

SUPPLEMENTARY MATERIAL

**Genetic diversity suggests two rather than three larch (*Larix* spp.) species across Russia's northern boreal forest**

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**Table S1.** Characterization of sites

Site	Latitude	Longitude	Elevation (m a.s.l.)	Sampled species	Biome	Mean annual T (°C)	Total annual P (mm)
NUR	59°37'N	59°15'E	750	LASI	NT	-0.20	850
YAM	67°26'N	69°20'E	9	LASI	FT	-6.3	430
TUR	64°17'N	100°13'E	557	LAGM	NT	-8.51	367
KHA	71°57'N	102°40'E	45	LAGM	FT	-12.32	210
CHO	70°30'N	147°11'E	71	LACA	FT	-13.38	211
BIL	68° 02'N	166°40'E	527	LACA	FT	-10.86	237

**NUR** refers to Northern Urals, **YAM** to Yamal Peninsula, **KHA** to Khatanga, **TUR** to Tura, **CHO** to Chokurdakh, **BIL** to Bilibino, LASI to *Larix sibirica*, LAGM to *Larix gmelini*, LACA to *Larix cajanderi*, NT to northern taiga, and FT to forest-steppe.

**Table S2.** Geographical distance between populations (in Km).

	YAM	KHA	TUR	CHO	BIL
NUR	1007	2335	2184	3904	4685
YAM		1380	1442	2919	3691
KHA			861	1566	2359
TUR				2069	2866
CHO					813

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**Table S3.** Details of the 12 microsatellite markers used in the study.

Multiplex	Locus	Repeat motif	Primer sequence (5'-3')	Allele size range (bp)	Fluorescent dye
1	bcLK056	(AG) <sub>20</sub>	F: ATGGGCTAAGGTATGTTTTACG R: TTGCCAACATCTATACCAAGTCT	174-200	ROX
	bcLK066	(TG) <sub>12</sub>	F: GCAACCGACAATGATTACATAG R: CTAAACTGAACCTTGCTCAAT	155-172	R6G
	bcLK228	(AG) <sub>18</sub>	F: CCCTAACCTAGAATCCAATAA R: GAGGAAGGCGACAAGTCATT	183-234	R6G
	bcLK260	(TG) <sub>14</sub> (AG) <sub>9</sub>	F: CTCCATAAGGGGCATCACAT R: TGGGCTCAAGTTGGACATTA	115-126	6-FAM
2	bcLK211	(CT) <sub>16</sub>	F: CCATTCTCCATAGGTTTCATTG R: ATGCTCCTTACTAAGTCAGATACAC	207-232	6-FAM
	bcLK224	(AG) <sub>17</sub>	F: GGAGAGGCCACTACTATTATTAC R: ATGCGTTCCTTCATTCTCT	152-168	6-FAM
	bcLK232	(AG) <sub>19</sub>	F: TGTGCTGGGTTGTTGTTAGA R: GGGTAATAGTTCAGTCTTTG	142-178	TAMRA
	bcLK253	(AG) <sub>17</sub>	F: AACACCATAGTGCAATGTGC R: TCCTCTTGTTGATGCCACTT	217-243	TAMRA
3	bcLK189	(AG) <sub>17</sub> AT(AG) <sub>6</sub>	F: ACCATACGCATACCCAATAGA R: AGTTTTCCCTTCCACACAAT	162-196	TAMRA
	bcLK225	(GA) <sub>20</sub>	F: CGTGGTCCCCTCCTCTAAA R: TGGCAGCTAAAGGATTAAGAA	180-213	6-FAM
	bcLK235	(TC) <sub>9</sub> (AC) <sub>2</sub> AG(AC) <sub>14</sub>	F: TTCACCTTGATCCTAGAGTTAGA R: AACCCCTAACCATATAATCCA	177-220	R6G
	bcLK263	(TC) <sub>20</sub>	F: CGATTGGTATAGTGGTCATTGT R: CCATCATACCTTCTTGAAGAG	205-255	ROX

