# Dramatic impact of future climate change on the genetic diversity and distribution of ecologically relevant Western Mediterranean *Carex* (Cyperaceae)

**Carmen Benítez-Benítez** [Corresp., 1] , **María Sanz-Arnal** [2] , **Malvina Urbani** [3] , **Pedro Jiménez-Mejías** [2] , **Santiago Martín-Bravo** [1]

[1] Department of Molecular Biology and Biochemical Engineering/Botany area, Universidad Pablo de Olavide, Seville, Seville, Spain

[2] Campus Cantoblanco/Department of Biology, Universidad Autónoma de Madrid, Madrid, Madrid, Spain

[3] Department of Chemistry and Pharmacy, University of Sassari, Sassari, Sardinia, Italy

Corresponding Author: Carmen Benítez-Benítez
Email address: cbenben1@upo.es

Anticipating the evolutionary responses of species to ongoing climate change is essential to propose effective management and conservation measures. The Western Mediterranean Basin constitutes one of the hotspots of biodiversity where the effects of climate change are expected to be more dramatic. Plant species with ecological relevance constitute ideal models to evaluate and predict the impact of climate change on ecosystems. Here we investigate these impacts through the spatio-temporal comparison of genetic diversity/structure (AFLPs), potential distribution under different future scenarios of climate change, and ecological space in two Western Mediterranean sister species of genus *Carex*. Both species are ecologically key in their riparian habitats, but display contrasting distribution patterns, with one widespread in the Iberian Peninsula and North Africa (*C. reuteriana*), while the other (*C. panormitana*) is a restricted, probably endangered, Central Mediterranean endemic. At present, we found a strong genetic structure driven by geography in both species, and lower values of genetic diversity and a narrower ecological space in *C. panormitana* than in *C. reuteriana*, although the allelic rarity was higher in the former. Future projections predict an overall dramatic reduction of suitable areas for both species under all climate change scenarios, which could be almost total for *C. panormitana*. In addition, gene diversity was inferred to decrease in all taxa, with genetic structure reinforcing in *C. reuteriana* by the loss of admixture among populations. Our findings stress the need for a reassessment of *C. panormitana* conservation status under IUCN Red List criteria and the implementation of conservation measures.

1  **Dramatic impact of future climate change on the genetic diversity and distribution of**

2  **ecologically relevant Western Mediterranean *Carex* (Cyperaceae)**

3  Carmen Benítez-Benítez [1*], María Sanz-Arnal [2], Malvina Urbani [3], Pedro Jiménez-Mejías [2], and

4  Santiago Martín-Bravo [1]

5  [1] Botany Area, Department of Molecular Biology and Biochemical Engineering. Universidad

6  Pablo de Olavide, Seville, 41013, Spain.

7  [2] Department of Biology, Universidad Autónoma de Madrid (UAM), Campus Cantoblanco,

8  Madrid, 28049, Spain.

9  [3] Department of Chemistry and Pharmacy. University of Sassari, Sassari, 1-07100, Italy.

10  Short title: Impact of climate change in *Carex*

11  Corresponding Author: Carmen Benítez-Benítez [1*]

12  Ctra. Utrera, 1, Seville, 41013, Spain.

13  Email address: cbenben1@upo.es

15  **Abstract**

16  Anticipating the evolutionary responses of species to ongoing climate change is essential to

17  propose effective management and conservation measures. The Western Mediterranean Basin

18  constitutes one of the hotspots of biodiversity where the effects of climate change are expected to

19  be more dramatic. Plant species with ecological relevance constitute ideal models to evaluate and

20  predict the impact of climate change on ecosystems. Here we investigate these impacts through

21  the spatio-temporal comparison of genetic diversity/structure (AFLPs), potential distribution

22  under different future scenarios of climate change, and ecological space in two Western

23  Mediterranean sister species of genus *Carex*. Both species are ecologically key in their riparian

24  habitats, but display contrasting distribution patterns, with one widespread in the Iberian

25  Peninsula and North Africa (*C. reuteriana*), while the other (*C. panormitana*) is a restricted,

26  probably endangered, Central Mediterranean endemic. At present, we found a strong genetic

27    structure driven by geography in both species, and lower values of genetic diversity and a

28    narrower ecological space in *C. panormitana* than in *C. reuteriana*, although the allelic rarity

29    was higher in the former. Future projections predict an overall dramatic reduction of suitable

30    areas for both species under all climate change scenarios, which could be almost total for *C.*

31    *panormitana*. In addition, gene diversity was inferred to decrease in all taxa, with genetic

32    structure reinforcing in *C. reuteriana* by the loss of admixture among populations. Our findings

33    stress the need for a reassessment of *C. panormitana* conservation status under IUCN Red List

34    criteria and the implementation of conservation measures.

35    **Keywords**: conservation genetics, ecological niche, global climate change, habitat loss,

36    Mediterranean Basin, restricted endemic, species distribution modeling

37    **1.  Introduction**

38    Nowadays, anthropogenically-driven global climate change (GCC herein) is one of the main

39    threats to life on our planet. The main conclusion from the Intergovernmental Panel on Climate

40    Change (IPCC, 2014) is that contemporary warming of land and ocean is irrefutably taking

41    place, and since the 1980s each successive decade has been warmer than any preceding one.

42    Projections of change in global mean temperature for the period 2016-2035 point to an increase

43    of 0.3-0.7ºC compared to the 1986-2005 period. By the end of this century (2081-2100),

44    estimates predict a higher frequency of extreme weather events and an increase of mean global

45    surface temperature of 0.3ºC-4.8ºC, depending on the emission and climate variability scenario

46    considered (IPCC 2013, 2014).

47        Many studies confirm that GCC has already affected the biota and ecosystems

48    (Parmesan, 2006; Johnson et al., 2017; Pecl et al., 2017; Ripple et al., 2017; García and Jordano,

49    2021). The responses of species populations to climate change can be categorized into three main

50    types: migration, extinction, and in situ adaptation (Christmas et al., 2016). Specifically, ongoing

51    GCC is inducing changes in the distribution of plant species with greater capacity for migration

52    to areas of higher latitude and/or altitude that may provide suitable environmental conditions

53    (niche conservatism, e.g., Jump and Peñuelas, 2005; Wiens et al., 2010; Morueta-Holme et al.,

54    2015; Christmas et al., 2016). However, migration rates for most species could be insufficient to

55    match the pace and magnitude of predicted climate changes (e.g., Loarie et al., 2009; Freeman

56    and Freeman, 2014; Morueta-Holme et al., 2015; González-Varo et al., 2017), leaving in situ

57    adaptation as the only alternative to extinction for these species. In species with restricted ranges,

58    low genetic variability and/or narrow ecological tolerance, genetic and phenotypic variation may

59    not provide enough adaptability to the new local conditions (Jump and Peñuelas, 2005; Aitken et

60    al., 2008; Aubin et al., 2016; Christmas et al., 2016; Gray, 2018).

61        Species distribution models (SDM, Guisan and Thuiller, 2005) are useful tools to predict

62    and compare present and future potential distribution of species (e.g., Blanco-Pastor et al., 2013;

63    Velásquez-Tibatá et al., 2013). This helps to assess species vulnerability under different GCC

64    future scenarios (e.g., Beaumont et al., 2008; Forester et al., 2013). While these methods do not

65    take into account population evolutionary potential, which may enable in situ adaptation

66    (Soberon and Peterson, 2005; Razgour et al., 2019), they are still useful to evaluate GCC impact

67    on extant populations under hypotheses of niche conservatism (Ackerly, 2003; Wiens and

68    Graham, 2005), which is the most common evolutionary response of lineages (Liu et al., 2012;

69    Lososová et al., 2020; Sanz-Arnal et al., 2021). They do not either consider habitat destruction

70    and fragmentation directly produced by human action. Furthermore, several studies have

71    projected current genetic diversity to future times, assuming the extinction of populations falling

72    outside the inferred potential distribution (Espíndola et al., 2012; Lima et al., 2017; Rizvanovic

73    et al., 2019), while others have projected future genetic structure based on molecular and

74    climatic data (Jay et al., 2012, 2015).

75        The Mediterranean Basin constitutes one of the Earth's hotspots of biodiversity and

76    harbors an exceptional plant diversity, featuring a high level of endemicity (Myers et al., 2000;

77    Mittermeier et al., 2011; Vargas, 2020). Unfortunately, this will likely be one of the regions most

78    affected by GCC (Fletcher and Zielhofer, 2013; IPCC, 2013; Guiot and Cramer, 2016; Lionello

79    and Scarascia, 2018; Cramer et al., 2018; Fenu et al., 2020; García and Jordano, 2021). As a

80    result of this, about 30% of the Mediterranean Basin hotspot could be losing its current climate

81    and turning into a non-analogous one, which could threaten about 30% of its endemic species,

82    assuming loss of analogue climate as a proxy for habitat loss (Bellard et al., 2014). Specifically,

83    the Western Mediterranean includes numerous areas that have been considered climatic refugia

84    during historical climatic oscillations from Miocene to Pleistocene (Médail and Diadema, 2009).

85    These refugia are reservoirs of unique genetic diversity and evolutionary potential due to the

86    long-term persistence of species, and therefore have high conservation priority (Médail and

87    Quézel, 1999; Médail and Diadema, 2009).

88        *Carex* L. (Cyperaceae) is a megadiverse angiosperm genus with several characteristics

89    that makes it an ideal model for the study of the effects of GCC on its species, populations and in

90    the ecosystems where it lives. With c. 2000 species it ranks among the three largest angiosperm

91    genera in the world (POWO, 2020; Roalson et al., 2021). It has an almost cosmopolitan

92    distribution although higher species diversity in temperate and cold areas of both hemispheres.

93    *Carex* diversification seems to have been historically favoured by global cooling periods

94    (Martín-Bravo et al., 2019), which lead to think that GCC could be negative for its species at

95    least from an evolutionary perspective. In the Western Mediterranean, as in many other world

96    regions, *Carex* species dominate a variety of plant communities, from wetland and river shores to

97    peat bogs and high mountain meadows. Some of these habitats are considered of special interest

98    and have conservation priority in the Directive 2013/32/EU. Therefore, responses of ecologically

99    important *Carex* species to climate changes could be probably decisive for the future persistence

100   of these habitats.

101       *Carex reuteriana* Boiss. and *C. panormitana* Guss. (sect. *Phacocystis*), are two endemic

102   sister species disjunctly distributed in the Western Mediterranean Basin (Luceño and Jiménez-

103   Mejías, 2008; Jiménez-Mejías et al., 2011), growing in creeks and river shores at medium

104   altitudes (Benítez-Benítez et al., 2018). *Carex reuteriana* comprises two subspecies: *C.*

105   *reuteriana* subsp. *reuteriana* from the centre to NW Iberian Peninsula and *C. reuteriana* subsp.

106   *mauritanica* (Boiss. & Reut.) Jim.-Mejías & Luceño from NW Africa (Morocco) to the S Iberian

107   Peninsula with populations on both sides of the Guadalquivir Valley (Sierra Morena and Betic

108   ranges; Jiménez-Mejías et al., 2011). The conservation status of *C. reuteriana* has not been

109   evaluated, although it is seemingly not endangered due to its relatively large distribution range

110   and high numbers of populations and individuals in many of them. On the other hand, *C.*

111   *panormitana* is a restricted Tyrrhenian endemic from Sardinia with a few additional small

112   populations in Sicily and Tunisia (Pignatti, 1982; Urbani et al., 1995; Gianguzzi et al., 2013;

113   Jiménez-Mejías et al., 2014). Regarding its conservation status, it has been listed under different

114   conservation categories according to a variety of regional and global red lists (Bilz et al., 2011;

115   Domina, 2011; Rossi et al., 2013; Urbani et al., 2013). Both species are conspicuous, tussock-

116  forming plants, which are ecologically relevant as they are dominant and characteristic taxa in

117  the plant communities (phytosociological ranks; Molina, 1996; Navarro et al., 2001; Rufo Nieto

118  and de la Fuente, 2011; Gianguzzi et al., 2013; Rodríguez-Guitián et al., 2017). Previous studies

119  revealed a strong genetic structure in both species driven by geography, with distinct genetic

120  clusters corresponding to disjunct populations (Jiménez-Mejías et al., 2011; Benítez-Benítez et

121  al., 2018).

122       In the present study, we analyse the genetic makeup and potential distribution in these

123  two ecologically relevant *Carex* sister species endemic to the Western Mediterranean Basin. We

124  examine the relationship between these factors in a comparative and geographic-temporal

125  framework in order to forecast the effects of GCC on these species. Thus, the main aims of this

126  study are to: (1) estimate and compare the genetic diversity/structure and potential distribution

127  within and between the species in the present and future; (2) tackle the hypothesis that pose a

128  negative relationship between range size, genetic diversity and ecological niche breadth on one

129  side, and vulnerability to environmental changes on the other; (3) relate the current and future

130  projected situation with the conservation status of both species.

131  **2.  Materials and methods**

132  *2.1 Analyses of Present Population Genetics*

133  We reanalysed the AFLP sampling that included 182 polymorphic loci used by Benítez-Benítez

134  et al. (2018), which consisted in 130 individuals from 18 different locations (69 individuals from

135  12 populations of *C. reuteriana* and 61 individuals from 6 populations of *C. panormitana*; Table

136  1), that representatively cover the range of both species fairly well.

137        Present gene diversity (Nei's diversity; Nei, 1978) at taxa and population level was

138  computed with AFLP$_{DAT}$ (Ehrich, 2006) as implemented in R v. 3.2.1 (R Core Development

139  Team, 2020). Since many *Carex* species often propagate vegetatively, including the two study

140  species (Luceño and Jiménez-Mejías, 2008; P. Jiménez-Mejías and M. Urbani, pers. comm.), we

141  tried to minimize sampling ramets from the same clone (genet) by selecting individuals at a

142  distance of at least 2m. The distribution of the number of pairwise genetic distance comparisons

143  among phenotypes and individuals within a species representing putative clones were inferred

144  with the clone function also in AFLP$_{DAT}$. The Arlequin function from AFLP$_{DAT}$ was used to

145    calculate gene diversity of populations at the ramet and genet levels before and after removing

146    putative clones, respectively. These clones were identified as phenotypes that differed in a

147    number of bands below the frequency of the error rate (Bonin et al., 2004). Frequency-down-

148    weighted marker values (DW) were also estimated as a measure of allele rarity (Schönswetter

149    and Tribsch, 2005).

