

Supplementary materials

Semerikov V.L., Semerikova S.A. Genetic variation and population history of three related fir species *Abies sachalinensis*, *A. nephrolepis* and *A. gracilis* (Pinaceae) revealed by nuclear microsatellites

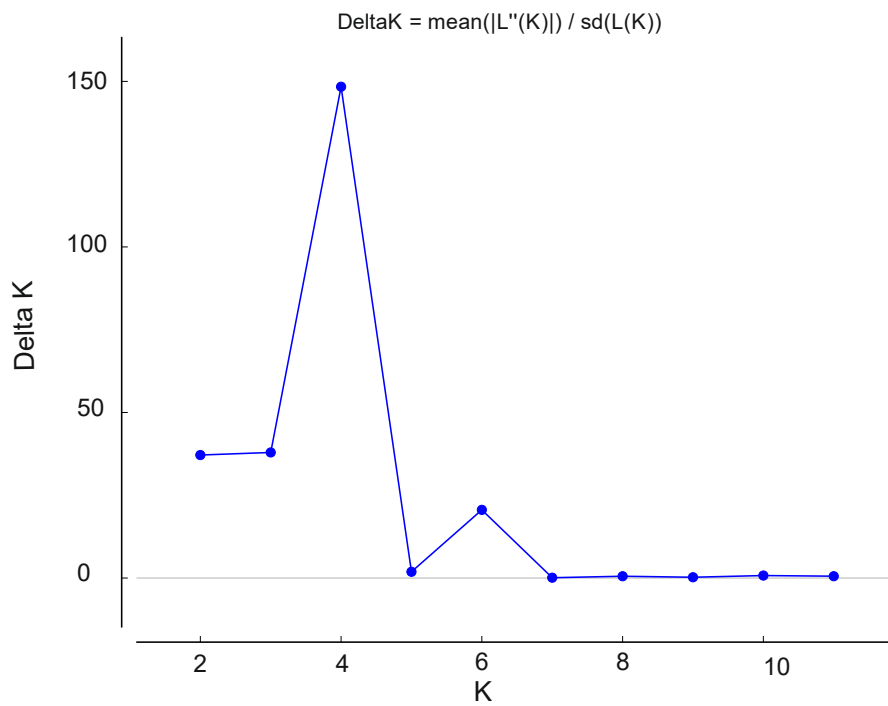
Table S1. Demographic parameters for six *Abies* population groups as estimated by DIYABC analyses with scenario 5.

Parameter	priors	mean	median	mode	q025	q975
N1	10-60000	46700	48000	50900	27400	59100
N2	10-60000	37400	37500	38100	20800	54800
N3	10-60000	24300	21600	12400	3930	56000
N4	10-60000	18600	16100	14600	5420	48800
N5	10-60000	39900	40200	40300	19500	58000
N6	10-2000	437	364	270	89	1280
t1	10-2000	459	368	184	39	1420
r1	0.001- 0.999	0.74	0.76	0.80	0.42	0.94
t2	10-5000	920	623	375	109	3530
t3	10-5000	2950	2960	2920	1050	4760
t4	10-5000	1620	1410	1180	369	4120
t5	10-20000	6840	6210	5880	2230	16300
μ_{mic_1}	$5 \cdot 10^{-5}$ – $5 \cdot 10^{-4}$	$1.59 \cdot 10^{-4}$	$1.42 \cdot 10^{-4}$	$1.09 \cdot 10^{-4}$	$6.62 \cdot 10^{-5}$	$3.43 \cdot 10^{-4}$
p_{mic_1}	0.1 – 0.3	0.22	0.23	0.30	0.12	0.30
sn_{mic_1}	$1 \cdot 10^{-8}$ – $1 \cdot 10^{-5}$	$2.63 \cdot 10^{-6}$	$1.92 \cdot 10^{-6}$	$7.09 \cdot 10^{-8}$	$5.75 \cdot 10^{-8}$	$8.51 \cdot 10^{-6}$

μ_{mic_2}	$1 \cdot 10^{-4} - 1 \cdot 10^{-3}$	$6.19 \cdot 10^{-4}$	$6.31 \cdot 10^{-4}$	$7.47 \cdot 10^{-4}$	$1.77 \cdot 10^{-4}$	$1.00 \cdot 10^{-3}$
p_{mic_2}	0.1 – 0.3	0.19	0.19	0.12	0.11	0.29
s_{nomic_2}	$1 \cdot 10^{-8} - 1 \cdot 10^{-5}$	$2.17 \cdot 10^{-6}$	$7.00 \cdot 10^{-7}$	$1.41 \cdot 10^{-8}$	$1.42 \cdot 10^{-8}$	$9.52 \cdot 10^{-6}$

N1 to N6 give the effective populations sizes for the Kuriles with Hokkaido, South Sakhalin, Central Sakhalin, North Sakhalin, *A. nephrolepis*, *A. gracilis*, respectively; t1, t2, t3, t4 and t5 reflect the time scale measured in generations, r1 reflect the rate of the North Sakhalin in the admixture origin of the Middle Sakhalin, μ_{mic_1} – mean mutation rate per generation of nuclear microsatellites; μ_{mic_2} – mean mutation rate of chloroplast microsatellites; p_{mic_1} – parameter of geometric distribution of the mutation model; s_{nomic_1} – mean rate of single nucleotide insertions/deletions.