**Table S4.** Characteristics of the sampled trees.

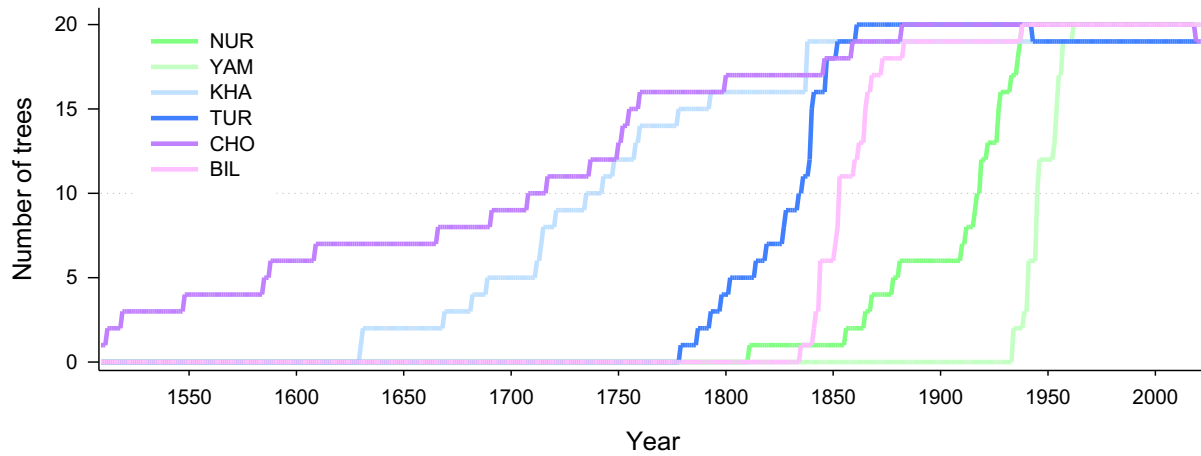
	Site	Cross-dated trees	Chronology start year	Chronology end year	Mean tree age (mean ± SD)	TRW in mm (mean ± SD)	dbh in cm (mean ± SD)	Tree height in m (mean ± SD)
LASI	NUR	20	1811	2020	112±34	0.98±0.56	20.25±6.28	7.05±1.92
	YAM	20	1945	2021	60±8	1.13±0.34	-	-
LAGM	KHA	19	1630	2023	300±55	0.31±0.15	22.3±2.25	11.7±1.89
	TUR	20	1779	2020	191±34	0.43±0.28	19.7±2.67	12.2±1.44
LACA	CHO	20	1509	2022	332±118	0.20±0.08	17.8±4.3	6.3±1.3
	BIL	20	1835	2023	164±22	0.52±0.21	22.2±50.2	10.7±1.15

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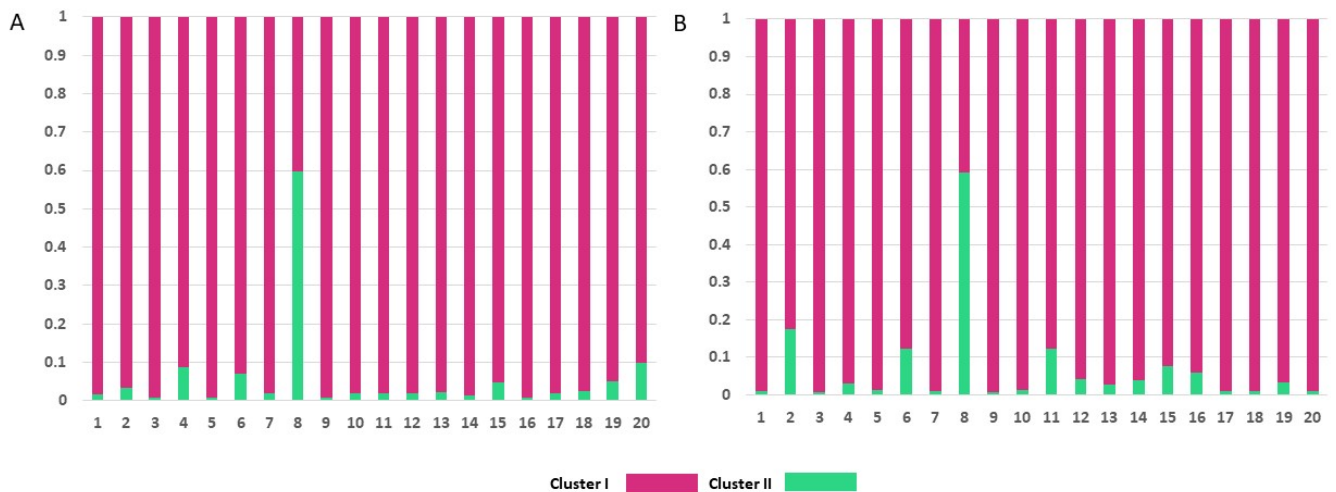
**Table S5.** Deviation from Hardy-Weinberg equilibrium: *p*-values and (degrees of freedom) for *L. sibirica*, *L. gmelinii* and *L. cajanderi* populations by locus. Values in bold represent significant deviation from Hardy-Weinberg equilibrium at  $\alpha = 0.05$ .

