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## Molecular footprints of local adaptation in two Mediterranean conifers

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1 Molecular footprints of local adaptation in two Mediterranean conifers

2  
3 Research Article

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28

29 Running head (max of 50 characters and spaces): Contrasting patterns of polymorphism in two

30 pines

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32

33 **ABSTRACT**

34 This study combines neutrality tests and environmental correlations to identify non-neutral  
35 patterns of evolution in candidate genes related to drought stress in two closely-related  
36 Mediterranean conifers, *Pinus pinaster* Ait. and *Pinus halepensis* Mill. Based on previous  
37 studies, we selected 12 amplicons covering six candidate genes that were sequenced in a large  
38 sample spanning the full range of these two species. Neutrality tests relatively robust to  
39 demography (*DHEW* compound test and *ML-HKA* test) were used to detect selection events at  
40 different temporal scales. Environmental associations between variation at candidate genes and  
41 climatic variables were also examined. These combined approaches detected distinct genes that  
42 may be targeted by selection, most of them specific to only one of the two conifers, despite their  
43 recent divergence (< 10 Ma). An exception was *4-coumarate: CoA ligase (4cl)*, a gene involved  
44 in the production of various important secondary products that appeared to play a role in local  
45 adaptation processes of both pines. Another remarkable result was that all significant  
46 environmental correlations involved temperature indices, highlighting the importance of this  
47 climatic factor as a selective driver on Mediterranean pines. The ability to detect natural  
48 selection at the DNA sequence level depends on the nature and the strength of the selection  
49 events, on the timescale at which they occurred and on the sensitivity of the methods to other  
50 evolutionary forces that can mimic selection (e.g. demography, population structure). Using  
51 complementary approaches can help to capture different aspects of the evolutionary processes  
52 that govern molecular variation at both intra- and interspecific levels.

53

54

## INTRODUCTION

55

56

57 Identifying candidate genes underlying genetic differences for adaptive traits can help to  
58 understand how species have adapted to their environment and to predict how they will respond  
59 to future climatic changes, which is a special concern in regions such as the Mediterranean  
60 Basin, where a substantial decrease in precipitation and a pronounced warming is expected in the  
61 near future (Petit, Hampe, and Cheddadi 2005; Giorgi and Lionello 2008). The ability to detect  
62 the footprints of natural selection in population DNA sequence samples depends on the nature  
63 and the strength of the selection events (Nielsen 2005), on the evolutionary scale at which they  
64 occur (Zhai, Nielsen, and Slatkin 2009) and on the sensitivity of the methods to other  
65 evolutionary forces that can mimic selection (e.g. demography, population structure; Biswas and  
66 Akey 2006).

67 Positive selection, which drives the increase in frequency of advantageous mutations, is  
68 of particular interest because it underlies local adaptation. Recent or on-going positive selection  
69 events can be detected using methods based on polymorphism within species (Biswas and Akey  
70 2006; Zhai, Nielsen, and Slatkin 2009). Recently, powerful methods based on site- and  
71 haplotype- frequency spectra that are relatively insensitive to demography or population  
72 structure have been developed (Zeng, Shi, and Wu 2007). Detecting selection events over a  
73 wider evolutionary scale (e.g. recurrent positive selection or ancient selective sweeps), can be  
74 efficiently done using methods contrasting within species polymorphism with among species  
75 divergence, as these methods are less sensitive to assumptions regarding recombination or  
76 demography. The *HKA* (Hudson-Kreitman-Aguadé) neutrality test (Hudson, Kreitman, and  
77 Aguade 1987) and its extensions (e.g. Wright and Charlesworth 2004) are among the most

78 powerful tests to detect positive selection (Zhai, Nielsen, and Slatkin 2009). In addition, the  
79 action of natural selection can be reflected in statistical associations between genetic and  
80 environmental data (Manel et al. 2003; Hancock et al. 2008; Coop et al. 2009). Several studies  
81 have shown that environmental heterogeneity influences the distribution of genetic diversity  
82 across plant populations (see Savolainen, Pyhäjärvi, and Knürr 2007, for forest trees; Nakazato,  
83 Bogonovich, and Moyle 2008; Montesinos et al. 2009). Detecting clinal genetic variation along  
84 environmental gradients can thus provide evidence for the action of selection (Gram and Sork  
85 2001; Vasemagi and Primmer 2005; Parisod and Christin 2008). Approaches that detect adaptive  
86 clinal variation are very attractive because they can directly link environmental gradients with  
87 genotypes and phenotypes. However, detecting environmental associations depends on the  
88 spatial scale examined and the associations have to be controlled for selectively neutral processes  
89 that can also generate clines (e.g. Storz 2002; Hancock et al. 2008; Coop et al. 2009; Keller et al.  
90 2009). Using environmental association approaches in conjunction with neutrality tests helps  
91 capturing different aspects of the evolutionary processes that govern molecular variation.

92         In the present study, we use the combined strategy outlined above to investigate patterns  
93 of polymorphism for a set of candidate genes related to drought stress in maritime pine (also  
94 known as cluster pine, *Pinus pinaster* Ait.), and in Aleppo pine (*Pinus halepensis* Mill.). *P.*  
95 *pinaster* is an economically important pine native to the occidental Mediterranean Basin and the  
96 European Atlantic front (Figure 1). This species is ecologically versatile, growing in a variety of  
97 substrates, in a wide range of elevations and under a range of Mediterranean and Atlantic climate  
98 regimes (semi-arid to very humid; Table 1). *P. halepensis*, a pine closely related to maritime  
99 pine, is one of the most abundant and widespread pine species of the Mediterranean Basin  
100 (Figure 1). This species, which also has a wide ecological breadth, is well adapted to dry

101 conditions as well as high-intensity fire regimes (Tapias et al. 2004), which makes it a species of  
102 choice for afforestation in xeric Mediterranean areas. These two conifers, because they have  
103 extensive and partially overlapping distributions across the Mediterranean Basin, may possibly  
104 display adaptation to similar sets of contrasted environmental conditions, *i.e.* regional climate  
105 types and spatial variability. Among the key environmental factors to *Pinus* distribution in  
106 Mediterranean climates, temperature and rainfall have been shown to constitute good biological  
107 descriptors (Richardson and Bond 1991; Soto et al. 2010). Additionally, several common garden  
108 studies have documented differences in drought tolerance and/or gene expression among  
109 Mediterranean pine provenances (for *P. pinaster* see Nguyen and Lamant 1989; Costa et al.  
110 1998; Chambel, Climent, and Alía 2007; Aranda et al. 2009; for *P. halepensis* see Atzmon,  
111 Moshe, and Schiller 2004; Sathyan, Newton, and Loopstra 2005; Voltas et al. 2008). Overall,  
112 these studies point to Mediterranean pines as an interesting system to study local adaptation  
113 mediated by abiotic stress response. In that context, studying allelic (SNP-allele and haplotype)  
114 frequency in drought-related candidate genes along temperature or precipitation clines can help  
115 to improve our understanding of pine adaptation to environmental heterogeneity.

116         Although *P. pinaster* and *P. halepensis* share various ecological requirements and may  
117 have responded to their environment in a similar manner, they present quite contrasted  
118 biogeographic and demographic histories that can also have a strong effect on the pattern of  
119 variation of the candidate genes examined. *Pinus pinaster* has a long-presence in the western  
120 Mediterranean Basin surviving the last glaciations in multiple refugia located in southeastern  
121 Spain, northern Africa and the Atlantic coast of Portugal (Bucci et al. 2007). In contrast, *P.*  
122 *halepensis* would have undergone long-range colonization of the western Mediterranean from  
123 ancient populations located in Greece and Turkey (Bucci et al. 1998; Morgante, Felice, and

124 Vendramin 1998; Grivet et al. 2009). In addition, the dynamics of *P. halepensis* populations  
125 throughout the Mediterranean Basin highly depend on forest fires. This species-specific  
126 information on population dynamics has to be taken into account when looking at the molecular  
127 footprint of selection.

128         Based on previous population genomic studies identifying drought tolerance genes  
129 potentially under selection (see Eveno et al. 2008; Grivet et al. 2009) as well as on gene  
130 expression studies identifying genes affected by drought stress (Watkinson et al. 2003; Rani et al.  
131 2009), we examine here patterns of nucleotide variation in an ortholog set of targeted candidate  
132 genes in *P. pinaster* and *P. halepensis*. We sample a broad geographic range of populations to: i)  
133 provide new evidence about positive selection acting on these genes, ii) identify the time scale at  
134 which selection events may have occurred, and iii) examine which environmental factors  
135 underlie molecular signatures of selection in both species. Our pluralistic approach provides  
136 insights on the adaptive strategy of two conifers that live under the same Mediterranean climate,  
137 but present distinct demographic, (re)colonization and life histories.

138

139

## MATERIALS AND METHODS

140

141 **Study species.** *Pinus pinaster* Ait.: Maritime pine populations have been assessed using various  
142 molecular markers: chloroplast and mitochondrial (e.g. Burban and Petit 2003; Bucci et al.  
143 2007), as well as nuclear (e.g. Salvador et al. 2000; Eveno et al. 2008). In particular, chloroplast  
144 markers were able to identify different gene clusters related to the history of the species (Bucci et  
145 al. 2007). Because of its economic importance, various programs of genetic improvement have  
146 been developed in *P. pinaster*, in particular for the Atlantic provenances. Within this framework,



147 several adaptive traits, such as growth, tolerance to drought and cold, and resistance to pests and  
148 diseases, have been the subject of genetic variability studies. Numerous approaches have been  
149 used to unravel the basis of quantitative traits in maritime pine: genetic (genetic cartography),  
150 physiologic (mechanisms implicated in traits), functional and structural genomic (candidate  
151 genes and proteins) and population genetic and genomic (genes under selection).

