

## Supplementary material

**Table S1:** Sampling of 136 individuals of the *Papaver alpinum* complex included here, with name codes as the three first letters of field populations. Coordinates as easternness (E) and northernness (N) in the Swiss Coordinate System. The 112 samples confirmed as native individuals of *P. occidentale* based on STRUCTURE analyses are indicated as such (Nat), whereas introduced samples (Int) and those genetically pertaining to outgroups *P. sendtneri* and *P. tatricum* (Out) are indicated. The mean read depth (DP) and proportion of SNPs with missing data (%NAs) are shown for each sample

Region	Code	E	N	Origin	DP	%NAs
Massif des Bornes	JAL1a	523494	94768	Nat	22.08	2.26
Massif des Bornes	JAL1c	523496	94770	Nat	15.09	3.55
Massif des Bornes	JAL2a	523440	94617	Nat	24.19	15.52
Massif des Bornes	JAL2c	523444	94618	Nat	1.30	3.65
Massif des Bornes	COL1a	524116	94177	Nat	9.98	0.57
Massif des Bornes	COL1c	524118	94175	Nat	20.39	1.01
Massif des Bornes	COL2a	523692	94427	Nat	12.37	4.55
Massif des Bornes	COL2c	523694	94429	Nat	10.17	1.35
Massif des Bornes	MOR1a	526723	97245	Nat	16.66	1.13
Massif des Bornes	MOR1c	526637	97151	Nat	18.26	3.82
Massif des Bornes	MOR2a	526463	97059	Nat	17.52	4.29
Massif des Bornes	MOR2c	526272	96927	Nat	13.04	0.87
Massif des Bornes	MOR3a	526855	95447	Nat	12.28	1.08
Massif des Bornes	MOR3c	527554	97427	Nat	12.60	1.16
Massif des Bornes	MOR4a	526240	96820	Nat	9.73	0.64
Massif des Bornes	MOR4c	526725	97249	Nat	31.69	1.37
Massif des Bornes	PTB1a	524117	94573	Nat	19.21	3.36
Massif des Bornes	PTB1c	524187	94628	Nat	12.80	4.07
Massif des Bornes	SOT1a	524007	95135	Nat	10.28	4.09
Massif des Bornes	SOT1d	523728	95348	Nat	16.28	3.29
Grammont	GRA1a	552594	134304	Nat	16.14	3.73
Grammont	GRA1c	552585	134230	Nat	6.19	1.01
Grammont	GRA2a	552599	134235	Nat	16.60	2.87
Grammont	GRA2c	552591	134217	Nat	13.19	4.33
Grammont	GRA3a	552588	134215	Nat	21.74	2.87
Grammont	GRA3c	552574	134229	Nat	11.02	0.77
Gummfluh	PIE1a	580347	143452	Nat	20.32	1.01
Gummfluh	PIE1c	580034	143270	Nat	25.12	1.28
Gummfluh	PIE2a	579999	143234	Nat	7.35	1.67
Gummfluh	PIE3a	579989	143225	Nat	10.04	1.55
Gummfluh	PIE3c	579991	143224	Nat	24.16	3.31
Gummfluh	SAL1a	579663	143048	Nat	7.09	1.77
Gummfluh	SAL1c	579610	143000	Nat	16.11	11.58
Gummfluh	SAL2a	579632	143206	Nat	9.47	1.13
Gummfluh	SAL2c	579650	143210	Nat	16.64	0.72
Jura	CUN1a	510788	158586	Int	13.67	1.77
Jura	TEN1a	513111	160593	Int	14.13	1.20
Jura	TEN1b	513113	160598	Int	14.20	2.11
Jura	TEN1c	513114	160593	Int	15.74	8.86