150         To further investigate the genetic structure found by Benítez-Benítez et al. (2018), a

151    phylogenetic tree of AFLP phenotypes was obtained with a Neighbor-Joining (NJ) analysis

152    based on Nei-Li distances including 1000 replicates to assess bootstrap support, as implemented

153    in PAUP v. 4.0b10 (Swofford, 2002). An analysis of molecular variance (AMOVA) was

154    conducted using ARLEQUIN v. 3.5.2.2 (Excoffier and Lischer, 2010) in which we also

155    calculated the fixation index $F_{st}$ (Wright, 1965). We conducted two partitions in order to examine

156    in detail the variation of genetic diversity, one considering the two species (*C. reuteriana* and *C.*

157    *panormitana*), and the other partition considering the four main genetic clusters previously found

158    by Benítez-Benítez et al. (2018): (1) *C. reuteriana* subsp. *reuteriana*, (2) *C. reuteriana* subsp.

159    *mauritanica*, (3) Sicilian-Tunisian populations of *C. panormitana*, and (4) Sardinian populations

160    of *C. panormitana*. We also used BAPS v. 6.0 (Corander et al., 2003) to look for possible

161    underlying fine structure, estimating the number of genetic clusters (K) by assigning individuals

162    and populations in undefined mixture clusters under a Bayesian framework. We ran the analysis

163    with a predefined 10 replicates from K=5 to K=8. Finally, Discriminant Analysis of Principal

164    Components (DAPC; Jombart, 2008) is a multivariate method that, unlike Principal Component

165    Analysis (PCA) and Discriminant Analysis (DA), maximizes the separation between groups

166    while minimizing variation within groups to identify genetic clusters (Jombart et al., 2010). It

167    was used to obtain a visual spatial assessment of genetic structure using the four main genetic

168    clusters previously defined as priors. In view of the weak genetic structure found within *C.*

169    *reuteriana* subsp. *reuteriana* (see results), a Mantel test was performed with GenAlEx v. 6.5

170    (Peakall and Smouse, 2012) to evaluate the correlation between genetic (Nei, 1972) and

171    geographic distances between its populations.

172         In order to enable the comparison of present genetic structure with that inferred for the

173    future for the taxonomically-driven partition considering three groups (*C. reuteriana* subsp.

174    *reuteriana*, *C. reuteriana* subsp. *mauritanica*, and *C. panormitana*), we conducted an analysis

175   with Structure v. 2.3.4 (Pritchard et al., 2000). For each taxon, we performed 10 independent

176   runs of 100,000 iterations each one, with a burn-in period of 1,000 for each value of K from 1 to

177   3. The best K was chosen comparing the probabilities for the K values inferred with Structure

178   Harvester (Earl and VonHoldt, 2012) and the graphic was performed with Structure Plot v. 2.0

179   (Ramasamy et al., 2014).

180   ***2.2 Potential species distribution and ecological niche modeling for present times***

181   We used the same occurrence dataset (316 georeferenced records of *C. reuteriana* subsp.

182   *reuteriana*, 118 of subsp. *mauritanica*, and 29 (all known records) of *C. panormitana*; Table S1)

183   and uncorrelated bioclimatic variables used in Benítez-Benítez et al. (2018): bio2 (mean diurnal

184   range), bio4 (temperature seasonality), bio15 (precipitation seasonality) and bio16 (precipitation

185   of wettest quarter). Distribution models were obtained for the three studied taxa: *C. reuteriana*

186   subsp. *reuteriana*, *C. reuteriana* subsp. *mauritanica*, and *C. panormitana*. We used three groups

187   (taxonomically-driven partition) rather than four (see genetic analyses) because of the low

188   number of occurrences for *C. panormitana*.

189         Biomod2 (Thuiller et al., 2009) implemented in R was used for SDM, testing six different

190   implemented modeling algorithms: classification tree analysis (CTA), Generalized Additive

191   Model (GAM), Generalized Boosted Regression Model (GBM), Generalized Linear Model

192   (GLM), Maximum Entropy Algorithm (MaxEnt), and Random Forest (RF). Thereafter, an

193   ensemble modeling was run including all algorithms in order to build more accurate projections

194   (Araújo and New, 2007; Forester et al., 2013). We randomly built three sets of pseudo-absences

195   and generated a data splitting (80% training data and 20% burn-in) to assess the models by cross-

196   validation, with two independent runs. We used True Skill Statistics (TSS; Allouche et al., 2006)

197   and Area Under the Curve (AUC; Swets, 1988) with a threshold > 0.7 as evaluation metrics for

198   building models.

199         Finally, we conducted a Principal Component Analysis (PCA; Janžekovič and Novak,

200   2012) of the retained bioclimatic variables using the prcomp function in the package ggplot2 in

201   R (Wickham, 2016) for visualizing the ecological niche occupied by each taxon (*C. reuteriana*

202   subsp. *reuteriana*, *C. reuteriana* subsp. *mauritanica*, and *C. panormitana*) under present

203   conditions.

204 **_2.3 Future projections of potential distribution, genetic diversity/structure, and environmental_**

205 **_niche_**

206 Future potential distribution was modeled with the same methodology as for the present (see

207 above). Future climate can be projected with different general circulation models (GCMs) which

208 are the primary source for studying the dynamics and components of the global climate system.

209 GCMs were selected following Parding et al. (2020): BCC-CMS2-MR, CanESM5, CNRM-

210 CM6-1, CNRM-ESM2-1, MIROC6 and MRI-ESM2-0 (data available in

211 https://www.worldclim.org/; Fick and Hijmans, 2017). These GCMs include four different

212 Representative Concentration Pathways (RCPs) addressed in the IPCC Fifth Assessment Report

213 (IPCC, 2014). We selected RCP2.6 and RCP8.5 to represent two extreme scenarios (an

214 optimistic with lowest greenhouse gas atmospheric concentration vs. a pessimistic with highest

215 concentration). In addition, two future temporal ranges (2041-2060, 2081-2100) were used to

216 project the set of GCMs. We have averaged the six different GCMs per each of the two scenarios

217 resulting from modeling analyses in a single raster layer for each of the two future temporal

218 ranges. This assembly accounts for uncertainty of future climatic conditions across the potential

219 distribution range of species, as shown by Wróblewska and Mirski (2018). We overlapped

220 present and future projections of potential distribution in a single map using QGIS v. 3.4.15

221 (QGIS Development Team, 2021), enabling the visualization of the potential loss and/or gain of

222 climatic suitable areas under different GCC scenarios.  Thus, SDM have been used to show how

223 the different Mediterranean regions where _C. reuteriana_ and _C. panormitana_ inhabit are

224 responding to the GCC comparing current distribution models against the future ones in order to

225 visualize the proportion of area loss/gain. It is important to note that this methodological

226 approach assumes no migration and that species ecological requirement would remain the same

227 (niche conservatism) in the future.

228 To estimate future gene diversity, we recalculated the values after removing those

229 sampled populations placed within the predicted lost range according to the inferred potential

230 distribution under the optimistic (RCP2.6) climate change scenario for 2081-2100. Therefore, we

231 assumed the extinction of populations located in unsuitable areas by future projections of SDM

232 (Espíndola et al., 2012; Lima et al., 2017; Rizvanovic et al., 2019). We did not obtain genetic

233 diversity values for the pessimistic (RCP8.5) 2081-2100 scenario, since all sampled populations

234 of *C. panormitana* and *C. reuteriana* subsp. *reuteriana* were predicted to go extinct (see results).

235 We used the spatial Bayesian clustering algorithm implemented in POPS v. 1.2 (Jay et

236 al., 2012, 2015) to infer population genetic structure in the future (2081-2100) also based on the

237 optimistic climate change scenario. We performed analyses for each taxon (*C. reuteriana* subsp.

238 *reuteriana*, *C. reuteriana* subsp. *mauritanica*, and *C. panormitana*) with and without admixture.

239 Two independent replicates were run for the best number of clusters (K=2) obtained in Structure

240 analyses for present times (see above), using genetic data from AFLPs, as well as spatial

241 coordinates of each population and quantitative bioclimatic variables as covariates. We selected

242 the same bioclimatic variables utilized in the future projections of SDM described above. For the

243 simulated data, we used 10,000 sweeps with a burn-in of 2,000 sweeps to run POPS. The

244 resulting output files were introduced in CLUMPP v. 1.1.2 (Jakobsson and Rosenberg, 2007) in

245 order to average two runs per each K. Subsequently, the outputs from CLUMPP were imported

246 in Distruct v. 1.1 (Rosenberg, 2004) to visualize the genetic structure for each independent

247 genetic cluster analysed.

248 Finally, we projected the future environmental space of each taxon. A PCA was

249 performed in the same way as for contemporary conditions, but removing those occurrences

250 located in areas of lost habitat as explained for the estimation of future genetic diversity

251 (optimistic scenario in 2081-2100).

**3. Results**

252

253 *3.1 Present genetic structure and diversity*

254 NJ analysis of AFLP phenotypes recovered three moderately to well-supported clades (Fig. 1a):

255 (1) *C. reuteriana* (88% Bootstrap [BS]), (2) Sicilian-Tunisian *C. panormitana* populations (75%

256 BS), and (3) Sardinian *C. panormitana* populations (100% BS). In turn, Sicilian and Tunisian

257 populations were recovered as sisters in well-supported distinct clades (98% BS Tunisia, 92%

258 BS Sicily). On the contrary, subspecies and populations of *C. reuteriana* were unresolved in a

259 polytomy.

260 AMOVA analysis results are shown in Table 2. The complete dataset considering the two

261 species revealed that 28.06% of the variation of genetic diversity is explained by differences

262   between the species, 37.22% by differences among populations within species, and 34.73% by

263   differences within populations. Considering each species separately, variation among

264   populations in *C. reuteriana* was considerably lower (39.82%) than in *C. panormitana* (68.76%),

265   so variation within populations showed the opposite pattern (60.18% vs. 31.24%, respectively).

266   When partitioning the four main genetic clusters previously found by Benítez-Benítez et al.

267   (2018), AMOVA analysis revealed 42.13% of the variation of genetic diversity is explained by

268   differences between groups, 21.46% by differences among populations within groups, and

269   36.42% by differences within populations. Regarding *C. reuteriana*, the differentiation between

270   populations was higher in subspecies *mauritanica* (37.02%) than in subspecies *reuteriana*

271   (20.36%). In *C. panormitana*, there was a stronger difference between Sicilian-Tunisian

272   populations (53.51%) than among Sardinian ones (41.4%).

273      DAPC analysis also confirmed the clear differentiation between the four genetic clusters

274   previously commented (Fig. 1b), and a perfect assignment of each individual to its a priori group.

275   However, BAPS analyses found a certain degree of additional, underlying genetic structure in *C.*

276   *reuteriana* subsp. *mauritanica* and *C. panormitana*, and suggested that six is the most accurate

277   number of genetic clusters (K=6; Fig. 1c). Three of these clusters corresponded to *C. reuteriana*:

278   (1) all six *C. reuteriana* subsp. *reuteriana* sampled populations; (2) four populations of *C.*

279   *reuteriana* subsp. *mauritanica*, two located in northern Africa (Morocco) and the other two from

280   the Betic ranges south of Guadalquivir Valley in southern Spain; and (3) the remaining two

281   subsp. *mauritanica* populations from Sierra Morena (north of Guadalquivir Valley). *Carex*

282   *panormitana* was also split into three clusters: (4) the four populations from Sardinia, (5) the

283   population from Sicily and (6) the population from Tunisia.

284      STRUCTURE retrieved two as the optimal number of genetic clusters for the three taxa

285   (K=2; Fig. 2a). *Carex reuteriana* subsp. *reuteriana* clusters lacked geographic structure and

286   presented admixture in all sampled populations.  The Mantel test was not significant for this

287   subspecies (p-value = 0.46; R2 = 0.001; Fig. S2 in Supplementary Material). On the contrary, *C.*

288   *reuteriana* subsp. *mauritanica* presented a clearer genetic structure, with the two clusters mostly

289   corresponding to populations from north of the Guadalquivir Valley and south of the valley

290   (Betic ranges) plus North Africa, respectively. Finally, the two genetic clusters in *C.*

291 *panormitana* corresponded, almost without admixture, to Sardinian populations and Sicilian-

292 Tunisian ones, respectively.

293       The distribution of the number of pairwise differences among AFLP individual

294 phenotypes in both species was unimodal for *C. reuteriana* while bimodal for *C. panormitana*

295 (Fig. S1). The latter indicated the existence of clones in this species. In congruence, three of the

296 four sampled Sardinian *C. panormitana* populations showed a significant presence of putative

297 ramets (18 of 38 sampled individuals), according to the clone function in $AFLP_{DAT}$. The final

298 AFLP error rate was 1.44% when clones were removed.

299       Finally, the analysis of the 130 sampled individuals from 18 populations revealed a high

300 genetic differentiation between *C. reuteriana* and *C. panormitana* with an $F_{st}$ value of 0.653.

301 Values were also high when considering *C. reuteriana* subspecies ($F_{st}$=0.46) and Sicilian-

302 Tunisian vs Sardinian populations of *C. panormitana* ($F_{st}$=0.765).

303       Values of present genetic (Nei´s) diversity for each taxon and sampled population are

304 shown in Table 1. *Carex reuteriana* s.l. (0.184), as well as both its subspecies (subsp. *reuteriana*:

305 0.142; subsp. *mauritanica*: 0.170), have higher genetic diversity than *C. panormitana*. For the

306 latter, the presence of putative clones was reflected in slightly different values at the genet

307 (0.133) and ramet (0.128) levels. These clones were only detected for Sardinian populations,

308 which was reflected in a very low genetic diversity in these populations (0.037 at genet and

309 0.032 at ramet level) in comparison with Sicilian-Tunisian counterparts (0.115). *Carex*

310 *panormitana* as a whole presented higher DW value (436.028) in comparison to both subspecies

311 of *C. reuteriana* (subsp. *reuteriana*: 154.041; subsp. *mauritanica*: 324.723), whilst *C. reuteriana*

312 s.l. retrieved the highest DW value (905.394). In addition, *C. reuteriana* subsp. *reuteriana*

313 displayed lower DW values than subsp. *mauritanica* in most of its populations (Table 1).