152 *Pinus halepensis* Mill.: Aleppo pine genetic variability has been studied with both  
153 chloroplast and nuclear markers (Bucci et al. 1998; Morgante, Felice, and Vendramin 1998;  
154 Grivet et al. 2009). A recent study revealed that the pattern of polymorphism observed in some  
155 candidate genes related to drought-tolerance in this species reflected long-range colonization and  
156 possibly natural selection during range expansion (Grivet et al. 2009). Various common garden  
157 studies have assessed Aleppo pine intraspecific variability in order to study the role of ecological  
158 factors in shaping adaptive strategies. Some experiments revealed adaptive variation to climate  
159 (total precipitation and dry season duration; Voltas et al. 2008) or reproductive features (Climent  
160 et al. 2008), highlighting thus the selective role of climate variables in determining population  
161 and family fitness in this species.

162

163 **Sampling.** Twelve populations of *P. pinaster* (77-122 individuals, depending on the gene; [Table](#)  
164 [S1](#)) and nine populations of *P. halepensis* (72-93 individuals; [Table S1](#)) were collected spanning  
165 the full range of each species ([Figure 1](#), [Table 1](#)). Populations were selected considering not only  
166 spatial distribution but also environmental heterogeneity in both species, prioritizing populations  
167 that represent contrasted environments ([Table 1](#)). Our sampling covers also different soil  
168 (siliceous, calcareous) and Mediterranean forest types. Finally, we included representations of  
169 the five traditional varieties or landraces described in maritime pine (Resch 1974): *mesogeensis*

170 (e.g. Olba), *atlantica* (e.g. Mimizan), *corteensis* (e.g. Pinia), *maghrebiana* (e.g. Tamrabta) and  
171 *renoui* (e.g. Tabarka), as well as all genecological groups normally considered in Aleppo pine:  
172 Western Europe, Eastern Europe and Northern Africa.

173 From each population, cones were collected from mother trees separated by at least 50 m  
174 without any phenotypic selection. Seeds from each mother tree were kept in individual paper  
175 bags and stored at 4 °C in a dry environment till DNA extraction (see below).

176

### 177 ***Spatial, environmental and genetic data.***

178 *Spatial and environmental data.* Three spatial variables were recorded for each population:  
179 altitude, latitude and longitude (Table 1). Eight climatic variables were considered: annual mean  
180 temperature (AMT), temperature seasonality (expressed as the standard deviation across months  
181 multiplied by 100; TS), maximum temperature of the warmest month (MTWM), minimum  
182 temperature of the coldest month (MTCM), annual precipitation (AP), precipitation of wettest  
183 month (PWM), precipitation of driest month (PDM), and precipitation seasonality (coefficient of  
184 variation; PS). Climatic data for *P. pinaster*'s Iberian populations were obtained from a  
185 functional phytoclimatic model based on raw data from meteorological stations (Gonzalo 2007).  
186 Climatic data for *P. pinaster*'s non-Iberian populations as well as for all *P. halepensis*'  
187 populations were obtained from the WorldClim – Global Climate Data at 5 minute resolution  
188 (Hijmans et al. 2005) (Table 1). Graphical pairwise correlations between these 11 spatial and  
189 environmental variables are presented in Figure S1.

190 *DNA extraction and candidate gene sequencing.* Genomic DNA from *P. pinaster* (haploid)  
191 megagametophytes was extracted with a modified Dellaporta et al. (1983) protocol. DNA  
192 extraction for *P. halepensis* was carried out as reported in Grivet et al. (2009).

193 Candidate genes related to drought tolerance were originally identified on the basis of  
194 functional studies performed in *Pinus taeda* and other conifers, or derived from model species  
195 such as *Arabidopsis thaliana*, as described elsewhere (González-Martínez et al. 2006; Eveno et  
196 al. 2008; Grivet et al. 2009; Wachowiak, Balk, and Savolainen 2009). Altogether the candidate  
197 genes selected for this study belong to three well-known and relatively small multigene families:  
198 the ASR (*lp31-Pt* and *lp33-Pt*), dehydrin (*dhn2-Pp*, *dhn2-Ps* and *dhn5-Ps*) and 4-coumarate:  
199 *CoA ligase* (*4cl-Pt*) families. The ASR family is named after the Abscisic acid (ABA), stress and  
200 ripening response (Frankel et al. 2006). These proteins are also induced by water deficit stress  
201 (WDS). The dehydrin gene, *dhn2-Pp*, previously described in maritime pine (Eveno et al. 2008),  
202 is not orthologous to the one described in Scots pine, i.e. *dhn2-Ps* (Wachowiak et al. 2009).

203 Previously published primer pairs of these putative candidate genes were transferred from  
204 *P. taeda* (*Pt*), *P. sylvestris* (*Ps*) or *P. pinaster* (*Pp*) to either *P. pinaster* or *P. halepensis* or both,  
205 and three new primer pairs, which overlap with pre-described amplicons, were also designed in  
206 order to extend the coverage of these target genes (Table S2). PCR conditions for the two pines  
207 studied here are given in Table S3. Outgroup sequences for each amplicon were obtained from  
208 GenBank: *P. taeda* for amplicons *lp31-Pt*, *lp33-Pt*, *dhn2-Pp* and *4cl-Pt*, and *P. sylvestris* for  
209 *dhn5-Ps* and one *dhn2-Ps* amplicon; or produced with our newly designed primers (*P. nigra* for  
210 the second *dhn2-Ps* amplicon) (Table S2). Sequence data from this article have been deposited  
211 with the EMBL/GenBank Data Libraries under accession nos. HM481479-HM483364.

212 PCR products were purified and sequenced from both ends following standard protocols  
213 (for *P. pinaster*, see Eveno et al. 2008; for *P. halepensis*, see Grivet et al. 2009). Multiple  
214 sequence alignments and manual adjustments were done using SeqMan v7 (DNASTAR  
215 Lasergene software) and BIOEDIT (<http://www.mbio.ncsu.edu/BioEdit/page2.html>).

216 *Chloroplast microsatellites*. To control for associations between candidate genes and  
217 environmental data that could be due to neutral processes, we included variation of chloroplast  
218 microsatellites (the only neutral genetic markers available for the two species at the wide range  
219 scale) as a covariate in the multivariate logistic regressions (see *Environmental associations*  
220 section below). We performed population-based Principal Component Analysis (PCA) on  
221 chloroplast markers, and kept the Principal Components (PCs) that explained the majority of the  
222 overall inertia of the data. For *P. pinaster*, the three first PCs of the 16 most common haplotypes  
223 (determined on the basis of five chloroplast microsatellites) – accounting for 74% of the overall  
224 variation – were extracted from the lattice dataset (430 records × 16 variables) of Bucci et al.  
225 (2007). For populations that did not match any of the 430 locations in this lattice, the mean of the  
226 closest 3-4 locations was computed (Table S4). For *P. halepensis*, PCs were computed in R (R  
227 Development Core Team) for each of the nine populations based on the 22 haplotypes  
228 determined from three chloroplast microsatellites (our unpublished data) and the three first PCs,  
229 which explain 82% of the overall variation, were used for subsequent analysis (Table S4).

230 Chloroplast microsatellites were also used to determine groups with similar evolutionary  
231 history to conduct neutrality tests (Figure 1). A previous study based on chloroplast  
232 microsatellites pointed at eight gene pools in *P. pinaster* (Bucci et al. 2007). Within the sampling  
233 used in the present study, Mimizan (Continental French lineage) and Pinia (Northern Italy and  
234 Corsican lineages) represent single lineages. Tabarka (Tunisia), Tamrabta (Moroccan Middle  
235 Atlas) and Sidi Meskour (Moroccan High Atlas) are all part of a North African lineage that  
236 combines western and eastern African origins. The rest of *P. pinaster* populations sampled are  
237 part of a wide Western Mediterranean lineage, except for Quatretonda and Oria that are  
238 considered marginal populations and may thus present a distinct evolutionary history (González-

239 Martínez et al. 2007a; Eveno et al. 2008). In *P. halepensis*, eastern Mediterranean populations  
240 (Elea in Greece and Shaharia in Israel) present a higher level of cpSSR diversity and substantial  
241 genetic differentiation from the rest and are considered single-population lineages (Grivet et al.  
242 2009); Zaouia Ifrane (Morocco) and Aures Beni Melloul (Algeria) form part of the North  
243 African group, while all four Spanish populations and the Italian population of Imperia belong to  
244 the Western Mediterranean group. These regions (North Africa and Western Mediterranean)  
245 define relatively homogeneous zones of the Mediterranean Basin in terms of soil and climate  
246 (Barbéro et al. 1998).

247

#### 248 ***Statistical analyses.***

249 *Gene diversity and divergence.* Number of segregating sites ( $S$ ), nucleotide diversity statistics  
250 ( $\theta_\pi$ , Tajima 1989;  $\theta_w$ , Watterson 1975), number of haplotypes ( $K$ ), and haplotypic diversity  
251 ( $H_e$ ) were computed for both North African and Western Mediterranean groups using scripts  
252 kindly provided by S.E. Ramos-Onsins (Department of Genetics, Faculty of Biology, University  
253 of Barcelona, Spain) and the program DnaSP v5 (Librado and Rozas 2009). Average divergence  
254 per site ( $K_{all}$ ) for each geographical group was computed between each of the pines and the  
255 outgroup *Pinus taeda*, as well as between *P. pinaster* and *P. halepensis* themselves, using scripts  
256 also provided by S.E. Ramos-Onsins.