(a)



(b)

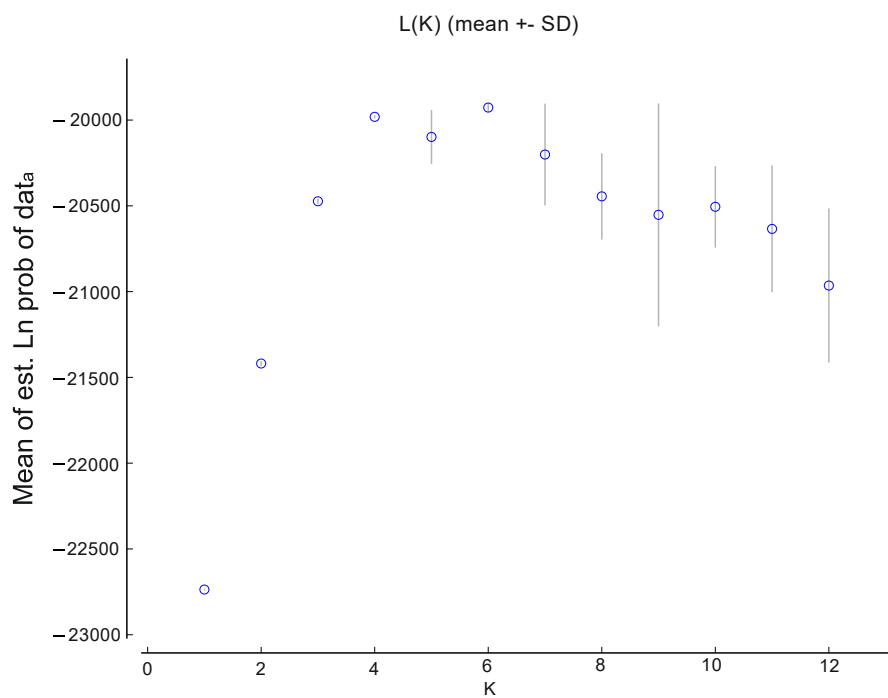


Fig. S1. The tests of the most likely number of clusters in the STRUCTURE analysis using 17 nSSR loci based on ΔK (Evanno et al., 2005) (a) or Ln P(D) (Pritchard et al., 2000) (b) approaches.

