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## Supplementary material

**Table S1.** Characteristics of the *Senecio pterophorus* populations used in this study and summary of genetic diversity metrics estimated as the percentage of polymorphic loci, *PLP*, the average gene diversity, *H<sub>j</sub>*, and band richness after rarefaction *Br(5)*. Populations are classified in sub-regional groups in the South African native range, Australia and Spain. n = number of individuals, NL= number of polymorphic AFLP loci.

Region/ Group <sup>1</sup>	Population name	Pop. Code	Origin <sup>2</sup>	Coordinates	Herbarium code	n	NL	PLP (%)	<i>H<sub>j</sub></i> (mean ± SE)	Br(5)
<b>SOUTH AFRICA</b>										
SA-1	Colchester	S06	N	33°41'S 25°49'E	BCN 78089	8	176	53.8	0.193 ± 0.010	1.342
SA-1	Grahamstown	S07	N	33°19'S 26°32'E	BCN 78090	9	190	58.1	0.191 ± 0.010	1.355
SA-1	Alexandria	S08	N	33°36'S 26°24'E	BCN 78091	9	231	70.6	0.237 ± 0.010	1.466
SA-1	Port Alfred	S09	N	33°36'S 26°52'E	BCN 78092	9	217	66.4	0.219 ± 0.010	1.409
SA-1	Stafford's Post	S16	N	30°31'S 29°46'E	BCN 78101	4	169	51.7	0.210 ± 0.010	----
SA-2	Franklin	S17	N	30°23'S 29°38'E	BCN 78110	4	187	57.2	0.256 ± 0.011	----
SA-2	Sidwadwenii	S20	N	31°24'S 28°50'E	----	6	194	59.3	0.232 ± 0.011	1.407
SA-2	Mqanduli	S21	N	31°50'S 28°46'E	----	4	188	57.5	0.258 ± 0.011	----
SA-2	Gwadana	S22	N	32°13'S 28°17'E	----	6	180	55.0	0.207 ± 0.010	1.374
SA-2	Nobokwe	S23	N	31°55'S 27°50'E	----	6	182	55.7	0.205 ± 0.010	1.361
SA-3	Fort Hare	S10	N	32°47'S 26°52'E	BCN 78093	9	243	74.3	0.253 ± 0.010	1.485
SA-3	Courtlands	S11	N	32°40'S 28°00'E	BCN 78094	4	208	63.6	0.284 ± 0.010	----
SA-3	Umtentu	S12	N	31°51'S 28°30'E	BCN 78095	5	207	63.3	0.257 ± 0.010	1.480
SA-3	Flagstaff	S13	N	31°11'S 29°26'E	BCN 78096	10	210	64.2	0.220 ± 0.010	1.408
SA-3	Mt. Alyliff	S14	N	30°50'S 29°15'E	BCN 78097	4	168	51.4	0.220 ± 0.011	----
SA-3	Bizana	S15	N	30°50'S 29°35'E	BCN 78098	4	188	57.5	0.240 ± 0.010	----
SA-3	Mount Frere	S18	N	30°57'S 28°57'E	BCN 78114	9	192	58.7	0.191 ± 0.010	1.341
SA-3	Antioch	S19	N	30°42'S 28°51'E	BCN 78116	7	188	57.5	0.211 ± 0.010	1.359
W. CAPE	Groenfontein kop	S01	E	33°47'S 18°52'E	BCN 78080	9	166	50.8	0.163 ± 0.010	1.259
W. CAPE	Cape Town	S02	E	34°07'S 18°23'E	BCN 78082	6	169	51.7	0.174 ± 0.010	1.275
W. CAPE	Elgin	S03	E	34°09'S 19°01'E	BCN 78083	5	203	62.1	0.244 ± 0.010	1.413
W. CAPE	Hermanus	S04	E	34°24'S 19°11'E	BCN 78085	6	196	59.9	0.212 ± 0.010	1.350
W. CAPE	Cape Town	S05	E	33°56'S 18°26'E	BCN 78086	7	220	67.3	0.244 ± 0.010	1.474
<b>AUSTRALIA</b>										
A-SYD	Doonside	A01	I	33°45'S 150°52'E	BCN 111744	6	158	48.3	0.181 ± 0.010	1.292
A-SYD	Newcastle	A02	I	32°52'S 151°41'E	BCN 111743	9	178	54.4	0.168 ± 0.010	1.267
A-EYRE	Port Lincoln	A03	I	34°33'S 135°49'E	BCN 111742	9	191	58.4	0.199 ± 0.010	1.361
A-EYRE	Wangary	A04	I	34°30'S 135°25'E	BCN 111741	10	201	61.5	0.194 ± 0.010	1.346
A-EYRE	Lincoln NP	A05	I	34°48'S 135°46'E	BCN 111740	10	194	59.3	0.120 ± 0.010	1.360
A-EYRE	Hincks NP	A06	I	33°55'S 136°14'E	BCN 111753	7	158	48.3	0.178 ± 0.011	1.290
A-ADE	Mt. Compass	A07	I	35°20'S 138°36'E	BCN 111752	6	179	54.7	0.209 ± 0.011	1.376
A-ADE	Cleland NP	A08	I	34°57'S 138°42'E	BCN 111750	6	182	55.7	0.218 ± 0.011	1.358
A-ADE	Warren CP	A09	I	34°40'S 138°51'E	BCN 111749	5	173	52.9	0.206 ± 0.010	1.343

