5	0.93	0.63
riv	219876.1	1	1	95	4.6	0.05	2	2	0.02	2	1	?	1	?	2.6	1	2	0.25	3	0	1.8	2.5	0.96	0.69
riv	219876.2	?	1	87	9.7	0.11	2	3	0.03	2	1	?	0	?	1.2	1	1	0.25	3	1	1.7	2.0	1.67	1.42
riv	219876.3	1	2	77	2.8	0.04	2	3	0.04	2	1	?	0	?	2.8	1	1	0.20	3	1	2.0	1.7	0.61	0.71
riv	AK-416-4	1	0	58	?	?	5	7	0.12	0	1	0	?	1.9	?	1	1	0.15	3	0	1.2	2.5	?	?
riv	MJ03.1.1	1	2	62	19.0	0.34	2	2	0.03	1	1	?	1	?	2.1	1	1	0.25	3	1	1.4	1.7	0.81	0.67
riv	MJ03.1.2	1	2	55	17.4	0.32	2	4	0.07	3	1	?	1	?	1.9	1	1	0.25	3	1	1.4	1.8	0.95	0.74
riv	MJ03.1.3	?	2	65	8.7	0.13	2	2	0.03	0	1	?	0	?	1.6	1	1	0.25	4	1	1.3	2.0	1.25	0.78
riv	MJ03.4.1	1	2	73	15.7	0.22	2	2	0.03	1	1	?	1	?	2.6	1	1	0.30	3	0	1.4	1.9	0.73	0.54
riv	MJ03.4.2	1	2	70	11.2	0.16	2	2	0.03	3	1	?	1	?	2.0	1	1	0.20	3	0	1.2	2.1	1.05	0.60
riv	MJ03.4.3	?	2	76	11.0	0.14	2	3	0.04	0	1	?	0	?	1.5	1	1	0.20	3	0	1.1	1.8	1.20	0.73
riv	TG03-30-1	1	2	14	1.5	0.11	2	1	0.07	3	1	?	1	?	2.3	1	1	0.40	3	2	1.8	2.6	1.13	0.78
riv	TG03-30-2	1	2	15	3.5	0.23	2	2	0.13	3	1	?	1	?	2.8	1	1	0.50	3	2	1.2	2.2	0.79	0.43
riv	TG03-30-3	1	2	22	1.7	0.08	2	3	0.14	3	1	?	1	?	3.0	1	1	0.40	3	2	1.6	3.1	1.03	0.53
riv	TMG-21-109	1	1	44	6.2	0.14	3	4	0.09	2	1	?	0	?	1.8	1	1	0.40	5	2	1.5	2.7	1.50	0.83

Taxon	*Specimen ID*	*1 Runners*	*2 Dev_stage*	*3 L_fl_stem*	*4 L_fl_ped*	*5 L_ped_l_fl*	*6 No_flowers*	*7 No_cauline*	*8 No_caul_l_fl*	*9 Pigments*	*10 Dens_stem*	*11 Sh_hyp_e*	*12 Sh_hyp_l*	*13 L_hyp_e*	*14 L_hyp_l*	*15 Hyp_gland*	*16 Dens_hyp*	*17 L_gland*	*18 No_cells_gland*	*19 Colour_gland*	*20 L_sepal*	*21 W_sepal*	*22 L_sep_l_hyp*	*23 W_sep_l_hyp*
riv	TMG-21-111	1	1	16	1.5	0.09	2	2	0.13	1	1	?	0	?	2.5	1	1	0.30	5	1	1.0	2.0	0.80	0.40
riv	TMG-21A-4	1	0	24	?	?	3	2	0.08	3	1	0	?	2.0	?	1	1	0.20	4	1	1.5	2.2	?	?
riv	CB99-049-1	0	1	54	1.5	0.03	2	1	0.02	0	0	?	0	?	1.5	1	1	0.20	5	1	1.2	1.9	1.27	0.80
riv	CB99-049-2	1	2	40	?	?	1	2	0.05	0	1	?	0	?	2.5	1	2	0.25	5	1	1.6	2.0	0.80	0.64
riv	CB99-049-3	?	1	18	3.9	0.22	2	2	0.11	0	1	?	0	?	1.7	1	2	0.15	3	0	1.6	2.0	1.18	0.94
riv	CB99-047-1	1	2	8	?	?	1	0	0.00	3	1	?	0	?	2.0	1	1	0.20	3	0	1.5	1.8	0.90	0.75
riv	CB99-047-2	?	2	27	5.9	0.22	2	2	0.07	3	0	?	0	?	2.3	1	1	0.25	4	0	1.4	2.0	0.87	0.61
riv	CB99-047-3	0	2	34	0.5	0.01	2	2	0.06	3	1	?	0	?	2.2	1	1	0.20	4	0	1.2	1.7	0.77	0.55
riv	CB99-045-1	1	0	31	?	?	2	2	0.06	0	1	0	?	1.3	?	1	1	0.10	3	0	1.9	2.4	?	?
riv	CB99-045-2	1	1	77	11.0	0.14	2	2	0.03	0	1	?	0	?	1.7	1	1	0.10	3	0	1.5	2.2	1.29	0.88
riv	CB99-045-5	1	0	115	?	?	2	4	0.03	0	0	0	?	2.0	?	1	1	0.10	3	1	1.5	2.5	?	?
riv	CB99-039-4	1	2	18	3.7	0.21	2	1	0.06	3	1	?	1	?	2.8	1	1	0.20	3	0	1.3	2.3	0.82	0.46
riv	CB99-039-3	1	2	28	0.6	0.02	2	1	0.04	3	1	?	1	?	1.9	1	1	0.10	3	0	1.5	2.3	1.21	0.79
riv	CB99-039-2	1	1	8	?	?	1	0	0.00	3	1	?	0	?	2.0	1	1	0.10	3	0	1.4	2.2	1.10	0.70
riv	AK-784-e	1	2	32	?	?	1	2	0.06	1	0	?	0	?	1.8	1	1	0.15	3	1	?	?	?	?
riv	AK-745-12a	1	0	27	?	?	2	2	0.07	1	0	0	?	1.3	?	1	1	0.10	3	1	1.1	2.0	?	?
riv	AK-745-12b	1	0	21	?	?	2	2	0.10	0	1	0	?	1.1	?	1	1	0.10	3	0	1.1	1.8	?	?
riv	AK-456-12	1	2	57	15.2	0.27	3	4	0.07	0	1	?	0	?	3.0	1	1	0.40	5	1	1.2	2.1	0.70	0.40
riv	AK-554-e	1	1	22	0.5	0.02	2	2	0.09	1	0	?	0	?	1.8	1	1	0.30	4	0	1.3	2.0	1.11	0.72
riv	AK-470-14	1	0	9	?	?	1	1	0.12	0	1	0	?	1.4	?	1	1	0.15	3	0	1.0	2.0	?	?
riv	AK-441-4	1	1	35	4.0	0.11	2	3	0.09	0	0	?	0	?	2.4	1	1	0.30	4	0	1.6	2.5	1.04	0.67
riv	AK-109-12	1	2	121	34.0	0.28	4	5	0.04	1	1	?	0	?	2.0	1	1	0.20	4	0	2.0	3.6	1.80	1.00
riv	AK-516-12	1	1	32	4.2	0.13	2	2	0.06	0	1	?	0	?	1.8	1	2	0.15	3	0	1.2	1.7	0.94	0.67
riv	AK-516-13	1	0	42	?	?	3	3	0.07	0	0	0	?	2.0	?	1	1	0.15	3	0	1.5	2.0	?	?
riv	AK-867-9	1	0	58	?	?	2	2	0.03	0	0	0	?	2.5	?	1	1	0.25	3	0	1.5	2.7	?	?
riv	AK-846-1	1	2	70	17.0	0.24	2	2	0.03	0	1	?	0	?	3.3	1	1	0.25	4	0	1.6	2.7	0.82	0.48
riv	AK-281-12	1	0	45	?	?	3	3	0.07	0	0	1	?	1.2	?	1	1	0.20	3	0	1.0	1.0	?	?