257 *Neutrality tests.* All neutrality tests were performed at the regional level (see group definition  
258 above) considering all sequenced gametes in each amplicon, using one sequence from another  
259 pine species as outgroup when appropriate, and considering all substitutions as well as only  
260 silent sites (except for the *MK* test where all sites must be used, see below). First, we conducted  
261 neutrality tests based on within-species population genetic data with (to determine ancestral

262 states) or without outgroup, including Tajima's  $D$  test (Tajima 1989), Fay and Wu's  $H$  normalized  
263 test (Zeng et al. 2006), both based on the site-frequency spectrum (SFS), Ewens-Watterson  $EW$   
264 homozygosity test (Watterson 1978), and the  $DHEW$  neutrality test (Zeng, Shi, and Wu 2007) – a  
265 compound test that combines the properties of  $D$ ,  $H$  normalized and  $EW$  tests – using scripts  
266 provided by K. Zeng (State Key Laboratory of Biocontrol and Key Laboratory of Gene  
267 Engineering of the Ministry of Education, Sun Yat-sen University, Guangzhou, China). Second,  
268 we used methods that compare patterns of polymorphism within species and divergence between  
269 species. The McDonald-Kreitman ( $MK$ ) test, which compares the ratio of nonsynonymous and  
270 synonymous mutations between and within species (McDonald and Kreitman 1991), was  
271 computed using DnaSP v5 (Librado and Rozas 2009).  $ML-HKA$  (Maximum-Likelihood  
272 multilocus Hudson-Kreitman-Aguadé) neutrality tests were computed using the  $mlhka$  program  
273 (Wright and Charlesworth 2004). This test is an extension of the  $HKA$  test that allows to test  
274 specific locus or groups of loci against a group of neutrally evolving genes for their levels of  
275 polymorphism and divergence. First, each amplicon was compared to all the rest and the  
276 selection parameter  $K$  was computed. The  $K$  parameter measures the degree to which diversity is  
277 increased or decreased with respect to divergence. Second, for significant tests, the analysis was  
278 repeated considering only amplicons from different genes in order to avoid potential linkage. All  
279 runs consisted in 100,000 cycles of the Markov chain; long runs of 1,000,000 cycles were also  
280 computed for significant tests as well as different starting values for the divergence time  
281 parameter ( $T$ ). However, no differences were found in the results and only basic runs are  
282 presented here. Standard likelihood ratio tests (LRTs) were used to compare among models  
283 considering one amplicon under selection at a time and the null model of no selection (degrees of  
284 freedom equal one). The  $ML-HKA$  test was performed using different outgroups to gain insights

285 on evolutionary times at which positive selective wave(s) may have taken place: i) with *P. taeda*  
286 as outgroup for both *P. pinaster* and *P. halepensis* amplicons. In this case, the time frame would  
287 correspond to the split between the *Trifoliae* section (to which *P. taeda* belongs) and the *Pinus*  
288 section (to which the Mediterranean pines belong) in the Oligocene (~25 Ma; Gernandt et al.  
289 2005; Gernandt et al. 2008). Three amplicons were discarded from these analyses because they  
290 had *P. sylvestris* or *P. nigra* as outgroups (two from *dhn2-Ps*, and one from *dhn5-Ps*); ii) with *P.*  
291 *halepensis* as outgroup for *P. pinaster* amplicons and *P. pinaster* as outgroup for *P. halepensis*  
292 amplicons. The time frame, in this case, would correspond to the diversification of  
293 Mediterranean piness (in the Miocene, ~10 Ma; Gernandt et al. 2008). One amplicon was  
294 discarded from this series of tests (*dhn2-Ps\_b*; see Table S2 for amplicon nomenclature) due to  
295 bad alignment between species and, thus, the possible amplification of a paralogous fragment in  
296 *P. halepensis* (*dhn2-Ps\_b* from *P. halepensis* had more similarity with the outgroup, *P. nigra*,  
297 than with its close relative *P. pinaster*).

298 *Environmental associations.* We tested if SNP-allele or haplotype frequencies at candidate loci  
299 correlated with climatic variables using logistic regression. We first carried out series of  
300 univariate logistic regressions to test for association between SNP/haplotype frequencies and  
301 environmental variables using the program SAM (Joost, Kalbermatten, and Bonin 2008). We  
302 considered a correlation as significant only when two likelihood ratio tests (G and Wald tests)  
303 rejected the null hypothesis of no association between the genetic and the environmental  
304 variables (at the 5% level). A strict Bonferroni correction was applied to correct for multiple  
305 testing of univariate models.

306 In a second step, whenever a SNP/haplotype was found significantly correlated with an  
307 environmental variable, we performed a multivariate logistic regression using neutral marker

308 PCs (see above) as covariates (together with the SNP and the environmental variables) to control  
309 for neutral processes (e.g. postglacial migrations, geographical isolation) that may have also  
310 generated clines in the absence of any local adaptation. Multiple logistic regressions were  
311 performed in *R* (R Development Core Team) using the *glm* function (assuming that allelic counts  
312 at SNPs were binomially distributed) for each SNP/haplotype separately. Model selection was  
313 carried out using the *drop1* function and likelihood ratio tests (LRTs). Whenever the models  
314 compared were not nested (and LRTs were thus not appropriate), we used Akaike's Information  
315 Criterion (AIC). Tests for environmental associations were performed at the amplicon level  
316 (counting the SNPs located within overlapping regions only once) and including only  
317 populations with more than three gametes sampled (average number of gametes sampled per  
318 population: 7.98 in *P. pinaster* and 9.27 in *P. halepensis*, see Table S1).

319

320

## RESULTS

321

### 322 Gene diversity and divergence

323 Overall primer transfer rates across the two pine species were high (91.6% for *P. pinaster* and  
324 83.3% for *P. halepensis*) and we obtained a total of 533 kbp and 380 kbp of sequence in *P.*  
325 *pinaster* and *P. halepensis*, respectively. All sequences represented putative orthologs  
326 (determined on the basis of similarities with available sequences in GenBank and construction of  
327 phylogenies including multiple gene members of the target families in different conifers) except  
328 probably for *dhn2-Ps\_b* in *P. halepensis* (see Methods). Maritime pine showed a higher level of  
329 gene diversity than Aleppo pine (Table 2), and this result held when considering only the nine  
330 orthologous amplicons in the two species (data not shown). In total, 131 SNPs (24 non-



331 synonymous) were detected in *P. pinaster* (4 to 27 per amplicon) and 65 SNPs (12 non-  
332 synonymous) in *P. halepensis* (1 to 21 per amplicon) (Table 2). There were only four shared  
333 polymorphisms (i.e. 2 % of polymorphic sites were shared) across species, with two of them  
334 (those within *4cl-Pt*) appearing only in one *P. pinaster* individual. Number of  
335 insertions/deletions was similar between the two species for the same locus, but these indels  
336 were not shared across species. None of them caused frame shifts. At the haplotype level, not  
337 only the number of haplotypes substantially differed between the two species (86 for *P. pinaster*  
338 vs. only 59 for *P. halepensis*) but also their frequency spectrum: *P. pinaster* had multiple  
339 common haplotypes along with some less frequent ones, while *P. halepensis* generally displayed  
340 one major haplotype together with some low-frequency ones (Figure S2). Finally, there was also  
341 a contrasted pattern of gene diversity between the regional groups defined by chloroplast  
342 microsatellites in *P. pinaster*: the Western Mediterranean group displayed higher nucleotide  
343 diversity than the North African group (average  $\theta_w$  per population of 0.0039 vs. 0.0022). The  
344 SNP and haplotypes detected were used to conduct neutrality tests, as well as to detect  
345 associations with environmental variables.

346 Divergence at the DNA sequence level was examined using two outgroups: *P. taeda*, a  
347 New World pine, and each of the Mediterranean pines as reference for the other (i.e. *P.*  
348 *halepensis* was used as outgroup for *P. pinaster* and *vice versa*). For both species, nucleotide  
349 divergence per site with *P. taeda* ( $K_{all} = 0.0397$  for *P. pinaster*;  $K_{all} = 0.0498$  for *P. halepensis*)  
350 was higher than with the other Mediterranean species ( $K_{all} = 0.0235$  for *P. pinaster* vs. *P.*  
351 *halepensis*) except for *dhn2-Pp\_b* in *P. pinaster* that displayed a slightly higher divergence  
352 between the Mediterranean pines than between each of them with *P. taeda*.

353

354 **Neutrality tests**

355 Neutrality tests rejected the null neutral model for distinct genes depending on the species and  
356 the geographic group (Table 3). The  $D$  and  $H_{norm}$  tests identified some genes departing  
357 significantly from expectation under the neutral model that are not detected by the more robust  
358  $DHEW$  test:  $lp31-Pt_a$  and  $lp31-Pt_b$  in the North African group for *P. pinaster*;  $lp33-Pp$  in the  
359 Western Mediterranean group for *P. halepensis*. As shown below, these two tests are probably  
360 reflecting demographical events and not selective processes. More relevantly, two fragments of  
361 the  $4cl-Pt$  gene were identified as potential targets of selection by  $DHEW$  tests:  $4cl-Pt_b$  in the  
362 Western Mediterranean group for *P. pinaster* and  $4cl-Pt_d$  in the North African group for *P.*  
363 *halepensis*. Considering all polymorphic sites or only silent sites did not change the qualitative  
364 results of the test (Table 3 and Table S5).