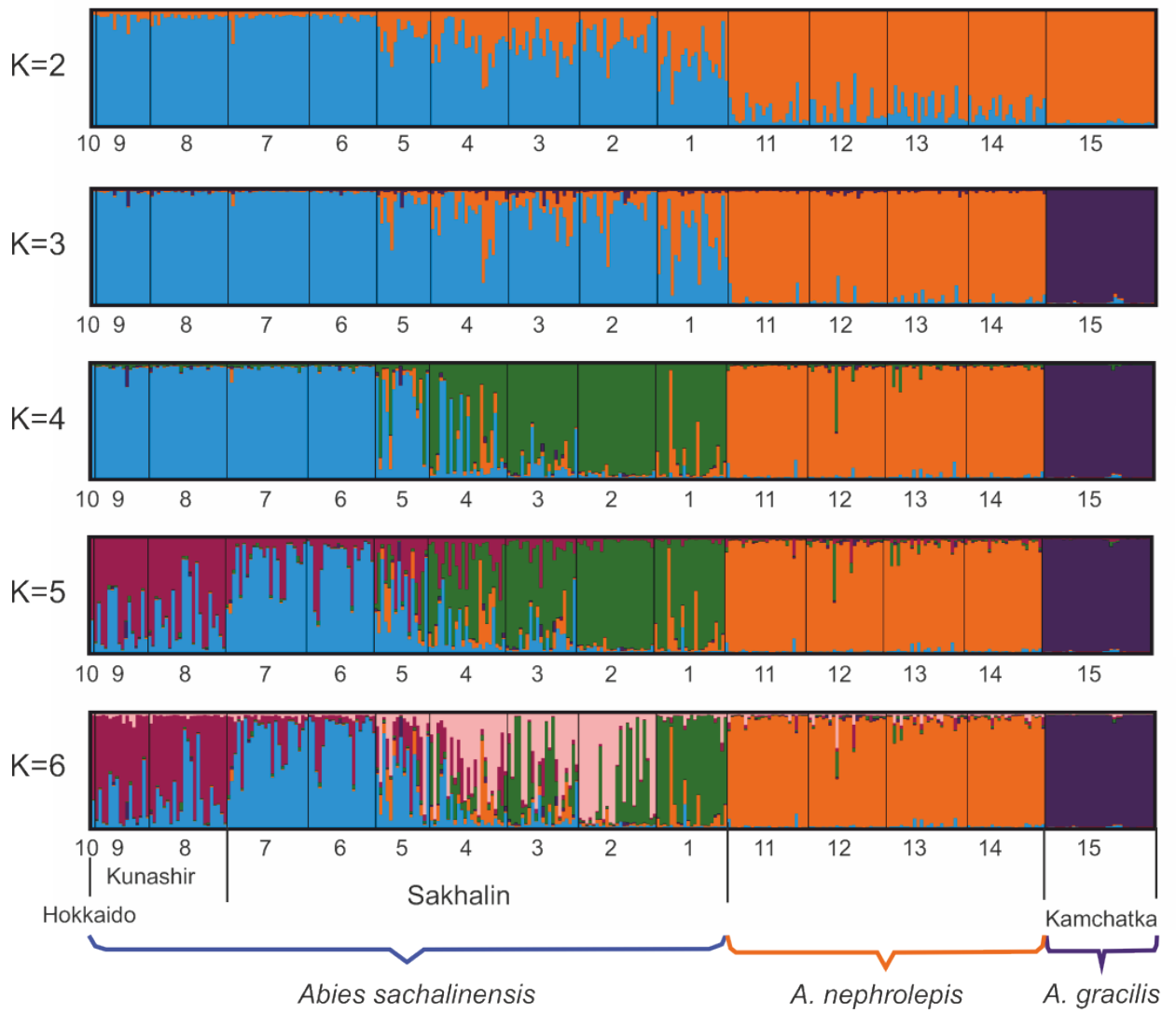


Fig. S2. Bayesian clustering of 15 studied populations at $K=2-6$.