314 ***3.2 Future genetic structure and diversity***

315 The POPS analyses projecting the future genetic structure did not detect any new genetic clusters

316 with respect to STRUCTURE analyses for present times (Fig. 2b), either implementing

317 admixture or non-admixture analyses. However, it revealed substantial changes in the genetic

318 structure of both subspecies of *C. reuteriana*. Thus, *C. reuteriana* subsp. *reuteriana* was

319 projected to almost completely lose one of its two current genetic clusters (except for one

320 individual). In *C. reuteriana* subsp. *mauritanica,* all Iberian sampled populations were assigned

321 to the same genetic cluster, while the other cluster would remain exclusively for Moroccan

322 populations, in both cases with no admixture between clusters. In contrast, *C. panormitana* was

323 projected to retain the same strong genetic structure found for present times, which was even

324 reinforced by the loss of the marginal admixture.

325       Future projections of genetic diversity removing populations affected by habitat loss

326 according to SDM results (see below; RCP2.6 for 2081-2100 in Fig. 3) yielded lower values of

327 genetic diversity when compared to present for all taxa, although only slightly for *C. reuteriana*

328 s.l. (*C. reuteriana* subsp. *reuteriana*: 0.107; *C. reuteriana* subsp. *mauritanica*: 0.164; *C.*

329 *panormitana*: 0.118 (genet), 0.100 (ramet)).  DW values were considerably higher in the Sicilian,

330 and, to a lesser extent, in the Tunisian population of *C. panormitana* than in the Sardinian ones

331 and both subspecies from *C. reuteriana* (Table 1).

332 **3.3 Species Distribution Modeling**

333 Projected potential distribution ranges of *C. reuteriana* and *C. panormitana* shifted according to

334 six GCMs in different time periods (2041-2060 and 2081-2100) and two RCPs scenarios

335 (RCP2.6 and RCP8.5). Both species were inferred to gain and lose suitable areas in response to

336 GCC under different scenarios (see projections for 2041-2060 in Fig. S2 in Supplementary

337 Material and Fig. 3b or 2081-2100). Herein, we will mainly comment on the results from 2081-

338 2100 since this scenario represents more severe climatic conditions in comparison with current

339 ones (Fig. 3b).

340       Future SDM revealed important losses of suitable areas for all taxa, which was reinforced

341 in the RCP8.5 scenario, especially for *C. panormitana*. Likewise, currently suitable areas

342 inferred to remain stable (current potential range overlapping with that inferred by future

343 models) were always reduced in the RCP8.5 with respect to RCP2.6. In *C. reuteriana* subsp.

344 *reuteriana* (Figs. 3a, 3b) climate change was predicted to produce the loss of around the half of

345 its currently suitable areas (41% in the RCP2.6 scenario and 57% in the RCP8.5 scenario),

346 including all the Central Iberian range, and, in the RCP8.5, also the NW Iberian quadrant. The

347 most stable areas (40% RCP2.6, 10% RCP8.5) would be located in the NW Iberian Peninsula.

348 Future suitable conditions (22% RCP2.6, 33% RCP8.5) could spread northwards of its current

349 distribution (Atlantic coast of North Spain and Western France; Fig. 3a). *Carex reuteriana* subsp.

350 *mauritanica* (Figs. 3c, 3d) displayed a predicted loss of potential area in its current range in

351 Sierra Morena (34% RCP2.6, 66% RCP8.5), while stable areas (53% RCP2.6, 24% RCP8.5)

352 could persist south of Guadalquivir Valley and in the Tingitan Peninsula. Future suitable areas

353 also extended to the north Atlantic coast of Portugal for both scenarios (13% RCP2.6, 10%

354 RCP8.5). *Carex panormitana* (Figs. 3e, 3f) yielded a remarkable reduction of its potential

355 distribution area under the two future climate scenarios (66% RCP2.6, 95% RCP8.5) with

356 respect to its current distribution range. The potentially future suitable areas were very low (8%

357 RCP2.6, 3% RCP8.5), mostly recovered in Balearic Islands (Fig. 3e, Fig. S3). A 26% of stable

358 areas were found in the coast of Tyrrhenian Islands (Corsica, Sardinia, and Sicily) for the

359 RCP2.6, whilst the RCP8.5 scenario only showed 1%.

360       PCAs showed (see Fig. S4) a similar environmental space both for present and future in

361 2081-2100 under RCP2.6 scenario, with also analogous percentages for the explained variances

362 along their PC1s (54.2% and 56.2%, respectively) and PC2s (27.8% and 23.5%, respectively).

363 *Carex reuteriana*, including its subspecies, displayed a wider environmental niche than *C.*

364 *panormitana* both in the present and the future.

365 **4. Discussion**

366 ***4.1 Geographically-driven strong genetic structure and contrasting patterns of genetic***

367 ***diversity***

368 The strong genetic structure for the present time (Figs. 1, 2a) supports the genetic clusters

369 previously obtained by Jiménez-Mejías et al. (2011) and Benítez-Benítez et al. (2018). AFLPs

370 revealed a slight differentiation between the two subspecies of *Carex reuteriana*, in congruence

371 with their allopatric distribution (Fig. 1), suggesting the importance of geographic speciation

372 during their differentiation (Cabej, 2012; Sobel, 2016). For the subspecies *reuteriana*, DAPC and

373 BAPS analyses recovered a single genetic cluster likely due to gene flow between its

374 populations, whilst for subspecies *mauritanica* two genetic clusters with geographical

375 congruence were identified (Figs. 1, 2a). Thus, the latter subspecies seems to have been

376 influenced by the role of Guadalquivir Valley as a barrier to dispersal since there exists a clear

377 genetic differentiation between Sierra Morena and Betic populations (Figs. 1c, 2a, Table 2). This

378 pattern was previously pointed out in other studies about the sect. *Phacocystis* (Jiménez-Mejías

379  et al., 2011; Benítez-Benítez et al., 2018), as well as in other Mediterranean plant groups (Ortiz

380  et al., 2008; Casimiro-Soriguer et al., 2010; Tremetsberger et al., 2016; Fernández i Marti et al.,

381  2018). By contrast, populations at both sides of the Strait of Gibraltar display a higher genetic

382  similarity (Figs. 1c, 2a), supporting this area as a single connected refuge (Marañón et al., 1999;

383  Arroyo et al., 2008; Rodríguez-Sánchez et al., 2008; Molina-Venegas, 2015). The higher DW

384  value and genetic diversity in the subspecies *mauritanica* (324.723, 0.170; see Table 1) than

385  subspecies *reuteriana* (154.041, 0.142; Table 1) seems to correspond with the higher genetic

386  structure found across the populations of the first subspecies. This higher allelic rarity identified

387  in the subspecies *mauritanica* from these southernmost, rear-edge populations of the Iberian

388  Peninsula could be a reflect of their long-term isolation and persistence in refugia during

389  Pleistocene glaciations (Médail and Diadema, 2009; Provan and Maggs, 2011; see Last Glacial

390  Maximum projections in Benítez-Benítez et al., 2018).

391       On the other hand, *C. panormitana* displayed a significant genetic structure between

392  Sicilian-Tunisian and Sardinian populations for all genetic analyses (Figs. 1, 2a), as shown in

393  other Tyrrhenian endemics (e.g., Bittkau and Comes, 2005; Molins et al., 2018). The genetic

394  similarity found across the Strait of Sicily in different group of plants (e.g., Fernández-Mazuecos

395  and Vargas, 2011; Lo Presti et al., 2011; De Castro et al., 2015; Tremetsberger et al., 2016), also

396  identified in *C. panormitana* (Fig. 1), suggests an important dispersal route between Sicily and

397  North of Africa. The genetic diversity in the Tyrrhenian *C. panormitana* is much lower than in

398  its mainland sister *C. reuteriana* (0.133 and 0.184 respectively, Table 1), supporting the finding

399  that species with wider distribution ranges combined with larger population sizes frequently

400  display higher levels of genetic diversity than restricted endemic plants (López-Pujol et al., 2009,

401  2013; García-Verdugo et al., 2015; Fernández-Mazuecos et al., 2016). Nonetheless, high genetic

402  diversity has been reported in some endemic species with narrow distributions from the

403  Mediterranean region (e.g., Mameli et al., 2008; Mayol et al., 2012; Fernández-Mazuecos et al.,

404  2016; Jiménez-Mejías et al., 2015). Specifically, *C. panormitana* displays striking contrasting

405  patterns between its disjunct populations, with lower genetic diversity but larger distribution

406  range in Sardinia, while higher diversity and distinctiveness but extremely reduced distribution

407  in Sicily and Tunisia (only one population each; Urbani et al., 1995, 2013). These higher DW

408  values could be due to a long-term persistence and isolation of Sicilian-Tunisian populations.

409  This agrees with Sicily and NE Tunisia serving as glacial refugia during the Last Glacial

410  Maximum (e.g., Schönswetter et al., 2003; Magri et al., 2006; Médail and Diadema, 2009;

411  Jiménez-Mejías et al., 2012; see Last Glacial Maximum projections in Benítez-Benítez et al.,

412  2018). Sardinian populations were the only that displayed a significant number of clones.

413  Therefore, the clonality detected within them could be probably responsible at least in part for its

414  low genetic diversity. This low genetic diversity in Sardinian populations could have been also

415  caused by a population bottleneck (see below).

416  *4.2 Future reduction of potential distribution and genetic diversity under GCC*

417       Our climatic predictions show that at the end of the century the loss of distribution range

418  will be clearly higher than the range gain for both Mediterranean species (Fig. 3; e.g., Casazza et

419  al., 2014; Al-Qaddi et al., 2017; Vessella et al., 2017; Kougioumoutzis et al., 2020). This could

420  convey ecological consequences because *C. reuteriana* and *C. panormitana* play important roles

421  within the ecosystem functioning of rivershores where they inhabit (Rodríguez-Guitián et al.,

422  2017). Although the more restricted *C. panormitana* seems to be more negatively affected by

423  climate change effects (Fig. 3e, 3f) than the more widespread *C. reuteriana* (Fig. 3a-d), their

424  potential distribution range will respond in similar ways under future GCC in terms of habitat

425  loss. Given the ecological dominance of these two species in their respectives ranges, their

426  disappearance could even alter the communities and boundaries of habitats that these species

427  help define (see Benítez-Benítez et al., 2021).

428       *Carex reuteriana* would maintain a larger distribution area (Fig. 3) and environmental

429  space (Fig. S4), as well as greater genetic diversity (Table 1) than *C. panormitana*, despite many

430  of its populations could be potentially wiped out in response to the GCC (Fig. 3a-d; Fig. S3).

431  Whether these populations would disappear, the dominant phytosociological associations (*Carici*

432  *reuterianae-Betulum celtiberica*, Rodríguez-Guitián et al., 2017 and *Caricetum tartessianae,*

433  Molina, 1996; Navarro et al., 2001; Rufo Nieto and de la Fuente, 2011) that forms part of the

434  Iberian riparian forests will be affected. *Carex reuteriana* subsp. *reuteriana* might be able to

435  migrate and change its distribution range (Bussotti et al., 2015) whilst conserve its ecological

436  niche according to the displacement of climatic suitability to northwards of its current

437  distribution range (e.g., Alsos et al., 2012; Wróblewska and Mirski, 2018). The relatively high

438  levels of genetic diversity and ecological width of species may also enable in situ local

439  adaptations, triggering high resilience to environmental changes and in turn buffering the loss of
440  its genetic diversity (Aubin et al., 2016; Bussotti and Pollastrini, 2017; Lima et al., 2017).
441  However, it has been reported that species might not be able to shift their distribution range
442  toward suitable conditions as fast as the GCC is taking place (Loarie et al., 2009) and thus their
443  survival could also depend on other factors (e.g., phenotypic plasticity, adaptive capacity,
444  dispersal or colonization ability; Hoffmann and Sgrò, 2011; Razgour et al., 2019). A significant
445  loss of suitable potential areas is predicted for both subspecies of *C. reuteriana,* although with
446  slight differences between them (Fig. 3a-d), whilst their genetic structure also could suffer
447  important changes in the future (2081-2100; Fig. 2). Specifically, the subspecies *mauritanica*
448  could undergo gene flow limitation across the Strait of Gibraltar, strengthening genetic structure
449  between Morocco and southernmost Iberian Peninsula populations (Fig. 2b; e.g., Escudero et al.,
450  2008; Ortiz et al., 2008; Terrab et al., 2008).  In contrast, populations at both sides of the
451  Guadalquivir Valley could increase their genetic admixture.

452      Otherwise, the more restricted *C. panormitana* seems to recover very little available
453  potential habitat and great habitat loss as well as reduction in its genetic diversity in the future
454  (Fig. 3; Table 1; Fig. S3). On the contrary, the current genetic structure of this Tyrrhenian
455  endemism (Sicilian-Tunisian vs. Sardinian populations, Fig. 2) could remain stable over time.
456  Predictions are especially alarming under the pessimist emission scenario (95% RCP8.5, Fig. 3f),
457  which indicate that this species could almost disappear in the future as a direct consequence of
458  the GCC. The extinction of *C. panormitana* will probably affect the functioning of the
459  ecosystem, as it dominates the riparian communities with *Carex pendula* forming a
460  phytosociological association (*Caricetum pendulo-panormitanae*, Gianguzzi et al., 2013). Our
461  findings support the hypothesis that local extinction rates appear to be higher in species with
462  restricted distribution, although it could also depend on their specific niche characteristics
463  (Lavergne et al., 2006; Gray, 2018). Specifically, the low genetic diversity found in *Carex*
464  *panormitana*, which would likely decrease in the future, foretells little capacity to adapt to the
465  new climatic conditions and therefore to modify its niche, which may contribute to its extinction
466  (Dagnino et al., 2020; Olave et al., 2019; Fig. 3e, 3f; Table 1; Fig. S4). However, a niche shift
467  during the Pliocene has been proposed for this lineage of plants (Benítez-Benítez et al., 2018),
468  which suggests that it may retain certain adaptation capacity when facing future climatic
469  changes.