365         None of the  $MK$  tests showed any departure from the null hypothesis of an equal ratio of  
366 nonsynonymous to synonymous variation within and between species (data not shown). The  $ML-$   
367  $HKA$  tests based on silent sites (with *P. taeda* as outgroup) revealed uncoupled patterns of  
368 polymorphism and divergence in only one amplicon in *P. pinaster* in the Western Mediterranean  
369 group ( $dhn2-Pp_b$ ), while in *P. halepensis* one amplicon in this same group ( $lp33-Pp$ ) and one in  
370 the North African group ( $4cl-Pt_b$ ) were significant (Table 3). These results still stood when  
371 analyses were restricted to only one amplicon per gene (in order to avoid potential linkage  
372 between fragments from the same gene) and when fragments potentially under selection were not  
373 used as control loci (data not shown). When all substitution sites were included in the analyses,  
374 three more genes were significant for *P. halepensis* in the Western Mediterranean group ( $dhn2-$   
375  $Ps_a$ ,  $4cl-Pt_a$ ,  $4cl-Pt_b$ ) (Table S5). In contrast, when Mediterranean pines were used as  
376 outgroup for each other, patterns of polymorphism and divergence either considering all sites

377 (Table S5) or silent sites (Table 3) seemed to evolve neutrally and a similar trend of the  
378 maximum likelihood estimate of the selection parameter (*ML-HKA*'s *K*) was observed in the two  
379 series of analyses.

380

### 381 **Environmental associations**

382 Environmental associations were examined at both the SNP and the haplotype level, and, overall,  
383 similar associations were detected. Nonetheless, a few correlations differed, with some found  
384 only at the haplotype level, which highlights how these two levels complement each other as  
385 haplotypes may reflect interactions among linked mutations. Within the two species, all  
386 significant associations detected between SNPs or haplotypes and climatic variables involved  
387 temperature indices as environmental variables.

388 As many as 23 significant associations were initially found in *P. pinaster* (non-corrected  
389 model as provided by SAM, see Methods). Only three associations remained after integrating  
390 neutral marker PCs as covariates, two of them with spatial variables (one with altitude, one with  
391 latitude) and one (*4cl-Pt\_c\_229*) with the minimum temperature of the coldest month (MTCM)  
392 (Figure 2; Table S6). At the haplotype level, initially 32 associations were found in maritime  
393 pine but only six remained in the corrected model: two (*4cl-Pt\_c\_A* and *4cl-Pt\_c\_B*) with  
394 altitude and one (*dhn5-Ps\_C*) with annual mean temperature (AMT), one (*dhn5-Ps\_E*) with  
395 maximum temperature of the warmest month (MTWM), and two (*4cl-Pt\_c\_A* and *4cl-Pt\_c\_B*)  
396 with minimum temperature of the coldest month (MTCM) (Figure 2; Table S7). In the case of *P.*  
397 *halepensis*, only one association was found by the corrected models, both at the SNP (between  
398 *4cl-Pt\_c\_131* and temperature seasonality, TS) and at the haplotype (*4cl-Pt\_c\_B* and TS) level  
399 (Figure 2; Tables S6 and S7).

400 In summary, association analysis identified two loci exhibiting significant correlations  
401 with temperature indices: *4cl-Pt\_c* that is associated with MTCM in *P. pinaster* and with TS in  
402 *P. halepensis* at both the SNP and haplotype levels, and *dhn5-Ps* that is associated with AMT  
403 and MTWM at the haplotype level in *P. pinaster* only.

404

## 405 DISCUSSION

406

407 In this study, we assessed the impact of natural selection on the same set of candidate genes  
408 related to drought tolerance in two widespread Mediterranean pine species. Our results revealed  
409 distinct selection patterns according to species, geographic regions and loci. Below, we discuss  
410 these findings in the light of the history of each species and the specificities of each of the  
411 methods used to reveal footprints of selection.

412

### 413 **Neutrality tests**

414 Neutrality tests examining selection events based on site- and haplotype-frequency spectrum  
415 identified distinct genes potentially targeted by selection. The *D* and/or *H<sub>norm</sub>* tests detected three  
416 loci departing from neutrality that were not detected by the *DHEW* compound tests. These results  
417 may be explained by the sensitivity of the *D* and *H<sub>norm</sub>* tests to demographic factors and different  
418 degrees of background selection (Zeng et al. 2006). Especially, Tajima's *D* is sensitive to  
419 background selection and population growth while the *H<sub>norm</sub>* is more sensitive to population  
420 shrinkage and subdivision. In a previous study in *P. halepensis* based on ten candidate genes, we  
421 have shown that this species has undergone historical bottlenecks and that the western  
422 populations of the species harbored some signatures of this demographic event (Grivet et al.

423 2009). In addition, based on the present data set and extensive coalescent simulation, we have  
424 found that observed values of  $D$  and  $H_{norm}$  for *P. pinaster* both in the Western Mediterranean and  
425 North African groups reject the standard neutral model and suggest past bottlenecks in this  
426 species too (see [Figure S3](#)). To test the robustness of the *DHEW* compound test, neutral  
427 coalescent simulations under realistic bottlenecks scenarios were further simulated in *P. pinaster*  
428 (1,000 coalescent simulations per scenario) and the significant values for this test were recorded.  
429 In all cases, the number of significant tests obtained was equal or lower than the number  
430 expected by chance (see [Figure S3](#)), highlighting the robustness of the *DHEW* test in the  
431 presence of bottleneck events and geographic population structure of magnitudes similar to the  
432 ones found in maritime and Aleppo pines. In addition to our simulations, the *DHEW* test has  
433 been shown to be robust to recombination and to have high sensitivity to detect positive selection  
434 (Zeng et al. 2007), as it combines powerful (and insensitive to recombination) haplotype-  
435 frequency spectrum tests (i.e the *EW* test) with SFS statistics, such as the  $D$  test that maintains  
436 power to detect positive selection across a wide period of time (Zeng et al. 2006; Zhai, Nielsen,  
437 and Slatkin 2009). Only two on-going events of selection were detected by the *DHEW* test, one  
438 in *P. pinaster* and one in *P. halepensis*. Both cases involved the *4cl-Pt* gene (albeit in different  
439 geographical regions and distinct amplicons), suggesting a potential role of *4cl* in local adaption  
440 in both pine species (see below).

441         Among the tests examining polymorphism within species and divergence among  
442 species, the *MK* test did not detect any loci under selection. While this test is somewhat robust to  
443 demography, it seems less powerful in detecting positive selection than *HKA* type tests (Zhai,  
444 Nielsen, and Slatkin 2009). The *ML-HKA* tests for both silent and all sites, using *P. taeda* as  
445 outgroup, identified three amplicons with uncoupled levels of polymorphism and divergence in

446 the two pines. Two genes (*dhn2-Pp\_b* in *P. pinaster* in the Western Mediterranean group and  
447 *4cl-Pt\_b* in *P. halepensis* in the North African group) showed high levels of diversity compared  
448 to divergence (selection parameter higher than one), a pattern compatible with balancing  
449 selection. One other gene (*lp33-Pp* in the Western Mediterranean group in *P. halepensis*) showed  
450 low diversity compared to divergence (selection parameter lower than one), which could reflect  
451 the transient reduction in variability occurring during a selective sweep. Three other genes  
452 showed uncoupled levels of polymorphism and divergence in *P. halepensis* when examining all  
453 sites, but not when examining silent sites alone. Two of these genes (*4cl-Pt\_a* and *4cl-Pt\_b* in the  
454 Western Mediterranean group) had an excess of nucleotide diversity, which could reflect recent  
455 balancing selection acting on non-synonymous sites, while for one gene (*dhn2-Pp\_a* in the  
456 Western Mediterranean group) purifying selection reducing diversity in non-synonymous sites  
457 could explain the observed pattern. Evidence for extensive purifying selection in conifers comes  
458 from an approximately four-fold nucleotide diversity at synonymous compared to non-  
459 synonymous sites in most species (see Table 1 in González-Martínez et al. 2010), including  
460 maritime ( $dN/dS = 0.169$ ) and Aleppo ( $dN/dS = 0.344$ ) pines (this study). Although  
461 demographical events can result in a significant *ML-HKA* test, its multilocus nature combined  
462 with the *HKA* framework should produce a more robust test than those based on comparing  
463 different aspects of polymorphism at a single locus (Wright and Charlesworth 2004).

464 In order to gain power by increasing sample size while taking the specific history of  
465 each species into account, we performed the neutrality tests in groups of populations that present  
466 similar evolutionary history (i.e. North African and Western Mediterranean groups). However,  
467 grouping populations may bias the output of the SFS-based neutrality tests as it can increase the  
468 proportion of singletons, leading to an excess of low frequency variants and thus to more

469 negative  $D$  (Städler et al. 2009). In our study, populations were grouped according to  
470 homogeneous gene pools (see Bucci et al. 2007 for *P. pinaster* and Grivet et al. 2009 for *P.*  
471 *halepensis*), the consequence of which should be that no substantial differences in the number of  
472 rare variants at the population and group levels are found. The extensive gene flow normally  
473 found in conifers with large and continuous distribution would also support this approach.  
474 Nevertheless, to check that our results were not biased because of population grouping, we  
475 performed neutrality tests at the population level too and found that values of  $D$  test at the group  
476 level were not more negative than at the single population level (data not shown). Moreover,  
477 results of the  $H_{nom}$  and  $DHEW$  tests should not be affected by the accumulation of singletons as  
478 the first is based on intermediary and high frequency variants while the second integrates all  
479 variants of the site frequency spectrum. Thus, our analyses appear reasonably robust to  
480 population grouping.