Vanil Noir	COM1a	577026	152436	Nat	9.78	5.68
Vanil Noir	COM1c	577055	152432	Nat	17.69	12.33
Vanil Noir	COM2a	577125	152334	Nat	16.80	1.45
Vanil Noir	COM2c	577189	152299	Nat	10.08	4.51
Vanil Noir	COM3a	577140	152353	Nat	11.38	1.55
Vanil Noir	COM3c	577180	152257	Nat	15.36	3.94
Vanil Noir	PAR1a	576800	151454	Nat	15.95	0.71
Vanil Noir	PAR1c	576820	151445	Nat	11.27	4.70
Vanil Noir	PAR2a	576842	151414	Nat	19.54	5.22
Vanil Noir	PAR2c	576830	151427	Nat	10.66	2.50
Vanil Noir	PAR3a	576849	151413	Nat	17.27	3.28
Vanil Noir	PAR3c	576851	151411	Nat	15.97	2.45
Vanil Noir	STJ1a	576436	151924	Nat	13.67	3.77
Vanil Noir	STJ1c	576445	151909	Nat	10.28	0.30
Vanil Noir	STJ2a	576450	151905	Nat	16.28	4.41
Vanil Noir	STJ2c	576440	151928	Nat	13.23	1.99
Vanil Noir	STJ3a	576472	151926	Nat	17.56	1.94
Vanil Noir	STJ3c	576483	151950	Nat	21.66	4.78
Vanil Noir	STJ4a	576554	151770	Nat	10.00	20.9
Vanil Noir	STJ4c	576687	151826	Nat	12.47	1.53
Vanil Noir	VEC1a	577021	152648	Nat	22.13	0.54
Vanil Noir	VEC1c	577004	152665	Nat	13.44	5.68
Vanil Noir	VEC2d	576970	152744	Nat	14.13	0.91
Vanil Noir	VEC2e	576932	152705	Nat	21.12	4.36
Vanil Noir	VEC3a	576877	152665	Nat	18.29	0.81
Vanil Noir	VEC3c	576854	152626	Nat	10.63	1.48
Vanil Noir	VEC4a	576799	152663	Nat	21.09	1.08
Vanil Noir	VEC4c	576783	152658	Nat	23.76	1.86
Dent de Savigny	RUT1a	584494	156069	Nat	23.92	3.11
Dent de Savigny	RUT1c	584554	156073	Nat	11.15	2.06
Dent de Savigny	RUT2a	584606	156028	Nat	9.79	1.50
Dent de Savigny	RUT2c	584623	156126	Nat	14.99	3.58
Dent de Savigny	RUT3a	584726	156032	Nat	16.70	0.72
Dent de Savigny	RUT3c	584807	156035	Nat	12.04	6.34
Dent de Savigny	SAV1a	583809	155591	Nat	23.14	0.74
Dent de Savigny	SAV1c	583832	155598	Nat	10.45	2.57
Dent de Savigny	SAV2a	583920	155659	Nat	29.93	5.68
Dent de Savigny	SAV2c	583871	155673	Nat	13.73	3.02
Spillgarten	FRO1a	599739	154462	Nat	21.78	2.52
Spillgarten	FRO1c	599689	154493	Nat	18.50	0.89
Spillgarten	FRO2a	599554	154550	Nat	21.86	0.38
Spillgarten	FRO2c	599533	154555	Nat	14.61	1.52
Spillgarten	FRO3a	599448	154555	Nat	14.39	1.53
Spillgarten	FRO3c	599356	154609	Nat	27.63	1.65
Spillgarten	FRO4a	599230	154542	Nat	25.57	0.37
Spillgarten	FRO4c	599256	154501	Nat	17.24	0.98
Spillgarten	GAN1a	598875	152925	Nat	14.72	98.64
Spillgarten	GAN1c	598856	153069	Nat	17.66	3.41
Spillgarten	GAN2a	598858	152946	Nat	11.42	2.48
Spillgarten	GAN2c	598878	152976	Nat	10.44	1.15
Spillgarten	GAN3a	598802	153036	Nat	9.70	1.30
Spillgarten	GAN3c	598763	152991	Nat	10.97	1.09
Spillgarten	GAN4c	598663	152997	Nat	15.32	2.90
Spillgarten	HFR1a	600367	154424	Nat	13.20	4.55
Spillgarten	HFR1c	600488	154282	Nat	12.90	1.01
Spillgarten	HFR2a	600517	154290	Nat	23.91	0.16
Spillgarten	HFR2c	600432	154194	Nat	14.83	0.32
Spillgarten	HFR3a	600479	154357	Nat	11.41	0.13
Spillgarten	HFR3c	600486	154339	Nat	14.48	0.32
Spillgarten	HFR4a	600455	154236	Nat	21.84	0.96
Spillgarten	HFR4c	600417	154258	Nat	17.44	0.64