riv	AK-811-12	1	1	20	11.0	0.55	2	3	0.15	0	1	?	0	?	2.2	1	1	0.10	3	0	1.9	2.5	1.14	0.86

Taxon	Specimen ID	24 W_l_sepal	25 Sh_sep_apex	26 L_petal	27 W_petal	28 W_l_petal	29 Sh_petal	30 L_gynoec	31 Dist_ubract	32 Dist_ubr_pet	33 W_ubract	34 L_ubract	35 W_L_ubract	36 No_lobes_ubr	37 Dist_lbract	38 Dist_lbr_pet	39 L_lbr_pet	40 L_lbract	41 W_lbract	42 No_lobes_lbr	43 Sh_lbr_apex	44 L_leaf	45 W_leaf	46 W_L_leaf
arc	65-195-1	0.48	1	4.2	1.1	0.26	1	?	1	0	1.6	2.7	0.59	1	?	?	?	?	?	?	?	4.9	6.3	1.29
arc	65-195-2	0.67	1	2.3	1.0	0.43	1	?	1	0	1.0	2.6	0.38	1	?	?	?	?	?	?	?	3.2	6.4	2.00
arc	65-195-3	0.43	1	4.2	2.0	0.48	1	?	1	1	3.0	3.9	0.77	2	?	?	?	?	?	?	?	5.0	6.2	1.24
arc	68-09K-1	0.61	1	4.1	1.9	0.46	1	?	1	1	5.8	5.2	1.12	5	1	1	7.5	3.8	?	3	?	4.2	7.6	1.81
arc	68-09K-2	0.61	1	3.0	1.3	0.43	1	?	?	?	?	?	?	?	?	?	?	?	?	?	?	3.8	8.4	2.21
arc	68-09K-3	0.52	1	3.8	1.2	0.32	1	?	1	1	4.8	3.6	1.33	5	?	?	?	?	?	?	?	5.2	6.3	1.21
arc	69-45K-1	0.55	1	4.9	2.3	0.47	1	?	1	0	1.0	3.2	0.31	1	1	0	?	3.8	1.3	1	?	5.2	6.8	1.31
arc	70-160y-1	0.52	1	3.5	1.7	0.49	1	4.3	1	0	1.3	7.0	0.19	1	1	1	9.0	?	?	?	?	4.0	7.5	1.88
arc	70-160y-2	0.78	1	?	?	?	?	3.8	1	1	2.2	5.0	0.44	1	?	?	?	?	?	?	?	5.2	5.4	1.04
arc	70-160y-3	0.78	0	?	?	?	?	3.8	?	?	?	?	?	?	?	?	?	?	?	?	?	2.8	4.3	1.54
arc	71-17-1	1.00	0	2.8	1.2	0.43	1	?	1	1	4.0	3.0	1.33	3	?	?	?	?	?	?	?	4.0	7.2	1.80
arc	71-17-2	0.50	0	3.1	1.2	0.39	1	?	?	?	?	?	?	?	1	1	19.0	3.5	4.5	3	1	4.5	7.5	1.67
arc	71-17-3	0.61	1	2.9	1.3	0.45	1	?	1	1	4.1	2.6	1.58	3	?	?	?	?	?	?	?	4.1	6.1	1.49
arc	72-162-1	0.59	0	3.3	1.1	0.33	1	3.4	1	1	4.6	3.6	1.28	5	?	?	?	?	?	?	?	3.4	6.4	1.88
arc	72-162-2	0.55	0	4.0	1.0	0.25	1	3.3	1	0	2.3	3.8	0.61	1	?	?	?	?	?	?	?	4.5	6.3	1.40
arc	MJ03.5.1	0.42	0	4.4	1.4	0.31	1	?	1	1	5.5	7.0	0.79	3	?	?	?	?	?	?	?	6.4	11.2	1.75
arc	MJ03.5.2	0.49	0	5.5	1.9	0.35	1	6.0	1	1	2.7	8.0	0.34	1	?	?	?	?	?	?	?	4.0	5.5	1.38
arc	MJ03.5.3	0.48	1	?	?	?	?	4.0	1	1	2.5	10.5	0.24	3	1	1	13.5	5.5	7.5	3	1	5.5	10.0	1.82
arc	MJ03.6.1	0.38	1	?	?	?	?	4.2	1	0	2.0	6.0	0.33	1	1	1	9.0	5.0	5.5	3	1	3.5	3.2	0.91
arc	MJ03.6.2	0.60	1	?	?	?	?	4.2	1	1	3.0	8.3	0.36	1	1	1	6.0	5.0	6.5	3	1	4.3	7.8	1.82
arc	MJ03.6.3	0.57	0	?	?	?	?	4.2	1	1	3.0	7.5	0.40	1	?	?	?	?	?	?	?	4.2	5.5	1.31
arc	TG03-46-1	0.80	0	2.9	1.0	0.34	0	?	1	0	1.9	7.3	0.26	1	?	?	?	?	?	?	?	5.1	6.0	1.18
arc	TG03-46-2	0.65	0	2.4	1.0	0.42	0	?	1	0	1.8	7.3	0.25	1	1	0	?	5.8	1.2	1	?	5.0	8.6	1.72
arc	TG03-46-3	0.46	0	3.1	1.1	0.35	0	?	1	0	4.9	9.5	0.52	2	?	?	?	?	?	?	?	6.0	8.2	1.37
arc	W79-84-1	0.67	0	3.4	1.2	0.35	1	2.3	1	0	1.0	4.0	0.25	1	1	0	?	13.0	2.7	1	?	3.6	7.5	2.11
arc	W79-84-2	0.50	1	?	?	?	?	4.0	1	0	1.6	3.8	0.42	1	?	?	?	?	?	?	?	3.8	7.3	1.95

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
arc	W79-84-3	0.51	0	?	?	?	?	3.1	1	0	0.8	3.5	0.23	1	?	?	?	?	?	?	?	3.4	5.6	1.65
arc	RE-01-11-1	0.54	0	4.7	1.7	0.36	1	?	1	0	3.1	6.6	0.47	1	?	?	?	?	?	?	?	5.2	8.3	1.60
arc	RE-01-11-2	0.45	0	3.2	1.0	0.31	1	?	1	0	2.0	4.4	0.45	1	?	?	?	?	?	?	?	5.1	6.9	1.35
arc	RE-01-11-3	0.67	0	4.7	1.9	0.40	1	?	?	?	?	?	?	?	?	?	?	?	?	?	?	4.7	6.3	1.34
bra	70-58_Pl_1	0.92	1	5.4	2.0	0.37	2	?	1	1	16.0	14.7	1.09	3	1	1	7.0	15.5	18.3	3	2	8.7	17.0	1.95
bra	70-58_Pl_2	0.37	0	4.5	1.9	0.42	2	4.3	1	1	8.7	9.5	0.92	3	1	1	29.0	14.5	26.0	7	1	?	?	?
bra	70-58_Pl_3	0.38	0	?	?	?	?	4.5	1	0	4.2	8.4	0.50	1	1	1	3.0	11.4	11.7	3	1	11.3	18.2	1.61
bra	72.1	0.50	1	2.9	2.1	0.72	2	?	1	1	1.8	2.3	0.78	2	1	1	2.5	4.8	7.4	5	1	4.8	10.3	2.15
bra	72.2	1.06	1	2.3	1.7	0.74	2	?	?	?	?	?	?	?	?	?	?	?	?	?	?	5.1	9.7	1.90
bra	72.3	0.92	0	4.2	2.4	0.57	2	?	?	?	?	?	?	?	?	?	?	?	?	?	?	6.8	11.6	1.71
bra	804.1	0.53	0	?	?	?	?	3.5	1	0	3.5	8.2	0.43	1	1	1	10.0	11.5	21.5	9	1	12.0	32.0	2.67
bra	804.2	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	10.0	21.0	2.10
bra	804.3	0.68	1	?	?	?	?	4.0	1	1	4.8	8.5	0.56	2	1	1	4.0	?	?	?	?	?	?	?
bra	3306	0.36	1	4.8	1.8	0.38	2	3.5	1	?	?	?	?	?	1	?	?	?	?	?	?	9.7	21.5	2.22
bra	MJ03.3.1	0.60	2	5.2	3.1	0.60	2	?	1	1	5.8	5.6	1.05	3	1	1	1.4	7.1	8.4	4	1	9.1	12.4	1.36
bra	MJ03.3.2	0.63	2	6.5	3.9	0.60	2	?	1	1	8.4	10.4	0.81	3	1	1	2.6	9.0	11.0	5	1	10.2	16.4	1.61
bra	MJ03.3.3	0.63	2	6.0	3.6	0.60	2	?	1	1	11.7	9.5	1.23	7	1	1	?	12.8	?	9	2	?	?	?