Region/ Group <sup>1</sup>	Population name	Pop. Code	Origin <sup>2</sup>	Coordinates	Herbarium code	n	NL	PLP (%)	H <sub>j</sub> (mean ± SE)	Br(5)
A-BM	Mt. Burr	A10	I	37°35'S 140°28'E	BCN 111748	4	205	62.7	0.269 ± 0.010	---
A-BM	Mt. Napier NP	A11	I	37°55'S 142°02'E	BCN 111747	8	220	67.3	0.232 ± 0.010	1.443
A-MEL	Hastings	A12	I	38°17'S 145°11'E	BCN 111746	9	177	54.1	0.140 ± 0.009	1.228
A-MEL	Gumbaya Park	A13	I	38°04'S 145°39'E	BCN 111745	2	142	43.4	0.116 ± 0.008	---
<b>EUROPE</b>										
<b>Spain</b>										
CAT-S	Cambrils	C01	I	41°04'N 1°04'E	BCN 111771	8	174	53.2	0.177 ± 0.010	1.289
CAT-N	Palafolls	C02	I	41°39'N 2°42'E	BCN 111770	9	202	61.8	0.207 ± 0.010	1.364
CAT-N	Calella	C03	I	41°37'N 2°39'E	BCN 111769	8	199	60.9	0.210 ± 0.010	1.357
CAT-N	Castellbisbal	C04	I	41°27'N 1°59'E	BCN 111768	6	183	56.0	0.211 ± 0.010	1.349
CAT-N	Castellar V.	C05	I	41°36'N 2°04'E	BCN 111767	5	150	45.9	0.161 ± 0.010	1.251
CAT-N	Bigues i Riells	C06	I	41°41'N 2°12'E	BCN 111766	2	158	48.3	0.170 ± 0.010	---
CAT-N	Sabadell	C07	I	41°31'N 2°07'E	BCN 111765	4	192	58.7	0.254 ± 0.010	---
CAT-N	Ripollet	C08	I	41°29'N 2°10'E	BCN 111764	6	158	48.3	0.162 ± 0.009	1.260
CAT-N	Matadepera	C09	I	41°35'N 2°01'E	BCN 111763	6	206	63.0	0.249 ± 0.011	1.415
CAT-N	Sant Llorenç NP	C10	I	41°36'N 2°05'E	BCN 111757	7	197	60.2	0.223 ± 0.010	1.394
CAT-N	Campins	C11	I	41°43'N 2°28'E	BCN 111756	4	174	53.2	0.237 ± 0.011	---
CAT-N	Montseny NP	C12	I	41°43'N 2°24'E	BCN 111755	3	146	44.6	0.206 ± 0.010	---
CAT-N	Viladecans	C13	I	41°17'N 2°02'E	---	8	178	54.4	0.181 ± 0.010	1.308
<b>Italy</b>										
ITA	Pietra Ligure	I01	I	44°08'N 8°16'E	BCN 111762	8	223	68.2	0.245 ± 0.010	1.440
ITA	Zucarello	I02	I	44°06'N 8°07'E	BCN 111761	9	209	63.9	0.236 ± 0.011	1.391
ITA	Pontedassio	I03	I	43°56'N 8°00'E	BCN 111760	8	203	62.1	0.236 ± 0.011	1.392
ITA	Arma di Taggia	I04	I	43°50'N 7°51'E	---	10	222	67.9	0.249 ± 0.011	1.454
ITA	Ventimiglia	I05	I	43°49'N 7°35'E	BCN 111759	8	205	62.7	0.239 ± 0.010	1.425
ITA	Vado Ligure	I06	I	44°16'N 8°25'E	BCN 111758	2	151	46.2	0.210 ± 0.010	---

<sup>1</sup> Abbreviation for sub-regional groups. In the South African native range: subgroups SA-1, SA-2 and SA-3 corresponding to lineages following a STRUCTURE analyses (see Fig. 4A). Populations were assigned to each sub-group based on the most frequent lineage. In Australia: A-SYD = Sydney area, A-EYRE = Eyre Peninsula, A-ADE = Adelaide area, A-BM = Barker-Mallee area, A-MEL = Melbourne area; In Spain: CAT-S = South Catalonia, CAT-N = North Catalonia.

<sup>2</sup> Origin: N = native, E = expanded, I = introduced.

**Table S2.** Primer descriptions, amplification conditions used in this study and GenBank accessions. °C, annealing temperature.

Regions	Primers	Sequences 5' → 3'	References <sup>1</sup>	°C	Genbank acc.
<i>ndhC-trnV<sup>UAC</sup></i>	ndhC	TAT TAT TAG AAA TGY CCA RAA AAT ATC ATA TTC	[1]	56	KU682190
	trnV <sup>(UAC)</sup> x2	GTC TAC GGT TCG ART CCG TA			
<i>rpL32-trnL<sup>UAG</sup></i>	rpL32F	CAG TTC CAA AA A AAC GTA CTT C	[1]	52	KU641238
	trnL <sup>(UAG)</sup>	CTG CTT CCT AAG AGC AGC GT			
<i>trnL-trnF</i>	trnL-e	GGT TCA AGT CCC TCT ATC CC	[2]	58	KU682189
	trnL-f	ATT TGA ACT GGT GCA ACG AG			
<i>trnT-trnLb</i>	trnTA2	CAA ATG CGA TGC TCT AAC CT	[3]	52	KU682191
	trnLb	TCT ACC GAT TTC GCC ATA TC			
<i>rpL16</i>	Rex2	GAT ATT CCC TTC ATT CTT CCT	[4,5]	52	KU605607
	rpL16F71	GCT ATG CTT AGT GTG TGA CTC GTT G			
<i>trnG</i>	3'-trnG <sup>UUC</sup>	GTA GCG GGA ATC GAA CCC GCA TC	[6]	52	KU641239
	5'-trnG2G	GCG GGT ATA GTT TAG TGG TAA AA			
<i>5'trnK</i>	trnK-3914F	TGG GTT GCT AAC TCA ATG G	[7]	52	KU605608
	matK-1168R	ATT GAA TGA ATT GAT CGT A			
<i>trnL</i>	trnL-c	CGA AAT CGG TAG ACG CTA CG	[2]	58	KU641240
	trnL-d	GGG GAT AGA GGG ACT TGA AC			