Spillgerten	HFR5a	600271	154210	Nat	15.59	1.52
Spillgerten	HFR5c	600286	154226	Nat	12.56	4.60
Spillgerten	HFR6a	600307	154160	Nat	10.85	0.38
Spillgerten	HFR6c	600167	154186	Nat	21.21	6.00
Spillgerten	HOL1a	599346	154100	Nat	11.30	4.88
Spillgerten	HOL1c	599325	154128	Nat	25.74	1.28
Spillgerten	HOL2a	599503	154137	Nat	11.07	0.69
Spillgerten	HOL2c	599732	154105	Nat	6.50	1.87
Spillgerten	VSP1a	599784	153988	Nat	11.97	0.74
Spillgerten	VSP1c	599838	153987	Nat	16.13	0.10
Spillgerten	VSP2a	599843	153989	Nat	23.82	2.50
Spillgerten	VSP2c	599879	153989	Nat	17.56	0.30
Spillgerten	VSP3a	599902	153995	Nat	25.50	0.59
Spillgerten	VSP3c	600008	153939	Nat	15.66	0.42
Spillgerten	VSP4a	600070	153910	Nat	12.65	0.23
Spillgerten	VSP4b	600167	153897	Nat	18.46	1.94
Lucerne	BLA1a	644462	182601	Out	16.39	0.65
Lucerne	BLA1c	644466	182597	Out	14.20	0.96
Lucerne	BLA2a	644472	182535	Out	9.40	2.77
Lucerne	BLA3a	644440	182711	Out	14.79	0.67
Lucerne	BLA3b	644439	182705	Out	13.73	2.55
Lucerne	BLA4a	644650	182748	Out	17.41	1.09
Lucerne	BLA5a	644674	182775	Out	10.77	1.42
Lucerne	BLA5b	644730	182954	Out	24.97	4.26
P. sendtneri	PSe1	659990	204424	Out	17.13	na
P. sendtneri	PSe2	659995	204419	Out	10.79	na
P. sendtneri	PSe3	659987	204414	Out	10.75	na
P. sendtneri	PSe4	659970	204403	Out	19.44	na
P. tatricum	PTa1_3	NA	NA	Out	14.88	4.16
P. tatricum	PTa2_3	NA	NA	Out	11.09	0.49
P. tatricum	PTa3_3	NA	NA	Out	14.48	5.39
P. tatricum	PTa4_3	NA	NA	Out	11.10	0.40
P. tatricum	PTa1a	NA	NA	Out	17.55	0.93
P. tatricum	PTa1b	NA	NA	Out	17.76	1.13
P. tatricum	PTa2a	NA	NA	Out	24.44	2.04
P. tatricum	PTa2b	NA	NA	Out	15.97	1.45