bra	MJ03.7.1	1.05	1	?	?	?	?	4.2	1	0	3.3	6.2	0.53	1	1	0	?	8.2	5.8	1	?	11.0	15.6	1.42
bra	MJ03.7.2	0.85	1	?	?	?	?	?	1	0	3.7	9.5	0.39	1	1	0	?	11.0	7.4	1	?	7.5	11.8	1.57
bra	MJ03.7.3	0.90	1	3.2	1.3	0.41	2	3.3	1	1	6.9	6.2	1.11	3	1	1	1.8	9.9	9.1	3	?	7.2	13.8	1.92
bra	MJ03.8.1	0.62	1	?	?	?	2	?	1	1	6.8	12.7	0.54	3	1	1	?	9.3	18.0	5	1	12.4	18.8	1.52
bra	MJ03.8.2	0.72	1	4.0	1.6	0.40	2	3.9	1	1	4.3	6.9	0.62	1	1	1	4.2	14.5	?	5	?	13.8	22.4	1.62
bra	MJ03.8.3	0.48	1	4.2	?	?	2	?	?	?	?	?	?	?	1	1	1.2	9.8	13.9	5	1	8.2	14.3	1.74
bra	SUP02-188-E1	0.58	1	4.1	1.4	0.34	1	?	1	0	1.0	2.5	0.40	1	1	1	1.0	5.6	6.0	3	2	8.3	13.8	1.66
bra	SUP02-188-E2	0.59	1	5.4	2.8	0.52	2	?	1	0	3.9	4.4	0.89	1	1	1	1.5	4.8	7.8	5	1	5.7	9.5	1.67
bra	SUP02-188-E3	0.72	1	3.6	2.2	0.61	2	?	1	1	6.0	5.4	1.11	3	1	1	2.4	5.7	5.9	3	1	7.6	12.8	1.68
bra	3189-1	0.75	0	?	?	?	?	3.5	1	1	9.9	6.7	1.48	3	1	1	11.2	7.8	14.2	5	2	10.7	19.0	1.78

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
bra	3189-2	0.85	0	4.0	2.3	0.58	2	2.4	1	1	3.3	3.5	0.94	1	1	1	2.8	7.2	10.8	5	2	8.9	16.8	1.89
bra	3189-3	0.57	1	2.6	1.2	0.46	2	2.1	1	0	4.8	4.1	1.17	3	1	1	1.4	5.9	3.8	3	2	9.0	17.6	1.96
bra	1826-1	0.58	0	3.4	3.5	1.03	2	?	1	1	8.8	6.2	1.42	5	1	1	3.4	9.7	12.8	6	2	12.8	22.6	1.77
bra	1826-2	0.68	1	4.0	1.9	0.48	2	4.2	1	1	16.0	12.4	1.29	3	1	1	10.0	15.9	33.6	7	2	13.2	23.0	1.74
bra	1069-1	0.63	1	4.6	2.7	0.59	2	?	1	1	7.6	3.9	1.95	3	1	1	4.3	7.5	15.8	7	2	8.3	17.2	2.07
bra	1069-2	0.82	1	5.2	2.0	0.38	1	?	1	1	10.8	6.4	1.69	5	1	1	9.4	11.4	26.0	7	1	13.9	20.8	1.50
bra	1069-3	1.00	1	5.5	2.8	0.51	2	?	1	1	5.8	3.4	1.71	3	?	?	?	?	?	?	?	11.5	21.2	1.84
bra	574a-1	0.47	0	4.0	1.8	0.45	2	?	1	1	5.4	3.7	1.46	3	1	1	9.2	7.7	15.8	7	2	10.2	18.6	1.82
bra	574a-2	0.59	2	3.9	1.9	0.49	2	?	1	1	13.4	6.6	2.03	5	1	1	5.5	9.0	12.0	7	1	8.2	16.8	2.05
bra	574a-3	0.48	0	3.2	1.4	0.44	2	?	1	0	4.6	4.6	1.00	3	1	1	2.6	8.3	11.2	5	2	7.0	14.5	2.07
bra	8121-1	0.73	1	5.9	3.4	0.58	2	?	1	1	8.8	7.4	1.19	3	1	1	1.7	8.4	13.4	5	1	7.4	15.0	2.03
bra	8121-2	0.78	0	5.2	3.1	0.60	2	?	1	1	5.3	3.5	1.51	3	1	1	0.8	5.7	10.6	5	1	7.3	10.8	1.48
bra	8121-3	0.74	2	6.0	3.9	0.65	2	?	1	1	5.0	4.6	1.09	2	1	1	2.6	7.5	11.8	5	1	7.1	13.4	1.89
fle	77-03_Pl_1	0.65	1	3.2	1.3	0.41	1	?	?	?	?	?	?	?	?	?	?	?	?	?	?	4.2	6.1	1.45
fle	77-03_Pl_2	0.63	1	3.2	1.0	0.31	0	?	1	0	0.7	1.9	0.37	1	?	?	?	?	?	?	?	4.0	5.8	1.45
fle	77-03_Pl_3	0.73	1	2.7	?	?	0	?	1	0	1.0	3.8	0.26	1	?	?	?	?	?	?	?	5.0	8.1	1.62
fle	04-01-1	0.74	1	?	?	?	?	2.6	1	0	1.0	5.7	0.28	1	1	?	?	?	?	?	?	3.5	6.1	1.74
fle	04-01-2	0.96	1	2.6	1.0	0.38	0	?	1	1	0.9	7.3	0.25	1	1	1	2.4	5.3	6.2	3	1	5.4	10.2	1.89
fle	04-01-3	0.56	2	?	?	?	?	2.3	1	0	3.2	8.3	0.29	1	?	?	?	?	?	?	?	5.2	7.4	1.42
fle	RE01-10-1	0.64	2	3.0	1.0	0.33	0	2.6	1	0	3.2	4.2	0.24	1	1	0	?	12.5	9.2	5	1	5.3	8.5	1.60
fle	RE01-10-2	0.62	1	3.2	1.2	0.38	0	?	1	0	1.3	4.5	0.20	1	1	0	?	7.6	2.8	1	0	4.5	7.8	1.73
fle	RE01-10-3	0.60	2	2.3	0.6	0.26	0	?	1	0	0.5	7.3	0.44	1	?	?	?	?	?	?	?	3.4	5.4	1.59
fle	RE2260-1	0.71	1	3.1	1.1	0.35	1	3.5	1	0	1.8	5.4	0.59	2	1	0	?	6.0	2.5	1	?	3.2	3.4	1.06
fle	RE2260-2	0.65	1	3.4	1.4	0.41	0	4.1	1	0	1.2	6.9	0.19	1	0	?	?	?	?	?	?	4.5	8.2	1.82
fle	RE-C1-1	0.45	0	3.0	0.8	0.27	0	?	1	0	0.9	1.6	0.31	1	1	0	?	6.3	2.1	1	?	2.8	4.3	1.54
fle	RE-C1-2	0.78	1	?	?	?	?	2.9	1	0	1.8	6.6	0.27	1	?	?	?	?	?	?	?	4.7	8.4	1.79
fle	RE-C1-3	0.81	0	2.5	0.9	0.36	0	2.2	1	0	1.9	3.8	0.32	1	?	?	?	?	?	?	?	5.7	9.2	1.61

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
fle	SUP02-154-E	0.71	2	3.8	0.9	0.24	0	?	1	0	0.4	2.0	0.45	1	?	?	?	?	?	?	?	2.9	4.8	1.66
fle	SUP02-155-8	0.71	1	3.4	0.8	0.24	0	?	1	0	?	5.2	0.35	1	?	?	?	?	?	?	?	3.5	6.2	1.77
fle	SUP02-155-9	0.71	1	3.6	1.9	0.53	2	?	1	0	?	3.6	0.53	2	1	1	2.3	3.0	4.5	3	0	3.0	4.4	1.47
fle	SUP02-155-10	0.86	1	3.4	1.4	0.41	1	?	1	0	1.2	1.4	0.29	1	1	1	2.4	3.4	5.1	3	0	3.1	4.8	1.55
fle	SUP02-163-E1	0.44	0	3.1	0.9	0.29	0	?	?	?	1.8	?	?	?	?	?	?	?	?	?	?	3.4	4.3	1.26
fle	SUP02-163-E2	0.39	0	2.0	0.5	0.25	0	?	?	?	3.4	?	?	?	?	?	?	?	?	?	?	3.9	6.2	1.59
fle	SUP02-163-E3	0.56	1	2.6	0.7	0.27	0	?	1	0	0.8	6.5	0.18	1	?	?	?	?	?	?	?	3.2	?	?