470        Although distribution models do not incorporate factors such as biotic interaction,

471    dispersal or adaptation into future projections, our results demonstrate the usefulness of

472    combining SDM and molecular genetic analysis to approach the future of species. Specifically,

473    the Mediterranean Basin is considered a vulnerable hotspot, where plant extinction is already

474    taking place (Médail, 2017; Orsenigo et al., 2018; IUCN, 2021) and as much as 3.000 species

475    (Malcolm et al., 2006) have been predicted to become extinct in the future under GCC scenarios

476    (Bellard et al., 2014). Likewise, the threat by desertification and expansion of arid regions

477    (IPCC, 2014) are also being induced by global warming. Those habitats which have been

478    inferred to remain mostly stable under ongoing GCC (e.g., parts of southernmost areas of Iberian

479    Peninsula, northern Africa, and Tyrrhenian Islands; Médail and Diadema, 2009) have been

480    considered as important refugia of current diversity (Temunovic et al., 2013). Nevertheless, the

481    permanence of species in these areas will depend not only on the future climatic conditions but

482    also the species ability to resist other threats like anthropogenic fragmentation or habitat loss

483    (Thomas et al., 2004; Malcolm et al., 2006; Newbold et al., 2015; Hoffmann et al., 2018).

484    *4.3 Conservation and survival issues in C. panormitana*

485        Our results express great concern about the conservation perspectives and future viability

486    of *Carex panormitana*. A review of different assessments of its conservation status clearly points

487    to a conflicting situation. Assessments at different geographical scales frequently result in the

488    application of different criteria and conservation categories due to considering different parts of

489    the taxon range. However, in the case of the restricted endemic *C. panormitana*, the whole range

490    was considered. On the one hand, it has been listed as a species with conservation priority for the

491    European Union in the Annex II of the Habitat Directive 92/43/CEE, and it has also been

492    catalogued as threatened in different regional red lists from Italy ("critically endangered (CR)"

493    by Conti et al., 1997; and "endangered (EN)" by Rossi et al., 2013; Urbani et al., 2013). On the

494    other hand, it has been classified as "least concern (LC)" in the European Red List of Vascular

495    Plants (Bilz et al., 2011) and at the global level in the IUCN Red List (Domina, 2011).

496    Importantly, the IUCN global assessment is based on a wrong distribution of the species

497    (Domina, 2011), which includes regions of Greece as part of the distribution range of *C.*

498    *panormitana*, whereas it is absent there (Jiménez-Mejías et al., 2014). This was probably due to a

499    misleading identification with the closely related *C. acuta* or *C. kurdica*, which is present in the

500  Balkan Peninsula (Jiménez-Mejías et al., 2014). Thus, *C. panormitana* requires, in view of our
501  results, a reassessment of its conservation status at the global level applying the IUCN criteria
502  and guidelines (IUCN, 2012, 2019; respectively).

503      The only known Sicilian population is located in the outskirts of Palermo city (Urbani et
504  al., 1995; 2013) along the shores of the Oreto River (Gianguzzi et al., 2013). This population
505  displays high genetic distinctiveness (see DW values; Table 1) and has important historical
506  value, as it is the type locality of the species (Gussone, 1844; see Jiménez-Mejías et al., 2014),
507  but its habitat is considered especially sensitive to disturbances (Thiébaut, 2006). The proximity
508  of this population to Palermo increases human pressure through different threats (e.g., urban
509  expansion, pollution of river water by agricultural and domestic activities, invasive species, etc.)
510  leading to habitat degradation and fragmentation (Gianguzzi et al., 2013). Moreover, a
511  fragmentation of this population and a decline in its size have been detected in recent years
512  (Gianguzzi et al., 2013). Habitat fragmentation and small population size could produce loss of
513  genetic diversity (Table 2) through processes like interruption of gene flow between
514  subpopulations, inbreeding and genetic drift. The latter process could also entail the loss of rare
515  alleles.

516      In view of our results, conservation measures should be urgently implemented to
517  safeguard the future of *C. panormitana* and the habitats where it lives. The reinforcement of
518  natural populations through the translocation of individuals between populations should be
519  avoided due to the strong genetic differentiation and distinctiveness found between Sicilian-
520  Tunisian and Sardinian populations. Accordingly, a specific conservation program should be
521  designed for *C. panormitana* which should include collection of seeds (and propagules) and ex-
522  situ storage in germplasm banks. Seed collecting (and ex situ growing of living individuals)
523  should be conducted separately for each of the three regions where this species inhabits
524  (Sardinia-Sicily-Tunisia), that should constitute different management units, to adequately
525  represent its genetic diversity and maintain its genetic structure. *Carex panormitana* displays
526  high levels of genetic diversity in Sicily and Tunisia, representing an important reservoir for
527  conservation of genetic resources, whilst Sardinian populations show an important genetic
528  impoverishment (Table 1). In some of the latter, the number of individuals could have severely
529  decreased due to river floods (M. Urbani, pers. comm.), perhaps producing bottlenecks that

530  would help to explain the low genetic diversity. Likewise, there are also at least one population

531  (Cantoniera Pirae´onni) in which overgrazing by cattle seems to be hindering flowering of

532  individuals (M. Urbani, pers. comm.), which could reduce sexual reproduction and therefore

533  perhaps affecting genetic diversity (e.g., Wu et al., 2010; Fernández-Mazuecos et al., 2016;

534  Souto and Tadey, 2019). Pursuant to the foregoing, it would be of paramount importance

535  investing on projects for biodiversity conservation, maintenance of the structure and ecosystem

536  functions, as well as decreasing the degree of disturbance in the habitat to guarantee its long-term

537  survival.

538      On the other side, the distribution range of *C. panormitana* is poorly known in Tunisia,

539  where its presence was not noted until a few years ago due to the confusion with other species of

540  *Carex* sect. *Phacocystis* (Jiménez-Mejías et al., 2014). Prospections would be also desirable in

541  NE Algeria, as one of the recently discovered Tunisian populations (Jiménez-Mejías et al., 2014)

542  is fairly close to the border (see Benítez-Benítez et al., 2018). Therefore, further field and/or

543  herbarium surveys are needed for this area of NW Africa to search for new populations which

544  may influence its conservation status.

545  **5. Conclusions**

546  Our results establish a clear genetic differentiation and strong structure both between and within

547  *C. panormitana* and *C. reuteriana* (including both its subspecies *reuteriana* and *mauritanica*).

548  The finding of genetic clusters according to disjunct areas suggests restricted gene flow among

549  populations and a significant role of geographical barriers. *Carex reuteriana* showed higher

550  levels of genetic diversity than *C. panormitana,* which presented the lowest values in Sardinia

551  probably due to the importance of vegetative reproduction. On the contrary, *C. panormitana*

552  displayed a greater genetic distinctiveness than both subspecies of *C. reuteriana*. Our future

553  scenarios of climate change forecast a reduction in the genetic admixture and diversity in most

554  populations of both species. In addition, SDM infer an overall loss of potential area for the three

555  taxa, especially for *C. panormitana* which could lose almost its entire distribution range and even

556  disappear under the most severe GCC scenario in the further future (RCP8.5 in 2081-2100).

557  These results, combined with the conflicting conservation assessments previously proposed for

558  *C. panormitana* and the extant threats to its persistence, support the urgent need to reassess

559     globally the conservation status of this Tyrrhenian restricted endemic and implement ex-situ/in-

560     situ conservation measures.

561          To sum up, this work displays how SDM in conjunction with molecular data can be used

562     to forecast the effects of GCC on the potential distribution and future dynamics of genetic

563     diversity and structure of species in the future. Therefore, this could be a useful approach for

564     conservation management and planning, helping the allocation of resources for priority species

565     and/or populations.

566     **Acknowledgments**

567     The authors thank P. Vargas for his support during AFLPs procedures.

568     **References**

569     Ackerly, D.D., 2003. Community Assembly, Niche Conservatism, and Adaptive Evolution in
570     Changing Environments. Int. J. Plant Sci. 164, S165–S184. https://doi.org/10.1086/368401
571     Aitken, S.N., Yeaman, S., Holliday, J.A., Wang, T., Curtis-McLane, S., 2008. Adaptation, migration
572     or extirpation: climate change outcomes for tree populations: Climate change outcomes for tree
573     populations. Evol. Appl. 1, 95–111. https://doi.org/10.1111/j.1752-4571.2007.00013.x
574     Allouche, O., Tsoar, A., Kadmon, R., 2006. Assessing the accuracy of species distribution models:
575     prevalence, kappa and the true skill statistic (TSS): Assessing the accuracy of distribution
576     models. J. Appl. Ecol. 43, 1223–1232. https://doi.org/10.1111/j.1365-2664.2006.01214.x
577     Al-Qaddi, N., Vessella, F., Stephan, J., Al-Eisawi, D., Schirone B., 2017. Current and future
578     suitability areas of kermes oak (*Quercus coccifera* L.) in the Levant under climate change. Reg.
579     Environ. Change 17, 143–156. https://doi.org/10.1007/s10113-016-0987-2
580     Alsos, I.G., Ehrich, D., Thuiller, W., Eidesen, P.B., Tribsch, A., Schönswetter, P., Lagaye, C.,
581     Taberlet, P., Brochmann, C., 2012. Genetic consequences of climate change for northern plants.
582     Proc. R. Soc. B. 279, 2042–2051. https://doi.org/10.1098/rspb.2011.2363
583     Araújo, M.B., New, M., 2007. Ensemble forecasting of species distributions. Trends in Ecol. Evol. 22,
584     42–47. https://doi.org/10.1016/j.tree.2006.09.010
585     Arroyo, J., Aparicio, A., Albaladejo, R.G., Muñoz, J., Braza, R., 2008. Genetic structure and
586     population differentiation of the Mediterranean pioneer spiny broom *Calicotome villosa* across
587     the Strait of Gibraltar. Biol. J. Linn. Soc. 93, 39–51. https://doi.org/10.1111/j.1095-
588     8312.2007.00916.x
589     Aubin, I., Munson, A.D., Cardou, F., Burton, P.J., Isabel, N., Pedlar, J.H., Paquette, A., Taylor, A.R.,
590     Delagrange, S., Kebli, H., Messier, C., Shipley, B., Valladares, F., Kattge, J., Boisvert-Marsh, L.,
591     McKenney, D., 2016. Traits to stay, traits to move: a review of functional traits to assess
592     sensitivity and adaptive capacity of temperate and boreal trees to climate change. Environ. Rev.
593     24, 164–186. https://doi.org/10.1139/er-2015-0072

594 Beaumont, L.J., Hughes, L., Pitman, A.J., 2008. Why is the choice of future climate scenarios for
595    species distribution modelling important?: Projecting species distributions under future climates.
596    Ecol. Lett. 11, 1135–1146. https://doi.org/10.1111/j.1461-0248.2008.01231.x

597 Bellard, C., Leclerc, C., Leroy, B., Bakkenes, M., Veloz, S., Thuiller, W., Courchamp, F., 2014.
598    Vulnerability of biodiversity hotspots to global change. Glob. Ecol. Biogeogr. 23, 1376–1386.
599    https://doi.org/10.1111/geb.12228

600 Benítez-Benítez, C., Escudero, M., Rodríguez-Sánchez, F., Martín-Bravo, S., Jiménez-Mejías, P.,
601    2018. Pliocene-Pleistocene ecological niche evolution shapes the phylogeography of a
602    Mediterranean plant group. Mol. Ecol. 27, 1696–1713. https://doi.org/10.1111/mec.14567

603 Benítez-Benítez, C., Martín-Bravo, S., Bjorå, C.S., Gebauer, S., Hipp, A.L., Hoffmann, M.H.,
604    Luceño, M., Pedersen, T.M., Reznicek, A., Roalson, E., Volkova, P., Yano, O., Spalink, D.,
605    Jiménez-Mejías, P., 2021. Geographical vs. ecological diversification in *Carex* section
606    *Phacocystis* (Cyperaceae): Patterns hidden behind a twisted taxonomy. J. Syst. Evol jse.12731.
607    https://doi.org/10.1111/jse.12731

608 Bittkau, C., Comes, H.P., 2005. Evolutionary processes in a continental island system: molecular
609    phylogeography of the Aegean *Nigella arvensis* alliance (Ranunculaceae) inferred from
610    chloroplast DNA. Mol. Ecol. 14, 4065–4083. https://doi.org/10.1111/j.1365-294X.2005.02725.x

611 Blanco-Pastor, J.L., Fernández-Mazuecos, M., Vargas, P., 2013. Past and future demographic
612    dynamics of alpine species: limited genetic consequences despite dramatic range contraction in a
613    plant from the Spanish Sierra Nevada. Mol. Ecol. 22, 4177–4195.
614    https://doi.org/10.1111/mec.12383

615 Bilz, M., Kell, S.P., Maxted, N., Landsdown, R.V., 2011. European Red list of Vascular Plants.
616    Publications Office of the European Union, Luxembourg.

617 Bonin, A., Bellemain, E., Bronken Eidesen, P., Pompanon, F., Brochmann, C., Taberlet, P., 2004.
618    How to track and assess genotyping errors in population genetics studies. Mol. Ecol. 13, 3261–
619    3273. https://doi.org/10.1111/j.1365-294X.2004.02346.x

620 Brummit, R.K., 2001. World geographical scheme for recording plant distributions, Biodiversity
621    Information Standards (TDWG), second ed. Hunt Institute for Botanical Documentation
622    Carnegie Mellon University, Pittsburgh, USA. https://www.tdwg.org/standards/  (accessed June
623    2021).