**Table S2:** Filtering of raw SNPs to generate dataset, with number of SNPs retained at each step

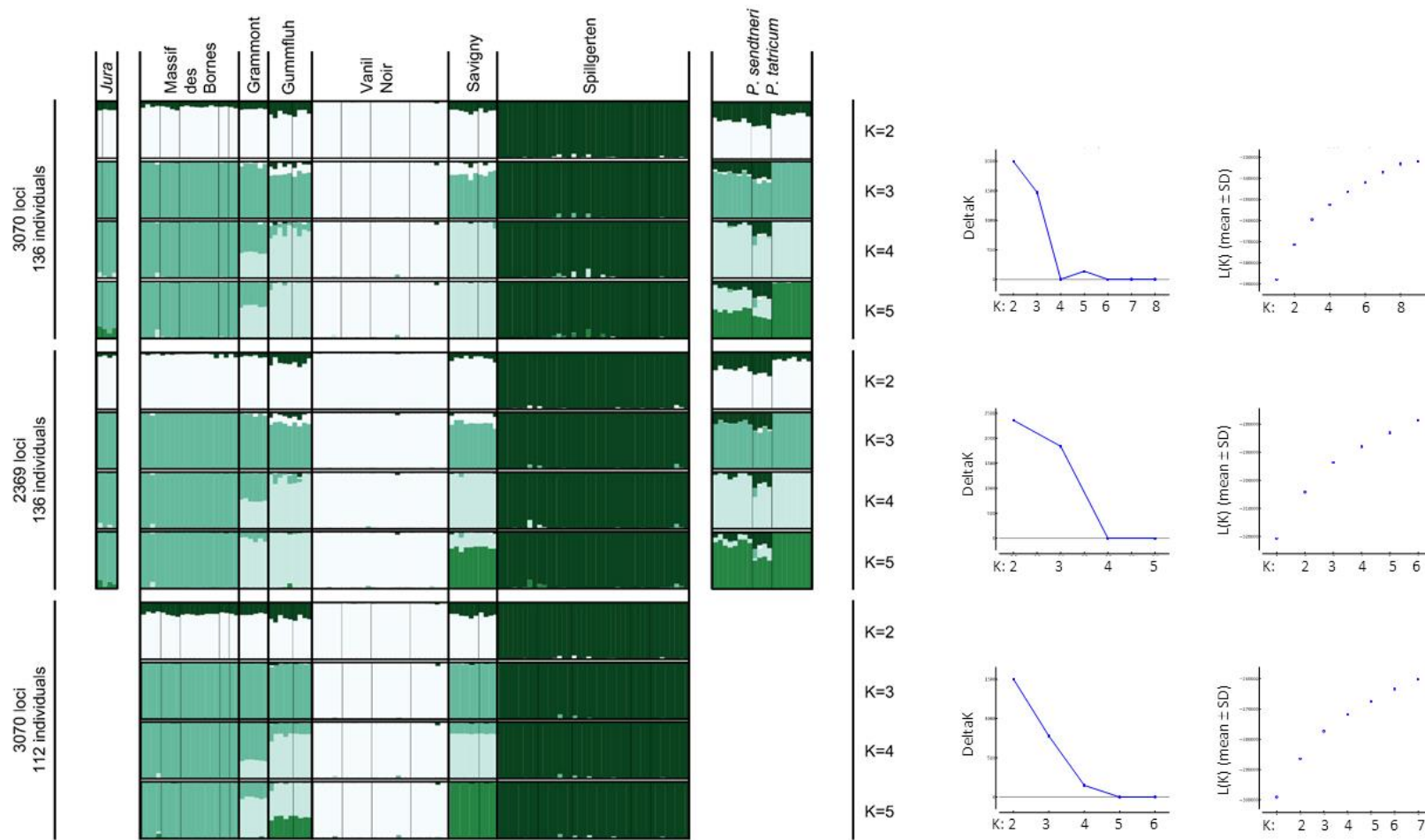
Filtering step	Number of SNPs
Total raw SNPs	338463
Removal of quality (Q<20), Min depth (<3), Mean depth (<10), Minor Allele Count (<3), Minor Allele frequency (<0.05) and missing data (>0.5)	45604
Removal of sites with too many NAs (0.2) per population	41350
Filter for allele balance and mapping quality	18251
Removal of loci with extreme high coverage	17676
Decomposition of complex SNPs	21314
Removal of indels, sites with missing data (0.9) and non-biallelic sites	18941
Removal of sites deviating from (global) Hardy-Weinberg (SNPs)	5912
Rad_haplotyper (independent ddRAD loci)	3070
Removal of putatively non-neutral ddRAD loci	2369

