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1 **Genetic diversity of maize landraces from the South-West of France**

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12 **Abstract**

13 From the 17th century until the arrival of hybrids in 1960s, maize landraces were cultivated in the South-West of
14 France, a traditional region for maize cultivation. A set of landraces were collected in this region between the
15 1950s and 1980s and were then conserved *ex situ* in a germplasm collection. Previous studies using molecular
16 markers on approx. twenty landraces for this region showed that they belonged to a Pyrenees-Galicia Flint genetic
17 group and originated from hybridization between Caribbean and Northern Flint germplasms introduced in Europe.
18 In this study, we assessed the structure and genetic diversity of 194 SWF maize landraces to elucidate their origin,
19 using a 50K SNP array and a bulk DNA approach. We identified two weakly differentiated genetic groups, one in
20 the Western part and the other in the Eastern part. We highlighted the existence of a longitudinal gradient along
21 the SWF area that was probably maintained through the interplay between genetic drifts and restricted gene flows,
22 rather than through differential climatic adaptation. The contact zone between the two groups observed near the
23 Garonne valley may be the result of these evolutionary forces. We found only few significant cases of
24 hybridization between Caribbean and Northern Flint germplasms in the region. We also found gene flows from
25 various maize genetic groups to SWF landraces. Thus, we assumed that SWF landraces had a multiple origin with
26 a slightly higher influence of Tropical germplasm in the West and preponderance of Northern Flint germplasm in
27 the East.

28

29 **Keywords:**

30 *Zea mays* L., landraces, genetic diversity, population genetic structure, French Pyrenees

31

32 Introduction

33 Maize was domesticated from teosinte, *Z. mays* L. subsp. *parviglumis*, about 9000 years ago in Southern Mexico
34 (1). Thereafter, it spread from the domestication center over North and South America (1-3). During these
35 expansions, maize evolved in contrasted environments, leading to distinct genetic groups adapted to new climates
36 such as cold temperatures and long days in the north and warmer temperatures in coastal Central America. After
37 the discovery of America by Columbus in 1492, maize was introduced in Europe for the first time in 1493 from
38 the Caribbeans to Spain (4-6). In the first half of the 16th century, a second introduction of maize is documented
39 in North-Eastern Europe from Northern Flint material originating from North America as suggested by an
40 illustration of Leonard Fuchs, a German herbalist, in 1542 (4, 7). Genetic and morphological differences between
41 European maize landraces were found in numerous studies. Studies based on morphological data separated
42 European maize landraces principally according to their earliness and morphological traits also related to flowering
43 time earliness (8, 9). Maize landraces from North-Eastern Europe were shown to be earlier than those from
44 Southern Europe. Molecular studies confirmed the major differentiation between maize from Northern and
45 Southern Europe (4, 7-11). Gauthier *et al.* (9) also detected, in their study, genetic differentiation between South-
46 Western (Northern Spain, Portugal and the Pyrenees) and South-Eastern (Greece and Italy) European landraces.
47 These results suggested that the landraces cultivated in the North, South-West and South-East of Europe resulted
48 from introductions of different maize landraces belonging to different American regions.

49 Molecular studies also showed that maize landraces cultivated at intermediate latitudes in Europe originated from
50 hybridizations between maize landraces from Caribbean, South American and North American landraces (4, 5, 7,
51 10-13). These authors observed genetic similarities between American Northern Flint landraces and landraces
52 from Northern Europe, and also between Caribbean and Southern Spain landraces, showing that the primary
53 introductions of maize landraces from America still have direct representatives in Europe. By analysing both
54 American and European landraces with SSR markers, Camus-Kulandaivelu *et al.* (10) structured them in 7 genetic
55 groups referred to as Mexican (MEX), Caribbean (CAR), Corn Belt Dent (CBD), Andean (AND), Northern Flint
56 (NF), Italian Flint (ITA) and Pyrenees-Galicia Flint groups. This shows that Pyrenees and Galician landraces
57 constitute an original landrace group compared to American genetic groups. Dubreuil *et al.* (7) found that maize
58 landraces cultivated in Pyrenees and Galicia display no close similarity with any of the American genetic group ;
59 but based on structure analyses, these landraces were shown to be intermediate between landraces from the South

60 of Spain and from the North of Europe. Recently Brandenburg *et al.* (12) analysed by resequencing first-cycle
61 inbred lines directly derived from American and European landraces and showed that Northern Flint and Southern
62 European material (notably from Spain) were the potential ancestors of Pyrenees and Galicia landraces.
63 Nevertheless, Mir *et al.* (11) argued that landraces from Pyrenees also displayed a hybrid origin between Northern
64 U.S Flint and Northern South-American landraces, with a predominance of the latter. Thus, all studies highlight
65 the importance of NF origin in the climatic adaptation of Pyrenees Galicia maize. There remains questions about
66 the geographic origin of this NF material: did it arrive directly from America or indirectly through NF landraces
67 from the North of Europe; these two ways for introduction of NF landraces were proposed by Tenailon and
68 Charcosset (13) on their map of introduction of maize in Europe. Following all the above information, it would be
69 highly beneficial to use genetic markers analyses to better understand the evolution of maize landraces located in
70 intermediate regions of Europe. Since maize is an outcrossing species, landraces are expected to display relatively
71 high levels of genetic diversity. To assess this diversity, molecular studies must thus include several individuals.
72 However, for large sets of landraces, molecular characterization based on several individuals per landrace is limited
73 by laborious and costly experimental processes. To overcome this problem, several studies on maize landraces
74 were done on bulks of several plants per landrace, for RFLP analysis (4, 9, 14, 15) and SSR analyses (7, 10, 11,
75 16-19). First, Dubreuil *et al.* (14) evaluated a method based on the RFLP analysis of balanced bulks of DNA from
76 several individuals. They found that allelic frequencies could be estimated with a high precision in bulks of 15
77 individuals. The major disadvantage of bulk DNA analysis was the loss of information on individual genotypes,
78 preventing access to variation at individual level and thus to genetic parameters such as Wright's fixation indices
79 (F_{IS} and F_{IT}). Nevertheless, bulking is highly efficient to estimate most parameter of interest regarding population
80 genetic structure and to make inference about the evolutionary history of populations. Recently, this bulk approach
81 was investigated on SNP markers in maize (20), leading to the development of a new method for allelic frequency
82 estimations (21).

83 In this report, we focus on the South-West of France (SWF), one of the main traditional maize cultivation areas in
84 Europe, as a case study for local scale analysis. Maize cultivation in SWF was first reported in 1626 in the 'Béarn'
85 region, and in 1628 and 1637 respectively in the towns of 'Bayonne' and 'Castelnaudary' (22). Based on historical
86 records, maize spread from its introduction in the South-West of France at the end of the 16th century and was
87 already largely cultivated in this area (from the Pyrenees to the Garonne Valley) at the end of the 17th century
88 (22). American hybrids were introduced from 1948 onwards in France and maize landraces were progressively
89 replaced by commercial American x European hybrids. The origin and genetic diversity of landraces cultivated in

90 SWF before the introduction of commercial hybrids are poorly known, although, as SWF includes the French
91 Pyrenean region, we could expect SWF landraces to exhibit similar characteristics to that of Pyrenees Galicia
92 landraces. The aims of this paper are (1) to assess the structure and genetic diversity of traditional maize landraces
93 cultivated in the South-West of France until 1960-1987, and (2) to determine genetic relationships between SWF
94 landraces with American and European maize landraces. To do so, we analysed the 50 K SNPs array diversity of
95 342 maize landraces, including 194 landraces collected in the South-West of France and conserved by INRA since
96 the 1960s, as well as 148 European and American maize landraces already analysed by Camus-Kulandaivelu *et*
97 *al.* (10) and Mir *et al.* (11) using SSR markers.

98 **Materials and methods**

99 **Plant material**

100 We studied one hundred and ninety-four maize landraces that had been collected between 1949 and 1987 (23, 24)
101 in the South-West of France (SWF, S1 Table) in the two French administrative regions “Nouvelle Aquitaine” (in
102 5 districts) and “Occitanie Pyrénées-Méditerranée” (in 9 districts). Since their collection, these landraces have
103 been preserved at the French Maize Biological Resource Center (CRB, Mauguio, France,
104 <https://urgi.versailles.inra.fr/siregal/siregal/grc.do>) and seed lots regenerated through four successive generations
105 of multiplication using between 100 and 200 full-sib ears for each landrace. Passport data including information
106 about the area of collection (continent, country and district) and geographical coordinates (latitude and longitude)
107 are available for each landrace although geographic coordinates are lacking for 36 of these 194 landraces (S1
108 Table).