fle	SUP02-180-8	0.87	0	2.7	1.3	0.48	0	?	1	0	0.6	6.8	0.26	1	1	1	2.7	6.8	7.9	3	1	7.5	10.5	1.40
fle	SUP02-180-9	0.63	1	3.1	1.7	0.55	1	?	1	0	1.6	8.8	0.39	1	0	?	?	?	?	?	?	4.6	5.5	1.20
fle	SUP02-180-10	1.21	1	3.4	1.3	0.38	0	?	1	0	3.9	2.6	0.31	1	1	0	?	7.6	5.3	2	1	7.1	10.7	1.51
fle	SUP02-181-8	0.63	1	2.5	1.0	0.40	0	?	1	0	1.9	1.7	0.35	1	1	1	5.6	6.3	6.4	3	0	5.3	8.0	1.51
fle	SUP02-181-9	0.75	1	2.4	0.9	0.38	0	?	1	0	?	5.2	0.31	2	1	1	12.0	7.6	8.7	4	0	5.6	7.6	1.36
fle	SUP02-181-10	0.80	1	2.8	1.4	0.50	0	?	1	0	?	7.6	0.51	3	1	1	3.4	7.8	7.3	4	0	4.5	6.6	1.47
fle	SUP02-265-E1	0.48	2	3.8	1.0	0.26	1	?	1	0	4.1	5.4	0.35	1	?	?	?	?	?	?	?	3.6	5.2	1.44
fle	SUP02-265-E2	0.44	2	3.4	1.2	0.35	1	?	?	?	1.8	?	?	?	?	?	?	?	?	?	?	3.5	5.6	1.60
fle	SUP02-265-E3	0.75	1	2.5	1.0	0.40	0	?	?	?	6.7	?	?	?	?	?	?	?	?	?	?	3.7	5.8	1.57
fle	TG03-39-1	0.50	0	?	?	?	?	3.0	1	0	1.1	5.3	0.77	2	?	?	?	?	?	?	?	4.3	6.4	1.49
fle	TG03-39-2	0.57	0	3.0	0.7	0.23	0	2.8	1	1	2.0	4.0	0.45	1	?	?	?	?	?	?	?	4.4	7.2	1.64
fle	TG03-39-3	0.62	1	3.1	0.9	0.29	0	2.2	1	1	1.0	3.8	1.76	5	?	?	?	?	?	?	?	4.0	6.2	1.55
fle	TG03-40-1	0.56	0	?	?	?	?	2.1	1	0	?	6.9	0.16	1	?	?	?	?	?	?	?	?	?	?
fle	TG03-40-2	0.57	1	2.8	1.0	0.36	0	?	1	0	2.2	4.7	0.43	2	?	?	?	?	?	?	?	3.4	5.8	1.71
fle	TG03-40-3	0.55	1	3.4	1.1	0.32	0	?	1	0	1.7	6.0	0.17	1	?	?	?	?	?	?	?	4.4	6.1	1.39
fle	TG03-42-1	1.00	0	?	?	?	?	2.9	?	?	4.7	?	?	?	?	?	?	?	?	?	?	4.3	6.0	1.40
fle	TG03-42-2	0.57	0	3.5	1.1	0.31	0	3.0	1	1	0.7	3.8	0.58	3	?	?	?	?	?	?	?	9.0	14.4	1.60
fle	TG03-42-3	0.53	1	3.2	1.0	0.31	0	?	1	1	?	3.5	0.49	1	?	?	?	?	?	?	?	4.3	6.2	1.44
fle	TG03-45-1	0.63	1	2.6	0.9	0.35	0	?	1	0	1.1	7.0	0.67	3	?	?	?	?	?	?	?	4.0	6.5	1.63
fle	TG03-45-2	0.55	1	3.2	0.9	0.28	0	?	1	0	3.4	2.3	0.30	1	?	?	?	?	?	?	?	?	?	?

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
fle	TG03-45-3	0.50	1	2.3	0.6	0.26	0	3.2	?	?	0.4	?	?	?	?	?	?	?	?	?	?	3.2	5.2	1.63
fle	SR-1-1	0.50	0	2.7	1.1	0.41	0	2.8	1	0	1.6	4.4	0.25	1	1	0	?	4.7	1.4	2	0	3.1	4.9	1.58
fle	SR-1-2	0.45	0	3.7	1.2	0.32	0	3.5	1	0	?	9.5	0.36	1	1	1	14.2	7.4	8.3	3	1	5.3	8.3	1.57
fle	SR-1-3	0.52	2	3.3	0.6	0.18	0	3.2	1	0	2.2	1.8	0.22	1	1	0	?	5.2	5.9	3	1	5.5	10.0	1.82
hyp	70-145.1	0.58	1	2.2	1.0	0.45	0	4.0	1	0	2.0	5.3	0.30	1	?	?	?	?	?	?	?	4.7	6.0	1.28
hyp	70-145.2	0.50	1	3.2	1.1	0.34	0	2.7	1	0	1.0	5.2	?	1	?	?	?	?	?	?	?	4.2	6.0	1.43
hyp	70-145.3	0.44	1	4.0	1.0	0.25	0	3.7	1	0	1.0	7.2	0.31	1	?	?	?	?	?	?	?	4.0	6.2	1.55
hyp	71-06.1	0.52	1	3.3	1.2	0.36	0	?	1	0	1.1	6.0	0.33	1	?	?	?	?	?	?	?	4.4	7.6	1.73
hyp	71-06.2	0.56	2	2.8	1.2	0.43	0	?	1	0	4.0	2.6	0.38	1	1	1	1.8	4.2	5.0	3	1	3.0	5.5	1.83
hyp	71-06.3	0.75	1	2.2	1.1	0.50	0	?	1	0	1.0	3.3	0.30	1	?	?	?	?	?	?	?	4.5	7.3	1.62
hyp	77-32.1	0.55	1	3.7	1.1	0.30	0	?	1	0	?	4.0	0.28	1	?	?	?	?	?	?	?	4.9	8.2	1.67
hyp	77-32.2	0.55	1	4.0	1.8	0.45	1	?	1	0	?	6.8	0.59	2	?	?	?	?	?	?	?	4.1	6.9	1.68
hyp	77-32.3	0.50	0	3.7	1.3	0.35	0	?	1	0	2.5	3.0	0.33	1	1	1	1.9	4.0	2.1	1	?	5.0	6.2	1.24
hyp	MJ03.2.1	0.70	0	2.9	1.0	0.34	0	?	1	0	1.1	?	?	?	?	?	?	?	?	?	?	3.7	3.5	0.95
hyp	MJ03.2.2	0.50	0	2.3	0.8	0.35	0	?	?	?	1.1	?	?	?	?	?	?	?	?	?	?	3.0	3.7	1.23
hyp	MJ03.2.3	0.63	1	3.0	1.4	0.47	0	?	1	0	0.9	3.5	0.71	1	0	?	?	?	?	?	?	3.7	4.6	1.24