**Table S3:** Partitioning of genetic structure among the 112 native individuals (I) of *Papaver occidentale* nested in field populations (S) and sampling regions (C) from hierarchical AMOVA on 3070 ddRAD loci

	<i>P. occidentale</i>	p-value
$F_{IS}$	-0.2015	1.0000+-0.0000
$F_{SC}$	0.0510	0.0000+-0.0000
$F_{CT}$	0.1217	0.0000+-0.0000
$F_{IT}$	-0.0015	0.9922+-0.0028

**Table S4:** Pairwise  $F_{ST}$  between the 19 native populations of *P. occidentale*. Significant differences are noted in bold

	COL	JAL	MOR	PTB	SOT	GRA	PIE	SAL	COM	PAR	STJ	VEC	RUT	SAV	FRO	GAN	HFR	HOL	VSP
COL	0																		
JAL	-0.007	0																	
MOR	<b>0.0601</b>	<b>0.0794</b>	0																
PTB	-0.027	-0.024	<b>0.0771</b>	0															
SOT	-0.042	-0.028	<b>0.0505</b>	-0.061	0														
GRA	<b>0.1647</b>	<b>0.173</b>	<b>0.1841</b>	<b>0.1597</b>	<b>0.1579</b>	0													
PIE	<b>0.1239</b>	<b>0.1364</b>	<b>0.1625</b>	<b>0.1304</b>	0.1132	<b>0.1983</b>	0												
SAL	<b>0.1334</b>	<b>0.14</b>	<b>0.1697</b>	0.1352	0.1192	<b>0.2021</b>	-0.017	0											
COM	<b>0.1069</b>	<b>0.1185</b>	<b>0.1462</b>	<b>0.1005</b>	<b>0.0967</b>	<b>0.1686</b>	<b>0.1347</b>	<b>0.1387</b>	0										
PAR	<b>0.1588</b>	<b>0.1688</b>	<b>0.1903</b>	<b>0.1618</b>	<b>0.1491</b>	<b>0.2214</b>	<b>0.1753</b>	<b>0.1808</b>	<b>0.0547</b>	0									
STJ	<b>0.137</b>	<b>0.1446</b>	<b>0.1652</b>	<b>0.1337</b>	<b>0.1236</b>	<b>0.1935</b>	<b>0.1547</b>	<b>0.1613</b>	<b>0.0313</b>	<b>0.0601</b>	0								
VEC	<b>0.1258</b>	<b>0.1341</b>	<b>0.16</b>	<b>0.1138</b>	<b>0.111</b>	<b>0.1772</b>	<b>0.1427</b>	<b>0.1543</b>	<b>0.0033</b>	<b>0.077</b>	<b>0.0488</b>	0							
RUT	<b>0.1478</b>	<b>0.1547</b>	<b>0.1729</b>	<b>0.1531</b>	<b>0.1353</b>	<b>0.2106</b>	<b>0.1704</b>	<b>0.1782</b>	<b>0.1458</b>	<b>0.1929</b>	<b>0.1742</b>	<b>0.1532</b>	0						
SAV	<b>0.1309</b>	<b>0.1409</b>	<b>0.1643</b>	<b>0.1462</b>	0.132	0.2076	<b>0.1547</b>	<b>0.1754</b>	<b>0.1432</b>	<b>0.1899</b>	<b>0.1654</b>	<b>0.1448</b>	<b>0.0323</b>	0					
FRO	<b>0.1256</b>	<b>0.1208</b>	<b>0.1516</b>	<b>0.1164</b>	<b>0.1027</b>	<b>0.1833</b>	<b>0.143</b>	<b>0.1497</b>	<b>0.1364</b>	<b>0.1799</b>	<b>0.162</b>	<b>0.1447</b>	<b>0.1663</b>	<b>0.1593</b>	0				
GAN	<b>0.1339</b>	<b>0.1266</b>	<b>0.1543</b>	<b>0.1218</b>	<b>0.1074</b>	<b>0.2013</b>	<b>0.1515</b>	<b>0.1603</b>	<b>0.1548</b>	<b>0.1952</b>	<b>0.1762</b>	<b>0.1592</b>	<b>0.1674</b>	<b>0.1552</b>	<b>0.0536</b>	0			
HFR	<b>0.1143</b>	<b>0.1061</b>	<b>0.1362</b>	<b>0.0979</b>	<b>0.0881</b>	<b>0.1611</b>	<b>0.1217</b>	<b>0.1302</b>	<b>0.1214</b>	<b>0.1587</b>	<b>0.1399</b>	<b>0.132</b>	<b>0.1435</b>	<b>0.1333</b>	<b>0.0072</b>	<b>0.0398</b>	0		
HOL	<b>0.1291</b>	<b>0.1289</b>	<b>0.1566</b>	<b>0.1179</b>	0.1024	0.1997	<b>0.1681</b>	<b>0.1729</b>	<b>0.1452</b>	<b>0.1978</b>	<b>0.1706</b>	<b>0.1545</b>	<b>0.1788</b>	<b>0.1748</b>	<b>0.0415</b>	<b>0.067</b>	<b>0.029</b>	0	
VSP	<b>0.1085</b>	<b>0.1031</b>	<b>0.1343</b>	<b>0.0971</b>	<b>0.0766</b>	<b>0.1644</b>	<b>0.133</b>	<b>0.1397</b>	<b>0.1255</b>	<b>0.1671</b>	<b>0.1423</b>	<b>0.1347</b>	<b>0.1488</b>	<b>0.1437</b>	<b>0.0193</b>	<b>0.0358</b>	<b>0.0071</b>	<b>0.0116</b>	0



