ON-LINE SUPPLEMENTARY MATERIAL

Pipenbaher, N., Kaligarič, M., Škornik, S., Ivajnšič, D., Ternjak, T., Šiško, M.: Genetic variability of *Linnaea borealis* – remnant of Eastern-Southeastern Alpine populations indicates a strong bottleneck and *in situ* glacial survival. Acta Botanica Croatica, DOI: 10.37427/botcro-2026-001.

On-line Suppl. Tab. 1. Nine microsatellite loci used in the study of *Linnaea borealis*.

Marker name	Forward and reverse primer sequence (5' - 3')	Motif	Size range (bp)
A5-F	ACA-CAC-TTT-TGA-GGG-CAT-CC	$(CA)_{14}$	172-186
A5-R	TGC-TTT-TCC-TTG-TGC-TTC-CT		
A102-F	CTT-CCA-CCA-CCC-CAA-TGT-A	$(CA)_{11}(AT)_{6}$	204-250
A102-R	TAA-CAA-CCA-CCT-TCG-TGT-GC		
A112-F	CCA-ACA-ACT-ACT-TCG-TCA-CTG	$(TC)_{12}(CA)_{13}(T)(AC)_{3}$	244-284
A112-R	TCC-AAG-AAT-GAG-ACC-ATC-AG		
B119-F	GAT-GGC-ACC-GAT-TGT-TTG	$(TC)_{17}$	214-248
B119-R	AAA-GGC-TGT-GAA-GTC-GTC-G		
C105-F	CCA-ATC-CAC-ACA-ACC-CTA-AC	$(CAA)_{7}(ATG)_{3}(CAG)_{4}(CAA)_{8}$	262-277
C105-R	ACC-TCT-CGC-AAG-CAT-CTT-C		
D7-F	CCT-TAC-GCT-TTG-GAG-ATG-TC	$(GAA)_{8}$	168-192
D7-R	GTG-AGG-CCA-CAG-AGA-AGA-TC		
D110-F	CCC-AGT-GTT-CAG-TGG-ATT-C	$(TC)_{6}CCA(CT)_{6}GTTT(CT)_{3}CA(CT)_{4}$	242-244
D110-R	GAT-GGT-GGT-GCT-TTG-TTG		
D110a-F	ACA-AAG-CAC-CAC-CAT-CAC	$(CTT)_{8}$	285-312
D110a-R	GCA-AAC-CTT-AGA-TAC-CAA-GTT-G		
D118-F	CGG-ACA-TAT-TCC-ACC-CAT-TC	$(TTC)_{3}TTT(TTC)_{8}$	177-193
D118-R	TCC-TGT-AAG-TTT-GGC-CGA-GA		

On-line Suppl. Tab. 2. The Evanno table output for *Linnaea borealis* material generated by the Structure Harvester V0.6.94 application (Earl and Vonholdt 2012).

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	|Ln''(K)|	Delta K
1	20	-2346.135	0.36889	NA	NA	NA
2	20	-2027.12	3.12319	319.015	38.74	12.404
3	20	-1746.845	2.62227	280.275	186.65	71.1788
4	20	-1653.22	1.14045	93.625	67.11	58.8451
5	20	-1626.705	2.3632	26.515	0.36	0.15234
6	20	-1600.55	8.97209	26.155	85.745	9.55686
7	20	-1660.14	9.01743	-59.59	62.605	6.94266
8	20	-1657.125	12.91266	3.015	20.775	1.60889
9	20	-1674.885	24.83712	-17.76	35.84	1.443
10	20	-1728.485	17.88414	-53.6	28.815	1.6112
11	20	-1753.27	13.48981	-24.785	5.62	0.41661
12	20	-1772.435	28.61237	-19.165	26.38	0.92198
13	20	-1765.22	17.37826	7.215	1.5	0.08631
14	20	-1759.505	19.1321	5.715	14.865	0.77697
15	20	-1768.655	25.49288	-9.15	16.785	0.65842
16	20	-1761.02	19.6957	7.635	11.14	0.56561
17	20	-1764.525	11.33216	-3.505	5.52	0.48711
18	20	-1762.51	13.75209	2.015	8.71	0.63336
19	20	-1769.205	21.23687	-6.695	0.94	0.04426
20	20	-1776.84	15.2404	-7.635	NA	NA

On-line Suppl. Tab. 3. Membership values to groups using STRUCTURE software (Pritchard et al. 2000).

Structure analysis K=3				
Accession	Population1	Population2	Population3	Membership treshold 0.9
AT_1	0.736	0.002	0.262	Admixed
AT_2	0.993	0.002	0.005	Population 1
AT_3	0.995	0.002	0.003	Population 1
AT_4	0.995	0.002	0.003	Population 1
AT_5	0.995	0.002	0.003	Population 1
AT_6	0.995	0.002	0.003	Population 1
AT_7	0.993	0.002	0.005	Population 1
AT_8	0.993	0.002	0.005	Population 1
AT_9	0.995	0.002	0.003	Population 1
AT_10	0.995	0.002	0.003	Population 1
AT_11	0.995	0.002	0.003	Population 1
AT_12	0.995	0.002	0.003	Population 1
AT_13	0.995	0.002	0.003	Population 1
SI_1	0.002	0.995	0.003	Population 2
SI_2	0.005	0.991	0.004	Population 2
SI_3	0.002	0.995	0.003	Population 2
SI_4	0.002	0.995	0.003	Population 2
SI_5	0.002	0.995	0.003	Population 2
SI_6	0.014	0.977	0.01	Population 2
SI_7	0.002	0.995	0.003	Population 2
SI_8	0.002	0.995	0.003	Population 2
SI_9	0.002	0.995	0.003	Population 2
SI_10	0.002	0.995	0.003	Population 2
SI_11	0.002	0.995	0.003	Population 2
SI_12	0.002	0.995	0.003	Population 2
SI_13	0.002	0.984	0.013	Population 2
SE_1	0.132	0.009	0.86	Admixed
SE_2	0.003	0.002	0.994	Population 3
SE_3	0.017	0.107	0.875	Admixed
SE_4	0.003	0.013	0.984	Population 3
SE_5	0.006	0.003	0.992	Population 3
SE_6	0.006	0.02	0.975	Population 3
SE_7	0.008	0.003	0.988	Population 3
SE_8	0.003	0.003	0.994	Population 3
SE_9	0.003	0.035	0.962	Population 3
SE_10	0.007	0.213	0.78	Admixed
SE_11	0.007	0.056	0.937	Population 3
SI_14	0.011	0.985	0.004	Population 2
AT_14	0.935	0.008	0.056	Population 1
SE_12	0.006	0.003	0.991	Population 3
SI_15	0.011	0.985	0.004	Population 2
AT_15	0.758	0.014	0.228	Admixed
SE_13	0.01	0.006	0.984	Population 3
SE_14	0.005	0.003	0.992	Population 3
SE_15	0.003	0.003	0.994	Population 3

