

SUPPLEMENTARY DATA

TABLE S1. List and location of the *Pinus pinaster* populations comprised in the present study. GG= genetic group (as identified by STRUCTURE; see main text); MTCM = mean temperature of the coldest month (°C); MTWM = mean temperature of the warmest month (°C); AMT= annual mean temperature (°C); CI = continentality index (°C); PWM = precipitation during the warmest quarter (mm); AP = annual mean precipitation (mm).

Population and abbreviation		Latitude	Longitude	GG	Altitude	MTCM	MTWM	AMT	CI	PWM	AP
Mimizan	Mimi	44°80'N	1°18'W	AF	37	3.2	24.8	13.3	21.6	232	1235
Pleucadec	Pleu	47°46'N	2°20'W	AF	80	2.5	21.9	11.2	19.4	154	804
Alto de la Llama	Alto	43°17'N	6°29'W	AIP	503	2.6	23.4	11.7	20.8	149	1137
Armayán	Arma	43°18'N	6°27'W	AIP	498	2.0	24.0	11.8	22.0	152	1112
Cadavedo	Cada	43°32'N	6°25'W	AIP	210	5.0	22.0	13.2	17.0	204	1316
Castropol	Cast	43°30'N	6°58'W	AIP	391	4.5	22.0	12.6	17.5	184	1179
Lamuño	Lamu	43°33'N	6°13'W	AIP	125	5.3	22.7	13.4	17.4	192	1282
Leiria	Leir	39°47'N	8°57'W	AIP	20	7.4	24.4	15.4	17.0	44	811
Puerto de Vega	Puer	43°32'N	6°37'W	AIP	121	4.9	22.6	13.4	17.7	194	1283
San Cipriano de Ribarteme	San	42°70'N	8°21'W	AIP	300	2.7	26.0	12.3	23.3	121	1600
Sierra de Barcia	Sier	43°31'N	6°29'W	AIP	240	4.7	22.4	13.0	17.7	192	1339
Pineta	Pine	41°58'N	9°20'E	CO	750	6.7	26.0	15.5	19.3	42	583
Pinia	Pini	42°10'N	9°27'E	CO	10	6.3	26.9	15.6	20.6	49	580
Oria	Oria	37°31'N	2°21'W	MO	1223	0.4	30.7	13.1	30.3	29	357
Tamrabta	Tamr	33°36'N	5°10'W	MO	1758	-4.6	30.4	10.7	35.0.	49	745
Arenas de San Pedro	Aren	40°11'N	5°60'W	MS	733	1.2	33.4	14.2	32.2	73	1318
Bayubas de Abajo	Bayu	41°31'N	2°52'W	MS	998	-1.4	29.6	10.6	30.9	96	553
Carbonero	Carb	41°10'N	4°16'W	MS	845	-0.7	31.3	12.3	32.0	72	435
Cenicientos	Ceni	40°16'N	4°29'W	MS	1100	1.3	28.8	12.4	27.5	60	794
Coca	Coca	41°15'N	4°29'W	MS	800	-0.6	31.2	12.3	31.8	77	454
Cuellar	Cuel	41°22'N	4°29'W	MS	830	-0.6	30.9	12.2	31.6	72	468
San Leonardo	SanL	41°50'N	3°30'W	MS	1096	-2.7	27.9	9.3	30.6	120	753
Valdemaqueda	Vald	40°30'N	4°18'W	MS	890	0.5	29.2	12.1	28.7	70	681

TABLE S2. Summary information of nuSSR markers used to estimate range-wide population genetic structure in *Pinus pinaster*. Name = locus name; Motif = SSR repeated motif; Label = fluorescent label; Min, Max = minimum and maximum allele sizes per locus; N = number of alleles per locus.