**Figure S1:** Barplots presenting the hierarchical genetic clustering of samples of *Papaver occidentale* among regions using STRUCTURE on different datasets: all 136 samples (incl. outgroups) vs 112 native samples of *P. occidentale* at all 3070 ddRAD loci vs 2369 ddRAD loci (i.e. after exclusion of 701 genic loci). On the right, evaluation of optimal number of clusters (K) according to  $\Delta K$  ('Evanno') method and the mean Ln probabilities. All datasets highlight similar genetic structure within *P. occidentale*.

**Supplementary Text S1: Species Distribution Modelling (SDM) based on present occurrence data used to evaluate the potential distribution range of *Papaver occidentale* at current time and describe putative locations of suitable habitats during the LGM, following Fragnière et al. (2020).**

Environmental variables likely playing a role in the distribution of *P. occidentale* distribution were selected from different available sources at the finest resolution (10 m; table). For SDM based here on presence at 28,209 coordinates across the currently occupied area, the following variable were used SLOPE, NORTHNESS, TEMP, PREC\_Sum, PREC\_Win, SUNSHINE, IRRAD, HOURS\_SUN and SCREES, following Fragnière et al. (2020). The indirect variable ELEVATION was neglected (Guisan et al. 2017) and temperature (TEMP), which is more direct and suitable for predictions across time, was privileged. SCREES explained most of the current distribution of *P. occidentale* and was removed from models to unmask the effect of other variables. As the original data for temperature at 1 km resolution was highly correlated with ELEVATION (R-squared value = 0.92, p-value < 0.001), TEMP was downscaled at a 10 m resolution based on ELEVATION. Multicollinear variables were removed (R-squared values > 0.6; Menard 2002) with a high variance inflation factor (VIF>5; Guisan et al. 2017).