109 To address questions about the origin of these landraces and to compare landraces from SWF with original
110 American material, we used a worldwide reference panel consisting of 64 European and 73 American maize
111 landraces (S2 Table) previously analysed using SSR markers by Camus-Kulandaivelu *et al.* (10). These authors
112 identified 7 genetic groups for these maize landraces that they termed the Andean (AND, $n=12$), Caribbean (CAR,
113 $n=26$), Mexican (MEX, $n=21$), Northern Flint (NF, $n=39$), Corn Belt Dent (CBD, $n=17$), Italian (ITA, $n=16$) and
114 Pyrenees-Galicia ($n=26$) groups. The Pyrenees-Galicia group consists of landraces from the Pyrenees (Spain and
115 France), from Northern Spain and from Portugal. Thus, in this study, we excluded the 22 landraces from the SWF
116 included in those 7 groups evidenced by Camus-Kulandaivelu *et al.* (10) to avoid duplicating the SWF landraces
117 ; so we gathered the remaining landraces from the Pyrenees-Galicia genetic group, such as landraces from Portugal
118 and Spain in a geographical landrace group named Pyrenees_Galicia_2 landrace group. To complement this
119 reference set, we added 2 landraces from Portugal and 9 landraces from South America previously analysed by
120 Mir *et al.* (11).

121

122 **DNA extraction and genotyping with 50K SNP array**

123 We assessed the nucleotide diversity of the 194 maize landraces collected in South-West France using the Maize
124 50K SNP array developed by Ganal *et al.* (20) and bulks of DNA representing each landrace. To this aim, DNA
125 was extracted from leaf disks collected on 15 individuals per landrace. To assess population diversity, we selected
126 the 30,068 Panzea markers (PZE-prefix SNPs) proven suitable for diversity analyses (20) and we predicted SNPs
127 allele frequencies using the method described in Arca *et al.* (21) briefly presented below. The approach consists
128 in a two-steps analysis of the relative fluorescence ratio for each allele. The first step consists in determining for
129 each SNP, whether a landrace is fixed for the A (or for the B) allele, by comparison with the distribution of ratio
130 of A vs. B fluorescence within a set of 327 inbred lines. If the SNP is declared polymorphic within the landrace,
131 the second step consists in estimating the allelic frequencies at this locus using a calibrated average curve
132 established from 1000 SNPs on polymorphic DNA pools controlled for their composition. Arca *et al.* (21) observed
133 that the mean absolute error (MAE) for allelic frequencies estimation at both steps was on average 7%. For the 82
134 American and the 66 European maize landraces used as a worldwide reference panel, we used the SNPs database
135 of Arca *et al.* (21) obtained using the same SNP array and following the same procedure. Combining these
136 different datasets, we finally obtained an allele frequency database for 23,412 SNP in which diversity was assessed
137 on 342 landraces.

138 **Diversity and genetic structure analysis of SWF landraces**

139 For each landrace, we estimated the allelic richness (A_r) and gene diversity (H_e , (25)) using a (26) script (S.
140 Nicolas, personal communication).

141 To assess the population genetic structure underlying our panel of SWF maize landraces, we used the software
142 ADMIXTURE v1.07 (27). This method assumes the existence of a predetermined number (K) of clusters and
143 estimates the fraction of ancestry of each accession in each of the K clusters (Q). It also infers SNP allele
144 frequencies of the ancestral landraces (P). The software requires individual genotypic data, while our SNP analysis
145 on DNA bulks provides allelic frequencies only. To obtain individual data, we thus simulated 5 haploid genotypes
146 per landrace. To limit linkage disequilibrium, this analysis was performed on a subset of 2500 SNPs chosen as
147 follows: first we divided the maize genetic map into 2500 non-overlapping windows; then, in each of these
148 windows, we randomly selected a single SNP. We explored K values ranging from K= 1 to K=13. The likely

149 number of genetic groups was estimated using the *DeltaK* parameter following method proposed by Evanno *et al.*
150 (28). Each landrace was assigned to a cluster when its fraction of ancestry in this cluster was higher or equal to
151 0.5. For $K > 2$, when ancestry fraction of a landrace in the different clusters was lower than 0.5, the landrace was
152 assigned to a composite group termed “mixed”.

153 **Relationship between landrace genetic structure, geographic and** 154 **climatic variables**

155 To describe the genetic structure of SWF landraces, we first looked for links between the genetic structure and the
156 geographic localization of the landraces. To this aim, we calculated pairwise genetic distances over the 194 maize
157 landraces using the modified Rogers’s distance (29, 30). On the corresponding genetic distance matrix, we
158 performed a principal coordinate analysis (PCoA) using R *ade4* package and estimated correlations between
159 landrace coordinates on the first axis of the PCoA and either (1) the longitude or (2) the latitude of their site of
160 collection. This analysis was based only on those 158 SWF landraces with available geographic coordinates. We
161 also looked for patterns of isolation by distance. To this aim, we performed a regression analysis between the
162 “genetic divergence matrix” which we estimated using the linearized $F_{ST} / (1 - F_{ST})$ values following Rousset (31),
163 and the pairwise geographic distance matrix calculated using latitude and longitude coordinates of the site of
164 collection of each landraces with spherical law of cosines formula (32). Pairwise F_{ST} values were calculated over
165 SWF landraces using the *Gst* estimate proposed by Nei (33). The statistical significance of the correlation between
166 these two matrices was evaluated using a Mantel test ((34), R *vegan* package).

167 We also explored relationships between the genetic structure and climatic variables. To this aim, we first retrieved
168 data for monthly precipitation and monthly minimum and maximum average temperatures from the
169 WORLDCLIM database (35). From these, we retained 12 variables: the mean monthly temperature and mean
170 monthly precipitation of the 6 months of maize cultivation in Europe, i.e., from May to October. We performed a
171 principal component analysis on these 12 variables with R *ade4* package. Doing this, we observed that the first
172 axis of this PCA explained 82.5% of the climatic variability observed for temperatures and precipitations covered
173 by our set of 158 SWF landraces. The climatic matrix distance between our 158 landraces was computed as the
174 Euclidian distance on this first PCA axis (*Ecodist* R package). Thereafter, we used the function *MRM* of the
175 *Ecodist* R package to perform a multiple regression of the genetic matrix on the geographical matrix and the

176 climatic matrix. We also compared through an ANOVA analysis, the climatic characteristics of the different
177 genetic groups identified using ADMIXTURE.

178 **Comparative analyses between SWF landraces and worldwide** 179 **maize genetic groups**

180 **Genetic diversity**

181 To compare allelic richness and gene diversity between well-known maize genetic groups and our set of SWF
182 landraces, we used results obtained using ADMIXTURE on our panel of 194 maize landraces for $K=2$ and
183 considered the seven genetic groups previously identified by Camus-Kulandaivelu *et al.* (10). Allelic richness and
184 genetic diversity (H_e) were estimated on each of these groups and, to compare allelic richness (A_r) among groups
185 of different sizes, we used the rarefaction method proposed by Petit *et al.* (36) with $n=1000$ resampling. To estimate
186 the expected heterozygosity (H_e) for each group we calculated the averaged values of allelic frequencies at the 23
187 K SNP over the landraces owing to each group. The H_e values were then averaged over SNPs. Pairwise
188 comparisons of A_r and H_e values between groups were carried out using Wilcoxon signed-rank tests across all the
189 23 K SNPs. Statistical analyses were computed using a R Core Team (26) script (S. Nicolas, personal
190 communication).

191 **Looking for footprints of hybridization between main maize genetic groups** 192 **in the origin of SWF landraces**

193 To determine whether SWF landraces originated from hybridizations between ancestral landrace groups of maize
194 s, we used the 3-populations test (37) implemented in the TreeMix software version 1.12 (38). This test compares
195 a focus population X to two reference populations Y and W , and calculates an f_3 statistic, $f_3(X; Y, W)$ defined as
196 the product of the difference in allele frequencies between population X and Y , and the difference in allele
197 frequencies between populations X and W . If the focal population X can be considered as resulting from an
198 admixture or hybridization event between population Y and W , the value of the f_3 -stat can be negative. A Z -score
199 value <-2 indicates significant mixture (37).