<sup>1</sup>References:

- [1] Shaw J, Lickey EB, Schilling EE, Small RL (2007) Comparison of whole chloroplast genome sequences to choose noncoding regions for phylogenetic studies in angiosperms: the tortoise and the hare III. *Am J Bot* 94:275–288
- [2] Taberlet P, Gielly L, Pautou G, Bouvet J (1991) Universal primers for amplification of three non-coding regions of chloroplast DNA. *Plant Mol Biol* 17:1105–1109
- [3] Cronn RC, Small RL, Haselkorn T, Wendel JF (2002) Rapid diversification of the cotton genus (*Gossypium*: Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes. *Am J Bot* 89:707–725
- [4] Sanz M, Schönswetter P, Vallès J, Schneeweiss GM, Vilatersana R (2014) Southern isolation and northern long-distance dispersal shaped the phylogeography of the widespread, but highly disjunct, European high mountain plant *Artemisia eriantha* (Asteraceae). *Bot J Linn Soc* 174:214–226
- [5] Jordan WC, Courtney MW, Neigel JE (1996) Low levels of infraspecific genetic variation at a rapidly evolving chloroplast DNA locus in North American duckweeds (Lemnaceae). *Am J Bot* 83:430–439
- [6] Shaw J, Lickey EB, Beck JT, Farmer SB, Liu W, Miller J, Siripun KC, Winder CT, Schilling EE, Small RL (2005) The tortoise and the hare II: relative utility of 21 noncoding chloroplast DNA sequences for phylogenetic analysis. *Am J Bot* 92:142–166
- [7] Johnson LA, Soltis DE (1995) Phylogenetic inference in Saxifragaceae sensu-stricto and *Gilia* (Polemoniaceae) using matK sequences. *Ann Missouri Bot Gard* 82:149–175

**Table S3.** Summary of the double scoring and error scoring rate. The percentages were calculated in relation to the total number of markers for each primer pair.

Primer combination	N° samples	Repetitions (%)	Repeatability (%)	Repeatability rang (%)	Error (%)
<i>EcoRI</i> -AGG/ <i>MseI</i> -CTC	44	12.05	97.00	82.35-100	3.00
<i>EcoRI</i> -ACT/ <i>MseI</i> -CAA	35	9.59	99.74	97.50-100	0.26
<i>EcoRI</i> -AAG/ <i>MseI</i> -CAA	33	9.04	97.20	82.61-100	2.80
<b>Mean</b>	37.33	10.22	97.98		2.02

**Table S4.** Proportion of assignment of Western Cape populations (South Africa expanded populations) and Australian populations to the native South African lineages with minimal log likelihood differences of 0, 1 and 2 based on a test implanted in AFLPOP. South African lineages: SA-1: southern lineage, SA-2: central lineage and SA-3: central/ northern lineage (see Fig. 4A). None = no assignment success

	WESTERN CAPE			AUSTRALIA		
	0	1	2	0	1	2
SA-1	42.4	36.4	33.4	9.0	4.5	3.4
SA-2	3.0	3.0	3.1	20.2	16.9	15.7
SA-3	54.6	51.5	42.4	70.8	57.3	46.1
None	0.0	9.1	21.2	0.0	21.3	34.8

**Table S5.** Proportion of assignment of populations from the three European colonization events to the native South African lineages and Australian sub-regions with minimal log likelihood differences of 0, 1 and 2 based on a test implanted in AFLPOP. South African lineages: SA-1: southern lineage, SA-2: central lineage and SA-3: central/northern lineage (following STRUCTURE analyses; see Fig. 4A). Australian sub-regions: A-SYD = Sydney populations, A-EYRE = Eyre Peninsula populations, A-ADE = Adelaide populations, A-BM = Barker-Mallee populations, A-MEL = Melbourne populations (see Fig. 1). None = no assignment success

	SPAIN (CAT-S)			SPAIN (CAT-N)			ITALY		
	0	1	2	0	1	2	0	1	2
SA-1	20.0	10.0	10.0	24.6	21.7	14.5	6.7	4.4	4.4
SA-2	0.0	0.0	0.0	11.6	5.8	5.8	4.4	4.4	0.0
SA-3	50.0	50.0	30.0	50.7	43.6	30.4	88.9	82.3	77.8
A-SYD	10.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
A-EYRE	0.0	0.0	0.0	8.7	2.9	2.9	0.0	0.0	0.0
A-ADE	20.0	20.0	20.0	1.5	1.4	0.0	0.0	0.0	0.0
A-BM	0.0	0.0	0.0	2.9	2.9	2.9	0.0	0.0	0.0
A-MEL	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
None	0.0	20.0	40.0	0.0	21.7	43.5	0.0	8.9	17.8

**Table S6.** Linear models testing differences in the metrics of genetic diversity, *PLP*, *Hj* and *Br(5)*, between the native region and each of the non-native regions (Western Cape in South Africa, Australia, Spain and Italy). *PLP* = percentage of polymorphic loci; *Hj* = average gene diversity; *Br(5)* = band richness after rarefaction to 5. Significant results at  $p < 0.05$  are indicated in bold.