Name	Motif	Label	Forward sequence	Reverse sequence	Min	Max	N
A6F03	(AC)17	VIC	CCTGAAAATCGACGGATCG	ATGGTATTTCGCGGGTTGC	258	272	8
rptest1	(ATC)7	NED	AGGATGCCTATGATATGCGC	AACCATAACAAAAGCGGTCG	131	171	18
Ctg4363	(AT)10	VIC	TAATAATTCAAGCCACCCCG	AGCAGGCTAATAACAACACGC	108	124	8
NZPR1078	(AC)10	PET	TGGTGATCAAGCCTTTCC	GTTGATGAGTGATGGCATGG	239	259	10
epi3	(TC)15	NED	AGCAACATTCCCTGGACAC	GGAATAATTGCAGTTGCAGTAGC	202	216	7
gPp14	(ATT)9	VIC	TATTGACGGTGTCTCTCCT	GACTTGACCTAAAGCATGG	215	237	8
pEST2669	(TA)19	NED	ATTGCTTCTGAAAGGGCATC	TCCCTTGGCACCATGTTAAT	202	229	6
epi5	(TA)9	PET	GGCGCGAACTACTTCATCTG	CAATGCTGACAAACCCAGAA	166	202	16
NZPR544	(CA)5(AC)12(TA)5	FAM	GCGATGTGCAACCCTGATA	TGCTATTCCGTAAAAACCC	340	359	8
ctg 275	(AT)16	FAM	ACGGAGATATATTGCTGGCG	AAAGAATAACGTGAAACAAACCC	259	269	6
epi6	(AT)9	FAM	CCCACCATGACAAGGTTGAT	CGCTGGGCTTGAACATCTA	161	185	11
ITPH4516	(CT)27	PET	TGATGCAAACAAGTTCCATG	AGCACTCGCTAAACTATGAAGG	223	238	6

TABLE S3. Size- dependent fitness components for male reproduction in 23 natural *Pinus pinaster* populations. GG = genetic Group; $m\mu$ = intercept of logistic regressions; $m\alpha$ = slope of logistic regressions; mTSFR = median threshold size for male reproduction; loCI,upCI = lower and upper 95% limits of Bayesian credible intervals for mTSFR; LVI = largest vegetative individual respect to male reproduction; SRI = smallest individual bearing male cones; mRAN = transition range (mLVI–mSRI); mVEG = number of vegetative individuals. na = not available.