481           Selective events appear to have affected distinct genes in *P. pinaster* and in *P.*  
482 *halepensis* despite their overlapping environment and close phylogenetic relationship, a result  
483 that may be connected to the different histories of the two pines that have likely resulted in  
484 different selective pressures. In *P. pinaster*, selective events were detected only within the  
485 Western Mediterranean group, while in *P. halepensis* footprints of selection were identified both  
486 in the Western Mediterranean and North African groups. These results point to different  
487 geographical selection pressures that may have led to the process of regional adaptation of the  
488 pines (see Barbéro et al. 1998 for a description of the different Mediterranean environmental  
489 zones; and Gómez and Zamora 2000; Nakazato, Bogonovich, and Moyle 2008; Montesinos et al.  
490 2009 for some examples on adaptive variation across heterogeneous environments). It is also  
491 noticeable that *P. pinaster* had lower levels of nucleotide variation within the North African

492 range. This fact can be attributed to population history and/or interpreted in the light of more  
493 extreme environmental conditions constraining population sizes and/or resulting in stronger  
494 selection in this range.

495

#### 496 **Environmental associations**

497 Environmental associations identified two loci that were correlated with temperature, suggesting  
498 the importance of this climatic variable as selective agent (Saxe et al. 2001; Jump et al. 2006).  
499 One of these genes was common for both pines (*4cl-Pt* correlated with MTCM in *P. pinaster* and  
500 with TS in *P. halepensis*), while the other gene association was only significant in *P. pinaster*  
501 (*dhn5-Ps* correlated with AMT and MTWM). Some of the correlations between genetic and  
502 climatic data in *P. pinaster* were due basically to the extreme values of a few North African  
503 populations (Sidi Meskour and Tamrabta for *4cl-Pt\_c*; Tabarka for *dhn5-Ps\_C*; see Figures 2 and  
504 3) and may not represent true adaptive responses to environmental gradients but local adaptation  
505 to particular environments or genetic drift due to population isolation (see references in  
506 Alleaume-Benharira, Pen, and Ronce 2006; Rosenblum, Hickerson, and Moritz 2007). In  
507 contrast, the other associations (*4cl-Pt\_c* in *P. halepensis* and *dhn5-Ps\_E* in *P. pinaster*) showed  
508 more robust patterns. For instance, *dhn5-Ps\_E* tended to be absent from populations  
509 characterized by the highest MTWM (Arenas de San Pedro in central Spain, Tamrabta in  
510 Moroccan Middle Atlas and Tabarka in coastal Tunisia) regardless of their geographical location  
511 (Table 1 and Figure 3).

512 Environmental correlations with allelic variation can be spuriously inflated by neutral  
513 processes that may also generate genetic clines, such as population history or population genetic  
514 structure. This is particularly true for forest trees that may have followed a postglacial



515 colonization pathway overlapping temperature and rainfall clines. Here, to control for  
516 confounding associations between candidate genes and environmental data, we included  
517 variation of chloroplast microsatellites as a covariate in the multivariate logistic regressions. In  
518 *P. pinaster*, the use of cpSSRs has allowed a more accurate description of genetic structure  
519 (Bucci et al. 2007) than previous studies based on biochemical markers, such as terpenes or  
520 allozymes (e.g. Baradat and Marpeau-Bezard 1988; Salvador et al. 2000). Recently, nuclear  
521 molecular data for a geographically limited set of populations (nuSSRs and SNPs) (Eveno et al.  
522 2008; our unpublished results) have identified similar gene pools as Bucci et al. (2007). More  
523 extensive sampling with highly-polymorphic biparentally-inherited nuclear markers could, in  
524 principle, reveal a more complex spatial genetic pattern affecting the outcome of some of the  
525 multivariate logistic regressions reported in this study. However, because the available  
526 chloroplast data set we used strongly reflects the species' history, they are expected to 'correct'  
527 for the presence of overall neutral genetic gradients. Accordingly, including these markers as  
528 covariates identified a substantial fraction of the correlations initially retained as significant as  
529 false positives (83.6 % in *P. pinaster* and 85.7% in *P. halepensis*) (Tables S6 and S7).

530

### 531 ***The dehydrin gene family***

532 Neutrality tests and environmental associations both point to dehydrins as potential targets of  
533 natural selection in *P. pinaster*. Some dehydrins were also suggested to be under selection in a  
534 study based on detection of outlier loci in this species (Eveno et al. 2008). Dehydrins displayed  
535 also non-neutral patterns of nucleotide diversity in *Pinus sylvestris* populations showing  
536 divergence for cold tolerance in Europe (Wachowiak et al. 2009) and were associated with  
537 carbon isotope discrimination (and, thus, potentially with drought tolerance) in *P. taeda*

538 (González-Martínez et al. 2008). Altogether these studies suggest the involvement of dehydrins  
539 in the adaptive response of pines to abiotic stress.

540 Dehydrins are part of a relatively small multigene family of intracellular stabilizers that  
541 plays a major role in cell protection against desiccation. These proteins are produced in response  
542 to any type of stress that causes dehydration at the cellular level, such as cold, drought or salinity  
543 (Close 1997). Changes in dehydrin gene expression have been reported in response to drought  
544 and/or cold stress in many plants such as cowpea (Ismail, Hall, and Close 1999), barley  
545 (Suprunova et al. 2004), wheat (Lopez et al. 2001), apple (Wisniewski et al. 2008), tomato  
546 (Weiss and Egea-Cortines 2009) and blueberry (Panta, Rieger, and Rowland 2001); while  
547 transgenic experiments confirmed the role of dehydrin genes in enhancing tolerance to drought  
548 or freezing stress in plants (e.g. in *Arabidopsis*, Puhakainen et al. 2004). In conifers, at least eight  
549 dehydrin genes have been identified in *Pinus sylvestris* (Joosen et al. 2006) and *Picea abies*  
550 (Yakovlev et al. 2008), and dehydrin expression has been shown to increase under wounding,  
551 cold and drought stress (Richard et al. 2000; Watkinson et al. 2003). Thus, it is not surprising to  
552 find in our study significant associations between dehydrins and temperatures, as critical low  
553 temperatures can cause tissue injury while high temperatures accompany dehydration, both  
554 stimulating the accumulation of dehydrins (Lewitt 1980; Ingram and Bartels 1996; Rizhsky,  
555 Liang, and Mittler 2002). Although our results, and others in *P. pinaster*, suggest that selection  
556 may have acted on some of the dehydrins tested, further genetic association and functional  
557 studies are necessary to confirm the role of dehydrins in local adaptation of this Mediterranean  
558 pine.

559

560 **The 4-coumarate: CoA ligase (*4cl*) gene**

561 There was converging evidence both from neutrality tests (*DHEW* in *P. pinaster* and both  
562 *DHEW* and *ML-HKA* in *P. halepensis*) and environmental associations that the *4-coumarate:*  
563 *CoA ligase (4cl)* gene may be under selection in the two Mediterranean pines studied.  
564 Preliminary results on phenotypical association corrected by neutral gradients in *P. pinaster* also  
565 point at *4cl-Pt*. Indeed, multiple regressions reveal significant associations between  
566 polymorphism in *4cl-Pt\_c* at the SNP and haplotype levels and total height in populations  
567 growing in sites characterized by dry and intermediate humidity (Table S8). The *4cl* family has  
568 been extensively studied in plants, where it is encoded by four to five genes in the fully  
569 sequenced genomes of *Arabidopsis*, rice and poplar (reviewed in Souza et al. 2008). The *4cl*  
570 gene is involved, among other processes, in the production of basic enzymes of the  
571 phenylpropanoid metabolism that are important metabolites acting as protectants against biotic  
572 and abiotic stresses (Rani et al. 2009). The *4cl* gene also encodes key enzymes in the  
573 biosynthesis of lignin and several studies have demonstrated its involvement in plant growth  
574 (e.g. Yun et al. 2005; Wagner et al. 2009; Yun et al. 2009). Thus, we expect that changes in *4cl*  
575 function would have significant repercussions on tree physiology and morphology. Implication  
576 of *4cl* in pine morphology and physiology has been shown in gene association studies (for *P.*  
577 *taeda* see González-Martínez et al. 2007b) as well as in gene suppression studies (for *P. radiata*  
578 see Wagner et al. 2009).

579

### 580 **Neutrality tests versus Environmental correlations**

581 The different approaches used in this study suggested different loci under selection within each  
582 of the two Mediterranean pine species. This fact has to be connected to the specificities of the  
583 statistical methods used, whose performance has been recently studied under various

584 demographic and recombination scenarios (Zeng et al. 2007; Zeng, Shi, and Wu 2007; Ramírez-  
585 Soriano et al. 2008; Zhai, Nielsen, and Slatkin 2009). Within-species site and haplotype  
586 frequency spectrum-based methods are suitable to detect ongoing or recently fixed selective  
587 sweeps - *EW* tending to be more powerful around the time when a selected mutation reaches  
588 fixation (Zeng, Shi, and Wu 2007). In contrast, tests comparing levels of (within-species)  
589 polymorphism and (among-species) divergence are able to detect the cumulative effects of  
590 positive selection events over a wider evolutionary scale. Within this category, the *ML-HKA* test  
591 is suitable to quantify the amount of selection in the genome and, due to its multilocus nature, it  
592 is expected to be more robust to changes in population size such as population bottlenecks and  
593 expansion than traditional tests (Wright and Charlesworth 2004). Simulations have shown that  
594 the *HKA* test is relatively insensitive to change of divergence time as most of its power comes  
595 from the transient reduction in variability occurring during selective sweeps (Zhai, Nielsen, and  
596 Slatkin 2009). However, we only obtained significant tests when using the less closely-related  
597 outgroup (i.e. a New World pine, *P. taeda*). This points to either lower power when divergence  
598 time from the outgroup is low or, alternatively, to selection events that took place before the split  
599 of the two Mediterranean pines considered. In our study, none of the *EW* neutrality tests were  
600 significant (data not shown), while both the *DHEW* and the *ML-HKA* tests revealed distinct  
601 genes potentially under selection. As a consequence, potential selective events detected by the  
602 neutrality tests assessed in this study would correspond to either on-going or relatively old  
603 selective events (i.e. before the diversification of the Mediterranean pines in the Miocene, ~10  
604 Ma; Gernandt et al. 2008).