624 Bussotti, F., Pollastrini, M., 2017. Observing Climate Change Impacts on European Forest: What
625    works and what does not in ongoing long-term monitoring networks. Front. Plant Sci. 8.
626    https://doi.org/10.3389/fpls.2017.00629

627 Bussotti, F., Pollastrini, M., Holland, V., Brüggemann, W., 2015. Functional traits and adaptive
628    capacity of European forests to climate change. Environ. Exp. Bot. 111, 91–113.
629    https://doi.org/10.1016/j.envexpbot.2014.11.006

630 Cabej, N.R., 2012. 18-Species and Allopatric Speciation, in: Cabej, N.R. (Ed.), Epigenetic Principles
631    of Evolution. Elsevier, pp 707-723. https://doi.org/10.1016/B978-0-12-415831-3.00018-5

632 Casazza, G., Giordani, P., Renato, B., Foggi, B., Viciani, D., Filigheddu, R., Farris, E., Bagella, S.,
633    Pisanu, S., Mariotti, M.G., 2014. Climate change hastens the urgency of conservation for range-

634    restricted plant species in the central-northern Mediterranean region. Biol. Conserv. 179, 129–

635    138. https://doi.org/10.1016/j.biocon.2014.09.015

636 Casimiro-Soriguer, R., Talavera, M., Balao, F., Terrab, A., Herrera, J., Talavera, S., 2010. Phylogeny

637    and genetic structure of *Erophaca* (Leguminosae), a East–West Mediterranean disjunct genus

638    from the Tertiary. Mol. Phylogenet. Evol. 56, 441–450.

639    https://doi.org/10.1016/j.ympev.2010.02.025

640 Christmas, M.J., Breed, M.F., Lowe, A.J., 2016. Constraints to and conservation implications for

641    climate change adaptation in plants. Conserv. Genet. 17, 305–320.

642    https://doi.org/10.1007/s10592-015-0782-5

643 Conti, F., Manzi, A., Pedrotti, F., 1997. Liste Rosse Regionali delle Piante d'Italia. WWF Italia.

644    Società Botanica Italiana, Università di Camerino, 139 pp.

645 Corander, J., Waldmann, P., Sillanpää, M.J., 2003. Bayesian Analysis of Genetic Differentiation

646    Between Populations. Genetics 163, 367–374. https://doi.org/10.1093/genetics/163.1.367

647 Cramer, W., Guiot, J., Fader, M., Garrabou, J., Gattuso, J.-P., Iglesias, A., Lange, M.A., Lionello, P.,

648    Llasat, M.C., Paz, A., Peñuelas, J., Snoussi M., Toreti, A., Tsimplis, N., Xoplaki, E., 2018.

649    Climate change and interconnected risks to sustainable developments in the Mediterranean. Nat.

650    Clim. Change 8, 972–980. https://doi.org/10.1038/s41558-018-0299-2

651 Dagnino, D., Guerrina, M., Minuto, L., Mariotti, M.G., Médail, F., Casazza, G., 2020. Climate change

652    and future of endemic flora in the South Western Alps: relationships between niche properties

653    and extinction risk. Reg. Environ. Change 20, 121. https://doi.org/10.1007/s10113-020-01708-4

654 de Castro, O., Véla, E., Vendramin, G.G., Gargiulo, R., Caputo, P., 2015. Genetic structure in the

655    *Genista ephedroides* complex (Fabaceae) and implications for its present distribution. Bot. J.

656    Linn. Soc. 177, 607–618. https://doi.org/10.1111/boj.12263

657 Domina, G., 2011. *Carex panormitana.* The IUCN Red List of Threatened Species 2011,

658    e.T188659A8649818. https://dx.doi.org/10.2305/IUCN.UK.2011-

659    1.RLTS.T188659A8649818.en. (accessed 10 June 2021).

660 Earl, D.A., vonHoldt, B.M., 2012. STRUCTURE HARVESTER: a website and program for

661    visualizing STRUCTURE output and implementing the Evanno method. Conservation Genet.

662    Resour. 4, 359–361. https://doi.org/10.1007/s12686-011-9548-7

663 Ehrich, D., 2006. AFLPDAT: a collection of r functions for convenient handling of AFLP data. Mol.

664    Ecol. Notes 6, 603–604. https://doi.org/10.1111/j.1471-8286.2006.01380.x

665 Escudero, M., Valcarcel, V., Vargas, P., Luceño, M., 2008. Strait of Gibraltar: an effective gene-flow

666    barrier for wind-pollinated *Carex helodes* (Cyperaceae) as revealed by DNA sequences, AFLP,

667    and cytogenetic variation. Am. J. Bot. 95, 745–755. https://doi.org/10.3732/ajb.2007342

668 Espíndola, A., Pellissier, L., Maiorano, L., Hordijk, W., Guisan, A., Alvarez, N., 2012. Predicting

669    present and future intra-specific genetic structure through niche hindcasting across 24 millennia.

670    Ecol. Lett. 15, 649-657. https://doi.org/10.1111/j.1461-0248.2012.01779.x

671 Excoffier, L., Lischer, H.E.L., 2010. Arlequin suite ver 3.5: a new series of programs to perform

672    population genetics analyses under Linux and Windows. Mol. Ecol. Resour. 10, 564–567.

673    https://doi.org/10.1111/j.1755-0998.2010.02847.x

674 Fenu, G., Bacchetta, G., Christodoulou, C.S., Cogoni, D., Fournaraki, C., Gian Pietro, G. del G.,
675    Gotsiou, P., Kyratzis, A., Piazza, C., Vicens, M., de Montmollin, B., 2020. A Common
676    Approach to the Conservation of Threatened Island Vascular Plants: First Results in the
677    Mediterranean Basin. Diversity 12, 157. https://doi.org/10.3390/d12040157
678 Fernández i Marti, A., Romero-Rodríguez, C., Navarro-Cerrillo, R.M., Abril, N., Jorrín-Novo, J.V.,
679    Dodd, R.S., 2018. Population genetic diversity of *Quercus ilex* subsp. *ballota* (Desf.) Samp.
680    reveals divergence in recent and evolutionary migration rates in the Spanish dehesas. Forests 9,
681    337. https://doi.org/10.3390/f9060337
682 Fernández-Mazuecos, M., Jiménez-Mejías, P., Martín-Bravo, S., Buide, M.L., Álvarez, I., Vargas, P.,
683    2016. Narrow endemics on coastal plains: Miocene divergence of the critically endangered genus
684    *Avellara* (Compositae). Plant. Biol. J. 18, 729–738. https://doi.org/10.1111/plb.12458
685 Fernández-Mazuecos, M., Vargas, P., 2011. Historical Isolation versus Recent Long-Distance
686    Connections between Europe and Africa in Bifid Toadflaxes (*Linaria* sect. *Versicolores*). PLoS
687    ONE 6, e22234. https://doi.org/10.1371/journal.pone.0022234
688 Fick, S.E., Hijmans, R.J., 2017. WorldClim 2: new 1-km spatial resolution climate surfaces for global
689    land areas. Int. J. Climatol 37, 4302–4315. https://doi.org/10.1002/joc.5086
690 Fletcher, W.J., Zielhofer, C., 2013. Fragility of Western Mediterranean landscapes during Holocene
691    rapid climate changes. CATENA 103, 16–29. https://doi.org/10.1016/j.catena.2011.05.001
692 Forester, B.R., DeChaine, E.G., Bunn, A.G., 2013. Integrating ensemble species distribution
693    modelling and statistical phylogeography to inform projections of climate change impacts on
694    species distributions. Diversity Distrib. 19, 1480–1495. https://doi.org/10.1111/ddi.12098
695 Freeman, B.G., Class Freeman, A.M., 2014. Reply to Rehm: Why rates of upslope shifts in tropical
696    species vary is an open question. Proc. Natl. Acad. Sci. 111, E1677–E1677.
697    https://doi.org/10.1073/pnas.1403753111
698 García, M.B., Jordano, P., 2021. Global Change Impacts, Consejo Superior de Investigaciones
699    Científicas, Madrid, 174 pp.
700 García-Verdugo, C., Sajeva, M., La Mantia, T., Harrouni, C., Msanda, F., Caujapé-Castells, J., 2015.
701    Do island plant populations really have lower genetic variation than mainland populations?
702    Effects of selection and distribution range on genetic diversity estimates. Mol. Ecol. 24, 726–
703    741. https://doi.org/10.1111/mec.13060
704 Gianguzzi, L., Cusimano, D., Ilardi, V., Romano, S., 2013. Distribution, ecology, vegetation and
705    conservation survey on the relictual population of *Carex panormitana* Guss. (Cyperaceae) in
706    Sicily (Italy). Webbia 68, 159–175. https://doi.org/10.1080/00837792.2013.853364
707 González-Varo, J.P., López-Bao, J.V., Guitián, J., 2017. Seed dispersers help plants to escape global
708    warming. Oikos 126, 1600–1606. https://doi.org/10.1111/oik.04508
709 Gray, A., 2018. The ecology of plant extinction: rates, traits and island comparisons. Oryx 53, 424–
710    428. https://doi.org/10.1017/S0030605318000315
711 Guiot, J., Cramer, W., 2016. Climate change: The 2015 Paris Agreement thresholds and
712    Mediterranean basin ecosystems. Science 354, 465–468. https://doi.org/10.1126/science.aah5015

713 Guisan, A., Thuiller, W., 2005. Predicting species distribution: offering more than simple habitat
714    models. Ecol. Lett. 8, 993–1009. https://doi.org/10.1111/j.1461-0248.2005.00792.x

715 Gussone, G., 1844. Florae Siculae Synopsis 2, Napoli, pp 575.

716 Hoffmann, A.A., Rymer, P.D., Byrne, M., Ruthrof, K.X., Whinam, J., McGeoch, M., Bergstrom,
717    D.M., Guerin, G.R., Sparrow, B., Joseph, L., Hill, S.J., Andrew, N.R., Camac, J., Bell, N.,
718    Reigler, M., Gardner, J.L., Williams, S.E., 2018. Impacts of recent climate change on terrestrial
719    flora and fauna: Some emerging Australian examples. Austral Ecol. 44, 3–27.
720    https://doi.org/10.1111/aec.12674

721 Hoffmann, A.A., Sgrò, C.M., 2011. Climate change and evolutionary adaptation. Nature 470, 479–
722    485. https://doi.org/10.1038/nature09670

723 IPCC, 2013. Climate Change 2013: The Physical Science Basis, in: Stocker, T.F., Qin, D., Plattner,
724    G.-K., Tignor, M., Allen, S.K., Boschung, J., Nauels, A., Xia, Y., Bex, V., Midgley, P.M. (Eds.),
725    Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel
726    on Climate Change. Cambridge University Press, Cambridge, United Kingdom and New York,
727    NY, USA, 1535 pp.

728 IPCC, 2014. Climate Change 2014: Synthesis Report, in: Core Writing Team, Pachauri, R.K., Meyer,
729    L.A. (Eds.), Contribution of Working Groups I, II and III to the Fifth Assessment Report of the
730    Intergovernmental Panel on Climate Change. IPCC, Geneva, Switzerland, 151 pp.

731 IUCN, 2012. IUCN Red List Categories and Criteria: Version 3.1. second ed Gland, Switzerland and
732    Cambridge, UK, 38 pp.

733 IUCN, 2021. The IUCN Red List of Threatened Species. Version 2021-2. https://www.iucnredlist.org
734    (accessed 19 September 2021).

735 IUCN Standards and Petitions Committee, 2019. Guidelines for Using the IUCN Red List Categories
736    and Criteria. Version 14, prepared by the Standards and Petitions Committee.
737    http://www.iucnredlist.org/documents/RedListGuidelines.pdf (accessed 19 September 2021).

738 Jakobsson, M., Rosenberg, N.A., 2007. CLUMPP: a cluster matching and permutation program for
739    dealing with label switching and multimodality in analysis of population structure.
740    Bioinformatics 23, 1801–1806. https://doi.org/10.1093/bioinformatics/btm233

741 Janžekovič, F., Novak, T., 2012. PCA - A Powerful Method for Analyze Ecological Niches, in:
742    Sanguansant, P. (Ed.), Principal component analysis-multidisciplinary applications, InTech,
743    Croatia, pp 128-142.

744 Jay, F., 2012. POPS: A Software for Prediction of Population Genetic Structure - Program
745    documentation and tutorial. University Joseph Fourier, Grenoble, France. http://membres-
746    timc.imag.fr/Olivier.Francois/pops.html (accessed 5 November 2020).

747 Jay, F., François, O., Durand, E.Y., Blum, M.G.B., 2015. POPS: A Software for Prediction of
748    Population Genetic Structure Using Latent Regression Models. J. Stat. Soft. 68.
749    https://doi.org/10.18637/jss.v068.i09

750 Jiménez-Mejías, P., Escudero, M., Guerra-Cárdenas, S., Lye, K.A., Luceño, M., 2011. Taxonomic
751    delimitation and drivers of speciation in the Ibero-North African *Carex* sect. *Phacocystis* river-
752    shore group (Cyperaceae). Am. J. Bot. 98, 1855–1867. https://doi.org/10.3732/ajb.1100120

Jiménez-Mejías, P., Fernández-Mazuecos, M., Amat, M.E., Vargas, P., 2015. Narrow endemics in European mountains: high genetic diversity within the monospecific genus *Pseudomisopates* (Plantaginaceae) despite isolation since the late Pleistocene. J. Biogeogr. 42:1455–1468. https://doi.org/10.1111/jbi.12507

Jiménez-Mejías, P., Luceño, M., 2011. Euro+Med Plantbase. The information resource for Euro-Mediterranean plant diversity. http://ww2.bgbm.org/EuroPlusMed/query.asp (accessed 16 April 2020).