On-line Suppl. Tab. 3. continued

Structure analysis K=3				
Accession	Population1	Population2	Population3	Membership treshold 0.9
R_1	0.004	0.003	0.992	Population 3
R_2	0.004	0.004	0.992	Population 3
R_3	0.004	0.003	0.992	Population 3
R_4	0.003	0.006	0.991	Population 3
R_5	0.003	0.006	0.991	Population 3
R_6	0.003	0.006	0.991	Population 3
R_7	0.006	0.005	0.989	Population 3
R_8	0.005	0.005	0.991	Population 3
R_9	0.005	0.005	0.991	Population 3
R_10	0.003	0.002	0.994	Population 3
R_11	0.003	0.002	0.994	Population 3
R_12	0.003	0.002	0.994	Population 3
R_13	0.005	0.005	0.991	Population 3
R_14	0.005	0.005	0.991	Population 3
R_15	0.005	0.005	0.991	Population 3
GB_1	0.004	0.004	0.992	Population 3
GB_2	0.004	0.055	0.941	Population 3
GB_3	0.004	0.022	0.974	Population 3
GB_4	0.005	0.004	0.992	Population 3
GB_5	0.011	0.006	0.983	Population 3
GB_6	0.005	0.004	0.991	Population 3
GB_7	0.003	0.005	0.992	Population 3
GB_8	0.045	0.002	0.952	Population 3
GB_9	0.008	0.004	0.988	Population 3
GB_10	0.003	0.007	0.99	Population 3
GB_11	0.004	0.008	0.988	Population 3
GB_12	0.056	0.008	0.937	Population 3
GB_13	0.004	0.005	0.991	Population 3

Admixed:5
Population1:13
Population2:15
Population3: 40

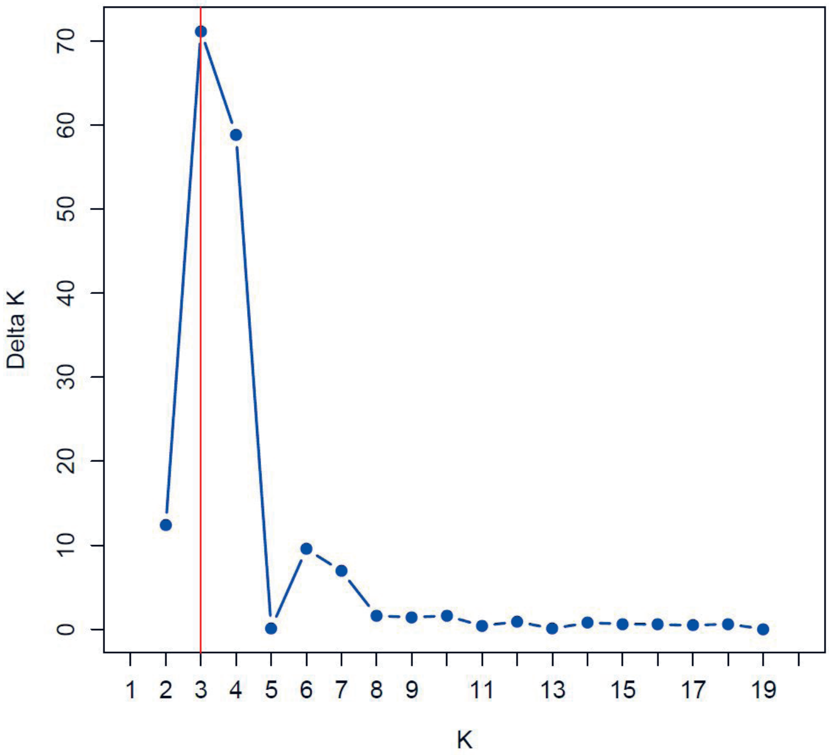
On-line Suppl. Tab. 4. The allele frequency divergence among groups (net nucleotide distance) and the average distances (expected heterozygosity) between individuals in the same group calculated by the STRUCTURE 2.3.4 software (Pritchard et al., 2000).

Allele-frequency divergence among populations (Net nucleotide distance):

Populations	1	2	3
1	–	0.4219	0.2547
2	0.4219	–	0.2134
3	0.2547	0.2134	–

Average distances (expected heterozygosity) between individuals in the same population:

Population 1	0.4375
Population 2	0.5267
Population 3	0.7293



On-line Suppl. Fig. 1. Graphical method, as in Evanno et al. (2005), allowing the detection of the number of groups on the *Linnaea borealis* dataset using Delta K (ΔK).