		<i>Value</i>	<i>Standard Error</i>	<i>t-value</i>	<i>p-value</i>
<i>PLP</i>	Intercept (South Africa native range)	<b>59.767</b>	<b>1.550</b>	<b>38.563</b>	<b>0.000</b>
	Western Cape	-1.407	3.324	-0.423	0.674
	Australia	-4.305	2.393	-1.799	0.078
	Spain	<b>-5.267</b>	<b>2.393</b>	<b>-2.201</b>	<b>0.032</b>
	Italy	2.067	3.100	0.667	0.508
<i>Hj</i>	Intercept (South African native range)	<b>0.2269</b>	<b>0.008</b>	<b>29.279</b>	<b>0.000</b>
	Western Cape	-0.019	0.017	-1.173	0.247
	Australia	<b>-0.040</b>	<b>0.012</b>	<b>-3.340</b>	<b>0.002</b>
	Spain	-0.023	0.012	-1.938	0.058
	Italy	0.009	0.015	0.577	0.566
<i>Br(5)</i>	Intercept (South African native range)	<b>1.402</b>	<b>0.018</b>	<b>78.058</b>	<b>0.000</b>
	Western Cape	-0.048	0.032	-1.499	0.143
	Australia	<b>-0.069</b>	<b>0.025</b>	<b>-2.726</b>	<b>0.009</b>
	Spain	<b>-0.070</b>	<b>0.027</b>	<b>-2.631</b>	<b>0.012</b>
	Italy	0.018	0.032	0.561	0.578

**Figure S1.** Summary of the AFLP data analyses conducted with the program STRUCTURE. The left graphs show the  $\Delta K$  for each  $K$  value. The right graphs show the mean similarity between runs for each  $K$  value. Circles represent the mean of all pairwise comparisons between ten runs and lines indicate the standard deviation. **A–B**, South African native range. **C–D**, South African native and expanded range. **E–F**, South Africa and Australia. **G–H**, South Africa, Australia and Spain. **I–J**, South Africa, Australia and Europe (Spain and Italy).