hyp	RE2957-1	0.86	1	3.2	1.3	0.41	0	3.0	1	0	?	6.0	0.18	1	1	0	?	7.2	1.4	1	?	4.0	6.2	1.55
hyp	RE2957-2	0.62	1	2.6	1.2	0.46	0	4.5	1	0	5.2	5.0	0.22	1	?	?	?	?	?	?	?	3.6	6.8	1.89
hyp	RE2957-3	0.67	2	2.8	1.1	0.39	0	5.2	1	0	2.2	4.9	0.18	1	?	?	?	?	?	?	?	3.4	6.0	1.76
hyp	TG03-28-1	0.61	1	?	?	?	?	3.7	0	?	?	?	?	?	1	0	?	3.9	2.6	3	1	6.1	9.9	1.62
hyp	TG03-28-2	0.55	1	2.5	1.0	0.40	0	2.8	1	0	1.7	6.0	0.87	5	?	?	?	?	?	?	?	4.8	7.4	1.54
hyp	TG03-28-3	0.55	0	3.0	0.9	0.30	0	3.0	1	0	?	3.0	0.73	1	?	?	?	?	?	?	?	3.2	4.5	1.41
hyp	TG03-31-1	0.60	0	?	?	?	?	3.4	1	0	1.5	6.0	?	1	1	1	5.5	4.3	5.0	3	1	4.2	7.1	1.69
hyp	TG03-31-2	0.65	1	2.1	1.0	0.48	0	3.0	1	0	?	5.0	0.34	1	?	?	?	?	?	?	?	3.7	7.0	1.89
hyp	TG03-31-3	0.52	1	3.8	1.3	0.34	0	3.6	1	0	?	2.7	?	1	?	?	?	?	?	?	?	6.0	8.0	1.33
hyp	TG03-34-1	0.65	2	3.4	0.9	0.26	0	?	1	0	2.1	4.0	0.38	1	1	0	?	7.4	1.8	1	?	3.6	7.6	2.11
hyp	TG03-34-2	0.60	1	3.3	1.4	0.42	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	4.3	6.8	1.58

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
hyp	TG03-34-3	0.54	1	2.8	1.2	0.43	0	?	?	?	1.9	?	?	?	?	?	?	?	?	?	?	3.1	5.2	1.68
hyp	TG03-41-1	0.46	1	3.1	1.0	0.32	0	?	1	0	1.3	6.2	0.34	1	?	?	?	?	?	?	?	4.0	6.8	1.70
hyp	TG03-41-2	0.55	1	3.2	0.9	0.28	0	?	?	?	1.1	?	?	?	?	?	?	?	?	?	?	3.0	5.2	1.73
hyp	TG03-41-3	0.46	0	3.1	1.4	0.45	0	?	1	0	?	4.0	0.48	1	1	1	2.1	4.1	2.8	1	?	5.1	6.2	1.22
hyp	TG03-43-1	0.48	0	3.8	1.0	0.26	0	?	1	0	0.5	5.1	0.25	1	1	1	6.0	6.9	3.8	2	?	5.1	7.3	1.43
hyp	TG03-43-2	0.57	1	3.5	1.5	0.43	0	?	1	0	?	3.9	0.28	1	1	1	4.1	5.9	5.2	3	1	5.8	10.4	1.79
hyp	TG03-44-1	0.50	1	4.1	1.1	0.27	0	?	?	?	1.2	?	?	?	?	?	?	?	?	?	?	4.1	6.6	1.61
hyp	TG03-44-2	0.55	1	3.9	1.3	0.33	0	?	1	0	1.2	1.8	0.28	1	1	0	?	4.0	1.2	1	?	3.5	5.3	1.51
hyp	TG03-44-3	0.48	1	3.1	0.9	0.29	0	?	1	0	1.4	3.7	?	1	1	0	?	6.1	1.7	1	?	?	?	?
hyp	TMG-24A-35	0.85	2	4.2	1.4	0.33	0	?	1	0	2.0	5.5	0.22	1	1	0	?	8.0	4.8	3	1	5.2	5.2	1.00
hyp	TMG-24C-35	0.82	1	2.7	1.3	0.48	0	?	1	0	1.7	3.3	0.36	1	1	0	?	4.9	1.4	1	1	4.1	8.4	2.05
hyp	TMG-24C-36	0.50	1	3.2	1.0	0.31	0	?	1	0	0.8	5.1	0.27	1	1	0	?	5.4	3.9	3	1	2.8	4.6	1.64
hyp	TMG-26-11B	0.50	0	2.5	0.8	0.32	0	?	1	0	2.4	3.8	0.53	3	?	?	?	?	?	?	?	2.6	3.9	1.50
hyp	TMG-26-11C	0.43	1	3.5	1.1	0.31	0	?	1	0	2.4	3.1	0.55	2	?	?	?	?	?	?	?	3.4	5.5	1.62
hyp	TMG-26-13C	0.41	0	2.7	1.0	0.37	0	?	1	0	2.2	3.5	0.23	1	1	0	?	4.3	0.5	1	1	3.8	6.3	1.66
hyp	TMG-27-E1	0.87	0	3.4	1.9	0.56	0	?	1	0	1.4	7.2	0.33	1	1	1	7.0	5.8	5.3	3	1	3.1	5.6	1.81
hyp	TMG-27-E2	0.95	1	3.2	2.4	0.75	0	?	1	0	?	6.5	0.37	2	1	1	6.5	6.4	8.0	3	0	4.9	10.4	2.12
hyp	TMG-27-E3	0.50	1	4.1	1.7	0.41	0	?	1	0	1.0	7.1	0.31	1	1	1	3.9	4.4	5.2	3	1	4.9	7.5	1.53
hyp	TMG-34-E1	0.68	1	3.3	1.2	0.36	0	?	1	0	3.4	4.0	0.35	1	?	?	?	?	?	?	?	3.8	6.8	1.79
hyp	TMG-34-E2	0.80	1	2.3	0.9	0.39	0	3.3	?	?	1.6	?	?	?	?	?	?	?	?	?	?	3.9	6.0	1.54
hyp	TMG-34-E3	0.60	0	?	?	?	?	2.8	1	0	1.8	2.8	0.36	1	?	?	?	?	?	?	?	3.9	6.2	1.59
hyp	AK-240-2	0.47	0	3.7	1.2	0.32	0	3.5	1	0	2.4	7.4	0.46	1	?	?	?	?	?	?	?	5.0	9.5	1.90
hyp	05-01-1	0.79	2	3.0	1.1	0.37	0	?	1	0	0.8	1.2	0.67	1	1	0	?	5.3	2.8	1	0	4.2	8.2	1.95
hyp	05-01-2	0.67	1	3.2	1.1	0.34	0	2.8	1	0	1.2	6.0	0.20	1	?	?	?	?	?	?	?	4.2	5.8	1.38
hyp	05-01-3	0.64	1	3.3	1.0	0.30	0	3.0	1	0	1.0	5.5	0.18	1	?	?	?	?	?	?	?	?	?	?