Jiménez-Mejías, P., Luceño, M., Lye, K.A., Brochmann, C., Gussarova, G., 2012. Genetically diverse but with surprisingly little geographical structure: the complex history of the widespread herb *Carex nigra* (Cyperaceae). J. Biogeogr. 39, 2279–2291. https://doi.org/10.1111/j.1365-2699.2012.02740.x

Jiménez-Mejías, P., Martín-Bravo, S., Amini-Rad, M., Luceño, M., 2014. Disentangling the taxonomy of *Carex acuta* s.l. in the Mediterranean basin and the Middle East: Re-evaluation of *C. panormitana* Guss. and *C. kurdica* Kük. ex Hand.-Mazz. Plant Biosystems 148, 64–73. https://doi.org/10.1080/11263504.2012.758675

Johnson, C.N., Balmford, A., Brook, B.W., Buettel, J.C., Galetti, M., Guangchun, L., Wilmshurst, J.M., 2017. Biodiversity losses and conservation responses in the Anthropocene. Science 356, 270–275. https://doi.org/10.1126/science.aam9317

Jombart, T., 2008. adegenet: a R package for the multivariate analysis of genetic markers. Bioinformatics 24, 1403–1405. https://doi.org/10.1093/bioinformatics/btn129

Jombart, T., Devillard, S., Balloux, F., 2010. Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. BMC Genet. 11, 94. https://doi.org/10.1186/1471-2156-11-94

Jump, A.S., Penuelas, J., 2005. Running to stand still: adaptation and the response of plants to rapid climate change. Ecol. Lett. 8, 1010–1020. https://doi.org/10.1111/j.1461-0248.2005.00796.x

Kougioumoutzis, K., Kokkoris, I.P., Panitsa, M., Trigas, P., Strid, A., Dimopoulos, P., 2020. Plant Diversity Patterns and Conservation Implication under Climate-Change Scenarios in the Mediterranean: The Case of Crete (Aegean, Greece). Divers. 12: 270. https://doi.org/10.3390/d12070270

Lavergne, S., Molina, J., Debussche, M., 2006. Fingerprints of environmental change on the rare mediterranean flora: a 115-year study. Global Change Biol. 12, 1466–1478. https://doi.org/10.1111/j.1365-2486.2006.01183.x

Lima, J.S., Ballesteros-Mejia, L., Lima-Ribeiro, M.S., Collevatti, R.G., 2017. Climatic changes can drive the loss of genetic diversity in a Neotropical savanna tree species. Glob. Change Biol. 23:4639–4650. https://doi.org/10.1111/gcb.13685

Lionello, P., Scarascia, L., 2018. The relation between climate change in the Mediterranean region and global warming. Reg. Environ. Change 18, 1481–1493. https://doi.org/10.1007/s10113-018-1290-1

Liu, H., Edwarsd, E.J., Freckleton, R.P., Osborne, C.P., 2012. Phylogenetic niche conservatism in C4 grasses. Oecologia 170: 835–845. https://doi.org/10.1007/s00442-012-2337-5

793 lo Presti, R.M., Oberprieler, C., 2011. The central Mediterranean as a phytodiversity hotchpotch:
794 phylogeographical patterns of the *Anthemis secundiramea* group (Compositae, Anthemideae)
795 across the Sicilian Channelz. J. Biogeogr. 38: 1109–1124. https://doi.org/10.1111/j.1365-
796 2699.2010.02464.x

797 Loarie, S.R., Duffy, P.B., Hamilton, H., Asner, G.P., Field, C.B., Ackerly, D.D., 2009. The velocity
798 of climate change. Nature 462, 1052–1055. https://doi.org/10.1038/nature08649

799 López-Pujol, J., Bosch, M., Simon, J., Blanché, C., 2009. Patterns of genetic diversity in the highly
800 threatened vascular flora of the Mediterranean Basin, in: Columbus, A., Kuznetsov, L. (Eds.),
801 Endangered Species: New Research. Nova Science Publishers, New York, pp 45–79.

802 López-Pujol, J., Martinell, M.C., Massó, S., Blanché, C., Sáez, L., 2013. The 'paradigm of extremes':
803 extremely low genetic diversity in an extremely narrow endemic species, *Coristospermum huteri*
804 (Umbelliferae). Plant Syst. Evol. 299, 439–446. https://doi.org/10.1007/s00606-012-0732-3

805 Lososová, Z., Divíšek, J., Chytrý, M., Götzenberger, L., Těšitel, J., Mucina, L., 2020.
806 Macroevolutionary patterns in European vegetation. J. Veg. Sci. 32: e12942.
807 https://doi.org/10.1111/jvs.12942

808 Luceño, M., Jiménez-Mejías, P., 2008. *Carex* (Cyperaceae). In: Castroviejo, S., Luceño, M., Galán,
809 A., Jiménez-Mejías, P., Cabezas, F., Medina, L. (Eds.), Flora Iberica. Plantas vasculares de la
810 Península Ibérica e Islas Baleares, vol. 18. CSIC, Madrid, pp 109–250.

811 Magri, D., Vendramin, G.G., Comps, B., Dupanloup, I., Geburek, T., Gömöry, D., Latałowa, M., Litt,
812 T., Paule, L., Roure, J.M., Tantau, I., Van Der Knaap, W.O., Petit, R.J., De Beaulieu, J., 2006. A
813 new scenario for the Quaternary history of European beech populations: palaeobotanical
814 evidence and genetic consequences. New Phytol. 171, 199–221. https://doi.org/10.1111/j.1469-
815 8137.2006.01740.x

816 Malcolm, J.R., Liu, C., Neilson, R.P., Hansen, L., Hannah, L., 2006. Global Warming and Extinctions
817 of Endemic Species from Biodiversity Hotspots. Conserv. Biol. 20, 538–548.
818 https://doi.org/10.1111/j.1523-1739.2006.00364.x

819 Mameli, G., Filigheddu, R., Binelli, G., Meloni, M., 2008. The Genetic Structure of the Remnant
820 Populations of *Centaurea horrida* in Sardinia and Associated Islands. Ann. Bot. 101, 633–640.
821 https://doi.org/10.1093/aob/mcn012

822 Marañón, T., Ajbilou, R., Ojeda, F., Arroyo, J., 1999. Biodiversity of woody species in oak
823 woodlands of southern Spain and northern Morocco. For. Ecol. Manag. 115, 147–156.
824 https://doi.org/10.1016/S0378-1127(98)00395-8

825 Martín-Bravo, S., Jiménez-Mejías, P., Villaverde, T., Escudero, M., Hahn, M., Spalink, D., Roalson,
826 E.H., Hipp, A.L., the Global Carex Group, Benítez-Benítez, C., P. Bruederle, L., Fitzek, E., A.
827 Ford, B., A. Ford, K., Garner, M., Gebauer, S., H. Hoffmann, M., Jin, X., Larridon, I.,
828 Léveillé-Bourret, É., Lu, Y., Luceño, M., Maguilla, E., Márquez-Corro, J.I., Míguez, M., Naczi,
829 R., A. Reznicek, A., R. Starr, J., 2019. A tale of worldwide success: Behind the scenes of *Carex*
830 (Cyperaceae) biogeography and diversification. J. Syst. Evol. 57, 695–718.
831 https://doi.org/10.1111/jse.12549

832 Mayol, M., Palau, C., Rosselló, J.A., González-Martínez, S.C., Molins, A., Riba, M., 2012. Patterns
833    of genetic variability and habitat occupancy in *Crepis triasii* (Asteraceae) at different spatial
834    scales: insights on evolutionary processes leading to diversification in continental islands. Ann.
835    Bot. 109, 429–441. https://doi.org/10.1093/aob/mcr298

836 Médail, F., 2017. The specific vulnerability of plant biodiversity and vegetation on Mediterranean
837    islands in the face of global change. Reg. Environ. Change 17: 1775–1790.
838    https://doi.org/10.1007/s10113-017-1123-7

839 Médail, F., Diadema, K., 2009. Glacial refugia influence plant diversity patterns in the Mediterranean
840    Basin. J. Biogeogr. 36, 1333–1345. https://doi.org/10.1111/j.1365-2699.2008.02051.x

841 Medail, F., Quezel, P., 1999. Biodiversity Hotspots in the Mediterranean Basin: Setting Global
842    Conservation Priorities. Conserv. Biol. 13, 1510–1513. https://doi.org/10.1046/j.1523-
843    1739.1999.98467.x

844 Mittermeier, R.A., Turner, W.R., Larsen, F.W., Brooks, T.M., Gascon, C., 2011. Global Biodiversity
845    Conservation: The Critical Role of Hotspots, in: Zachos, F.E., Habel, J.C. (Eds.), Biodiversity
846    Hotspots. Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 3–22. https://doi.org/10.1007/978-
847    3-642-20992-5_1

848 Molina, A., 1996. Sobre la vegetación de los humedales de la Península Ibérica (1. *Phragmiti-
849    Magnocaricetea*). Lazaroa 16, 27–88.

850 Molina-Venegas, R., 2015. Una flora entre dos continentes, el punto caliente de diversidad vegetal
851    Bético-Rifeño en el Mediterráneo occidental. Chronica naturae 5, 16–25.

852 Molins, A., Bacchetta, G., Rosato, M., Rosselló, J.A., Mayol, M., 2018. Molecular phylogeography of
853    *Thymus herba-barona* (Lamiaceae): Insight into the evolutionary history of the flora of the
854    western Mediterranean islands. Taxon 60, 1295–1305. https://doi.org/10.1002/tax.605006

855 Morueta-Holme, N., Engemann, K., Sandoval-Acuña, P., Jonas, J.D., Segnitz, R.M., Svenning, J.-C.,
856    2015. Strong upslope shifts in Chimborazo's vegetation over two centuries since Humboldt.
857    Proc. Natl. Acad. Sci. 112, 12741–12745. https://doi.org/10.1073/pnas.1509938112

858 Myers, N., Mittermeier, R.A., Mittermeier, C.G., da Fonseca, G.A.B., Kent, J., 2000. Biodiversity
859    hotspots for conservation priorities. Nature 403, 853–858. https://doi.org/10.1038/35002501

860 Navarro, G., Molina, J.A., Moreno, P.S., 2001. Vegetación acuática y helofítica del Sistema Ibérico
861    septentrional, centro de España. Acta Bot. Malac. 26, 143–156.
862    https://doi.org/10.24310/abm.v26i0.7405

863 Nei, M., 1972. Genetic Distance between Populations. Am. Nat. 106, 283–292.

864 Nei, M., 1978. Estimation of average heterozygosity and genetic distance from a small number of
865    individuals. Genetics 89, 583–590. https://doi.org/10.1093/genetics/89.3.583

866 Newbold, T., Hudson, et al., 2015. Global effects of land use on local terrestrial biodiversity. Nature
867    520, 45–50. https://doi.org/10.1038/nature14324

868 Olave, M., Marín, A.G., Avila, L.J., Sites, J.W., Morando, M., 2019. Disparate Patterns of
869    Diversification Within Liolaemini Lizards, in: Rull, V., Carnaval, A. (Eds.), Neotropical
870    Diversification: Patterns and Processes, Fascinating Life Sciences. Springer, Cham, pp. 765–790.

871 Orsenigo, S., Montagnani, C., Fenu, G., Gargano, D., Peruzzi, L., Abeli, T., Alessandrini, A.,
872      Bacchetta, G., Bartolucci, F., Bovio, M., Brullo, C., Carta, A., Castello, M., Cogoni, D., Conti,
873      F., Domina, G., Foggi, B., Rossi, G., 2018. Red Listing plants under full national responsibility:
874      Extinction risk and threats in the vascular flora endemic to Italy. Biol. Conserv. 224, 213–222.
875      https://doi.org/10.1016/j.biocon.2018.05.030
876 Ortiz, M.Á., Tremetsberger, K., Terrab, A., Stuessy, T.F., García-Castaño, J.L., Urtubey, E., Baeza,
877      C.M., Ruas, C.F., Gibbs, P.E., Talavera, S., 2008. Phylogeography of the invasive weed
878      *Hypochaeris radicata* (Asteraceae): from Moroccan origin to worldwide introduced populations.
879      Mol. Ecol. 17, 3654–3667. https://doi.org/10.1111/j.1365-294X.2008.03835.x
880 Parding, K.M., Dobler, A., McSweeney, C.F., Landgren, O.A., Benestad, R., Erlandsen, H.B.,
881      Mezghani, A., Gregow, H., Räty, O., Viktor, E., El Zohbi, J., Christensen, O.B., Loukos, H.,
882      2020. GCMeval – An interactive tool for evaluation and selection of climate model ensembles.
883      Clim. Serv. 18, 100167. https://doi.org/10.1016/j.cliser.2020.100167
884 Parmesan, C., 2006. Ecological and Evolutionary Responses to Recent Climate Change. Annu. Rev.
885      Ecol. Evol. Syst. 37, 637–669. https://doi.org/10.1146/annurev.ecolsys.37.091305.110100
886 Peakall, R., Smouse, P.E., 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software
887      for teaching and research-an update. Bioinformatics 28, 2537–2539.
888      https://doi.org/10.1093/bioinformatics/bts460
889 Pecl, G.T., Araújo, M.B., Bell, J.D., Blanchard, J., Bonebrake, T.C., Chen, I.-C., Clark, T.D., Colwell,
890      R.K., Danielsen, F., Evengård, B., Falconi, L., Ferrier, S., Frusher, S., Garcia, R.A., Griffis, R.B.,
891      Hobday, A.J., Janion-Scheepers, C., Jarzyna, M.A., Jennings, S., Lenoir, J., Linnetved, H.I.,
892      Martin, V.Y., McCormack, P.C., McDonald, J., Mitchell, N.J., Mustonen, T., Pandolfi, J.M.,
893      Pettorelli, N., Popova, E., Robinson, S.A., Scheffers, B.R., Shaw, J.D., Sorte, C.J.B., Strugnell,
894      J.M., Sunday, J.M., Tuanmu, M.-N., Vergés, A., Villanueva, C., Wernberg, T., Wapstra, E.,
895      Williams, S.E., 2017. Biodiversity redistribution under climate change: Impacts on ecosystems
896      and human well-being. Science 355, eaai9214. https://doi.org/10.1126/science.aai9214
897 Pignatti, S., 1982. Flora d'Italia. Volume Terzo. Edagricole, Bologna, 723 pp.
898 POWO, 2020. Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew.
899      http://www.plantsoftheworldonline.org/ (accessed 5 April 2021).
900 Pritchard, J.K., Stephens, M., Donnelly, P., 2000. Inference of Population Structure Using Multilocus
901      Genotype Data. Genetics 155, 945–959. https://doi.org/10.1093/genetics/155.2.945
902 Provan, J., Maggs, C.A., 2011. Unique genetic variation at a species´s rear edge is under threat from
903      global climate change. Proc. R. Soc. B 279(1726), 39–47.
904      https://doi.org/10.1098/rspb.2011.0536
905 QGIS Development Team, 2021. QGIS Geographic Information System. Open Source Geospatial
906      Foundation Project. http://qgis.osgeo.org/ (accessed 16 May 2021).
907 R Core Development Core Team, 2020. R: A language environment for statistical computing. R
908      Foundation for Statistical Computing, Vienna, Austria.