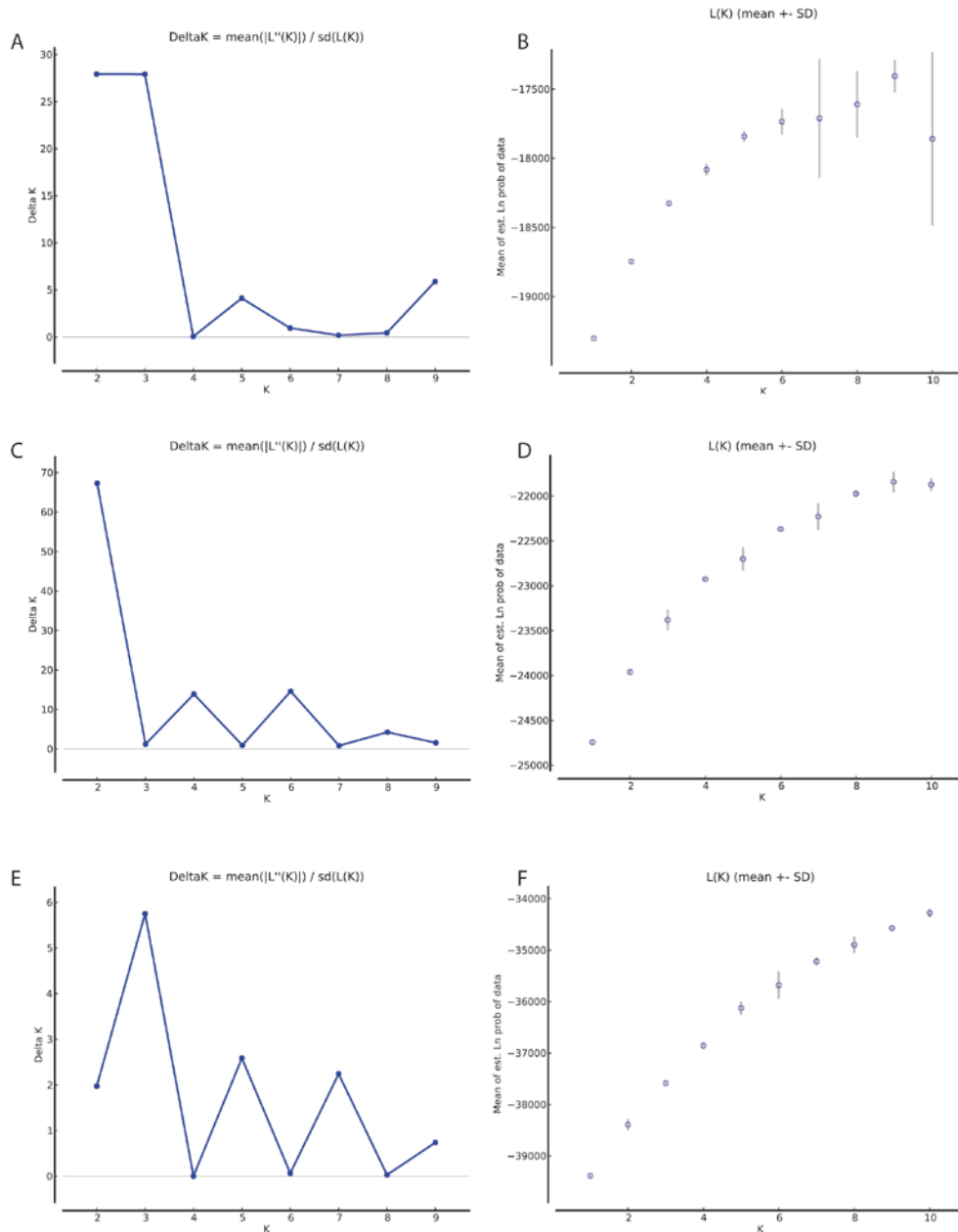
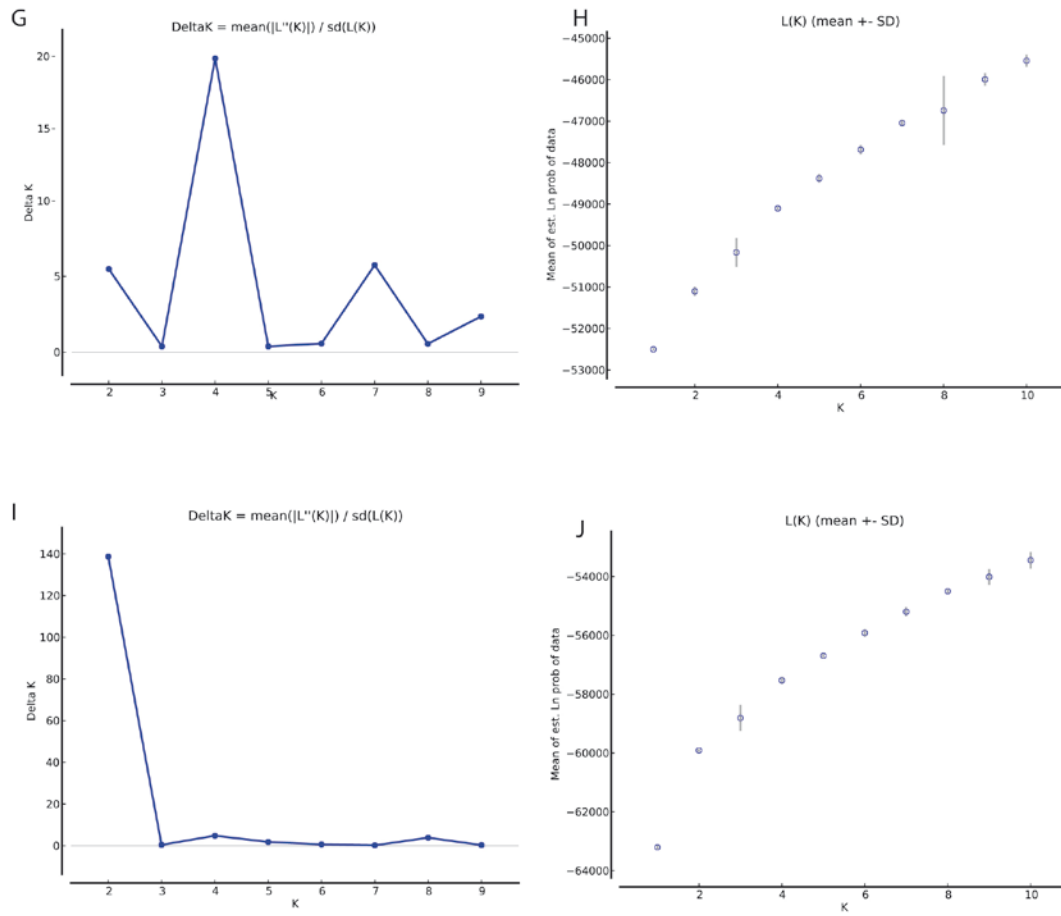
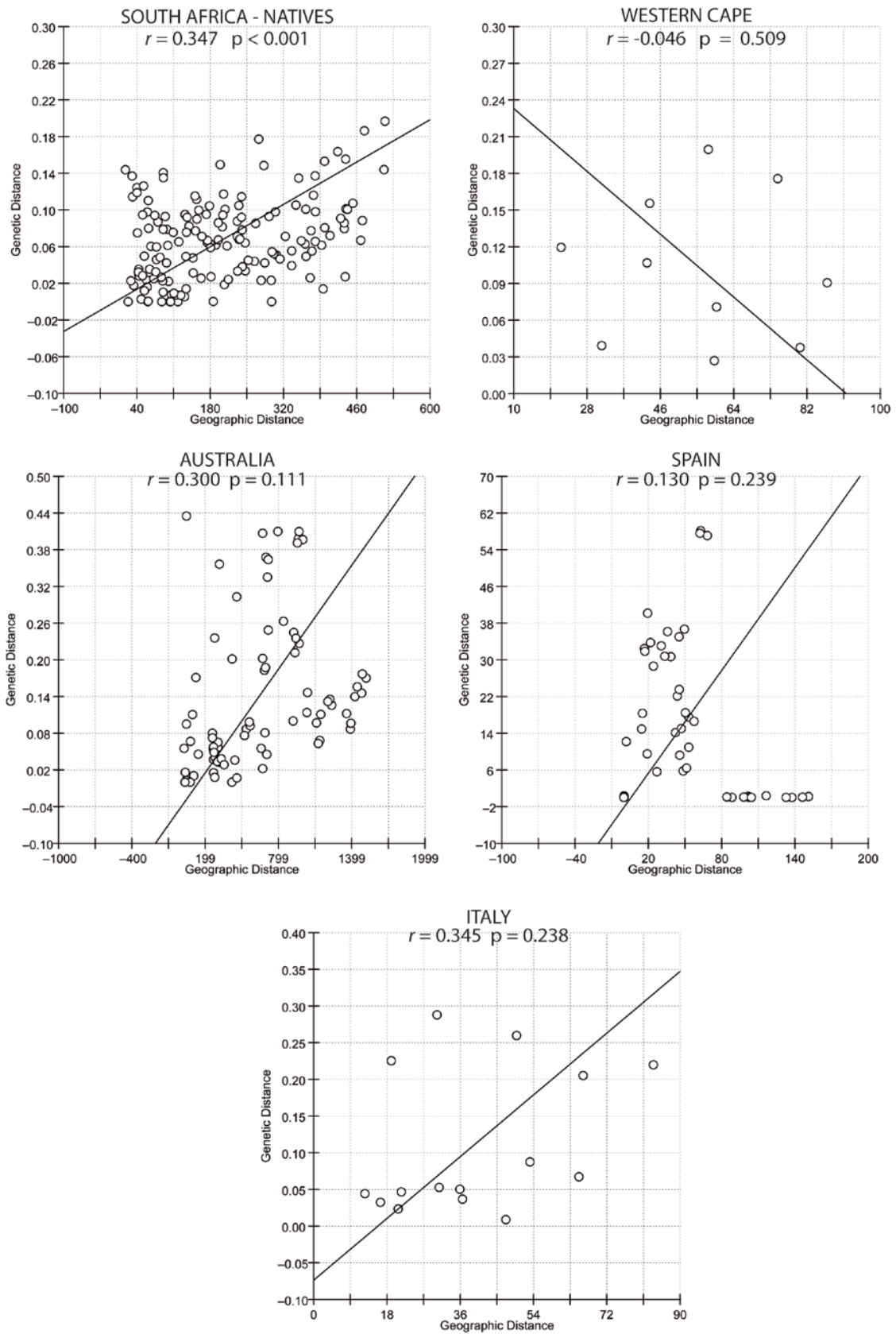