hyp	05-03-1	1.00	1	1.7	0.8	0.47	0	?	1	0	4.0	4.2	0.95	2	1	1	3.9	4.8	6.4	3	0	3.0	5.2	1.73
hyp	05-03-2	0.67	1	2.5	0.9	0.36	0	?	1	0	1.2	6.9	0.17	1	1	1	4.4	5.2	6.2	3	0	5.1	8.2	1.61

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
hyp	05-03-3	0.50	1	2.9	1.1	0.38	0	?	1	0	1.0	5.5	0.18	1	1	0	?	6.6	6.4	3	1	5.2	8.3	1.60
hyp	CB99-038-1	0.76	2	2.4	1.2	0.50	0	?	1	0	1.0	4.1	0.24	1	?	?	?	?	?	?	?	4.0	6.5	1.63
hyp	CB99-038-2	0.65	1	4.3	1.2	0.28	0	?	1	0	2.4	6.7	0.36	1	?	?	?	?	?	?	?	5.9	8.2	1.39
hyp	CB99-038-3	0.70	0	3.7	1.1	0.30	0	3.2	1	0	1.9	5.6	0.34	1	?	?	?	?	?	?	?	3.6	4.8	1.33
hyp	CB99-027-1	0.64	1	4.0	1.9	0.48	1	?	1	0	1.6	5.6	0.29	1	?	?	?	?	?	?	?	3.3	5.1	1.55
hyp	CB99-027-2	0.76	2	3.0	1.5	0.50	0	?	1	0	1.5	5.3	0.28	1	?	?	?	?	?	?	?	3.6	4.8	1.33
hyp	CB99-027-3	0.45	2	3.9	1.7	0.44	1	?	1	0	1.5	4.5	0.33	1	1	0	?	7.0	1.8	1	0	5.2	6.7	1.29
hyp	G-6842-1	0.61	2	2.4	1.2	0.50	0	?	1	0	1.0	2.7	0.37	1	?	?	?	?	?	?	?	2.3	3.2	1.39
hyp	G-6842-2	0.76	2	3.0	0.8	0.27	0	?	1	0	1.2	3.2	0.38	1	?	?	?	?	?	?	?	3.1	4.0	1.29
hyp	G-6842-3	0.61	0	2.7	1.1	0.41	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	2.3	3.2	1.39
riv	3189.1	0.57	1	?	?	?	?	4.4	1	0	3.4	7.2	0.47	1	?	?	?	?	?	?	?	3.5	6.2	1.77
riv	3189.2	0.50	0	?	?	?	?	4.5	1	0	1.8	3.0	0.60	1	?	?	?	?	?	?	?	5.9	10.0	1.69
riv	3189.3	0.68	1	?	?	?	?	4.3	1	0	2.2	6.4	0.34	1	?	?	?	?	?	?	?	7.4	11.5	1.55
riv	219876.1	0.72	0	4.3	2.6	0.60	0	?	1	0	0.9	3.9	0.23	2	?	?	?	?	?	?	?	4.4	7.9	1.80
riv	219876.2	0.85	2	4.2	1.3	0.31	0	?	1	0	3.2	6.8	0.47	2	?	?	?	?	?	?	?	5.3	10.0	1.89
riv	219876.3	1.18	1	?	?	?	?	3.9	1	0	1.0	3.4	0.29	2	?	?	?	?	?	?	?	5.4	11.3	2.09
riv	AK-416-4	0.48	1	4.1	2.4	0.59	2	?	1	0	1.8	5.0	0.36	1	1	1	10.0	8.0	8.3	3	2	4.6	7.2	1.57
riv	MJ03.1.1	0.82	1	2.4	0.6	0.25	0	3.0	1	0	2.3	6.2	0.37	1	1	1	11.8	5.7	?	5	?	4.2	9.7	2.31
riv	MJ03.1.2	0.78	1	2.7	1.0	0.37	0	3.3	1	0	3.3	6.2	0.54	1	1	1	8.2	?	?	?	?	4.1	9.3	2.27
riv	MJ03.1.3	0.63	1	?	?	?	?	2.5	1	0	2.8	8.9	0.31	1	?	?	?	?	?	?	?	5.2	8.4	1.62
riv	MJ03.4.1	0.74	0	?	?	?	?	3.4	1	1	5.9	6.8	0.87	2	0	?	?	?	?	?	?	4.4	7.4	1.68
riv	MJ03.4.2	0.57	0	1.4	1.1	0.79	0	3.2	1	0	2.6	8.0	0.33	1	0	?	?	?	?	?	?	4.2	9.1	2.17
riv	MJ03.4.3	0.61	0	?	?	?	?	2.3	1	0	2.8	8.1	0.35	1	0	?	?	?	?	?	?	3.5	?	?
riv	TG03-30-1	0.69	1	?	?	?	?	4.1	1	0	4.6	6.2	0.74	1	?	?	?	?	?	?	?	3.0	5.8	1.93
riv	TG03-30-2	0.55	1	?	?	?	?	3.8	1	0	1.8	4.0	0.45	1	?	?	?	?	?	?	?	3.1	5.8	1.87
riv	TG03-30-3	0.52	1	4.2	1.3	0.31	0	3.9	1	1	2.2	4.0	0.55	1	?	?	?	?	?	?	?	4.5	7.6	1.69
riv	TMG-21-109	0.56	1	4.5	2.7	0.60	1	4.0	1	0	1.0	3.1	0.32	1	1	0	?	8.8	4.5	3	1	5.4	7.2	1.33

Taxon	*Specimen ID*	*24 W_l_sepal*	*25 Sh_sep_apex*	*26 L_petal*	*27 W_petal*	*28 W_l_petal*	*29 Sh_petal*	*30 L_gynoec*	*31 Dist_ubract*	*32 Dist_ubr_pet*	*33 W_ubract*	*34 L_ubract*	*35 W_L_ubract*	*36 No_lobes_ubr*	*37 Dist_lbract*	*38 Dist_lbr_pet*	*39 L_lbr_pet*	*40 L_lbract*	*41 W_lbract*	*42 No_lobes_lbr*	*43 Sh_lbr_apex*	*44 L_leaf*	*45 W_leaf*	*46 W_L_leaf*
riv	TMG-21-111	0.50	2	3.7	1.0	0.27	0	3.1	1	0	3.6	6.9	0.52	2	?	?	?	?	?	?	?	4.3	7.5	1.74
riv	TMG-21A-4	0.68	1	3.5	1.7	0.49	0	?	1	1	1.3	2.5	0.52	1	1	1	1.6	3.7	1.5	1	1	3.9	6.9	1.77
riv	CB99-049-1	0.63	1	2.1	1.1	0.52	0	?	1	1	3.7	4.4	0.84	1	?	?	?	?	?	?	?	2.7	3.0	1.11
riv	CB99-049-2	0.80	2	?	?	?	?	4.0	?	?	?	?	?	?	?	?	?	?	?	?	?	3.8	7.8	2.05
riv	CB99-049-3	0.80	2	3.0	1.5	0.50	0	?	1	1	2.1	3.5	0.60	2	?	?	?	?	?	?	?	4.2	7.1	1.69
riv	CB99-047-1	0.83	2	?	?	?	?	4.0	?	?	?	?	?	?	?	?	?	?	?	?	?	2.6	4.2	1.62
riv	CB99-047-2	0.70	1	3.4	1.2	0.35	0	3.7	1	1	4.0	4.4	0.91	1	?	?	?	?	?	?	?	3.1	6.4	2.06
riv	CB99-047-3	0.71	1	2.8	0.8	0.29	0	4.1	1	1	1.7	4.0	0.43	1	?	?	?	?	?	?	?	3.7	6.4	1.73
riv	CB99-045-1	0.79	0	3.2	1.6	0.50	1	?	1	1	9.4	4.7	2.00	5	?	?	?	?	?	?	?	4.3	7.5	1.74
riv	CB99-045-2	0.68	0	3.8	1.4	0.37	0	?	1	1	5.2	3.2	1.63	3	?	?	?	?	?	?	?	3.4	6.0	1.76
riv	CB99-045-5	0.60	0	3.0	1.8	0.60	1	?	1	1	7.0	4.3	1.63	5	?	?	?	?	?	?	?	4.7	9.6	2.04
riv	CB99-039-4	0.57	2	3.0	0.8	0.27	0	4.7	1	1	3.6	3.8	0.95	2	?	?	?	?	?	?	?	3.2	8.0	2.50
riv	CB99-039-3	0.65	1	3.0	1.7	0.57	2	2.5	1	0	1.5	4.4	0.34	1	?	?	?	?	?	?	?	3.6	7.0	1.94
riv	CB99-039-2	0.64	2	3.8	1.6	0.42	1	?	?	?	?	?	?	?	?	?	?	?	?	?	?	4.3	7.2	1.67
riv	AK-784-E	?	?	?	?	?	?	3.1	?	?	?	?	?	?	?	?	?	?	?	?	?	3.4	6.0	1.76
riv	AK-745-12a	0.55	2	3.1	1.3	0.42	0	?	1	1	3.0	3.9	0.77	1	?	?	?	?	?	?	?	3.9	7.8	2.00