200 We also tested two scenarios for the origin of SWF landraces. In the first one, we made the hypothesis that SWF
201 landraces originated from hybridizations between landraces of Caribbean and Northern Flint (NF) groups as
202 proposed in previous articles. In the second scenario, we assumed that SWF landraces originated from
203 hybridizations between maize landraces belonging to unknown groups we thus wanted to identify. For example,
204 to determine whether SWF landraces originated from hybridization between landraces belonging from NF and
205 MEX groups, we performed TreeMix 3-population tests using the combination of three populations analysed
206 formed by a focal SWF landrace, with one NF and one MEX landraces as potential ancestors of the focal landraces.
207 To analyse these two scenarios of origin, we performed all combinations of three landraces formed by (1) a focal
208 SWF landrace (194 landraces) and two landraces from American groups; (2) a focal SWF landrace (194 landraces)
209 and two landraces from European groups; and (3) a focal SWF landrace (194 landraces) and one landrace from an
210 American group and one landrace from a European group. This resulted in 1,807,304 tests.

211 To analyse more broadly the genetic proximity between SWF landraces and worldwide maize genetic groups, we
212 also performed a principal component analysis (PCA) with ade4 R package using SNP data from 342 maize
213 landraces. To perform this analysis, we only used the 72 American landraces representing for the most part the 4
214 main historical maize genetic groups (i.e. MEX, AND, CAR and NF groups). The European maize landraces
215 (including the SWF landraces) were added as supplementary data. Due to their recent origins, the landraces of
216 CBD group (39) were also added as supplementary data. We used the modified Rogers' distance between each
217 SWF landrace and each American landrace in order to identify the closest American maize genetic group.

218 **Results**

219 Among the 23412 SNPs analysed, 378 exhibited missing data for at least one landrace; they were consequently
220 discarded from analyses leaving 23034 SNPs. Among them, 15 were monomorphic on all the landraces considered
221 in this study ($n=342$). At landrace level, the proportion of polymorphic loci varied from 13.5% for IPK60, a
222 German Northern Flint landrace, to 92.8% for EPZMV23, a landrace from Spain. On average, the proportion of
223 polymorphic loci within landrace was 68.7%.

224 **Genetic diversity and population structure**

225 The proportion of polymorphic SNPs in landraces from the South-West of France varied between 34% and 86%,
226 with an average value of 70%. Averaged over SNPs, the mean allelic richness (Ar) per landrace was 1.70, and
227 varied from 1.33 to 1.86. Mean gene diversity (H_e) was 0.22 per landrace (min = 0.12; max = 0.27, Fig 1, S1
228 Table).

229

230 **Fig 1. Genetic diversity analysis of SWF landraces.** Histogram of (a) allelic richness and (b) expected
231 heterozygosity values estimated for each of the 194 landraces.

232

233 Using the software ADMIXTURE on the whole set of SWF landraces, we identified a stratification in two major
234 groups (the maximal deltaK value occurred at $K=2$, S1 Fig). As shown on Fig 2, the two groups distinguished
235 landraces located in the Eastern part of the South-West of France from those located in the Western part. The first
236 group which was named 'East South-West France' (S-SWF) included 65 landraces. Most of these landraces were
237 collected in the Eastern districts such as Ariège, Tarn and Haute-Garonne; but ten of them were collected in
238 Western districts of SWF (i.e., from districts such as Pyrénées Atlantiques, Hautes-Pyrénées, Landes and Gironde).
239 The second group referred to hereafter as 'West South-West France' (W-SWF) included 126 landraces mostly
240 originating from the Hautes-Pyrénées, Pyrénées-Atlantiques and Landes districts. Twenty-three landraces from
241 this group were nevertheless collected in the Eastern part of the area. Interestingly, most of the landraces collected
242 in the Haute-Garonne and Ariège districts exhibited patterns of admixture between W-SWF and E-SWF groups.

243 At K=3, we observed a third group mostly composed of the 10 landraces that were assigned to E-SWF group at
244 K=2 but located in the western part of the region (S2 Fig).

245

246 **Fig 2. Geographical representation of the 158 maize landraces from the South-West of France (36**
247 **landraces having no geographical coordinates were not plotted).** The districts of collection sites are
248 represented with administrative numbers. Landraces for which pie-diagram had both blue and cyan colors
249 exhibited mixed genetic origins between E-SWF and W-SWF groups.

250

251 PCoA on allele frequencies revealed the same pattern of population structure. The first axis (representing 13% of
252 the total inertia) separated landraces located in the Western part (W-SWF cyan colour in Fig 3a) from those located
253 in the Eastern part (E-SWF dark blue colour in Fig 3a). The second PCoA axis of Fig 3a (representing 6.3% of
254 total inertia) highlighted variation among E-SWF landraces. Six landraces, assigned to the third group identified
255 with ADMIXTURE at K=3 (S2 Fig) were indeed strongly differentiated from the majority of E-SWF landraces on
256 the PCoA plan 1-2.

257

258 **Fig 3. Spatial genetic structuration analysis of SWF landraces.** (a) Principal coordinate analysis on SNP data
259 using Rogers 'genetic distance matrix estimated among the 194 landraces. (b) Longitudinal and (c) latitudinal
260 gradient analyses on SNP data of 158 landraces from South-West France using coordinates values on the first axis
261 of PCoA analysis. SWF landraces were colored according to their assignation to E-SWF and W-SWF groups
262 identified with admixture analysis at K=2. (d) Isolation by distance (IBD) analysis of 158 landraces from South-
263 West France using $F_{ST} / (1 - F_{ST})$ matrix for genetic differentiation estimated following Rousset (1997) and
264 geographical distance matrix estimated for each pair of landraces. R= coefficient of correlation. ***= p-
265 value<0.001.

266

267 We analysed the genetic diversity of each of these two groups. The allelic richness of W-SWF was significantly
268 higher than that of E-SWF: $A_r=1.718$ and $A_r= 1.679$ respectively (Wilcoxon's signed-rank test, $p\text{-value} < 10^{-15}$;

269 Table 1). On the other hand, the E-SWF group exhibited a higher level of gene diversity compared to the W-SWF
 270 group: $H_e=0.290$ and $H_e=0.273$ respectively (p -value $< 10^{-15}$ using Wilcoxon's signed-rank test). This discrepancy
 271 between A_r and H_e indicates that allelic frequencies are more balanced in E-SWF than in W-SWF. The W-SWF/E-
 272 SWF differentiation explained a low but significant proportion of the overall genetic diversity: $F_{ST}=0.026$ (p -
 273 value $< 10^{-15}$ based on permutation test over landraces). The mean F_{ST} between pairs of landraces was 0.104 and
 274 0.168 for the W-SWF and E-SWF groups, respectively. This shows that the E-SWF landraces are, on average,
 275 more differentiated from each other than the W-SWF landraces.

276

277 **Table 1. Allelic richness (A_r) and gene diversity (or expected heterozygosity, H_e) for the two SWF groups**
 278 **identified with admixture at $K=2$ and the 7 genetic groups previously identified in Camus-Kulandaivelu *et***
 279 ***al.* (10).**

Group.Name	Population Size	Allelic richness (A_r)	Expected heterozygosity (H_e)
Andean	12	1.75	0.31
Caribbean	25	1.72	0.32
Corn Belt Dent	15	1.75	0.33
Pyrenees_Galicia_2	9	1.76	0.30
Italian flint	17	1.66	0.29
Mexican	22	1.71	0.33
Northern flint	37	1.52	0.27
W-SWF	129	1.72	0.27
E-SWF	65	1.68	0.29

280 A_r values were calculated using rarefaction method as in (36), with 1000 resampling of 9 landraces without
 281 replacement in each group; except for Andes group for which we obtained only 220 possible resampling of 9

282 landraces. We used a Wilcoxon signed-rank test to analyze statistical differences between peers of H_e (or pair of
283 A_r) values estimated for the 9 groups. All comparisons for pair of H_e (and pair of A_r) were significant (p -value<
284 0.009); except for comparison between H_e of ITA and SWEF groups (p -value= 0.45) and comparison between
285 A_r of Andean and Corn Belt Dent groups. E-SWF= East South-West France; W-SWF= West South-West France.

286

287 **Relationships between geographic distribution, climate variables** 288 **and population structure**

289 To determine the main factors underlying the genetic structure observed in SWF landraces, we looked for a
290 relationship between genetic variation and either the geographical origin of the landraces or the climatic
291 characteristics of their site of origin. To this aim, we first looked for associations between (i) landrace coordinates
292 on the first axis of the PCoA (Fig 3a) performed on the SNPs and (ii) either latitude or longitude coordinates of
293 their prospection sites. As shown on Figs 3b and c, linear regression analyses evidenced significant correlations
294 with both longitudinal ($r=0.72$; p -value < 10^{-15}) and latitudinal coordinates ($r=0.5$; p -value = 10^{-10}), highlighting
295 the existence of both longitudinal and latitudinal genetic gradients. We also identified a significant correlation
296 between the pairwise $F_{ST} / (1 - F_{ST})$ ratio and pairwise geographic distances ($r=0.38$, p -value < 10^{-15} , Fig 3d). This
297 result clearly marks a pattern of isolation by distance.