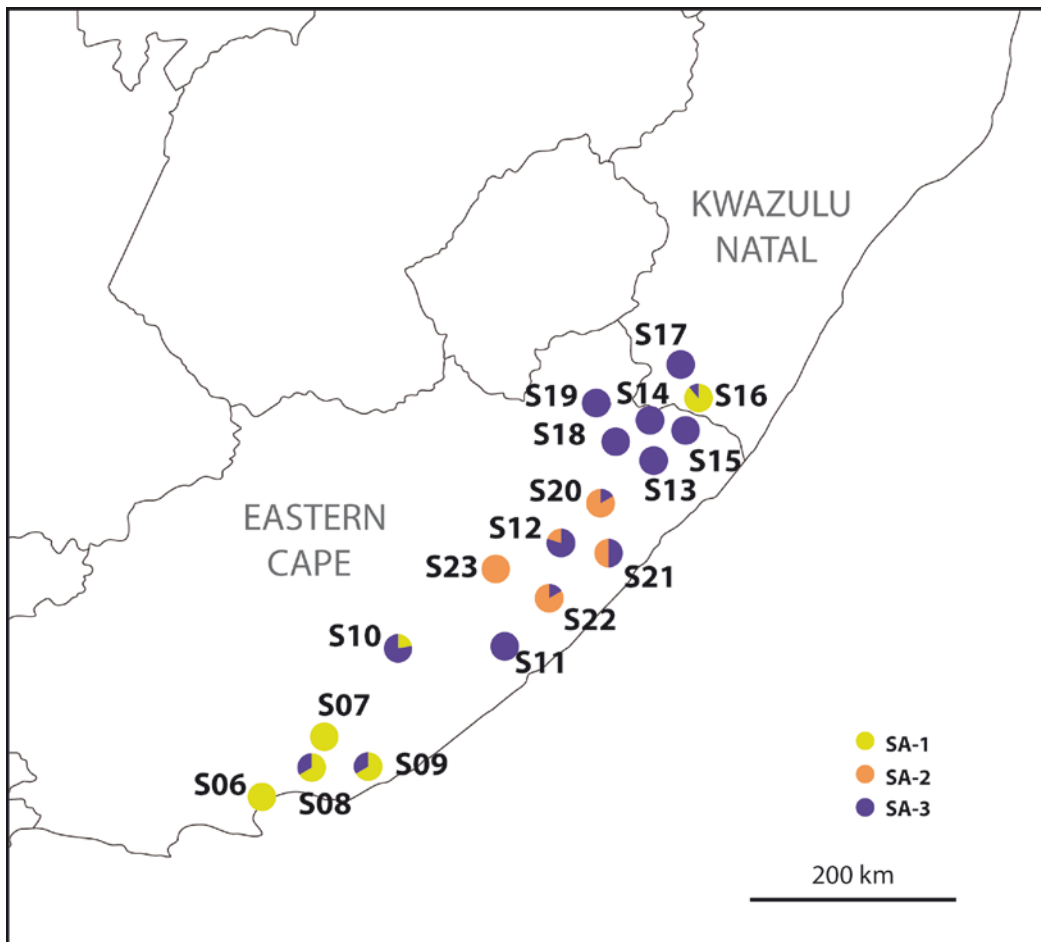
Figure S1 (continued)



