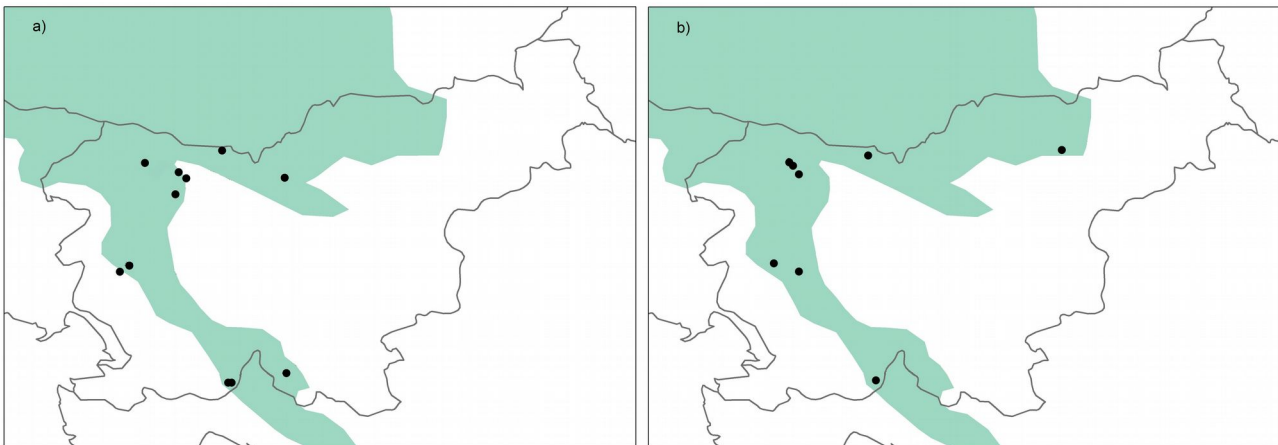


Supplementary material

Fig. S1 – Geographic location of the sampled populations in Slovenia. (a) Populations tested using isoenzymes; (b) populations tested using SSRs. The green area represents the Norway spruce distribution range across Slovenia (source: EUFORGEN - [http:// www.euforgen.org/species/picea-abies/](http://www.euforgen.org/species/picea-abies/)).



Westergren M, Bozic G, Kraigher H (2018).

Genetic diversity of core vs. peripheral Norway spruce native populations at a local scale in Slovenia
iForest – Biogeosciences and Forestry – doi: [10.3832/ifor2444-011](https://doi.org/10.3832/ifor2444-011)

Fig. S2 - The Norway spruce population of Smrekova Draga (SD), Slovenia, located along an inverted vegetation gradient occurring in a Karst sinkhole.



Tab. S1 - Pairwise F_{ST} values (above diagonal) and p-values for genotypic differentiation (below diagonal) among Norway spruce populations based on 13 polymorphic isoenzyme loci. Statistically significant departures from zero (F_{ST}) at $\alpha = 0.05$ are marked with an asterisk (*). (UTL): upper tree line populations; (INV): vegetation inversion populations. For population codes see Tab. 1.

	LIP^{UTL}	PP^{UTL}	VE^{UTL}	GS^{UTL}	TR^{INV}	VP^{INV}	SD^{INV}	TB	LP	LED	SMR
LIP^{UTL}		0.013	0.002	0.008	0.014	0.016	0.000	0.013	0.008	0.009	0.006
PP^{UTL}	0.060		0.016	0.034*	0.021	0.024	0.016	0.011	0.009	0.015	0.000
VE^{UTL}	0.256	0.091		0.000	0.005	0.002	0.006	0.000	0.000	0.000	0.007
GS^{UTL}	0.015	0.001	0.788		0.007	0.001	0.018	0.014	0.013	0.004	0.021
TR^{INV}	0.000*	0.002	0.288	0.493		0.005	0.030*	0.015	0.016	0.009	0.008
VP^{INV}	0.002	0.009	0.520	0.427	0.020		0.027	0.015	0.009	0.000	0.018
SD^{INV}	0.031	0.018	0.485	0.016	0.000*	0.003		0.019	0.004	0.017	0.019
TB	0.274	0.251	0.264	0.187	0.000*	0.004	0.000*		0.010	0.003	0.003
LP	0.049	0.009	0.348	0.026	0.000*	0.167	0.396	0.019		0.007	0.011
LED	0.023	0.055	0.509	0.100	0.000*	0.709	0.036	0.102	0.032		0.008
SMR	0.627	0.686	0.054	0.010	0.002	0.000*	0.000*	0.769	0.001*	0.006	

Tab. S2 - Pairwise F_{ST} values (above diagonal) and p-values for genotypic differentiation (below diagonal) among Norway spruce populations based on six SSR loci. Statistically significant departures from zero (F_{ST}) at $\alpha = 0.05$ are marked with an asterisk (*). (UTL): upper tree line populations; (INV): vegetation inversion populations. For population codes see Tab. 1.

	LIP^{UTL}	CJ^{UTL}	SD^{INV}	VP^{INV}	SIJ	JER	CV
LIP^{UTL}	-	0.009	0.003	0.010	0.000	0.005	0.004
CJ^{UTL}	0.002*	-	0.003	0.017*	0.008	0.001	0.007
SD^{INV}	0.071	0.369	-	0.014*	0.007	0.005	0.004
VP^{INV}	0.000*	0.000*	0.008	-	0.015*	0.017*	0.021*
SIJ	0.633	0.004	0.003*	0.011	-	0.001	0.005
JER	0.016	0.066	0.013	0.010	0.309	-	0.007
CV	0.002*	0.117	0.138	0.003*	0.002*	0.014	-