298 Examining climate characteristics from May to October in the collection sites of our set of SWF landraces, we
299 observed that landraces belonging to the E-SWF group were from sites associated with higher temperature and
300 weaker precipitation than W-SWF landraces (S3 Table). Differences in monthly temperatures and precipitations
301 between E-SWF and W-SWF landraces were low, but significant variations were observed from June to August
302 for temperature and during September and October for precipitations (see S3 Table, in bold). To explore how much
303 genetic differentiation between SWF landraces could be explained by geographic distance instead of climatic
304 distance, we performed a multiple linear regression of both geographic and climatic data matrices with the genetic
305 data matrix. Results showed a significant relationship only for the geographic matrix (p -value=0.01 for
306 geographical values VS p -value= 0.67 for climatic values), which suggests that the demographic history (instead
307 of selection) of these populations is the main factor driving population differentiation.

308 **Genetic diversity of SWF landraces compared to the main maize**

309 **genetic groups**

310 As shown in Table1, the two genetic groups identified in the South-West of France using ADMIXTURE exhibited
311 larger allelic richness (A_r) and gene diversity (H_e) than the Northern Flint group, but lower allelic richness and
312 gene diversity than the Corn Belt Dent (CBD), Andean (AND) and Caribbean (CAR) groups. H_e values were
313 higher for MEX than for E-SWF and W-SWF groups, whereas the A_r of MEX was higher than the A_r of E-SWF
314 group and lower than that of W-SWF group.

315 **Do SWF landraces originate from hybridization between known maize**

316 **genetic groups?**

317 We used treeMix 3-population test to determine whether SWF landraces result from hybridization events between
318 historical maize genetic groups. Two different scenarios of hybridization were considered. The first scenario
319 assumes that SWF landraces originated from hybridization events between Caribbean and Northern Flint
320 landraces. We distinguished Northern Flint landraces from North America (NFA) from those from Northern
321 Europe (NFE) and we analysed two hypotheses: SWF landraces originate from (1) an hybridization between
322 Caribbean landraces and Northern Flint landraces previously introduced in Europe (NFE), or (2) an hybridization
323 between Caribbean landraces and American Northern Flint landraces (NFA) independently introduced in the
324 South-West of France. To do this, we performed TreeMix 3-populations tests on all combinations of a focal SWF
325 landrace with each of the Caribbean landraces included in our analysis and each of the NF landraces representing
326 either the Northern America (NFA) or Northern Europe (NFE) groups (resulting in 43640 tests for the CAR x
327 NFA scenario and 126100 tests for the CAR x NFE scenario; Figs 4a and b, S4 Table). Negative f_3 -stat values,
328 suggestive of a hybridization event between CAR and NFE, were detected for triplets involving five landraces
329 from the E-SWF group and three landraces from the W-SWF group (922 triplets). The f_3 -stat values suggestive of
330 a hybridization event between CAR and NFA landraces were observed for the same set of SWF landraces (284
331 triplets). This test was thus unable to determine the implication of NFE versus NFA in hybridization events. When
332 looking for Z -score < -2 (S4 Table), four landraces of the E-SWF group and PPS1236 of the W-SWF group had
333 significant triplets with both NFA and NFE landraces; while PPS363 of the W-SWF group had significant triplets
334 with only NFE landraces. These results suggest that only 6 SWF landraces can be considered as originating from

335 hybridization events between landraces from NF (either Northern America or those introduced in Europe) and
336 CAR groups. The relevant CAR landraces in these analyses were located in various geographic regions: Caribbean
337 Islands (13 landraces), Northern South America (1 landrace from Venezuela), Costa Rica (1 landrace) and
338 Southern Spain (3 landraces).

339

340 **Fig 4. Histogram of f_3 -stat values estimated by TreeMix three-population test.** Each f_3 -stat corresponds to
341 triplet for a focal SWF landrace with two landraces from two different genetic groups such as Caribbean (CAR),
342 Northern flint (NF), Mexican (MEX), Andean (AND), Italian (ITA), Corn Belt Dent (CBD) and
343 Pyrenees_Galicia_2 groups. (a) Histogram for combinations of SWF landraces with CAR and American Northern
344 flint (NFA) landraces. (b) Histogram for combinations of SWF landraces with CAR and European Northern flint
345 (NFE) landraces. (c) Histogram for other combinations. Red color indicated negative values for triplets of
346 landraces, showing that some SWF landraces could have originated from mixture events of landraces from other
347 genetic groups.

348

349 In a second step, we used three-mix tests to test whether SWF landraces originated from hybridizations between
350 any of the historical genetic groups. This led us to analyse 1329094 different triplets. Over those, only 204
351 exhibited both negative values for the f_3 -stat parameter and Z -score < -2 (Fig 4c, S4 Table). Interestingly, all these
352 triplets included one NF landrace as one of the ancestor of the SWF landraces (S4 Table), the second ancestral
353 landrace belonging either to the MEX, AND or ITA groups. For SWF landraces, we detected such a hybridization
354 footprint for only 4 landraces. These 4 landraces from the South-West of France were also implied in the triplets
355 showing signal of hybridization events between CAR and NF landraces (S4 Table). We also observed 4 other SWF
356 landraces that showed signals for hybridization events between landraces from at least two genetic groups. It
357 concerned (1) 2 landraces of E-SWF showing signals for hybridization events between landraces from only NF
358 and AND groups (PPS1248 and PPS1249); (2) one landrace of W-SWF showing signals for hybridization events
359 between landraces only from NF and MEX groups; and (3) 1 landrace of W-SWF (PPS616) showed signals for
360 hybridization events between landraces of NF and landraces from either MEX or ITA groups (S4 Table). All these
361 results suggested that few landraces from the SWF (1) originated from hybridization events between landraces
362 from NF and either CAR or MEX or AND maize genetic groups, (2) the NF germplasm played important role in

363 the evolution of these SWF landraces and (3) maize landraces of ITA group showed genetic similarity with some
364 SWF landraces.

365 We did not observe signals for hybridization events including CBD landraces as one of the ancestors of the SWF
366 landraces, suggesting either that these were not influenced by CBD landraces after their introduction in Europe, or
367 that we could not evidence it with the TreeMix 3-population test.

368

369 **Genetic proximity between SWF landraces and maize from Europe and** 370 **America**

371 As we detected only few clear evidences of hybridization events in SWF landrace origins using a TreeMix 3-
372 population test, we performed a PCA on SNPs for the whole set of 342 maize landraces (Fig 5, S2 Table). Fig 5
373 shows the position of the different groups on the first and second axes of the PCA. The first axis (19.7% inertia)
374 mainly separated Northern Flint landraces from Tropical landraces (AND, CAR, MEX) while the second axis
375 (6.4% inertia) mainly separated South American from Caribbean landraces. As expected, we observed that most
376 European NF landraces were close to American NF landraces, and that landraces from Southern Spain were close
377 to those from the Caribbean Islands. The two SWF groups occupied a central position on the first PCA plan (Fig
378 5) but somewhat separated on the two first axes. Landraces of the E-SWF group were more dispersed compared
379 to W-SWF landraces that appeared more grouped. On the first axis, E-SWF landraces appeared closer to the NF
380 group than did W-SWF landraces. On the contrary, W-SWF landraces were closer to tropical landraces (AND,
381 CAR and MEX) than to NF landraces (Fig 5). Looking for relationships between landraces from Europe, we found
382 that landraces from the SWF were closer to Pyrenees_Galicia_2 and European Northern Flint landraces (NFE)
383 than to Italian flint landraces.

384

385 **Fig 5. PCA analysis on SNP data of 72 American maize landraces with 260 maize landraces from Europe**
386 **and those of CBD as supplementary data.** Labels indicate landrace country of origins (see Table_S2). South-
387 West France landraces were colored according to their admixture result at K=2 allowing to distinguish East (in
388 blue) and West South-West France (in cyan) genetic groups. The remaining American and European landraces
389 were colored according to their genetic groups previously identified by Camus-Kulandaivelu et al. (2006) : Corn

390 Belt Dent in red, Caribbean in green, Northern flint in yellow, Mexican in brown, Italian Flint in orange, Andean
391 in magenta, Pyrenees_Galicia_2 in grey. The 9 landraces from South America and 2 landraces from Portugal
392 studied by Mir et al (2017) were colored in black.