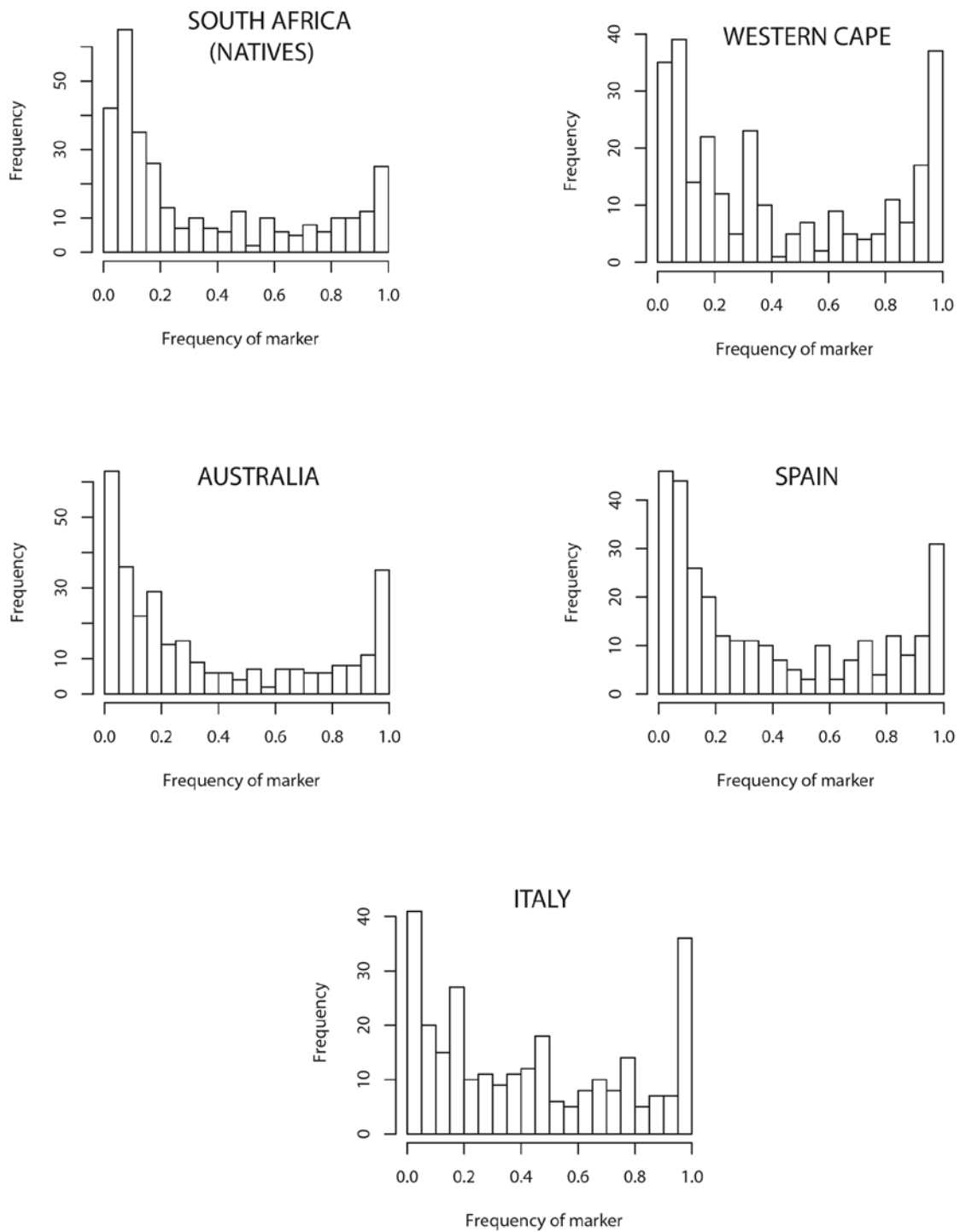
**Figure S2.** Relationship between genetic distance ( $F_{ST}$  values) and geographical distance (km) for population pairs within regions



**Figure S3.** Results of BAPS analysis ( $K = 3$ ) using AFLP markers in native South African samples of *Senecio pterophorus*. Colors identify genetically distinct clusters. South African lineages: SA-1: southern lineage, SA-2: central lineage and SA-3: central/northern lineage.



**Figure S4.** Marker frequency distribution for each of the five ranges studied. Only polymorphic markers are included.



**Figure S5. A**, Marker frequency distribution for each of the five Australian sub-regions studied. **B**, Marker frequency distribution for each of the Spanish sub-regions studied. Only polymorphic markers are included. Australian sub-regions: A-SYD = Sydney area, A-EYRE = Eyre Peninsula area, A-ADE = Adelaide area, A-BM = Barker-Mallee area, A-MEL = Melbourne area; Spanish sub-regions: CAT-N= North Catalonia, CAT-S= South Catalonia.