605         Last generation tests, such as *DHEW* or *ML-HKA*, are powerful for detecting positive  
606 selection and are relatively insensitive to other evolutionary forces, but still do not integrate

607 recombination rate, a factor that can produce substantial biases (Nielsen et al. 2007; Ramírez-  
608 Soriano et al. 2008), nor provide insights on selection drivers. Methods based on correlation  
609 between genetic and environmental data are appealing because they aim at understanding  
610 species-specific adaptations and processes that connect an organism to its environment by  
611 looking at allelic frequencies or the genetic structure of populations (Foll and Gaggiotti 2006;  
612 Joost, Kalbermatten, and Bonin 2008). These correlation methods are also more appealing than  
613 methods based on detection of outliers (e.g. Eveno et al. 2008) as they target particular selection  
614 drivers and provide a hypothesis testing framework. In addition, they are well suited for high-  
615 throughput genotyping even for non-model species (Namroud et al. 2008; Eckert et al.  
616 forthcoming). However, correlation methods are not without limitations, as it may be challenging  
617 to find the environmental factors that are relevant for each species adaptation and associations  
618 have to be controlled for historical and demographical processes, in particular for allelic clines  
619 produced by postglacial migrations in Europe and the Americas.

620 Together, neutrality tests and environmental association approaches complement each  
621 other by looking at different evolutionary scales and types of selection. In our study, they  
622 detected a relatively-high number of genes showing non-neutral patterns of evolution, a result  
623 that can be attributed to a selection of candidate genes based on earlier studies (González-  
624 Martínez et al. 2006; Eveno et al. 2008; Grivet et al. 2009). This fact supports a candidate gene  
625 approach with targeted genes, at least for organisms that have large genomes (e.g. conifers),  
626 which, so far, preclude dense genome-wide sampling.

627

628 **Conclusion**

629 Our pluralistic approach revealed a dynamic action of natural selection in space and time within  
630 maritime and Aleppo pines (Felsenstein 1976; see Vasemagi and Primmer 2005 for other  
631 examples). Selection events along with environmental associations were detected; some of these  
632 events differ between the two species reflecting individual histories (recolonization,  
633 demography, adaptation) while others are shared, which translates partly as a common history of  
634 these closely-related and partially sympatric Mediterranean pines. The simultaneous search for  
635 patterns of selection in two closely-related species can help understanding the evolutionary  
636 forces responsible for adaptive responses, and thus provides an effective way of assessing the  
637 degree of local adaptation, a key factor to integrate in future management and conservation  
638 strategies (Wright and Gaut 2005).

639

## SUPPLEMENTARY MATERIAL

640

641

642 **Table S1.** Sampling size per amplicon (six putative candidate genes) and per population for *P.*  
643 *pinaster* and *P. halepensis*.

644 **Table S2.** Characteristics of the primers used to amplify the candidate genes in *P. pinaster* and  
645 *P. halepensis*.

646 **Table S3.** PCR conditions for amplicon amplification (six putative candidate genes) for *P.*  
647 *pinaster* and *P. halepensis*.

648 **Table S4.** First three Principal Components (PCs) of the chloroplast haplotype frequency for *P.*  
649 *pinaster* and *P. halepensis*.

650 **Table S5.** Polymorphism, divergence and neutrality tests (all sites) in *P. pinaster* and *P.*  
651 *halepensis* for the phylogeographical groups defined with chloroplast microsatellites.

652 **Table S6.** SAM output (uncorrected models) showing the significant associations (at 5%)  
653 between a given allele (SNP) at a given locus and a given environmental variable for *P. pinaster*  
654 and *P. halepensis*.

655 **Table S7.** SAM output (uncorrected models) showing the significant associations (at 5%)  
656 between a given haplotype and a given environmental variable for *P. pinaster* and *P. halepensis*.

657 **Table S8.** Phenotypic data for *P. pinaster* populations (unpublished data kindly provided by R.  
658 Alía and P.H. Garnier-Géré).

659 **Figure S1.** Graphical pairwise relationships between the 11 spatial and environmental variables  
660 recorded.

661 **Figure S2.** Haplotype distribution in *P. pinaster* and *P. halepensis* for the nine common  
662 amplicons.

663 **Figure S3.** Demographic inferences in *P. pinaster* using multilocus coalescent simulation of  
664 genetic bottleneck scenarios.  
665



666

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679

680

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688

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**Table 1.** Spatial coordinates and climatic variables for *P. pinaster* and *P. halepensis* populations.

Population	Country	Spatial variables			Climatic variables							
		Altitude (m)	Latitude (degrees)	Longitude (degrees)	AMT (°C)	TS	MTWM (°C)	MTCM (°C)	AP (mm)	PWM (mm)	PDM (mm)	PS
<i>P. pinaster</i>												
Arenas de San Pedro	Spain	733	40.194822	-5.116213	14.2	668.9	33.4	1.4	1318	199	12	60.8
Cazorla	Spain	1100	37.919675	-2.925765	11.5	650.2	30.6	-1.4	1257	179	11	58.3
Coca	Spain	800	41.254705	-4.497827	12.3	655.9	31.2	-0.6	454	55	15	30.0
Cómpeta	Spain	903	36.834265	-3.953989	14.0	512.1	27.5	4.7	899	132	5	64.1
Olba	Spain	1002	40.173309	-0.622966	12.4	600.7	28.3	0.6	509	63	24	31.5
Oria	Spain	1223	37.531165	-2.351138	13.1	633.1	30.6	0.4	357	46	5	46.2
Quatretonda	Spain	435	38.971645	-0.358844	15.3	553.7	30.3	3.8	777	120	9	52.1
Mimizan	France	19	44.134167	-1.303056	13.2	490.9	24.9	3.1	1235	149	62	24.3
Pinia	France	15	42.021083	9.464861	15.6	515.5	27.0	6.3	585	80	8	49.6
Tabarka	Tunisia	121	36.958397	8.703792	17.7	573.4	31.8	6.7	916	162	4	72.3
Tamrabta	Morocco	1758	33.600000	-5.016667	11.8	665.3	31.3	-3.2	721	96	8	54.4
Sidi Meskour	Morocco	1931	31.439375	-6.903864	11.4	711.3	32.5	-5.2	514	71	5	56.4
<i>P. halepensis</i>												
Cabanellas	Spain	210	42.235556	2.790000	14.8	575.5	27.4	3.9	713	97	35	26.0
Carratraca	Spain	650	36.841111	-4.834444	15.7	568.6	30.6	4.4	693	106	3	69.4
S'avall	Spain	10	39.287222	3.047778	16.8	525.9	28.7	6.8	566	92	5	54.7
Tarrasa	Spain	117	41.466667	2.100000	15.9	551.1	27.7	5.8	619	83	29	29.5
Imperia	Italy	109	43.900000	8.050000	15.1	550.5	27.5	4.6	804	107	18	38.5
Zaouia Ifrane	Morocco	1512	33.570000	-5.140000	11.5	668.7	31.2	-3.8	849	123	8	57.4

Aures Beni Melloul	Algeria	936	35.166667	6.833333	13.4	657.2	31.2	-0.1	375	53	10	36.1
Elea	Greece	155	37.766667	21.533333	16.7	592.0	30.8	5.4	808	150	6	77.1
Shaharia	Israel	236	31.600000	34.833333	20.0	496.4	31.8	8.0	397	100	0	116

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AMT: annual mean temperature; TS: temperature seasonality (STD \*100); MTWM: maximum temperature of the warmest month; MTCM: minimum temperature of the coldest month; AP: annual precipitation; PWM: precipitation of the wettest month; PDM: precipitation of the driest month; PS: precipitation seasonality (CV \*100).

**Table 2.** Gene diversity (all sites) for 12 amplicons from six putative candidate genes across the twelve *P. pinaster* populations and the nine *P. halepensis* populations.