Pop	GG	$m\mu \pm \text{s.e.}$	$m\alpha \pm \text{s.e.}$	mTSFR	loCI	upCI	mLVI	mSRI	mRAN	%mVEG
Mimi	AF	-10.72 ± 5.91 × 10 ⁻²	4.15 × 10 ⁻² ± 2 × 10 ⁻⁴	258.2	220.1	291.1	378	146	232	4.2
Pleu	AF	-8.40 ± 3.43 × 10 ⁻²	3.00 × 10 ⁻² ± 1 × 10 ⁻⁴	283.6	264.4	294.8	327	120	207	2.8
Alto	AIP	-7.19 ± 4.39 × 10 ⁻²	2.77 × 10 ⁻² ± 2 × 10 ⁻⁴	234.2	217.0	258.7	300	134	166	1.5
Arma	AIP	-9.78 ± 2.71 × 10 ⁻²	4.15 × 10 ⁻² ± 2 × 10 ⁻⁴	248.4	232.6	267.9	313	118	195	7.0
Cada	AIP	-5.86 ± 3.22 × 10 ⁻²	2.36 × 10 ⁻² ± 1 × 10 ⁻⁴	226.7	209.3	250.4	231	78	153	1.1
Cast	AIP	-4.81 ± 2.95 × 10 ⁻²	2.22 × 10 ⁻² ± 1 × 10 ⁻⁴	230.0	203.5	252.5	410	94	316	4.1
Lamu	AIP	-8.88 ± 5.13 × 10 ⁻²	3.56 × 10 ⁻² ± 2 × 10 ⁻⁴	232.1	209.4	248.3	257	113	144	1.5
Leir	AIP	-8.68 ± 3.72 × 10 ⁻²	3.61 × 10 ⁻² ± 1 × 10 ⁻⁴	260.4	248.0	271.8	376	100	276	0.8
Puer	AIP	-9.30 ± 6.27 × 10 ⁻²	4.18 × 10 ⁻² ± 2 × 10 ⁻⁴	247.2	217.5	271.4	280	126	154	4.9
San	AIP	-11.61 ± 7.56 × 10 ⁻²	5.21 × 10 ⁻² ± 3 × 10 ⁻⁴	227.1	209.2	244.0	267	137	130	2.6
Sier	AIP	-4.96 ± 4.14 × 10 ⁻²	2.16 × 10 ⁻² ± 2 × 10 ⁻⁴	233.4	217.1	248.8	282	119	163	4.3
Pine	CO	na	na	na			467	127	340	na
Pini	CO	-6.23 ± 4.67 × 10 ⁻²	2.51 × 10 ⁻² ± 2 × 10 ⁻⁴	238.2	215.4	263.9	347	111	236	1.9
Oria	MO	-8.59 ± 3.06 × 10 ⁻²	3.56 × 10 ⁻² ± 1 × 10 ⁻⁴	231.9	219.8	243.8	338	101	237	4.9
Tamr	MO	-9.54 ± 4.84 × 10 ⁻²	3.47 × 10 ⁻² ± 2 × 10 ⁻⁴	296.6	273.1	316.7	383	105	278	3.2
Aren	MS	-7.49 ± 3.55 × 10 ⁻²	3.14 × 10 ⁻² ± 1 × 10 ⁻⁴	240.2	226.0	252.7	392	112	280	6.3
Bayu	MS	-8.12 ± 3.04 × 10 ⁻²	3.21 × 10 ⁻² ± 1 × 10 ⁻⁴	239.1	229.7	255.3	361	108	253	4.2
Carb	MS	-8.38 ± 6.01 × 10 ⁻²	3.64 × 10 ⁻² ± 3 × 10 ⁻⁴	228.8	213.0	249.8	290	117	173	8.3
Ceni	MS	-6.03 ± 4.93 × 10 ⁻²	2.86 × 10 ⁻² ± 2 × 10 ⁻⁴	208.6	172.1	246.4	353	132	221	1.8
Coca	MS	-9.13 ± 4.27 × 10 ⁻²	3.35 × 10 ⁻² ± 2 × 10 ⁻⁴	250.8	237.2	269.7	296	118	178	10.3
Cuel	MS	-7.07 ± 3.17 × 10 ⁻²	3.01 × 10 ⁻² ± 1 × 10 ⁻⁴	246.8	228.6	264.4	345	106	239	3.3
SanL	MS	-9.77 ± 4.18 × 10 ⁻²	4.00 × 10 ⁻² ± 2 × 10 ⁻⁴	229.7	207.7	255.7	283	80	203	4.4
Vald	MS	-6.92 ± 3.93 × 10 ⁻²	2.93 × 10 ⁻² ± 2 × 10 ⁻⁴	225.6	200.9	242.3	272	111	161	4.1

TABLE S4. Size-dependent fitness components for female reproduction in 23 natural *Pinus pinaster* populations. GG = genetic Group; f μ = intercept of logistic regressions; f α = slope of logistic regressions; fTSFR = median threshold size for female reproduction; loCI,upCI = lower and upper 95% limits of Bayesian credible intervals for fTSFR; fLVI = largest vegetative individual respect to female reproduction; fSRI = smallest individual bearing female cones; fRAN = transition range (fLVI–fSRI), fVEG = number of vegetative individuals. na not available.