### A. Australian sub-regions

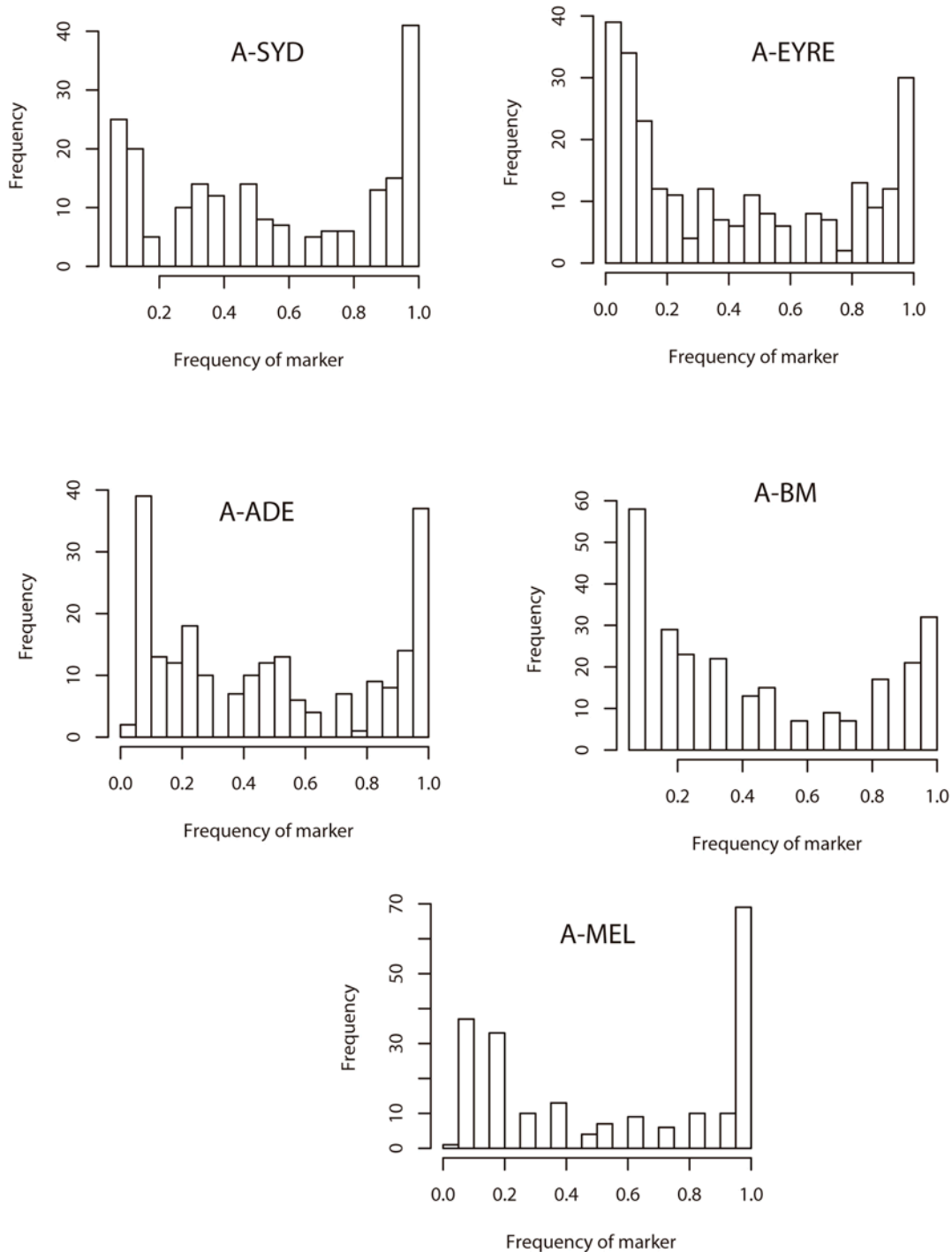
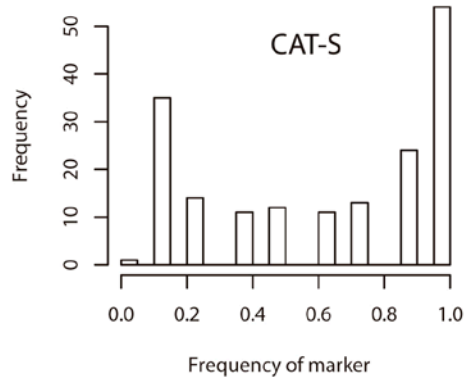
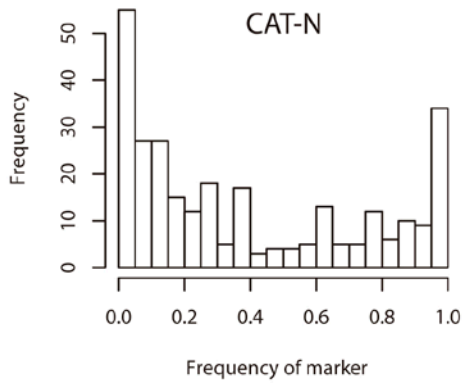


Figure S5 (continuation)

**B. Spanish sub-regions**



**Figure S6. A**, Total metric tons (Tn) of unwashed wool imported from Australia and South Africa to Spain from 1951 to 1986 **B**, Percentage of imported wool from Australia and South Africa in comparison to total amount imported (Estadística del comercio exterior de España 1951-1989)