riv	AK-745-12b	0.61	2	2.5	1.1	0.44	0	?	1	1	3.4	3.5	0.97	1	?	?	?	?	?	?	?	3.9	8.0	2.05
riv	AK-456-12	0.57	1	3.3	1.4	0.42	1	3.4	1	0	3.2	8.2	0.39	1	1	1	17.2	4.7	7.0	3	2	6.0	10.6	1.77
riv	AK-554-e	0.65	2	3.7	1.8	0.49	1	?	1	0	1.2	4.4	0.27	1	?	?	?	?	?	?	?	3.7	6.0	1.62
riv	AK-470-14	0.50	2	2.5	0.9	0.36	0	?	?	?	?	?	?	?	?	?	?	?	?	?	?	4.0	6.7	1.68
riv	AK-441-4	0.64	1	4.2	1.6	0.38	1	?	1	1	2.5	4.4	0.57	1	?	?	?	?	?	?	?	4.1	8.4	2.05
riv	AK-109-12	0.56	1	5.1	1.2	0.24	0	5.0	1	0	0.6	3.0	0.20	1	1	1	6.0	10.2	5.4	1	0	5.7	12.2	2.14
riv	AK-516-12	0.71	0	2.6	1.3	0.50	0	?	1	1	4.5	4.4	1.02	1	?	?	?	?	?	?	?	3.4	6.4	1.88
riv	AK-516-13	0.75	2	3.1	1.5	0.48	0	?	1	0	1.7	4.0	0.43	1	1	1	7.6	3.1	5.7	3	1	4.0	8.6	2.15
riv	AK-867-9	0.56	1	3.4	2.0	0.59	1	?	1	1	8.6	6.5	1.32	3	?	?	?	?	?	?	?	5.5	9.8	1.78
riv	AK-846-1	0.59	2	3.0	1.2	0.40	0	4.5	1	1	6.0	7.9	0.76	1	?	?	?	?	?	?	?	6.5	11.4	1.75
riv	AK-281-12	1.00	0	?	?	?	?	?	1	0	1.3	3.0	0.43	1	1	1	8.5	4.9	7.4	3	2	7.0	12.6	1.80
riv	AK-811-12	0.76	2	5.4	2.1	0.39	1	?	1	1	3.2	4.7	0.68	2	?	?	?	?	?	?	?	5.0	9.2	1.84

Taxon	*Specimen ID*	*47 Dist_inc*	*48 Sh_inc*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*	*51 Str_sheath*	*52 Sh_sheath*	*53 Fri_sheath*
arc	65-195-1	2.4	0	5	1	1	2	1
arc	65-195-2	1.5	0	5	1	1	2	1
arc	65-195-3	3.0	0	5	1	1	?	1
arc	68-09K-1	3.6	1	5	1	1	2	1
arc	68-09K-2	2.1	1	5	1	1	2	1
arc	68-09K-3	2.7	1	5	2	1	1	2
arc	69-45K-1	2.8	1	5	1	1	1	1
arc	70-160y-1	2.0	1	5	1	1	1	1
arc	70-160y-2	2.4	1	3	1	1	0	1
arc	70-160y-3	1.4	1	3	1	1	0	1
arc	71-17-1	2.4	1	5	0	0	1	1
arc	71-17-2	2.2	1	5	1	1	1	1
arc	71-17-3	2.7	1	5	?	1	2	1
arc	72-162-1	2.1	1	5	1	1	1	1
arc	72-162-2	2.2	1	5	1	1	2	1
arc	MJ03.5.1	2.5	1	4	1	1	1	1
arc	MJ03.5.2	2.0	1	3	1	1	1	1
arc	MJ03.5.3	2.8	1	5	1	1	1	1
arc	MJ03.6.1	1.2	1	3	1	1	1	1
arc	MJ03.6.2	2.0	1	5	1	1	1	1
arc	MJ03.6.3	2.0	0	3	1	1	2	1
arc	TG03-46-1	2.2	0	3	0	1	1	1
arc	TG03-46-2	2.0	1	5	1	1	1	1
arc	TG03-46-3	3.2	1	5	1	1	1	1
arc	W79-84-1	1.9	0	5	1	1	2	1
arc	W79-84-2	2.1	1	4	2	1	2	1
arc	W79-84-3	1.1	1	3	1	0	2	1

Taxon	*Specimen ID*	*47 Dist_inc*	*48 Sh_inc*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*	*51 Str_sheath*	*52 Sh_sheath*	*53 Fri_sheath*
arc	RE-01-11-1	2.1	2	5	2	1	1	2
arc	RE-01-11-2	1.7	1	5	2	1	1	2
arc	RE-01-11-3	2.5	2	2	1	1	2	2
bra	70-58_Pl_1	4.2	1	5	1	1	1	1
bra	70-58_Pl_2	?	?	?	?	?	?	?
bra	70-58_Pl_3	4.9	2	7	1	?	?	?
bra	72.1	2.4	1	7	2	2	1	1
bra	72.2	2.1	1	7	2	2	1	1
bra	72.3	3.1	1	7	2	2	2	1
bra	804.1	6.5	2	9	2	2	2	1
bra	804.2	6.0	2	9	2	2	2	1
bra	804.3	?	?	?	?	?	?	?
bra	3306	6.8	2	9	2	1	2	1
bra	MJ03.3.1	4.2	1	7	2	0	0	1
bra	MJ03.3.2	5.9	2	6	2	0	0	1
bra	MJ03.3.3	?	?	?	?	?	?	?
bra	MJ03.7.1	7.5	1	5	1	2	2	1
bra	MJ03.7.2	2.5	1	5	2	2	1	1
bra	MJ03.7.3	3.8	1	5	1	1	2	1
bra	MJ03.8.1	7.1	1	7	1	2	1	1
bra	MJ03.8.2	5.9	1	7	1	2	2	1
bra	MJ03.8.3	3.3	1	7	1	1	2	1
bra	SUP02-188-E1	4.6	2	5	2	1	0	2
bra	SUP02-188-E2	3.3	1	5	2	0	1	1
bra	SUP02-188-E3	4.4	2	5	2	0	0	1
bra	3189-1	6.7	2	7	2	2	2	1
bra	3189-2	5.7	2	7	2	2	0	1

Taxon	*Specimen ID*	*47 Dist_inc*	*48 Sh_inc*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*	*51 Str_sheath*	*52 Sh_sheath*	*53 Fri_sheath*
bra	3189-3	5.2	1	7	2	2	0	1
bra	1826-1	7.3	2	5	2	2	0	1
bra	1826-2	7.3	2	5	2	2	?	?
bra	1069-1	4.7	2	7	2	1	0	1
bra	1069-2	7.2	2	7	1	1	0	1
bra	1069-3	7.4	0	7	1	1	0	1
bra	574a-1	7.3	2	11	2	1	2	1
bra	574a-2	4.6	1	9	1	2	1	1
bra	574a-3	3.8	2	9	2	2	2	1
bra	8121-1	3.5	2	5	2	2	2	1
bra	8121-2	3.5	1	7	2	2	2	1
bra	8121-3	3.7	0	7	1	2	2	1
fle	77-03_Pl_1	2.2	0	5	1	0	0	1
fle	77-03_Pl_2	2.1	0	4	0	0	2	1
fle	77-03_Pl_3	1.9	0	5	0	0	1	1
fle	04-01-1	2.2	0	5	0	?	?	?
fle	04-01-2	3.2	0	5	0	0	0	1
fle	04-01-3	2.6	0	5	1	1	0	1
fle	RE01-10-1	2.4	0	5	0	1	1	2
fle	RE01-10-2	2.5	1	5	0	1	1	1
fle	RE01-10-3	1.9	1	3	0	0	1	1
fle	RE2260-1	1.4	0	5	0	1	0	1
fle	RE2260-2	2.1	1	5	1	1	1	1
fle	RE-C1-1	1.2	0	3	0	0	0	1
fle	RE-C1-2	1.5	0	3	0	0	0	1
fle	RE-C1-3	2.5	0	3	0	0	1	1
fle	SUP02-154-E	1.3	0	5	0	0	0	1
fle	SUP02-155-8	1.6	0	5	0	2	2	1
fle	SUP02-155-9	1.5	1	3	0	2	2	1
fle	SUP02-155-10	1.7	0	5	1	2	2	1
fle	SUP02-163-E1	1.3	0	5	1	?	?	?
fle	SUP02-163-E2	1.4	1	3	0	1	0	1
fle	SUP02-163-E3	?	?	3	1	?	?	?
fle	SUP02-180-8	4.6	1	5	1	1	0	1
fle	SUP02-180-9	2.4	1	5	1	2	1	1
fle	SUP02-180-10	4.2	0	5	1	1	1	1
fle	SUP02-181-8	3.4	0	5	1	2	2	1
fle	SUP02-181-9	5.1	0	5	0	2	2	1
fle	SUP02-181-10	1.8	0	5	0	2	2	1
fle	SUP02-265-E1	2.5	0	5	0	?	?	?