908 Ramasamy, R., Ramasamy, S., Bindroo, B., Naik, V., 2014. STRUCTURE PLOT: a program for
910  drawing elegant STRUCTURE bar plots in user friendly interface. SpringerPlus 3, 431.
911  https://doi.org/10.1186/2193-1801-3-431

912 Razgour, O., Forester, B., Taggart, J.B., Bekaert, M., Juste, J., Ibáñez, C., Puechmaille, S.J., Novella-
913  Fernandez, R., Alberdi, A., Manel, S., 2019. Considering adaptive genetic variation in climate
914  change vulnerability assessment reduces species range loss projections. Proc. Natl. Acad. Sci.
915  116, 10418–10423. https://doi.org/10.1073/pnas.1820663116

916 Ripple, W.J., Wolf, C., Newsome, T.M., Galetti, M., Alamgir, M., Crist, E., Mahmoud, M.I.,
917  Laurance, W.F., 15,364 scientist signatories from 184 countries, 2017. World Scientists'
918  Warning to Humanity: A Second Notice. BioScience 67, 1026–1028.
919  https://doi.org/10.1093/biosci/bix125

920 Rizvanovic, M., Kennedy, J.D., Nogués-Bravo, D., Marske, K.A., 2019. Persistence of genetic
921  diversity and phylogeography structure of three New Zealand forest beetles under climate
922  change. Divers. Distrib. 25,142–153. https://doi.org/10.1111/ddi.12834¡

923 Roalson, E.H., Jiménez-Mejías, P., et al., 2021. A framework infrageneric classification of *Carex*
924  (Cyperaceae) and its organizing principles. J. Syst. Evol. 59, 726–762.
925  https://doi.org/10.1111/jse.12722

926 Rodríguez-Guitián, M.A., Real, C., Romero-Franco, R., Álvarez-Hurtado, A., 2017.
927  Phytosociological framework and conservation value of supratemperate riparian birch forest of
928  the Northwestern Iberian Peninsula. Lazaroa 3, 87–126 https://doi.org/10.5209/LAZA.56061

929 Rodríguez-Sánchez, F., Pérez-Barrales, R., Ojeda, F., Vargas, P., Arroyo, J., 2008. The Strait of
930  Gibraltar as a melting pot for plant biodiversity. Quat. Sci. Rev. 27, 2100–2117.
931  https://doi.org/10.1016/j.quascirev.2008.08.006

932 Rosenberg, N.A., 2004. DISTRUCT: a program for the graphical display of population structure. Mol.
933  Ecol. Notes 4, 137–138. https://doi.org/10.1046/j.1471-8286.2003.00566.x

934 Rossi, G., Montagnani, C., Gargano, D., Peruzzi, L., Abeli, T., Ravera, S., Cogoni, A., Fenu, G.,
935  Magrini, S., Gennai, M., Foggi, B., Wagensommer, R.P., Venturella, G., Blasi, C., Raimondo,
936  F.M., Orsenigo, S., 2013. Lista rossa della flora Italiana. 1. Policy species e altre specie
937  minacciate, in: Rossi, G., Montagnani, C., Gargano, D., Peruzzi, L., Abeli, T., Ravera, S.,
938  Cogoni, A., Fenu, G., Magrini, S., Gennai, M., Foggi, B., Wagensommer, R.P., Venturella, G.,
939  Blasi, C., Raimondo, F.M., Orsenigo, S. (Eds.), Red list of Italian flora 1. Policy species and
940  other threatened species. Comitato Italiano IUCN, Ministero dell'Ambiente e della Tutela del
941  Territorio e del Mare, Italy, 55 pp.

942 Rufo Nieto, L., De la Fuente García, V., 2011. Vegetación serial de la cuenca del Río Tinto (Huelva,
943  España): pastos, prados y comunidades rupícolas. Lazaroa 32, 73–89.
944  https://doi.org/10.5209/rev_LAZA.2011.v32.37253

945 Sanz-Arnal, M., Benítez-Benítez, C., Jiménez-Mejías, P., Miguez, M., Martín-Bravo, S., 2021. Are
946  Cenozoic relicts also climatic relicts? Insights from the macroecological evolution of the giant
947  sedges of *Carex* sect. *Rhynchocystis* (Cyperaceae). Am. J. Bot. https://doi.org/10.1002/ajb2.1788

948 Schönswetter, P., Paun, O., Tribsch, A., Niklfeld, H., 2003. Out of the Alps: colonization of Northern
949    Europe by East Alpine populations of the Glacier Buttercup *Ranunculus glacialis* L.
950    (Ranunculaceae). Mol. Ecol. 12, 3373–3381. https://doi.org/10.1046/j.1365-294X.2003.01984.x
951 Schönswetter, P., Tribsch, A., 2005. Vicariance and dispersal in the alpine perennial *Bupleurum*
952    *stellatum* L. (Apiaceae). Taxon 54, 725–732. https://doi.org/10.2307/25065429
953 Sobel, J.M., 2016. Speciation, Geography of, in: Kliman, R.M., (Ed.), Encyclopedia of Evolutionary
954    Biology. Academic Press, pp 183–191. https://doi.org/10.1016/B978-0-12-800049-6.00333-4
955 Soberon, J., Peterson, A.T., 2005. Interpretation of Models of Fundamental Ecological Niches and
956    Species' Distributional Areas. Biodiv. Inf. 2, 1–10. https://doi.org/10.17161/bi.v2i0.4
957 Souto, C.P., Tadey M., 2019. Livestock effects on genetic variation of creosote bushes in Patagonian
958    rangelands. Environ. Conserv. 26, 59–66. https://doi.org/10.1017/S0376892918000280
959 Swets, J., 1988. Measuring the accuracy of diagnostic systems. Science 240, 1285–1293.
960    https://doi.org/10.1126/science.3287615
961 Swofford, D.L., 2002. PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods).
962    Version 4. Sinauer Associates, Sunderland, Massachusetts.
963 Temunović, M., Frascaria-Lacoste, N., Franjić, J., Satovic, Z., Fernández-Manjarrés, J.F., 2013.
964    Identifying refugia from climate change using coupled ecological and genetic data in a
965    transitional Mediterranean-temperate tree species. Mol. Ecol. 22, 2128–2142.
966    https://doi.org/10.1111/mec.12252
967 Terrab, A., Schönswetter, P., Talavera, S., Vela, E., Stuessy, T.F., 2008. Range-wide phylogeography
968    of *Juniperus thurifera* L., a presumptive keystone species of western Mediterranean vegetation
969    during cold stages of the Pleistocene. Mol. Phylogenet. Evol. 48, 94–102.
970    https://doi.org/10.1016/j.ympev.2008.03.018
971 Thiébaut, G., 2006. Aquatic Macrophyte Approach to Assess the Impact of Disturbances on the
972    Diversity of the Ecosystem and on River Quality. Internat. Rev. Hydrobiol. 91, 483–497.
973    https://doi.org/10.1002/iroh.200610868
974 Thiers, B., 2020. Index Herbariorum: A global directory of public herbaria and associated staff. New
975    York Botanical Garden's Virtual Herbarium. http://sweetgum.nybg.org/science/ih/ (accessed 18
976    June 2021).
977 Thomas, C.D., Cameron, A., Green, R.E., Bakkenes, M., Beaumont, L.J., Collingham, Y.C., Erasmus,
978    B.F.N., de Siqueira, M.F., Grainger, A., Hannah, L., Hughes, L., Huntley, B., van Jaarsveld,
979    A.S., Midgley, G.F., Miles, L., Ortega-Huerta, M.A., Peterson, A.T., Phillips, O.L., Williams,
980    S.E., 2004. Extinction risk from climate change. Nature 427, 145–148.
981 Thuiller, W., Lafourcade, B., Engler, R., Araújo, M.B., 2009. BIOMOD - a platform for ensemble
982    forecasting of species distributions. Ecography 32, 369–373. https://doi.org/10.1111/j.1600-
983    0587.2008.05742.x
984 Tremetsberger, K., Ortiz, M.Á., Terrab, A., Balao, F., Casimiro-Soriguer, R., Talavera, M., Talavera,
985    S., 2016. Phylogeography above the species level for perennial species in a composite genus.
986    AoB PLANTS 8, plv142. https://doi.org/10.1093/aobpla/plv142

987 Urbani, M., Calvia, G., Pisanu, S., 2013. *Carex panormitana* Guss, in: Rossi, G., Foggi, B., Gennai,
988    M., Gargano, D., Montagnani, C., Orsenigo, S., Pedrini, S. (Eds.), Schede per una Lista Rossa
989    della Flora vascolare e crittogamica Italiana, 45, pp 134–136.

990 Urbani, M., Gianguzzi, L., Ilardi, V., 1995. Notes on the distribution and ecology of *Carex*
991    *panormitana* Guss. (Cyperaceae). Giorn. Bot. Ital. 129, 186.

992 Vargas, P., 2020. The Mediterranean Floristic Region: High Diversity of Plants and Vegetation
993    Types, in: Goldstein, M.I., Dellasala, D.A. (Eds.), Encyclopedia of the World's Biomes.
994    Elsevier, pp. 602–616. https://doi.org/10.1016/B978-0-12-409548-9.12097-4

995 Velásquez-Tibatá, J., Salaman, P., Graham, C.H., 2013. Effects of climate change on species
996    distribution, community structure, and conservation of birds in protected areas in Colombia. Reg.
997    Environ. Change 13, 235–248. https://doi.org/10.1007/s10113-012-0329-y

998 Vessella, F., Tirado-López, J., Cosimo Simeone, M., Schirone, B., Hidalgo, P.J., 2017. A tree species
999    range in the face of climate change: cork oak as a study case for the Mediterranean biome. Eur. J.
1000    Forest Res. 136, 555–569. https://doi.org/10.1007/s10342-017-1055-2

1001 Wickham, H., 2016. *ggplot2*: Elegant Graphics for Data Analysis. Springer-Verlag New York. ISBN
1002    978-3-319-24277-4. https://ggplot2.tidyverse.org/ (accessed 3 May 2021).

1003

1004 Wiens, J.J., Ackerly, D.D., Allen, A.P., Anacker, B.L., Buckley, L.B., Cornell, H.V., Damschen, E.I.,
1005    Jonathan Davies, T., Grytnes, J.-A., Harrison, S.P., Hawkins, B.A., Holt, R.D., McCain, C.M.,
1006    Stephens, P.R., 2010. Niche conservatism as an emerging principle in ecology and conservation
1007    biology: Niche conservatism, ecology, and conservation. Ecol. Lett. 13, 1310–1324.
1008    https://doi.org/10.1111/j.1461-0248.2010.01515.x

1009 Wiens, J.J., Graham, C.H., 2005. Niche Conservatism: Integrating Evolution, Ecology, and
1010    Conservation Biology. Annu. Rev. Ecol. Evol. Syst. 36, 519–539.
1011    https://doi.org/10.1146/annurev.ecolsys.36.102803.095431

1012 Wright, S., 1965. The Interpretation of Population Structure by F-Statistics with Special Regard to
1013    Systems of Mating. Evol. 19, 395–420.

1014 Wróblewska, A., Mirski, P., 2018. From past to future: impact of climate change on range shifts and
1015    genetic diversity patterns of circumboreal plants. Reg. Environ. Change 18, 409–424.
1016    https://doi.org/10.1007/s10113-017-1208-3

1017 Wu, J., Gao, Y., Bao, X., Gao, H., Jia, M., Li, J., Zhao, N., 2010. Genetic variation among *Stipa*
1018    *grandis* P. Smirn populations with different durations of fencing in the Inner Mongolian Steppe.
1019    Rangel. 32(4), 427–434. https://doi.org/10.1071/RJ09038

1020

1021

# Figure 1

Figure 1

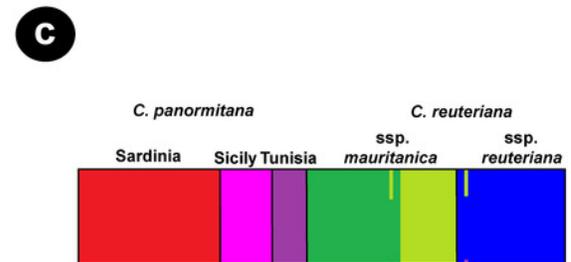
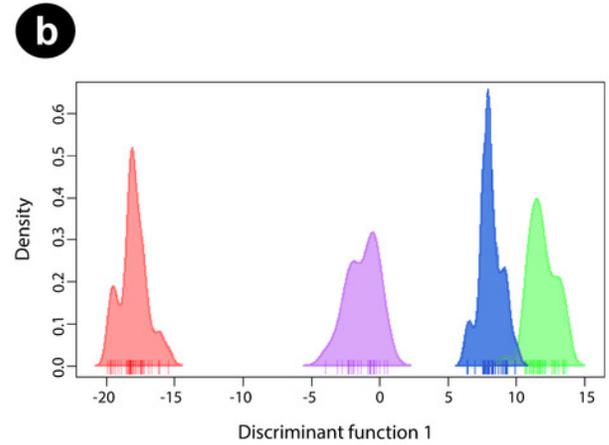
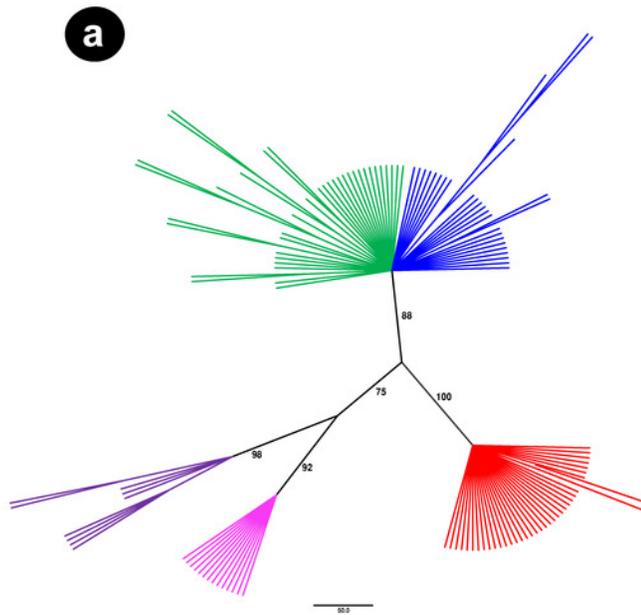
**Main results of the analyses of present genetic structure in *C. reuteriana-C. panormitana.*** (a) Neighbor-joining tree based on Nei-Li genetic distances obtained from AFLP phenotype for all sampled individuals; numbers above branches indicate bootstrap values (>50%); (b) DAPC scatter plot showing the discriminant function (axis x) and density (axis y) across two principal components; (c) BAPS admixture bars obtained for all sampled individuals, each represented by a bar. Colours represent the taxonomic or geographic adscription of samples: *C. reuteriana* subsp. *reuteriana* (blue), *C. reuteriana* subsp. *mauritanica* (green), and *C. panormitana* (red -Sardinia-, pink -Sicily-, and purple -Tunisia-). In DAPC (**b**), purple represents both Sicilian and Tunisian populations of *C. panormitana*; and lines below each density plot represent individuals. In BAPS (**c**), two shades of green are used to represent underlying geographic structure found within *C. reuteriana* subsp. *mauritanica* (dark green -Iberian Peninsula-, light green-North Africa-).