Amplicon	<i>P. pinaster</i>							<i>P. halepensis</i>						
	<i>N</i>	<i>L</i>	<i>S</i>	$\theta_\pi$	$\theta_w$	<i>K</i>	<i>He</i>	<i>N</i>	<i>L</i>	<i>S</i>	$\theta_\pi$	$\theta_w$	<i>K</i>	<i>He</i>
<i>lp31-Pt</i>														
<i>a</i>	122	456	12	6.26	4.89	6	0.717	79	353	3	2.48	1.72	4	0.460
<i>b</i>	111	560	7	3.91	2.37	3	0.446	74	488	7	3.93	2.94	4	0.464
<i>lp33-Pp</i>	97	449	9	4.29	3.89	9	0.798	90	375	1	0.17	0.53	2	0.065
<i>dhn2-Pp</i>														
<i>a</i>	120	472	12	6.06	4.74	11	0.807	89	448	2	0.20	0.88	3	0.088
<i>b</i>	85	596	21	8.42	7.03	11	0.811	93	346	4	0.55	2.26	5	0.105
<i>dhn2-Ps</i>														
<i>a</i>	92	743	27	8.10	7.13	14	0.899	na	na	na	na	na	na	na
<i>b</i>	80	513	15	5.92	5.90	14	0.855	92	457	11	1.93	4.73	6	0.204
<i>dhn5-Ps</i>	77	449	4	4.00	1.81	5	0.735	na	na	na	na	na	na	na
<i>4cl-Pt</i>														
<i>a</i>	91	551	13	5.67	4.64	4	0.678	88	461	10	5.88	4.30	13	0.805
<i>b</i>	92	256	7	3.56	5.37	5	0.291	79	688	21	10.67	6.18	13	0.793
<i>c</i>	87	543	4	0.69	1.46	4	0.341	78	528	3	2.47	1.15	5	0.697
<i>d</i>	na	na	na	na	na	na	na	72	452	3	2.80	1.37	4	0.484
<i>Total</i>	1054	5588	131	-	-	86	-	834	4596	65	-	-	59	
<i>Mean</i>	-	-	-	5.17	4.48	-	0.671	-	-	-	3.11	2.61	-	0.416

$N$ : number of sequences;  $L$ : total analyzed length in base pair;  $S$ : polymorphic sites;  $\theta_{\pi}$ : Tajima's nucleotide diversity  $\times 10^{-3}$  (Tajima 1989) and  $\theta_w$ : Watterson's nucleotide diversity (Watterson 1975) per site ( $\times 10^{-3}$ );  $K$ : number of haplotypes;  $He$ : haplotype diversity; na: amplicons that failed to transfer across species.



**Table 3a.** Polymorphism, divergence and neutrality tests (silent sites) in *P. pinaster* for the phylogeographical groups defined with chloroplast microsatellites (see text for details).

Amplicon	<i>S</i>	<i>D</i>	<i>H<sub>norm</sub></i>	<i>DHEW</i> <i>P</i> -value	<i>ML-HKA's K</i> ( <i>P. taeda</i> )	<i>K<sub>s</sub></i> ( <i>P. taeda</i> )	<i>ML-HKA's K</i> ( <i>P. halepensis</i> )	<i>K<sub>s</sub></i> ( <i>P. halepensis</i> )
Western Mediterranean <sup>a</sup>								
<i>lp31-Pt</i>								
<i>a</i>	8	2.172	-0.635	0.958	0.961	38.350	1.292	20.310
<i>b</i>	6	1.834	-1.380	0.913	0.698	44.250	0.720	24.360
<i>lp33-Pp</i>								
<i>dhn2-Pp</i>	6	1.133	0.911	0.984	0.696	60.060	1.839	15.990
<i>a</i>	7	0.269	-0.853	0.406	1.605	38.160	1.307	31.580
<i>b</i>	19	0.186	0.825	0.727	3.256 *	31.940	1.975	39.720
<i>dhn2-Ps</i>								
<i>a</i>	15	0.631	0.703	0.562	ptna	ptna	phna	phna
<i>b</i>	8	-0.126	0.232	0.209	ptna	ptna	d	d
<i>dhn5-Ps</i>								
<i>a</i>	2	1.960	0.136	0.907	ptna	ptna	phna	phna
<i>4cl-Pt</i>								
<i>a</i>	2	0.422	0.067	0.610	0.307	31.480	0.250	26.870
<i>b</i>	2	-1.041	-3.173 *	0.014 *	0.741	43.930	0.446	41.220
<i>c</i>	1	0.214	0.565	0.663	0.542	23.080	0.000	1.190
<i>d</i>	na	na	na	na	na	na	na	na
North Africa <sup>b</sup>								
<i>lp31-Pt</i>								
<i>a</i>	7	-0.276	-3.065 *	0.336	0.878	39.300	0.952	22.280

<i>b</i>	6	-2.046	-3.813	0.073	0.820	44.250	0.880	26.150
<i>lp33-Pp</i>	5	0.014	0.926	0.899	0.614	57.860	1.946	13.040
<i>dhn2-Pp</i>								
<i>a</i>	4	0.799	-0.554	0.615	0.868	36.610	0.792	28.620
<i>b</i>	13	1.095	0.361	0.718	2.036	32.780	1.362	33.600
<i>dhn2-Ps</i>								
<i>a</i>	6	0.190	-0.232	0.322	ptna	ptna	phna	phna
<i>b</i>	6	-1.116	-1.223	0.085	ptna	ptna	d	d
<i>dhn5-Ps</i>	2	0.688	-0.809	0.540	ptna	ptna	phna	phna
<i>4cl-Pt</i>								
<i>a</i>	8	2.797	0.411	0.995	1.279	39.160	0.442	28.880
<i>b</i>	3	2.266	0.090	0.982	1.303	48.190	1.017	34.730
<i>c</i>	2	0.201	0.387	0.494	1.039	25.240	0.000	3.410
<i>d</i>	na	na	na	na	na	na	na	na

*D*: Tajima's *D* (Tajima 1989);  $H_{norm}$ : Fay and Wu's normalized *H* (Zeng et al. 2006); *DHEW* test: compound test (Zeng et al. 2007); *ML-HKA*'s *K*: Selection parameter of the Maximum-Likelihood multilocus Hudson-Kreitman-Aguadé neutrality tests (Wright and Charlesworth 2004); the species used as outgroup is given in parenthesis; *S*: number of segregating sites;  $K_s$ : average proportion of nucleotide differences between species per silent site  $\times 10^{-3}$ .

na: amplicons that failed to transfer across species; ptna: *P. taeda* outgroup sequence not available; phna: *P. halepensis* outgroup sequence not available; d: discarded because possible paralog.

*P*-values [P neutrality test (neutral)  $\leq$  P neutrality test (observed)]: 0 < \*\*\* < 0.001 < \*\* < 0.01 < \* < 0.05

<sup>a</sup> Western Mediterranean: Arenas de San Pedro, Cazorla, Coca, C mpeta and Olba.

<sup>b</sup> North Africa: Tabarka, Tamrabta and Sidi Meskour.

**Table 3b.** Polymorphism, divergence and neutrality tests (silent sites) in *P. halepensis* for the phylogeographical groups defined with chloroplast microsatellites (see text for details).

Amplicon	<i>S</i>	<i>D</i>	<i>H<sub>norm</sub></i>	<i>DHEW</i> <i>P</i> -value	<i>ML-HKA's K</i> ( <i>P. taeda</i> )	<i>K<sub>s</sub></i> ( <i>P. taeda</i> )	<i>ML-HKA's K</i> ( <i>P. pinaster</i> )	<i>K<sub>s</sub></i> ( <i>P. pinaster</i> )
Western Mediterranean <sup>a</sup>								
<i>lp31-Pt</i>								
<i>a</i>	2	1.689	-1.714	0.860	0.597	34.590	0.452	20.960
<i>b</i>	4	0.535	-0.948	0.501	0.889	48.280	1.380	23.090
<i>lp33-Pp</i>								
<i>dhn2-Pp</i>	1	-0.629	-4.343 *	0.270	0.145 *	69.100	0.361	14.020
<i>a</i>	0	nps	nps	nps	nps	55.770	nps	44.020
<i>b</i>	0	nps	nps	nps	nps	57.180	nps	38.220
<i>dhn2-Ps</i>								
<i>a</i>	na	na	na	na	na	na	na	na
<i>b</i>	2	-0.595	0.317	0.382	ptna	ptna	d	d
<i>dhn5-Ps</i>								
<i>a</i>	na	na	na	na	na	na	na	na
<i>4cl-Pt</i>								
<i>a</i>	6	0.752	-1.222	0.599	2.236	43.260	1.618	22.500
<i>b</i>	16	2.386	-0.320	0.985	2.279	52.000	1.242	30.660
<i>c</i>	2	1.701	-1.305	0.867	1.350	31.970	2.976	9.440
<i>d</i>	3	2.324	-0.981	0.965	0.674	54.780	ppna	ppna
North Africa <sup>b</sup>								
<i>lp31-Pt</i>								
<i>a</i>	2	1.818	-1.053	0.898	0.819	34.140	1.123	12.710

<i>b</i>	2	1.882	0.602	0.909	0.530	49.000	0.924	22.700
<i>lp33-Pp</i>	0	nps	nps	nps	nps	69.410	nps	9.550
<i>dhn2-Pp</i>								
<i>a</i>	1	-0.774	0.289	0.313	0.329	56.280	0.525	19.310
<i>b</i>	1	-1.147	0.160	0.189	0.215	57.320	0.205	33.600
<i>dhn2-Ps</i>								
<i>a</i>	na	na	na	na	na	na	na	na
<i>b</i>	0	nps	nps	nps	ptna	ptna	d	d
<i>dhn5-Ps</i>	na	na	na	na	na	na	na	na
<i>4cl-Pt</i>								
<i>a</i>	4	1.306	-0.201	0.791	2.072	44.030	1.815	22.450
<i>b</i>	14	2.316	0.044	0.981	3.251 *	50.760	1.951	31.290
<i>c</i>	2	1.077	0.221	0.834	1.665	27.720	3.309	5.200
<i>d</i>	3	-1.494	-6.584	0.009 **	0.860	60.020	ppna	ppna

*D*: Tajima's *D* (Tajima 1989);  $H_{norm}$ : Fay and Wu's normalized *H* (Zeng et al. 2006); *DHEW* test: compound test (Zeng et al. 2007); *ML-HKA*'s *K*: Selection parameter of the Maximum-Likelihood multilocus Hudson-Kreitman-Aguadé neutrality tests (Wright and Charlesworth 2004); the species used as outgroup is given in parenthesis; *S*: number of segregating sites;  $K_s$ : average proportion of nucleotide differences between species per silent site  $\times 10^{-3}$ .