Locus	NUR	YAM	TUR	KHA	CHO	BIL
bcLK066	0.175 (28)	0.497 (78)	0.467 (28)	0.274 (36)	0.966 (36)	<b>0.040</b> (36)
bcLK189	0.827 (21)	0.290 (21)	0.297 (21)	<b>0.009</b> (21)	0.965 (36)	0.187 (28)
bcLK224	0.160 (28)	<b>&lt;0.001</b> (3)	0.894 (21)	0.864 (28)	0.864 (28)	<b>0.040</b> (10)
bcLK225	<b>0.022</b> (28)	<b>&lt;0.001</b> (45)	0.933 (231)	0.534 (105)	<b>&lt;0.001</b> (120)	0.077 (78)
bcLK228	0.716 (28)	0.228 (105)	0.683 (91)	0.107 (78)	0.314 (78)	<b>&lt;0.001</b> (36)
bcLK232	<b>0.004</b> (10)	0.583 (21)	0.205 (15)	1.000 (55)	0.087 (21)	<b>0.004</b> (6)
bcLK235	0.907 (36)	<b>0.003</b> (136)	0.198 (91)	<b>0.034</b> (136)	0.526 (66)	<b>0.015</b> (21)
bcLK253	<b>&lt;0.001</b> (36)	<b>0.003</b> (6)	0.202 (10)	<b>0.001</b> (10)	<b>0.020</b> (10)	<b>0.004</b> (6)
bcLK260	<b>0.036</b> (36)	0.169 (45)	0.862 (55)	0.349 (91)	0.601 (91)	0.123 (28)

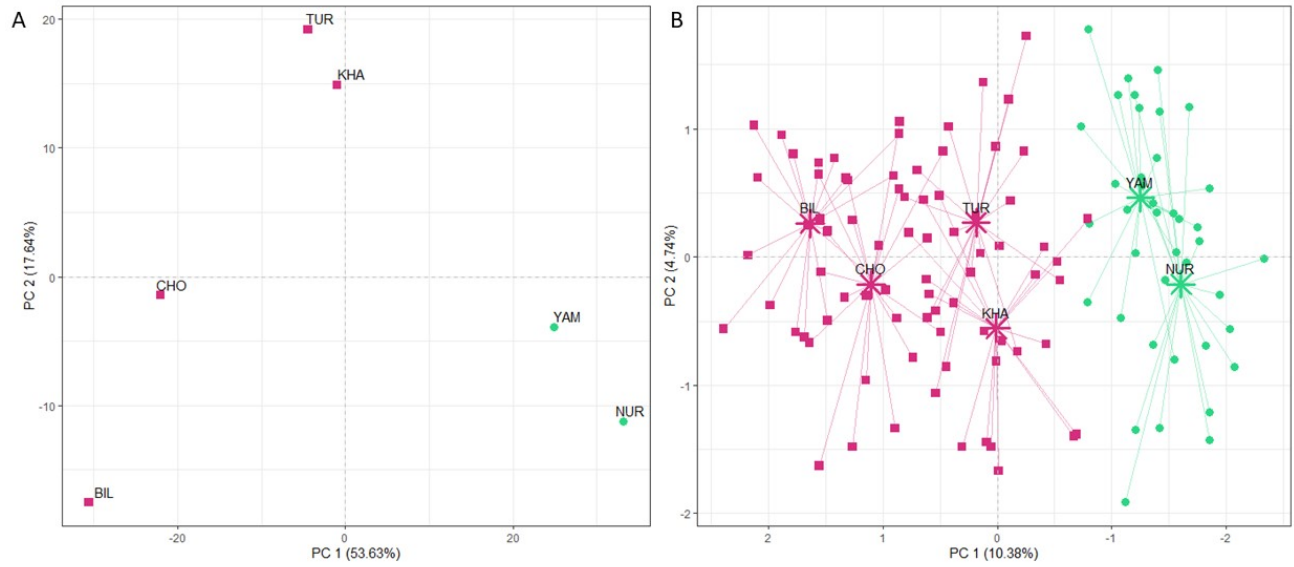
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**Figure S1.** Sample depth at each population. The dotted line represents the year in which sample depth reached 50%. **NUR** refers to Northern Urals, **YAM** to Yamal Peninsula, **KHA** to Khatanga, **TUR** to Tura, **CHO** to Chokurdakh, and **BIL** to Bilibino.



**Figure S2.** Bayesian clustering analysis of the **TUR** (A) and **KHA** (B) populations based on nine nuclear microsatellite loci. Barplots indicate estimated assignment of each individual into two  $K$  clusters.



**Figure S3.** Principal component analysis (PCA) plot showing the first two principal components. Colors used in the PCA plot correspond to the result of STRUCTURE analysis at  $K=2$ . A) PCA plot displaying all *Larix* populations analyzed in the present study. B) PCA plot displaying all *Larix* individuals analyzed in the present study. **NUR** refers to Northern Urals, **YAM** to Yamal Peninsula, **KHA** to Khatanga, **TUR** to Tura, **CHO** to Chokurdakh, and **BIL** to Bilibino.