# Figure 2

Figure 2

**Population genetic structure analyses.** (a) Population genetic structure for present times inferred by STRUCTURE, and (b) for future conditions (2081-2100) under RCP2.6 climate scenario projected with POPS. Circles indicate sampled populations of *C. reuteriana* subsp. *reuteriana*, *C. reuteriana* subsp. *mauritanica*, and *C. panormitana.* Colours are as in Fig.1 and represent the identified genetic groups (K=2 for the three taxa). Pie charts show the proportion of individuals in each population assigned to each of the two genetic groups.

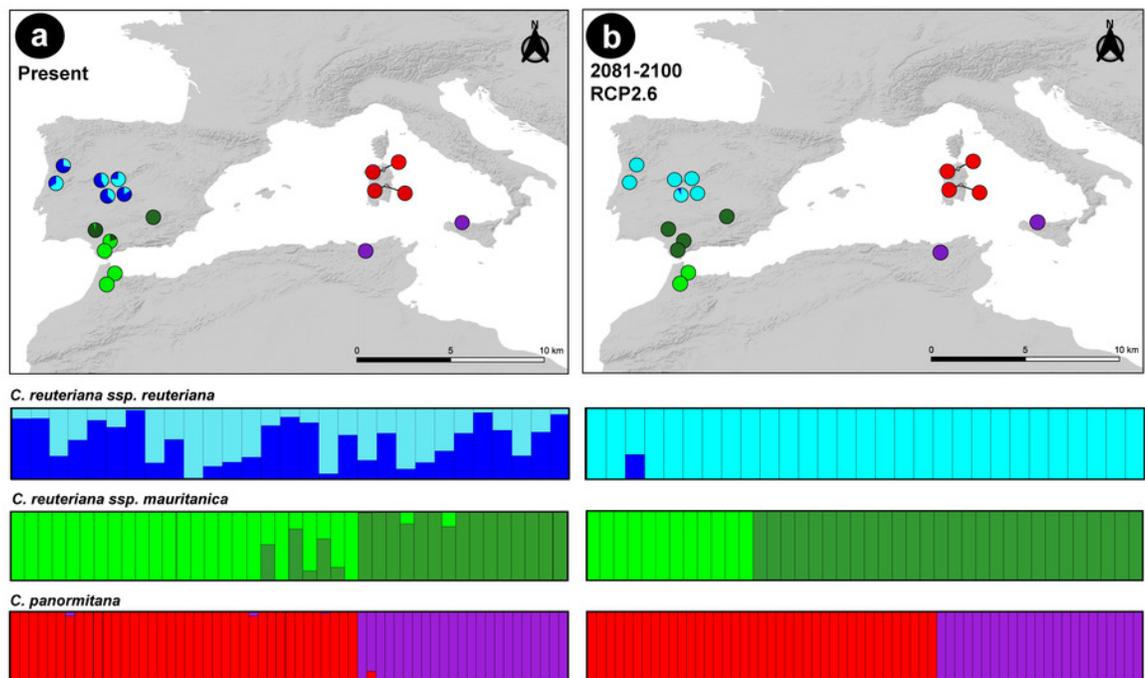



Table 1

**Geographic location and voucher of each sampled population of *C. reuteriana* (two subspecies) and *C. panormitana*, average gene diversity at ramet and genet level for present and future (2081-2100) under RCP2.6 GCC scenario, and allelic rarity levels (DW).** Labelling of the populations specifies the taxa (REU = *Carex reuteriana* subsp. *reuteriana;* MAU = *Carex reuteriana* subsp. *mauritanica;* PAN = *Carex panormitana*), and the TDWG botanical country abbreviation (Brummitt, 2001) [MOR = Morocco, POR = Portugal, SAR = Sardinia, SIC = Sicily, SPA = Spain, TUN = Tunisia]. Herbarium acronyms are according to Index Herbariorum (Thiers, 2020). Populations inferred as extinct (IAE) under RCP2.6 scenario for 2081-2100 are not included in the genetic diversity calculation.

| Taxon/ Population | Locality | Voucher/ Herbarium | Number of individuals | Longitude/ Latitude | DW present (genet) | Mean gene diversity ± SD (present; ramet level) | Mean gene diversity ±SD (present; genet level) | Mean gene diversity ± SD (future; ramet level) | Mean gene diversity ±SD (future; genet level) |
|---|---|---|---|---|---|---|---|---|---|
| *C. reuteriana* | | | 69 | | 905.394 | 0.184 | | 0.176 | |
| *C. reuteriana* ssp. *reuteriana* | | | 29 | | 154.041 | 0.142 | | 0.107 | |
| **REU_POR-TM_1** | Portugal, Tras os Montes, Lamego, Bigorne, Petrarouca | M. Escudero *et al.,* 37ME07 (UPOS-7374) | 6 | -7.88/41.03 | 13.558 | 0.106 ± 0.064 | | | |
| **REU_POR-BL_2** | Portugal, Beira Litoral, Coimbra, Lousã | M. Escudero *et al.,* 60ME07 (UPOS-7373) | 7 | -8.23/40.10 | 11.873 | 0.083 ± 0.048 | | | |
| **REU_SPA-Av_3** | Spain, Ávila, Sierra de Gredos, Las Chorreras del Tormes | J.M. Marín, 5504JMM (UPOS-1004) | 5 | -5.16/40.34 | 25.219 | 0.110 ± 0.069 | | IAE | |
| **REU_SPA-CcN_4** | Spain, Cáceres, Valley of Jerte | P. Jiménez-Mejías & I. Pulgar, 24PJM13 (UPOS- | 4 | -5.75/40.22 | 9.278 | 0.114 ± 0.077 | | IAE | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | 5449) | | | | | |
| **REU_SPA-CcS_5** | Spain, Cáceres, Ibor river | P. Jiménez-Mejías *et al.,* 24PJM13 (UPOS-5449) | 4 | -5.44/39.62 | 21.162 | 0.183 ± 0.122 | IAE |
| **REU_SPA-To_6** | Spain, Toledo, Navalucillos | P. Jiménez-Mejías *et al.,* 60PJM13 (UPOS-5479) | 3 | -4.66/39.64 | 9.189 | 0.158 ± 0.120 | IAE |
| ***C. reuteriana* ssp. *mauritanica*** | | | 40 | | 324.723 | 0.170 | 0.164 |
| **MAU_SPA-Se_7** | Spain, Sevilla, El Ronquillo, Rivera de Huelva | P. Jiménez-Mejías, 35PJM07 (UPOS-7372) | 7 | -6.17/37.67 | 21.125 | 0.155 ± 0.089 | |
| **MAU_SPA-CaGu_8** | Spain, Cádiz, El Gastor, Guadalete river | P. Jiménez-Mejías, 34PJM07 (UPOS-7371) | 5 | -5.45/36.88 | 8.625 | 0.100 ± 0.063 | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **MAU_SPA-CaAl_9** | Spain, Cádiz, Alcornocales Natural Park, | P. Jiménez-Mejías & I. Pulgar, 17PJM07 (UPOS) | 8 | -5.59/36.55 | 24.108 | 0.084 ± 0.048 | | | |
| **MAU_SPA-J_10** | Spain, Jaén, Despeñaperros | P. Jiménez-Mejías & L. Reina, 67PJM09 (UPOS) | 8 | -3.06/38.39 | 25.558 | 0.103 ± 0.058 | IAE | | |
| **MAU_MOR-Lao_11** | Morocco, Tanger, Rif, Oued Laou | A.J. Chaparro *et al.,* 8AJC05 (UPOS-1637) | 5 | -5.30/35.14 | 13.032 | 0.131 ± 0.081 | | | |
| **MAU_MOR-Lou_12** | Morocco, Tanger, Rif, Oued Loukos | A.J. Chaparro *et al.,* 3AJC05 (UPOS-1630) | 7 | -5.44/35.03 | 24.417 | 0.114 ± 0.066 | | | |
| ***C. panormitana*** | | | 61 | | 436.028 | 0.128 | 0.133 | 0.118 | 0.100 |
| **Tunisia-Sicily** | | | 23 | | 114.057 | 0.115 | | | |
| **PAN_TUN_13** | Tunisia, Jendouba, El Feija National Park | P. Jiménez-Mejías & J.E. Rodríguez, 132PJM13 (UPOS-6636) | 9 | 8.31/ 36.49 | 36.949 | 0.067 ± 0.038 | IAE | | |
| **PAN_SIC_15** | Italy, Sicily, Fiume Oreto | D. Cusimano s.n. (SS) | 14 | 13.34/ 38.09 | 51.900 | 0.077 ± 0.041 | | | |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Sardinia** | | | 38 | | 110.234 | 0.032 | 0.037 | | |
| **PAN_SAR-Bau_16** | Italy, Sardinia, Bau Mela river, Villagrande | M. Urbani, 2013 (SS) | 9 | 9.42/39.98 | 11.239 | 0.024 ± 0.015 | 0.033 ±0.022 | 0.024 ± 0.015 | 0.033 ±0.022 |
| **PAN_SAR-Pira_17** | Italy, Sardinia, Cantoniera, Pirae´onni, Villagrande | M. Urbani, 2013 (SS) | 10 | 9.40/ 40.02 | 7.471 | 0.026 ± 0.016 | 0.031±0.021 | 0.026 ± 0.016 | 0.031±0.021 |
| **PAN_SAR-Ber_18** | Italy, Sardinia, Ramacaso river, Berchidda | M. Urbani, 2013 (SS) | 8 | 9.24/ 40.82 | 7.934 | 0.023 ± 0.015 | | | |
| **PAN_SAR-Cal_19** | Italy, Sardinia, Miriacheddu river, Calangianus | M. Urbani, 2013 (SS) | 11 | 9.26/ 40.89 | 7.577 | 0.012 ± 0.008 | 0.028±0.030 | 0.012 ± 0.008 | 0.028±0.030 |

Table 2

**AMOVA analyses for AFLPs data.** The first group includes for comparisons the *Carex reuteriana-C. panormitana* complex and for each species separately. The second group compares the four AFLPs groups found.

| Grouping compared and source of variation | d.f. | Sum of Squares | Variance components | Percentage of variation |
|---|---|---|---|---|
| **1 - Whole dataset (2 groups: *C. reuteriana* s.l. vs. *C. panormitana*)** | | | | |
| Among groups | 2 | 622.957 | 6.24105 | 28.06% |
| Among pops. | 15 | 800.836 | 6.46433 | 37.22% |
| Within pops. | 112 | 798.007 | 7.12506 | 34.73% |
| ***C. reuteriana* s.l.** | | | | |
| Among pops. | 10 | 369.104 | 4.65780 | 39.82% |
| Within pops. | 57 | 593.411 | 10.41071 | 60.18% |
| ***C. panormitana*** | | | | |
| Among pops. | 3 | 44.146 | 1.16277 | 68.76% |
| Within pops. | 55 | 204.596 | 3.71993 | 31.24% |
| **2- Whole dataset (4 groups: *C. reuteriana* ssp. *reuteriana* vs. *C. reuteriana* spp. *mauritanica* vs. *C. panormitana* (Sicily + Tunisia) vs. *C. panormitana* (Sardinia)** | | | | |
| Among groups | 3 | 920.170 | 8.24129 | 42.13% |
| Among pops. | 14 | 503.623 | 4.19747 | 21.46% |
| Within pops. | 112 | 798.007 | 7.12506 | 36.42% |
| ***C. reuteriana* ssp. *reuteriana*** | | | | |
| Among pops. | 5 | 117.297 | 2.70605 | 20.36% |
| Within pops. | 23 | 243.393 | 10.58230 | 79.64% |
| ***C. reuteriana* ssp. *mauritanica*** | | | | |
| Among pops. | 5 | 251.807 | 6.05238 | 37.02% |
| Within pops. | 34 | 350.018 | 10.29464 | 62.98% |
| ***C. panormitana* (Sicilian-Tunisian populations)** | | | | |
| Among pops. | 1 | 90.374 | 7.64231 | 53.51% |
| Within pops. | 21 | 139.452 | 6.64059 | 46.49% |
| ***C. panormitana* (Sardinian populations)** | | | | |
| Among pops. | 3 | 44.146 | 1.35354 | 41.40% |
| Within pops. | 34 | 65.144 | 1.91599 | 58.60% |

# Figure 3

Figure 3

**Predicted changes of potential distribution inferred by Biomod**. Projections comparing present and future times (2081-2100) under RCP2.6 (top maps) and RCP8.5 (bottom maps) climatic change scenarios for (a, b) *C. reuteriana* subsp. *reuteriana,* (c, d) *C. reuteriana* subsp. *mauritanica*, and (e, f) *C. panormitana.* Future projections represent the consensus SDM averaged across six GCMs. Percentages indicate the proportion of potential range inferred to be gained, lost, or to remain stable in the future in comparison with the present, according to the following colour scheme: red areas are currently suitable areas predicted to be lost, orange areas are currently suitable areas projected to remain stable, and green areas are currently unsuitable areas projected to become suitable. Black dots represent current occurrences of each taxon used for SDM.

**2081-2100**