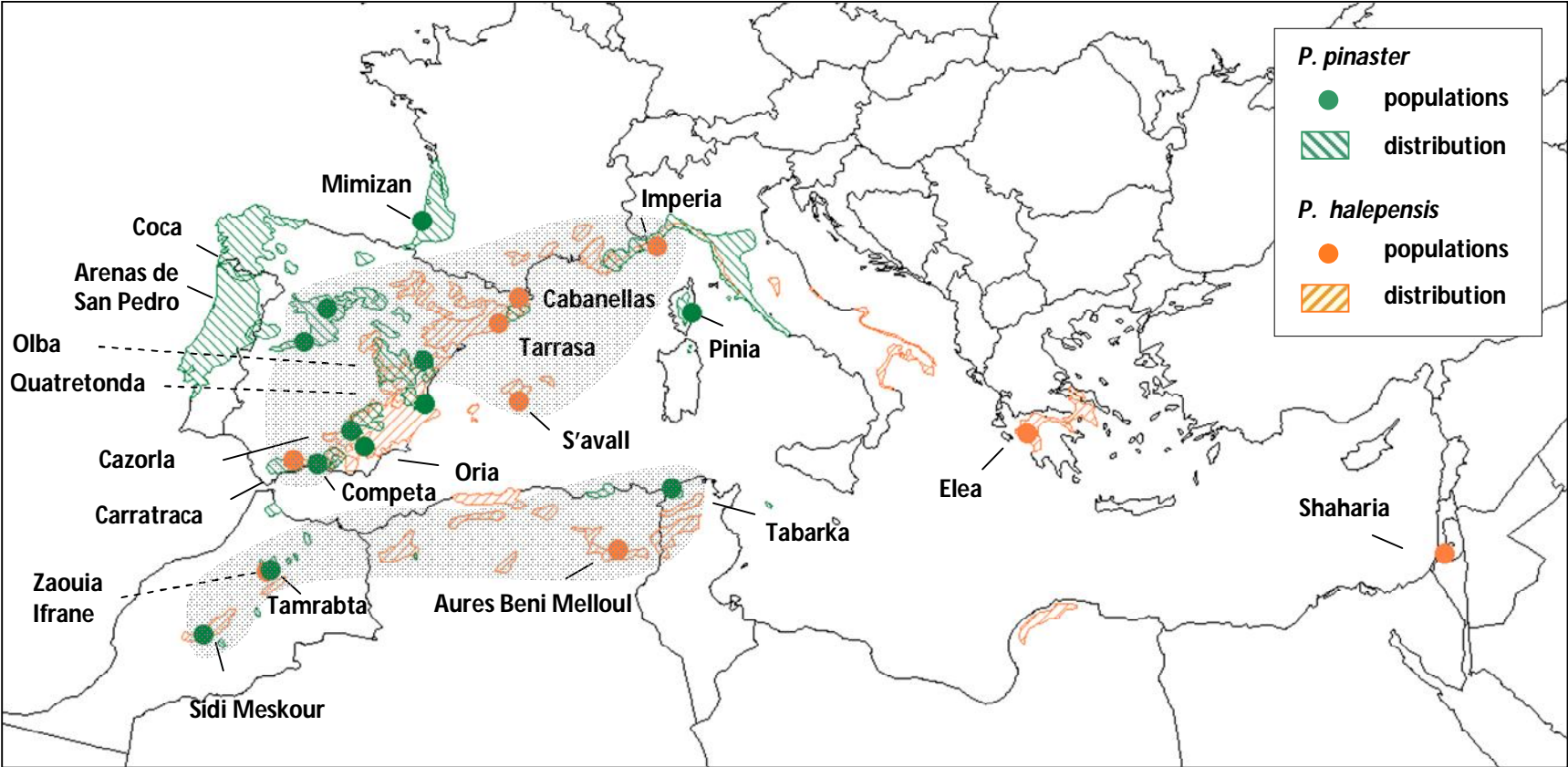
na: amplicons that failed to transfer across species; ptna: *P. taeda* outgroup sequence not available; ppna: *P. pinaster* outgroup sequence not available; d: discarded because possible paralog; nps: monomorphic fragment.

*P*-values [P neutrality test (neutral)  $\leq$  P neutrality test (observed)]: 0 < \*\*\* < 0.001 < \*\* < 0.01 < \* < 0.05

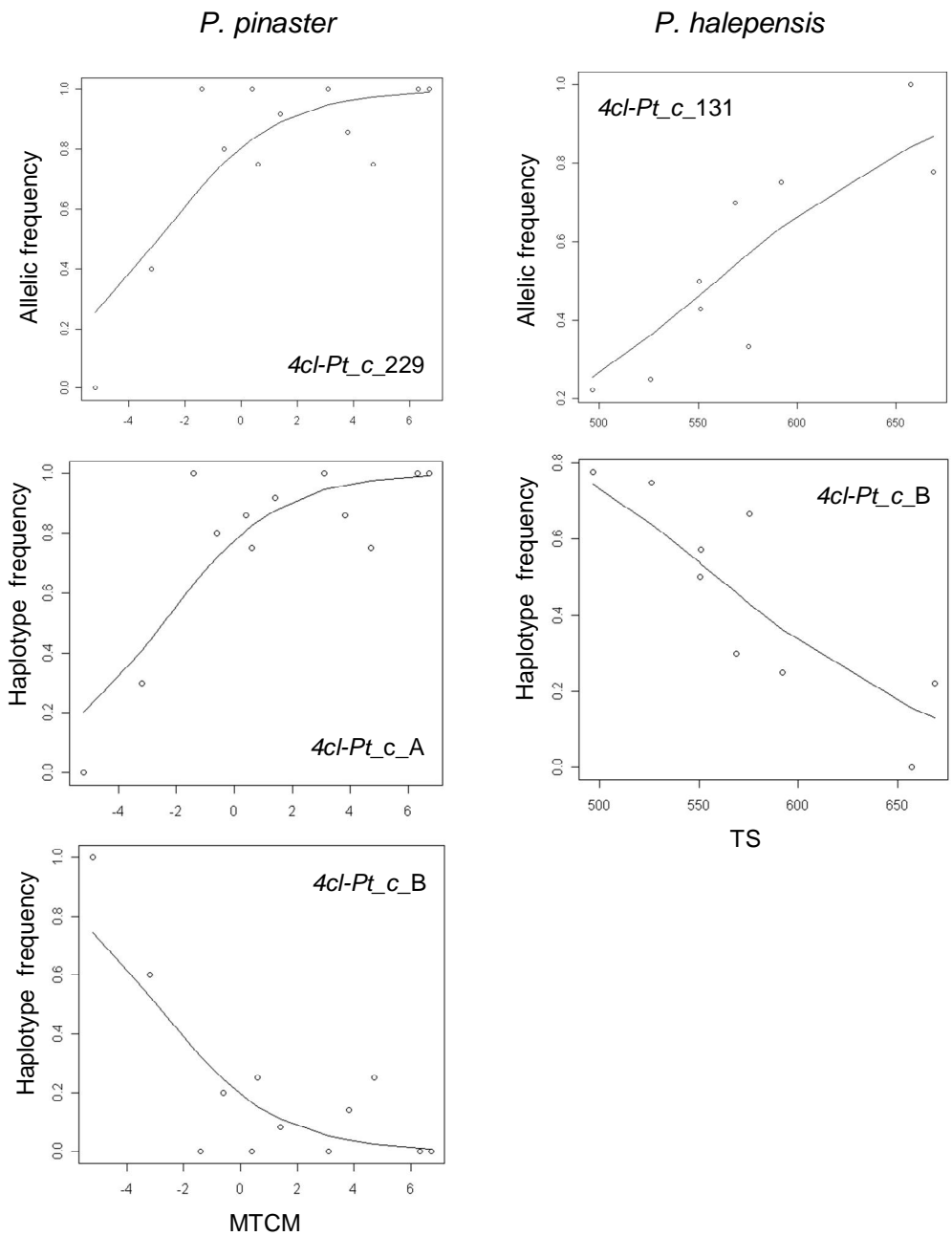
<sup>a</sup> Western Mediterranean: Cabanellas, Carratraca, Imperia, S'avall and Tarrasa.

<sup>b</sup> North Africa: Aures Beni Melloul and Zaouia Ifrane.

**Figure 1.** Location of the 12 *P. pinaster* and the 9 *P. halepensis* populations and the distribution of the two species. Grey areas represent the two groups (Western Mediterranean and North African) defined by chloroplast SSRs (see text for details).



**Figure 2.** Predicted and observed patterns of clinal variation at *4cl-Pt\_c*. Sigmoid curves denote the clines in either allelic (SNP position given) or haplotypic (haplotypes represented by capital letters) frequencies under a logistic regression model. The logistic regression model uses a climatic variable (MTCM or TS) after controlling for neutral processes (i.e. using the PCs of neutral molecular markers as covariates) for *P. pinaster* and *P. halepensis*. MTCM: minimum temperature of the coldest month; TS: temperature seasonality.



**Figure 3. Upper section:** *dhn5-Ps* haplotype distribution showing the proportion of haplotypes C (in grey), E (in black) and all others (in white) in *P. pinaster*. The size of the pie is proportional to the sample size at each location. **Lower section:** expected (sigmoid curves) and observed covariation in haplotype frequencies of *dhn5-Ps\_C* and *dhn5-Ps\_E* and climatic variables. Expected curves were obtained under a logistic regression model including a single environmental variable (AMT or MTWM) after controlling for neutral processes (i.e. using the PCs of neutral molecular markers as covariates) for *P. pinaster*. AMT: annual mean temperature; MTWM: maximum temperature of the warmest month.