Pop	GG	f μ ± s.e.	f α ± s.e.	fTSFR	loCI	upCI	fLVI	fSRI	fRAN	%fVEG
Mimi	AF	-6.79 ± 2.23 × 10 ⁻²	2.00 × 10 ⁻² ± 1 × 10 ⁻⁴	316.8	301.2	346.9	404	129	249	2.1
Pleu	AF	-5.75 ± 1.71 × 10 ⁻²	2.15 × 10 ⁻² ± 1 × 10 ⁻⁴	258.0	236.3	280.9	422	115	212	7.4
Alto	AIP	-5.47 ± 2.22 × 10 ⁻²	1.16 × 10 ⁻² ± 1 × 10 ⁻⁴	426.6	368.0	522.8	403	126	174	0
Arma	AIP	-5.32 ± 2.32 × 10 ⁻²	1.51 × 10 ⁻² ± 1 × 10 ⁻⁴	381.7	341.0	451.0	391	92	221	0
Cada	AIP	-6.42 ± 3.05 × 10 ⁻²	1.43 × 10 ⁻² ± 1 × 10 ⁻⁴	458.4	399.0	531.9	470	138	93	0
Cast	AIP	-5.53 ± 2.59 × 10 ⁻²	1.55 × 10 ⁻² ± 1 × 10 ⁻⁴	363.6	299.4	418.7	410	84	326	1.4
Lamu	AIP	-4.97 ± 1.76 × 10 ⁻²	1.33 × 10 ⁻² ± 1 × 10 ⁻⁴	385.9	336.2	426.8	430	100	157	0
Leir	AIP	-5.26 ± 1.96 × 10 ⁻²	1.06 × 10 ⁻² ± 1 × 10 ⁻⁴	490.4	399.4	576.8	448	100	276	0
Puer	AIP	-6.62 ± 3.02 × 10 ⁻²	1.39 × 10 ⁻² ± 1 × 10 ⁻⁴	450.6	391.5	524.0	429	149	131	0
San	AIP	-4.31 ± 2.27 × 10 ⁻²	1.66 × 10 ⁻² ± 1 × 10 ⁻⁴	262.7	228.1	303.4	353	78	189	2.6
Sier	AIP	-5.16 ± 3.42 × 10 ⁻²	0.96 × 10 ⁻² ± 1 × 10 ⁻⁴	480.2	381.3	578.9	364	118	164	0
Pine	CO	na	na	na			467	263	204	na
Pini	CO	-8.44 ± 6.33 × 10 ⁻²	2.77 × 10 ⁻² ± 2 × 10 ⁻⁴	368.8	294.0	448.9	458	147	200	0
Oria	MO	-5.08 ± 1.48 × 10 ⁻²	1.84 × 10 ⁻² ± 1 × 10 ⁻⁴	284.7	256.3	310.2	366	85	253	2.1
Tamr	MO	-6.40 ± 1.73 × 10 ⁻²	2.22 × 10 ⁻² ± 1 × 10 ⁻⁴	276.8	259.0	300.3	383	78	305	6.4
Aren	MS	-5.77 ± 1.99 × 10 ⁻²	1.85 × 10 ⁻² ± 1 × 10 ⁻⁴	325.9	293.1	371.9	400	112	280	1.6
Bayu	MS	-4.46 ± 1.25 × 10 ⁻²	1.80 × 10 ⁻² ± 1 × 10 ⁻⁴	246.9	233.0	269.6	366	94	267	3.5
Carb	MS	-5.26 ± 2.49 × 10 ⁻²	2.20 × 10 ⁻² ± 1 × 10 ⁻⁴	233.2	211.2	271.3	314	99	191	6.3
Ceni	MS	-5.43 ± 2.53 × 10 ⁻²	1.95 × 10 ⁻² ± 1 × 10 ⁻⁴	287.2	242.7	333.5	364	111	242	1.8
Coca	MS	-5.41 ± 3.47 × 10 ⁻²	1.65 × 10 ⁻² ± 1 × 10 ⁻⁴	306.4	241.0	501.0	367	82	214	0
Cuel	MS	-6.37 ± 2.08 × 10 ⁻²	2.49 × 10 ⁻² ± 1 × 10 ⁻⁴	229.5	203.3	281.8	383	72	273	3.3
SanL	MS	-5.71 ± 2.07 × 10 ⁻²	2.00 × 10 ⁻² ± 1 × 10 ⁻⁴	285.2	236.7	335.7	349	103	180	0
Vald	MS	-6.54 ± 3.04 × 10 ⁻²	1.84 × 10 ⁻² ± 1 × 10 ⁻⁴	339.7	260.6	423.3	377	99	173	0

TABLE S5. Associations of environmental variables (first column) with reproductive life-history traits (second column) in *Pinus piaster*. Corrected values indicate slopes, standard errors and *P*-values for the association after including neutral genetic structure corrections (i.e. likelihood ratio test between a full model and a reduced model with just neutral genetic structure); uncorrected values indicate association parameters without correcting for neutral genetic structure (i.e. just environmental data and traits data in the model).