393

394 As a second way to identify genetic proximity between landraces, we used a heatmap representation with R gg2plot
395 function to visualize the result of genetic distance estimation between SWF landraces and the 82 American
396 landraces (S3 Fig). The heatmap representation of genetic distances showed that the 194 landraces from SWF were
397 closer to 4 Chilean (PPS949 from AND, PPS941 from CBD, PPS961 from NF and PPS938 from MEX groups), 2
398 CBD (PI214189 and PI280061) and 2 NF (PI213793 and PI401755) landraces from North of America than
399 landraces from others American countries. These results suggested an introduction of Northern Flint and CBD
400 landraces from Northern America into the SWF genepool, as well as exchanges of maize landraces between Chile
401 and SWF. Comparing the genetic distances of the two SWF groups with the American accessions, we did not
402 evidence any clear difference between the genetic origins of the two groups from the South-West of France, except
403 that E-SWF landraces appeared to be close to landraces from the NF group and that W-SWF landraces were closer
404 to Tropical landraces (S3 Fig).

405

406 **Discussion**

407 **Validity and limitations of bulk DNA analysis with the 50 K SNP** 408 **array**

409 The usefulness of the bulk DNA approach in genetic diversity investigations has been proven in numerous studies
410 (8, 14, 17, 18, 21, 40). The major constraint observed for the use of this pooled DNA analysis is the loss of
411 information about genetic variation at the individual level (8, 15). As a result, genetic parameters such as
412 individual's heterozygosity and Wright's F_{IS} fixation indices (30, 33) cannot be estimated directly. Bulk analysis
413 also limits the use of classic genetics tools that require individual information such as the softwares ADMIXTURE
414 (27), GENEPOP (41), HZAR (42) and STRUCTURE (43). As a result, we chose to estimate genetic parameters
415 and to use software tools that do not require individual genotype information to characterize and analyse these
416 landraces, except for the use of the ADMIXTURE software for which we simulated genetic haplotypes (27).

417 Despite these constraints, the genetic proximities we revealed between American and European landraces using
418 the 50K SNPs on DNA bulks were in accordance with what is known about the main paths of maize introductions
419 in Europe. Indeed, our PCA analysis allowed distinguishing the main historical maize genetic groups previously
420 identified by Camus-Kulandaivelu *et al.* (10). For instance, the genetic similarity between maize landraces from
421 the South of Spain and Caribbean landraces corroborates the introduction of maize by Columbus from the
422 Caribbean Islands to Spain (4-6). We also detected strong genetic proximity between Northern Flint and landraces
423 from the North of Europe, in accordance with the introduction of maize landraces from Northern America to
424 Northern Europe as suggested by an illustration of Leonard Fuchs, a German herbalist, in 1542 (4, 7).

425 **Diversity and genetic structure of maize landraces from the SWF**

426 Using a genetic database of 23412 SNP markers to analyse the genetic diversity of maize landraces that were
427 collected in the South-West of France circa 50 years ago, we were able to identify two main groups of landraces,
428 one located in the Eastern side and one in the Western side of the South-West of France. However, although these
429 two groups were identified through different analyses (ADMIXTURE, PCoA), the genetic differentiation between
430 them was relatively low ($F_{ST} = 0.03$) and indicated that each group contains an important genetic variability.

431 The geographical repartition of the two groups and their low divergence led us to propose two hypotheses for the
432 origin and evolution of maize landraces in the South-West of France. The first hypothesis was that these landraces
433 originated from the same ancestral group of landraces and were then differentiated into 2 groups under the effect
434 of genetic drift and reduced gene flow. This hypothesis was supported by the results obtained in our analysis of
435 the pairwise genetic distance matrix between landraces, which revealed patterns of isolation by distance (IBD).
436 We highlighted such a longitudinal gradient along SWF using a multivariate technique (PCoA) based on a genetic
437 distance matrix with SNP data from 158 landraces, which led to a significant correlation coefficient between the
438 first PCoA axis and the longitudinal coordinates of their prospection sites. Multivariate approaches have been used
439 in many studies to analyze environmental or genetic gradients in landraces analysis (44-46). For their study of
440 human genetic variation, Menozzi *et al.* (45) presented a synthetic map with the use of principal components (PCA)
441 to condense information from many alleles and concluded that genetic gradients were suggestive of historical
442 migrations across continents. However, Novembre and Stephens (46) found that PCA correlating with
443 geographical did not necessarily reflect specific migration events but may instead have simply reflected isolation
444 by distance.

445 The second hypothesis was that each of the identified genetic groups originated from a distinct ancestral group of
446 maize landraces that were introduced in SWF. This second hypothesis was however invalidated by the low level
447 of differentiation observed between the two groups. Our results therefore support the conclusions of a previous
448 analysis on some of these populations using SSR data suggesting that SWF landraces originated from a single
449 genetic group of maize closest to the ancestors of the Pyrenees-Galicia group ($F_{ST} = 0.03$ between the
450 Pyrenees_Galicia_2 group and each of the groups from the South-West of France) (4, 7, 8, 10).

451 The geographical distribution of maize landraces in SWF could also be the result of a diversifying selection. The
452 occurrence of a genetical longitudinal gradient along the Pyrenees area as observed in this study has been reported
453 for several species (47-50). Gradients, such as altitude or longitude, play an important role in the Pyrenees, as they
454 shape the existing proportion of suitable habitats along the mountains (48, 49). Valbuena-Ureña *et al.* (50)
455 emphasized that longitude is an important gradient to take into account in the Pyrenees, because the influence of
456 the Atlantic ocean provides cooler and wetter climate westwards than in Eastern areas, which are more influenced
457 by the Mediterranean climate.

458 We found differences for temperature and precipitation between Eastern and Western parts of the SWF, but
459 regression analysis showed that climatic variations did not explain genetic variability observed between SWF

460 landraces, when considering geographical covariates. Since climate variation are geographically structured with
461 longitude and latitude, we still cannot exclude completely the involvement of climatic variation in the
462 differentiation of SWF landraces into two genetic groups; our results rather suggest that demography (restriction
463 of gene flow and genetic drift) is the main driver of population differentiation between maize landraces in this
464 region. This is supported by the longitudinal and latitudinal gradients that we observed on the first axis of PCA,
465 which is determined by a large number of SNPs. However, the genetic differences observed for SWF landraces
466 could be also explained by impact of farmer's practices. The management of seeds and farmer's exchanges in
467 different valleys limited by hilly mountains probably contributed to differentiate SWF landraces in different
468 districts. Already, the ethnobotanical survey realized in 2012-2013 with farmers in the Pyrenean area did not reveal
469 major differences in farmer's practices between the East and West parts of the Pyrenees (51).

470 **The use of genome wide analysis to infer the origin of SWF**

471 **landraces**

472 **The role of hybridization**

473 Building on previous works, our first assumption was that SWF landraces originated from a hybridization between
474 maize landraces belonging to Caribbean and Northern Flint genetic groups and that the hybridization occurred
475 earlier in Spain before introduction of maize in the South-West of France. Several studies on genetic diversity of
476 European and American maize landraces (Dubreuil et al., 2006; Rebourg et al., 2003; Revilla Temiño et al., 2003)
477 highlighted a Pyrenees-Galicia flint group made up of European landraces including a small sample of landraces
478 from the South-West of France and landraces from the North of Spain. This original landrace group was
479 hypothesized to originate from hybridizations between landraces of Caribbean and Northern flint groups; however
480 less than 30 landraces from Pyrenees-Galicia were used in these previous studies. In our study, using a much larger
481 data set of 194 maize landraces from the SWF, the origin for SWF landraces was more precisely analysed. Our
482 PCA analysis showed genetic proximity between landraces from the Western part of the South-West of France
483 and some maize landraces from Spain and Portugal, supporting genetic relationship mentioned between landraces
484 from Pyrenees and Galicia in previous studies of maize landraces named as Pyrenees-Galicia flint group (Camus-
485 Kulandaivelu et al., 2006; Dubreuil et al., 2006; Gauthier et al., 2002). Based on historical documents, the
486 introduction of maize in the South-West of France was reported by Renoux (22) as originating from Spain. In her

487 study, Vouette (52) reported the name of maize in the Pyrenees valleys as "wheat from Spain", as given by
488 Bonnafous (1836). Similarly, the first mention of maize in the mercuriales of Verfeuil (near Toulouse) in 1637
489 indicates the name of "millet of Spain" (53). The vernacular names do not allow finding the genetic origin of the
490 maize landraces, but gave indications of where the maize landraces came from before their introduction in a given
491 country. The introduction of SWF maize from Spain in the 17th century is also justified by the coasting trade
492 practiced by fisherman from fishing ports of Atlantic coast of France and Spain (Mauro, 1968). In his work on
493 relations between Spain and the South of France in the 17th century, Mauro (54) cited the route of maize that left
494 from the West part to progress towards the East part of South-West of France. The progression of maize from West
495 to East is consistent with the greater genetic allelic richness observed in the W-SWF group than in the E-SWF
496 group. The lower allelic richness of E-SWF compared to the former group can also be explained by their proximity
497 to NF which is the less diverse genetic group as observed in our allelic richness and gene diversity analysis and as
498 found by Gauthier *et al.* (9) and Dubreuil *et al.* (7).