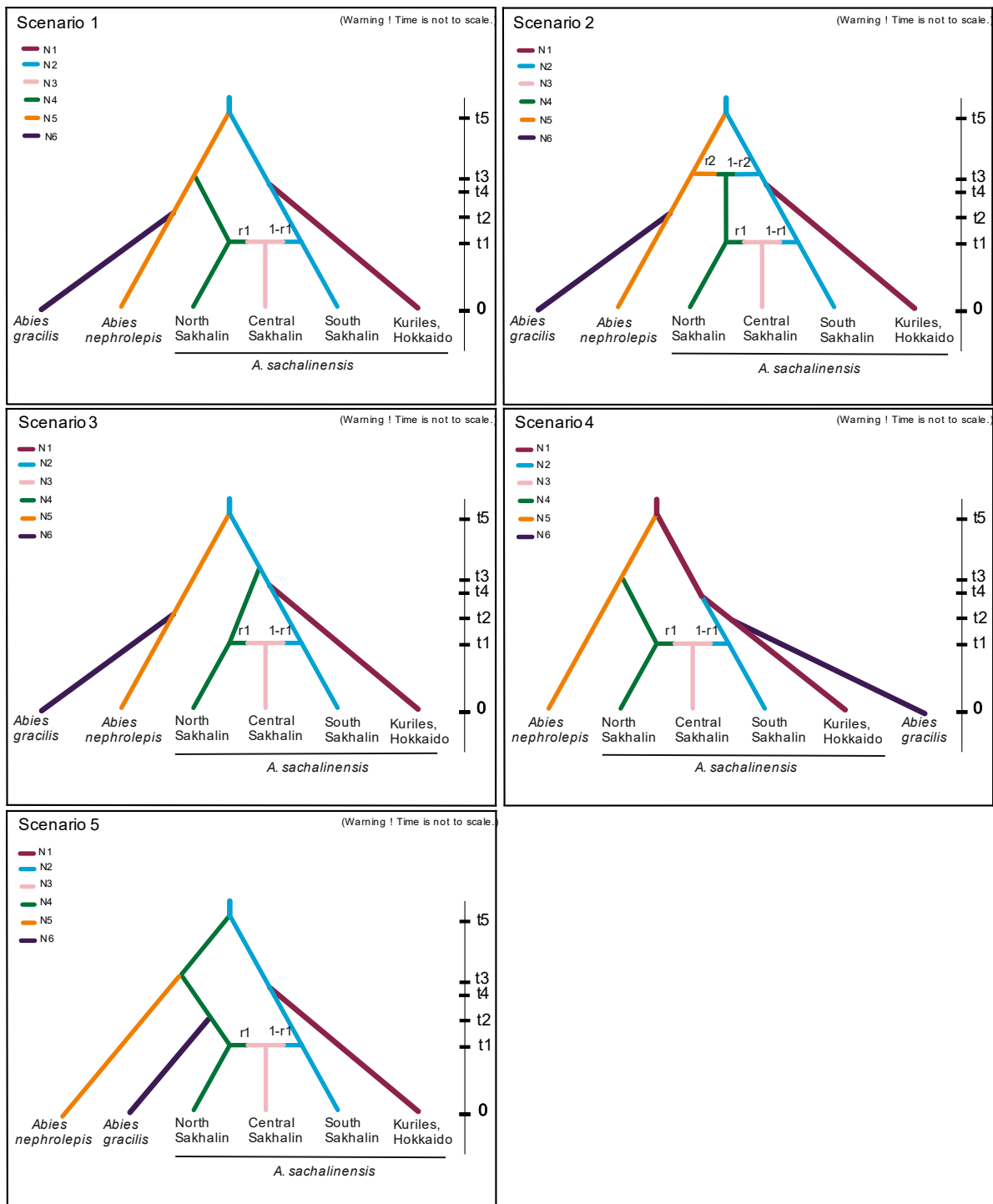


Fig. S3. Alternative demographic scenarios for three *Abies* species analyzed using DIYABC. N1 – N6 correspond to the effective size of the considered six population groups: N1 Hokkaido with Kuriles, N2 South Sakhalin, N3 Central Sakhalin, N4 Northern Sakhalin, N5 *A. nephrolepis*, N6 *A. gracilis*. t_1 , t_2 , t_3 , t_4 , t_5 correspond to the age of demographic events (population divergence or hybridization), r_1 and r_2 correspond to the contribution each of the two parent groups participating in the hybrid formation of a new group.

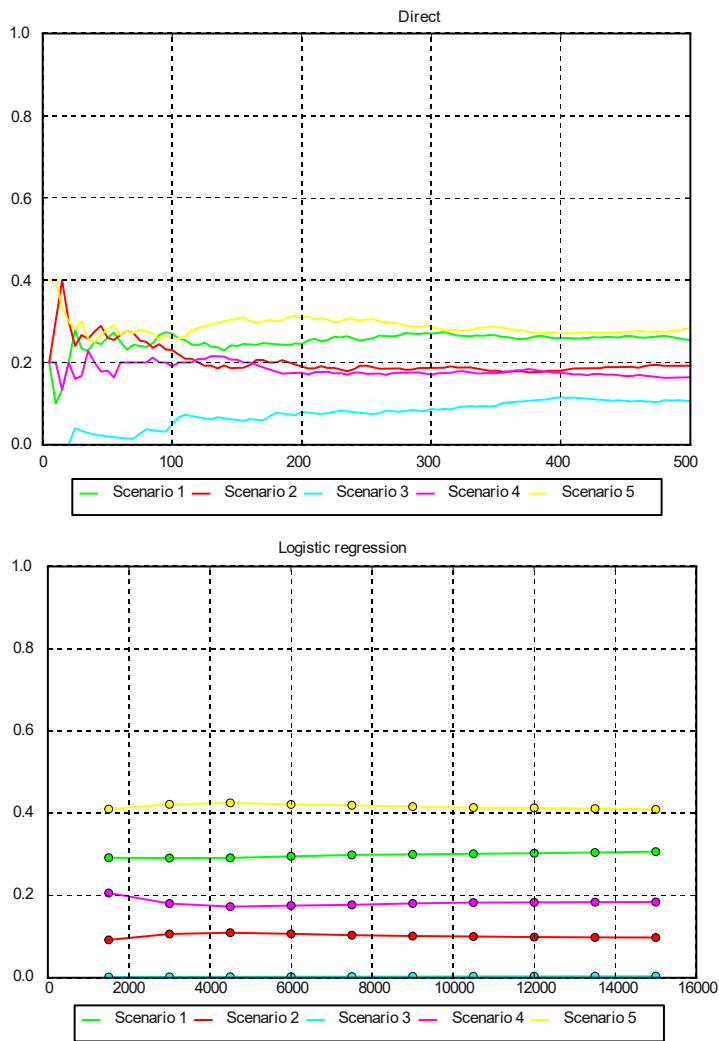


Fig. S4. The posterior probability of five tested demographic scenarios, computed with direct estimate (top) and with logistic regression approach (bottom).