	Trait	Corrected			Uncorrected		
		Slope	P-value		Slope	P-value	
Alt	fTSFR	-2.02×10^{-1} \pm 7.02×10^{-2}	0.011	-9.87×10^{-2} \pm 3.13×10^{-2}	0.005		
	mTSFR	-3.37×10^{-2} \pm 1.86×10^{-2}	0.090	1.39×10^{-3} \pm 9.22×10^{-3}	0.881		
	H	-4.06×10^{-2} \pm 3.06×10^{-2}	0.205	-4.68×10^{-2} \pm 9.77×10^{-3}	0.000		
	%M	-2.21×10^{-2} \pm 1.54×10^{-2}	0.171	-1.90×10^{-2} \pm 6.65×10^{-3}	0.010		
	% F	1.57×10^{-2} \pm 1.24×10^{-2}	0.223	1.33×10^{-2} \pm 4.75×10^{-3}	0.011		
Lat	fTSFR	-8.22×10^{-5} \pm 1.97×10^{-4}	0.682	-7.02×10^{-5} \pm 5.81×10^{-5}	0.241		
	mTSFR	-5.23×10^{-5} \pm 4.45×10^{-5}	0.258	2.09×10^{-6} \pm 1.45×10^{-5}	0.887		
	H	1.84×10^{-5} \pm 7.31×10^{-5}	0.805	-1.14×10^{-6} \pm 2.25×10^{-5}	0.960		
	%M	2.01×10^{-5} \pm 3.67×10^{-5}	0.593	-6.81×10^{-7} \pm 1.24×10^{-5}	0.957		
	% F	-1.95×10^{-5} \pm 2.90×10^{-5}	0.512	1.96×10^{-7} \pm 8.80×10^{-6}	0.982		
Long	fTSFR	2.08×10^{-5} \pm 1.41×10^{-4}	0.885	6.58×10^{-5} \pm 5.81×10^{-5}	0.271		
	mTSFR	5.50×10^{-5} \pm 3.01×10^{-5}	0.087	-8.97×10^{-5} \pm 1.43×10^{-5}	0.537		
	H	1.84×10^{-5} \pm 5.22×10^{-5}	0.729	6.02×10^{-5} \pm 1.79×10^{-5}	0.003		
	%M	-1.24×10^{-5} \pm 2.63×10^{-5}	0.645	1.61×10^{-5} \pm 1.18×10^{-5}	0.189		
	% F	1.16×10^{-5} \pm 2.09×10^{-5}	0.585	-1.08×10^{-5} \pm 8.42×10^{-6}	0.214		
AMT	fTSFR	30.58 \pm 16.22	0.079	29.46 \pm 10.76	0.013		
	mTSFR	-4.59 \pm 4.07	0.277	-1.63 \pm 3.01	0.595		
	H	9.24 \pm 6.24	0.159	10.26 \pm 4.12	0.022		
	%M	6.86 \pm 2.88	0.031	6.46 \pm 2.16	0.007		
	% F	-4.87 \pm 2.37	0.058	-4.31 \pm 1.57	0.012		
MTCM	fTSFR	29.43 \pm 7.48	0.001	20.01 \pm 3.99	0.000		
	mTSFR	-0.91 \pm 2.49	0.719	-1.20 \pm 1.42	0.407		
	H	8.36 \pm 3.31	0.023	7.67 \pm 1.44	0.000		
	%M	4.83 \pm 1.56	0.007	3.99 \pm 0.85	0.000		
	% F	-3.35 \pm 1.33	0.024	-2.72 \pm 0.63	0.000		
MTWM	fTSFR	-18.34 \pm 6.06	0.009	-14.18 \pm 3.66	0.001		
	mTSFR	-2.19 \pm 1.72	0.221	-0.19 \pm 1.16	0.872		
	H	-5.14 \pm 2.52	0.059	-5.61 \pm 1.30	0.000		
	%M	-2.12 \pm 1.33	0.132	-2.32 \pm 0.85	0.013		
	% F	1.52 \pm 1.08	0.177	1.78 \pm 0.59	0.006		
CI	fTSFR	-14.08 \pm 3.39	0.001	-9.71 \pm 1.91	0.000		
	mTSFR	-0.72 \pm 1.15	0.542	0.21 \pm 0.69	0.762		
	H	-3.97 \pm 1.53	0.020	-3.78 \pm 0.67	0.000		
	%M	-1.94 \pm 0.79	0.026	-1.75 \pm 0.45	0.001		
	% F	1.37 \pm 0.65	0.052	1.27 \pm 0.31	0.001		
AP	fTSFR	4.22×10^{-2} \pm 5.85×10^{-2}	0.482	1.13×10^{-1} \pm 4.28×10^{-2}	0.015		
	mTSFR	2.47×10^{-3} \pm 1.40×10^{-2}	0.862	-6.57×10^{-3} \pm 1.19×10^{-2}	0.586		
	H	3.09×10^{-2} \pm 2.06×10^{-2}	0.153	4.69×10^{-2} \pm 1.53×10^{-2}	0.006		
	%M	7.67×10^{-3} \pm 1.10×10^{-2}	0.495	2.00×10^{-2} \pm 9.22×10^{-3}	0.043		
	% F	-1.23×10^{-2} \pm 8.28×10^{-3}	0.157	-1.77×10^{-2} \pm 6.09×10^{-3}	0.009		
PDM	fTSFR	1.14 \pm 5.19 $\times 10^{-1}$	0.044	5.54 $\times 10^{-1}$ \pm 2.66 $\times 10^{-1}$	0.050		
	mTSFR	1.47×10^{-1} \pm 1.35×10^{-1}	0.294	-1.11×10^{-2} \pm 7.05×10^{-2}	0.877		
	H	2.39×10^{-1} \pm 2.12×10^{-1}	0.277	2.61×10^{-1} \pm 9.27×10^{-2}	0.011		
	%M	1.81×10^{-1} \pm 1.02×10^{-1}	0.096	9.66×10^{-2} \pm 5.64×10^{-2}	0.102		
	% F	-1.85×10^{-1} \pm 7.49×10^{-2}	0.026	-8.79×10^{-2} \pm 3.81×10^{-2}	0.032		