**Table.** Environmental variables initially selected for current SDM of *P. occidentale*.

Abbreviation	Variable type	Unit	Source	Native resolution	Resolution used in SDM
SLOPE	terrain inclination	Degrees (°)	From DEM	2 m	Upscaled to 10 m, median value
NORTHNESS	Slope aspect on the south-north axis	No unit, a real number between -1 (south) and 1 (north)	From DEM, cosinus of the slope aspect	2 m	Upscaled to 10 m, median value
TEMP	Mean yearly mean temperature (norm, 1981-2010)	degrees °C	TnormY8110 (Meteoswiss, 2018)	1000 m	Downscaled to 10 m, using DEM to improve resolution (strong negative linear relationship between ELEVATION and TEMP, R-squared value = 0.92, p-value < 0.001 ***. TEMP was thus calculated as a function of ELEVATION, see Online Resource 4)
PREC_Win	Mean winter precipitation (norm, 1981-2010)	Milimeters (mm)	RnormM8110, mean for December, January and February (Meteoswiss, 2018)	1000 m	Downscaled to 10m, using bicubic spline interpolation to get a smooth result
SUNSHINE	Mean yearly relative sunshine duration (norm, 1981-2010)	Percent (%)	SnormY8110 (Meteoswiss, 2018)	1000 m	Downscaled to 10m, using bicubic spline interpolation to get a smooth result
IRRAD	Total irradiance during one day at the solstice (21 of June)	Wh / m2 /day	From DEM with r.sun (Solar irradiance and irradiation model) in GRASS GIS (Neteler and Mitasova, 2013)	10 m	10 m
HOURS_SUN	Hours of sun during one day at the solstice (21 of June)	Hours (h)	From DEM with r.sun (Solar irradiance and irradiation model) in GRASS GIS	10 m	10 m
SCREES	Landcover : area with Calcareous screes	Presence-absence (1-0)	Area delimited using GEOCOVER and orthophotos with a 100 m buffer.	NA, vector data.	Rasterized to 10 m

## Model selection, calibration and validation

Pseudo-absence data (or background data) representative of random environmental conditions across the studied area were generated as to equal the number of presences (i.e. 28,209).

Following comparison of general linear and additive models (Fraginière et al. 2020), we here used a General Additive Model (GAM) with logit as link function and included nonlinear smooth functions of environmental variables (k set to 2) in the SDM (Guisan et al. 2002; Hastie et al. 2017). All environmental variables were initially included in the models and their significance estimated to remove some superfluous variables and build to the most parsimonious model based on the Akaike information criterion (AIC) and Bayesian information criterion (BIC; Atkinson 1980; Sakamoto et al. 1986).

As our data were strongly spatially autocorrelated, cross validation techniques such as the 10-fold cross validation (Rodriguez et al. 2009; Lever et al. 2016) and Monte-Carlo cross validation (Shao 1993; Xu and Liang 2001) were unsuitable. We therefore designed a spatial cross validation (Pohjankukka et al. 2017; Roberts et al. 2017) and split the studied area into two blocks along the W-E axis to use data within one block to train the model while data from the second block validated the model, and vice versa. This procedure was repeated along the N-S axis and environmental variables underlying overfitting were accordingly removed. Cross validation was analyzed with a ROC curve (Hanley and McNeil 1982), plotting the true positive rate against false positive rate for each validation dataset next to the full model ROC curve and using the area under the curve (AUC) and mean squared residuals (MSR) to evaluate the model performance.

The validated GAM model predicting *P. occidentale* habitat suitability across screes of its native distribution included four significant environmental variables (SLOPE, TEMP, NORTHING, PREC\_Win; p-value < 0.001) and explained 58.64 % of the total variance. The mean AUC of the validation datasets during the spatial cross validation was 0.9 and a best threshold from the ROC curve estimated at 0.55.

## References

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