499

500 **The influence of Northern Flint landraces**

501 NF landraces played an important role in the evolution of SWF maize landraces and more generally in the
502 adaptation of maize in Europe (4, 6) and in the development of CBD germplasm (55). Our TreeMix 3-population
503 analysis allowed us to confirm Northern flint landraces influence in the evolution of SWF landraces. For all
504 admixture events highlighted in this analysis, SWF landraces displayed a mixed origin between NF landraces with
505 either CAR, AND, MEX or ITA landrace groups. There are two possible ways to explain the presence of NF marks
506 in the genome of SWF landraces: either directly from a secondary introduction from North America (NFA), or
507 introduced from the North of Europe (NFE) as reviewed by Tenailon and Charcosset (2011). Revilla *et al.* (1998)
508 supported the NFA hypothesis by suggesting that NF landraces could have been introduced into the North of Spain
509 at several times from the beginning of the 17th century. Later, Brandenburg *et al.* (2017) found that European flint
510 inbred lines, i.e. first-cycle inbred lines directly derived from landraces after few generations of selfing, were
511 issued from an admixture between inbred lines belonging to European Northern Flint landraces and those derived
512 from Southern Spain lines. Our TreeMix 3-population test was not able to distinguish the involvement of NFA
513 versus NFE in the origin of SWF landraces. This is probably due to the genetic similarity between NFA and NFE
514 ($F_{ST}=0.04$). However, our PCA analysis showed a closer genetic proximity between maize landraces from the

515 Eastern part of SWF and Northern flint landraces located in the North of Europe (NFE), supporting the scenario
516 involving some gene flow from European Northern flint landraces.

517 **The influence of maize landraces from the south of America**

518 We found genetic relationships between maize landraces from SWF and maize landraces from the South America.
519 Mir *et al.* (11) showed that maize landraces from SWF had a Northern South America origin, but our study does
520 not allow us to really assess this path of introduction, as only four maize landraces from the North of South America
521 were used in this studies: VEN405 from CAR, VEN736 from ITA, ANTI392 and PANA168 both from AND
522 groups. These landraces were also found to be probable ancestors for SWF landraces in TreeMix 3-population test
523 (Supp. Table 4); but our PCA analysis showed only evidence for genetic similarity between W-SWF landraces
524 and those from the Northern South-America. It is possible that our study did not capture very well genetic
525 relationships between SWF landraces and these expected Northern South-American parental landraces identified
526 by Mir *et al.* (11), because of a limited sample of maize landraces from South America. In consequence, we had
527 difficulty to evidence relationships between SWF landraces with Northern South America landraces. Note that
528 American landraces introduced in Europe evolved in America during about 500 years, which limits the ability of
529 TreeMix 3-population test to detect hybridization events between SWF and Northern South American landraces.

530 Our collection of landraces from SWF presented the lowest genetic differentiation with landraces from Chile
531 (except for CHZMO8050) compared to the remaining landraces from America. All these Chilean landraces have
532 been shown to originate from different genetic groups (10), with a probable replacement of traditional landraces
533 with relatively recent introduction of Northern US materials (3). Genetic relatedness between Chilean and SWF
534 landraces may be due to the introduction of SWF genepools into Chile or vice-versa. Interestingly, the Spanish
535 (especially Basques and Andalusians) and also other Europeans such as French people (mainly coming from SWF)
536 immigrated mainly to Chile in the second half of the 19th century, although Basque presence in Chile began in the
537 conquistador period. Also exchanges between the Basque country and the South West of France have taken place
538 in both directions and for a few centuries (https://en.wikipedia.org/wiki/Immigration_to_Chile, march 2020).

539 **The influence of CBD landraces**

540 Finally, our PCA analysis showed genetic proximity between 10 landraces from SWF and landraces belonging to
541 the Corn Belt Dent genetic group (CBD). CBD is a group of maize landraces identified in previous studies as

542 resulting from hybridizations between Northern Flint and U.S Southern Dent materials (39, 55). The presence of
543 CBD genomic traces in SWF can be explained by the recent introduction of American hybrid seeds in Europe,
544 since hybrids are CBD. Indeed, from 1948, with the Marshall plan, the first American hybrids were tested in France
545 (22). Then, from 1957 onwards, the first hybrids created by INRA were developed in France; they were double
546 hybrids with at least one American line. Farmers 'adoption of hybrids was fairly rapid (56). These 10 landraces,
547 showing a genetic proximity with CBD group on the PCA analysis, shaped a specific group with admixture
548 analysis at $k=3$. Introgression of CBD germplasm into local landraces has also been observed in Central Italy with
549 very variable effects (57).

550 **The different scenarios for SWF landrace origin**

551 More generally, it is thought that the South-West of France has been submitted to several introductions of maize
552 of various genetic origins, as already reported for Spanish maize landraces (6) and in Portugal (11, 58). Evidence
553 for subsequent admixture between the genetic groups involved in these introductions were observed in this study
554 with TreeMix 3-populations tests, PCA analyses and genetic distance analyses. In our TreeMix 3-population test,
555 we found only few landraces from the South-West of France that originated from hybridization events between
556 American and European landraces. Signals for hybridization events occurring in SWF landraces could probably
557 have been obscured by the combined effect of the high genetic diversity within landraces and the relatively low
558 F_{ST} between landrace genetic groups. The fact that SWF landraces were already hybridized before their
559 introduction in the South-West of France could have also influenced TreeMix analysis results, as we initially had
560 assumed that SWF landraces were similar to the landraces of the Pyrenees-Galicia group.

561 All these results above allowed us to describe at least two scenarios of origin that take into account the influence
562 of Northern Flint landraces from the North of Europe predominantly in the Eastern part and the genetic proximity
563 of W-SWF landraces with Tropical landraces. For the first scenario, we postulated that, after the introduction of
564 hybridized maize landraces from Spain (Caribbean x Northern Flint landraces), the NFE landraces spread from the
565 North to the Eastern part of SWF where they hybridized together. The arrival of NFE landraces could have been
566 followed by successive gene flows of maize landraces from Mexican and Andean groups introduced from America,
567 through the Atlantic harbours to the west part of SWF.

568 In the second scenario for the origin of SWF landraces, we hypothesized that the first maize landraces introduced
569 in the South-West of France displayed predominantly Northern Flint ancestries as do Galician landraces (11).

570 Thus, these landraces spread from the Western to the Eastern parts of the South-West of France. Thereafter,
571 Tropical landraces (from Mexican, Caribbean and Andean genetic groups) were introduced in the Western part of
572 SWF. Presence of genetic marks from Tropical landraces also occurred through seed exchanges between
573 Mediterranean trademen from Italy, France, Spain and Portugal at the end of the sixteenth century (11, 12). Revilla
574 Temiño *et al.* (5), Patto *et al.* (58), Brandenburg *et al.* (12) and Mir *et al.* (11) found that the South of Europe has
575 been submitted to maize landraces introductions from both the Caribbean islands and South America.

576 **Conclusion**

577 Assessing the population genetic structure and diversity of a collection of crop accessions is the best way to
578 develop an efficient management strategy and to improve breeding programs. Here we used DNA bulk analyses
579 with a 50K SNP array to investigate the diversity and population structure for a panel of 194 maize landraces
580 collected 30 to 60 years ago in the South-West of France. In this study, we assumed that the maize landraces from
581 the South-West of France originated mostly from hybridizations between landraces of Caribbean and Northern
582 flint groups. Introduced around 1626 through Atlantic harbours such as Bayonne, these SWF landraces have
583 probably been submitted posteriorly to gene flows from landraces belonging to various countries of America and
584 Europe, as expected by Revilla Temiño *et al.* (5) for maize landraces from Spain and Patto *et al.* (58) for those
585 from Portugal. A single mixture of NF and CAR landraces is not sufficient to explain the genetic origin of SWF
586 maize.

587 The differentiation between W-SWF and E-SWF ($F_{ST}=0.026$) observed among SWF landraces with admixture
588 analysis can result from demographic processes with influences of gene flow (isolation by distance) and genetic
589 drift. Adaptation processes related to farmer's practices could not be completely excluded. This would require a
590 study associating genetic studies and morphological characterization to ethnobotanical surveys with old farmers
591 who still remember maize cultivation in the 60s.