fle	SUP02-265-E2	1.4	0	5	1	0	0	1
fle	SUP02-265-E3	1.1	1	5	0	0	0	1
fle	TG03-39-1	1.4	1	5	1	0	0	1
fle	TG03-39-2	2.2	0	5	1	0	0	1
fle	TG03-39-3	2.1	0	5	1	1	1	1
fle	TG03-40-1	?	?	?	?	1	1	1
fle	TG03-40-2	2.0	1	3	1	1	1	1
fle	TG03-40-3	1.9	1	5	1	1	1	1
fle	TG03-42-1	2.7	0	5	1	1	0	1
fle	TG03-42-2	5.5	1	5	1	1	0	1
fle	TG03-42-3	1.9	1	5	1	0	0	1
fle	TG03-45-1	1.9	0	3	0	1	2	1
fle	TG03-45-2	?	?	?	?	0	0	1
fle	TG03-45-3	1.3	1	3	1	0	1	1

Taxon	*Specimen ID*	*47 Dist_inc*	*48 Sh_inc*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*	*51 Str_sheath*	*52 Sh_sheath*	*53 Fri_sheath*
fle	SR-1-1	1.6	0	5	0	1	0	1
fle	SR-1-2	3.0	0	5	0	1	2	1
fle	SR-1-3	3.0	0	5	0	1	0	1
hyp	70-145.1	2.1	0	3	1	0	0	1
hyp	70-145.2	2.0	0	3	0	1	1	1
hyp	70-145.3	2.0	1	5	1	1	1	1
hyp	71-06.1	2.6	1	5	1	1	0	1
hyp	71-06.2	0.8	1	5	1	1	1	1
hyp	71-06.3	2.5	1	5	1	1	0	1
hyp	77-32.1	2.7	0	3	0	0	2	1
hyp	77-32.2	2.3	0	3	1	0	2	1
hyp	77-32.3	2.0	1	3	1	0	0	1
hyp	MJ03.2.1	1.7	1	3	1	2	2	1
hyp	MJ03.2.2	1.3	0	5	1	1	2	1
hyp	MJ03.2.3	2.6	1	5	1	1	1	1
hyp	RE2957-1	2.5	0	5	0	0	0	1
hyp	RE2957-2	2.0	0	5	0	0	0	1
hyp	RE2957-3	1.4	0	5	0	0	0	1
hyp	TG03-28-1	3.0	0	3	1	0	1	1
hyp	TG03-28-2	2.2	1	5	1	0	2	1
hyp	TG03-28-3	1.5	0	3	1	0	3	1
hyp	TG03-31-1	2.0	0	3	0	0	1	1
hyp	TG03-31-2	2.0	1	5	1	1	2	1
hyp	TG03-31-3	2.7	1	3	1	1	0	1
hyp	TG03-34-1	2.5	0	5	1	0	2	1
hyp	TG03-34-2	2.0	0	3	0	0	0	1
hyp	TG03-34-3	1.6	1	5	0	0	2	1
hyp	TG03-41-1	1.9	0	3	1	1	1	1
hyp	TG03-41-2	1.2	0	3	0	1	2	1
hyp	TG03-41-3	3.0	1	3	1	0	2	1
hyp	TG03-43-1	1.9	1	5	1	1	0	1
hyp	TG03-43-2	3.0	1	5	1	1	1	1
hyp	TG03-44-1	2.0	0	3	0	1	2	1
hyp	TG03-44-2	1.2	1	5	0	1	1	1
hyp	TG03-44-3	?	?	?	?	1	1	1
hyp	TMG-24A-35	2.4	0	3	1	1	0	1
hyp	TMG-24C-35	2.3	1	5	1	0	0	1
hyp	TMG-24C-36	0.8	0	5	0	0	0	1
hyp	TMG-26-11B	0.8	1	3	1	0	1	1
hyp	TMG-26-11C	1.7	0	3	1	0	0	1
hyp	TMG-26-13C	1.5	0	5	2	0	1	1
hyp	TMG-27-E1	1.3	0	5	1	1	0	1
hyp	TMG-27-E2	2.3	0	5	1	0	0	1
hyp	TMG-27-E3	2.5	0	5	1	0	0	1
hyp	TMG-34-E1	1.9	0	5	0	0	0	1
hyp	TMG-34-E2	1.7	1	3	1	0	0	1
hyp	TMG-34-E3	1.7	0	5	1	0	0	1
hyp	AK-240-2	2.5	0	5	1	0	0	1
hyp	05-01-1	2.4	0	5	0	1	2	1
hyp	05-01-2	1.8	0	5	0	1	0	1
hyp	05-01-3	?	?	?	?	0	0	1
hyp	05-03-1	1.4	0	5	0	1	1	1
hyp	05-03-2	2.4	0	5	1	0	0	1
hyp	05-03-3	2.3	1	5	0	1	0	1

Taxon	*Specimen ID*	*47 Dist_inc*	*48 Sh_inc*	*49 No_lobes_leaf*	*50 Sh_leaf_apex*	*51 Str_sheath*	*52 Sh_sheath*	*53 Fri_sheath*
hyp	CB99-038-1	2.2	0	3	0	2	0	1
hyp	CB99-038-2	2.7	0	5	1	1	0	1
hyp	CB99-038-3	1.8	1	5	1	0	1	1
hyp	CB99-027-1	1.7	0	5	0	2	0	1
hyp	CB99-027-2	1.3	0	3	1	1	1	1
hyp	CB99-027-3	2.4	0	3	0	1	1	1
hyp	G-6842-1	1.2	0	3	0	1	1	1
hyp	G-6842-2	1.4	0	3	0	1	0	1
hyp	G-6842-3	1.1	0	5	0	1	2	1
riv	3189.1	1.8	2	5	0	2	1	1
riv	3189.2	3.4	2	4	1	2	2	1
riv	3189.3	4.2	2	5	1	2	2	1
riv	219876.1	2.2	1	5	0	2	1	1
riv	219876.2	2.4	2	5	1	2	2	1
riv	219876.3	2.6	1	5	1	1	1	1
riv	AK-416-4	1.9	1	5	0	1	2	1
riv	MJ03.1.1	1.9	2	5	1	2	1	1
riv	MJ03.1.2	1.8	2	5	0	2	2	1
riv	MJ03.1.3	1.8	1	5	1	2	2	1
riv	MJ03.4.1	1.9	2	5	1	2	1	1
riv	MJ03.4.2	2.1	2	5	1	2	2	1
riv	MJ03.4.3	1.6	2	5	0	2	2	1
riv	TG03-30-1	2.7	0	5	1	1	1	1
riv	TG03-30-2	1.3	1	5	1	1	2	1
riv	TG03-30-3	1.7	0	5	1	1	2	1
riv	TMG-21-109	1.6	1	5	1	0	1	1
riv	TMG-21-111	1.2	0	5	0	0	2	1
riv	TMG-21A-4	1.8	1	5	1	0	2	1
riv	CB99-049-1	1.3	1	3	1	2	2	1
riv	CB99-049-2	1.9	1	5	1	2	2	1
riv	CB99-049-3	1.4	2	5	2	2	0	0
riv	CB99-047-1	1.1	1	3	1	1	2	1
riv	CB99-047-2	0.9	2	5	1	2	2	1
riv	CB99-047-3	1.8	2	5	0	2	2	1
riv	CB99-045-1	1.5	2	5	0	1	2	1
riv	CB99-045-2	1.0	2	5	1	1	2	1
riv	CB99-045-5	1.8	2	5	0	1	2	1
riv	CB99-039-4	1.8	0	5	2	1	2	1
riv	CB99-039-3	1.2	0	5	0	1	2	1
riv	CB99-039-2	2.3	0	5	1	1	2	1
riv	AK-784-e	1.5	2	5	0	0	0	0
riv	AK-745-12a	1.6	1	5	1	1	2	1
riv	AK-745-12b	1.7	1	5	1	1	2	1
riv	AK-456-12	3.0	1	5	1	0	0	1
riv	AK-554-e	1.0	1	5	0	0	2	1
riv	AK-470-14	1.1	0	3	1	1	0	0
riv	AK-441-4	2.6	0	5	1	1	0	0
riv	AK-109-12	3.2	2	5	2	2	2	1
riv	AK-516-12	1.3	2	5	0	1	1	1
riv	AK-516-13	1.8	2	5	1	1	2	1
riv	AK-867-9	2.2	2	5	1	0	0	1
riv	AK-846-1	2.7	2	5	1	1	2	1
riv	AK-281-12	2.6	2	5	1	1	2	1
riv	AK-811-12	1.9	1	5	2	2	2	1