TABLE S6. Number of trees per population included in the molecular marker analysis and average of individual assignment probability for each of the optimal K=6 clusters (C1 through C6) representing five geographical genetic groups (GG) in *Pinus pinaster*.

Population	<i>N</i>	C1	C2	C3	C4	C5	C6	GG
Mimi	19	0.74	0.01	0.02	0.01	0.06	0.15	AF
Pleu	21	0.67	0.02	0.03	0.01	0.12	0.16	AF
Alto	9	0.14	0.01	0.59	0.02	0.09	0.14	AIP
Arma	9	0.08	0.01	0.70	0.02	0.14	0.05	AIP
Cada	10	0.09	0.00	0.82	0.01	0.04	0.04	AIP
Cast	10	0.12	0.01	0.80	0.01	0.04	0.03	AIP
Lamu	9	0.10	0.01	0.73	0.01	0.10	0.06	AIP
Leir	24	0.19	0.01	0.24	0.01	0.42	0.13	AIP
Puer	8	0.05	0.01	0.76	0.04	0.10	0.05	AIP
San	12	0.15	0.01	0.51	0.02	0.25	0.06	AIP
Segu	21	0.12	0.01	0.50	0.01	0.23	0.13	AIP
Sier	10	0.21	0.01	0.41	0.02	0.13	0.21	AIP
Pine	10	0.05	0.03	0.03	0.80	0.05	0.04	CO
Pini	14	0.01	0.02	0.02	0.92	0.01	0.01	CO
Oria	29	0.10	0.54	0.07	0.03	0.16	0.11	MO
Tamr	24	0.01	0.95	0.01	0.01	0.01	0.01	MO
Aren	27	0.14	0.02	0.09	0.03	0.34	0.38	MS
Bayu	27	0.22	0.01	0.07	0.03	0.14	0.53	MS
Carb	6	0.28	0.04	0.11	0.06	0.20	0.31	MS
Ceni	9	0.30	0.01	0.13	0.02	0.19	0.35	MS
Coca	19	0.26	0.08	0.13	0.06	0.26	0.22	MS
Cuel	28	0.34	0.02	0.07	0.01	0.20	0.36	MS
Rodo	8	0.16	0.02	0.03	0.02	0.42	0.35	MS
SanL	20	0.14	0.06	0.07	0.06	0.11	0.56	MS
Vald	16	0.11	0.01	0.05	0.03	0.36	0.44	MS
Total	399							