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737 **List of supplementary figures:**

738 **S1 Fig. Plot of DeltaK of the log likelihood from the admixture analysis on SWF landraces SNP data.**

739 Group numbers varied from K=1 to K=13.

740

741 **S2 Fig. Bar-plot for K=2 to K=5 for admixture analysis with the 194 SWF maize landraces.** At K=2, we

742 differentiated W-SWF (in cyan) and E-SWF (in blue) genetic groups. At K=3, 15 landraces (in dark-grey)

743 previously assigned to E-SWF group at K=2 constituted a group distinguished from E-SWF and W-SWF groups.

744 At K=4, we observed a fourth group consisting of about 10 landraces located principally in “Lot” and in “Lot et

745 Garonne” districts. At K=5, landraces from Gironde (in turquoise) differ from W-SWF groups ; Landraces from

746 “Lot” and “Lot et Garonne” districts were integrated again in E-SWF group and we observed differentiation

747 between landraces from the third group at K=3.

748

749 **S3 Fig. Heat-map of Rogers ‘genetic distance values between the 194 landraces from SWF and the 82**

750 **landraces from America.** American landraces were sorted by latitude of their collection sites and colored as per

751 their genetic groups previously identified by Camus-Kulandaivelu et al. (2006). We also sorted SWF landraces

752 using their ancestries values on W-SWF group obtained with admixture analysis at K=2 ; thus SWF landrace

753 numbers from 0 to 65 represent the E-SWF landrace group and SWF landrace numbers from 66 to 194 represent

754 W-SWF landrace group. Corn Belt Dent in red, Caribbean in green, Northern flint in yellow, Mexican in brown,

755 Italian Flint in orange, Andean in magenta and the 9 landraces from South America studied by Mir et al (2017)

756 in black.

757

758

759 [List of supplementary tables:](#)

760 **S1 Table. Combination of passport data (column 1 to 5), genetic diversity analysis (column 6 and 7) and**
761 **admixture analysis at K=2 (column 8 to 10) performing on SNP data of the 194 maize landraces from the**
762 **South-West of France.** W-SWF= "West South-West France»; E-SWF =" East South-West France".

763

764 **S2 Table. Passport information and PCA analysis result on SNP data of 342 maize landraces.**

765

766 **S3 Table. Climatic variations between E-SWF and W-SWF groups from May to October.** This table
767 contained mean of temperature and mean of precipitation for W-SWF and E-SWF groups from May to October.
768 We shaded in bold months for which differences for mean temperatures between the two groups were
769 significant (p -value<5%). Same thing was doing for precipitation.

770

771 **S4 Table. TreeMix 3-population test results.** This table represents a summary of TreeMix 3-population test
772 results performed using all combinations of three landraces shaped by one landrace from SWF considered as
773 tested population, and two other landraces (pop2 and pop3) considered as potential ancestors of the tested
774 landraces. We only represented the results of three landraces for which f_3 -stat values were negative with
775 $Zscore < -2$. E-SWF= East South-West France, W-SWF= West South-West France.

776

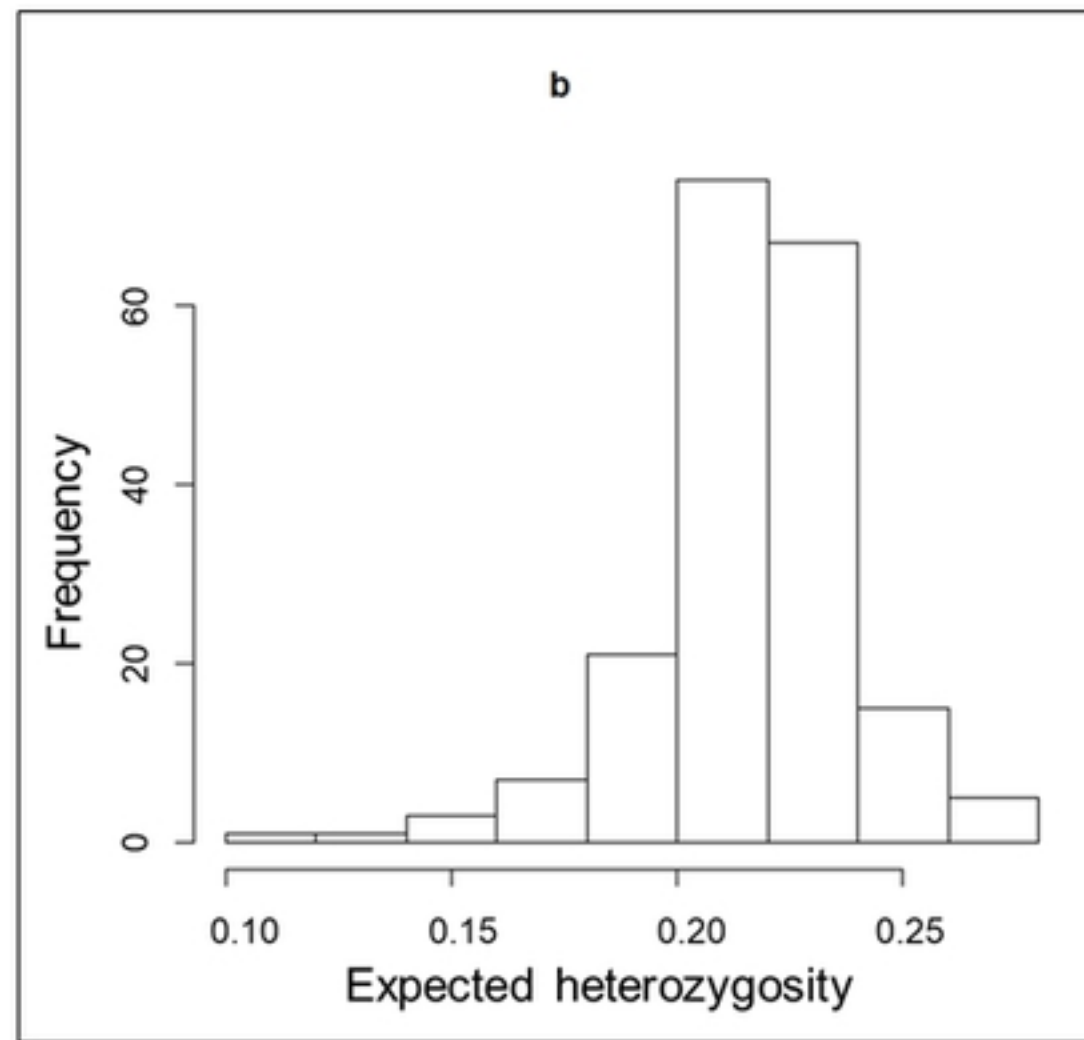
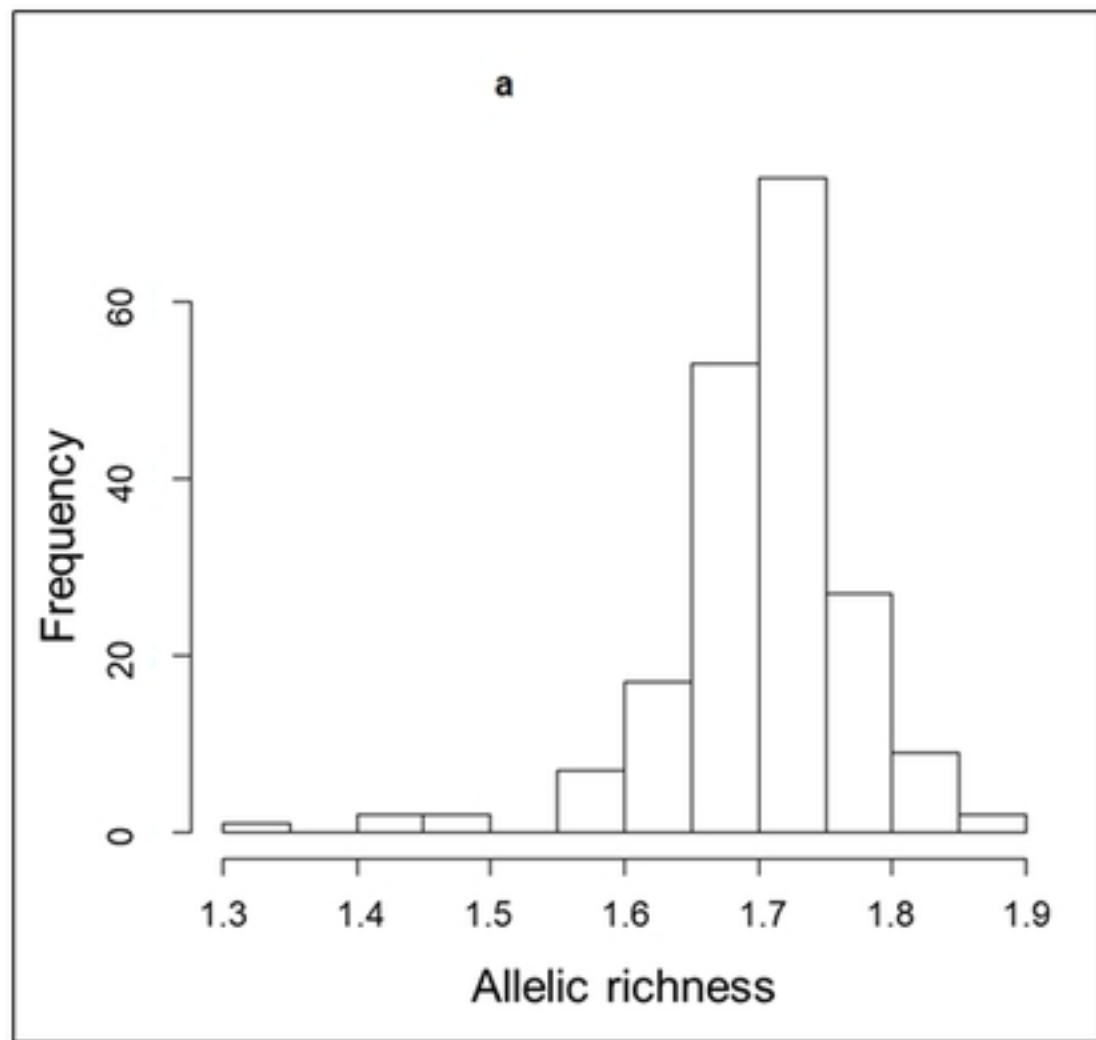


Fig1

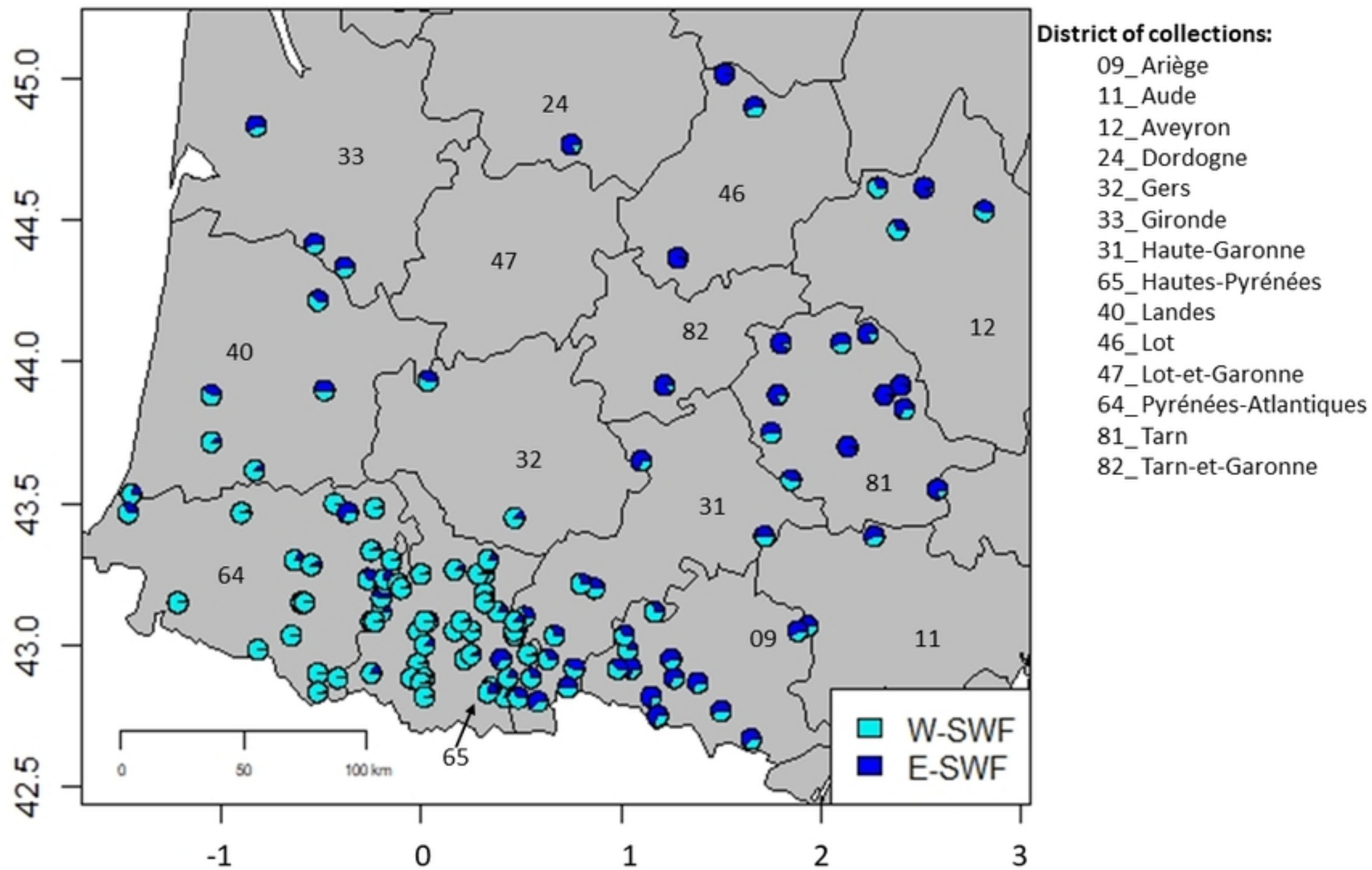
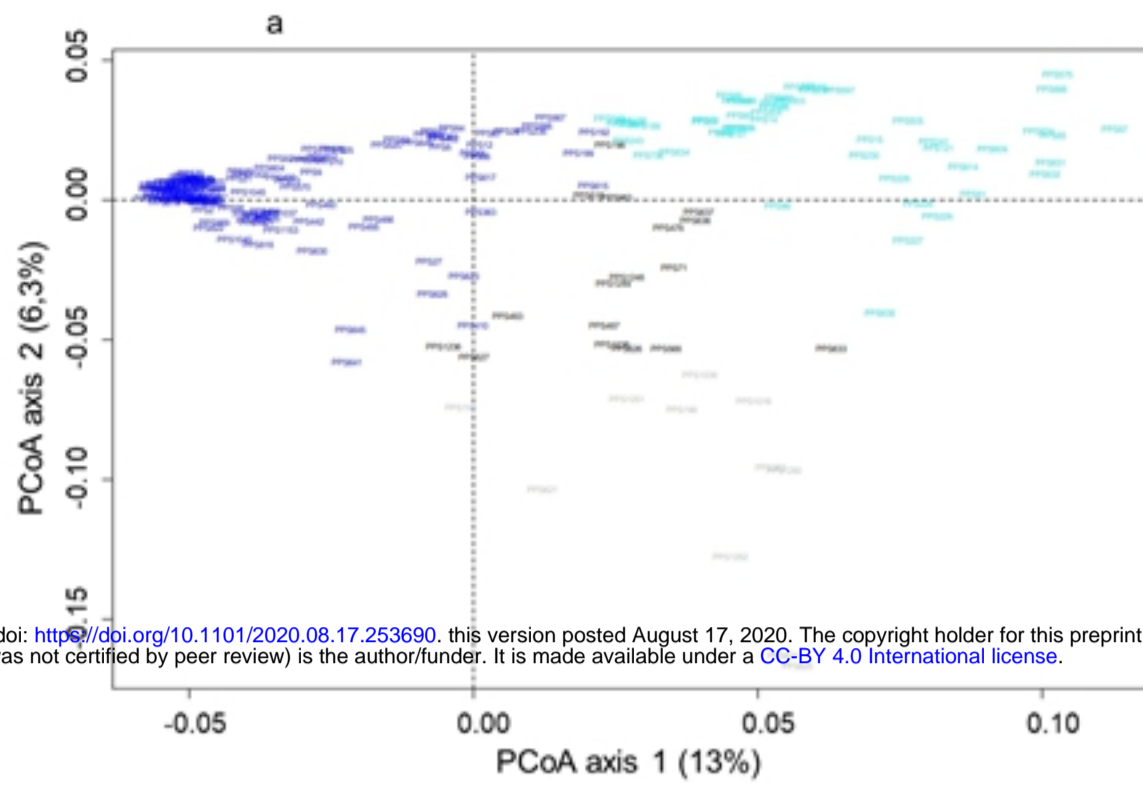


Fig2



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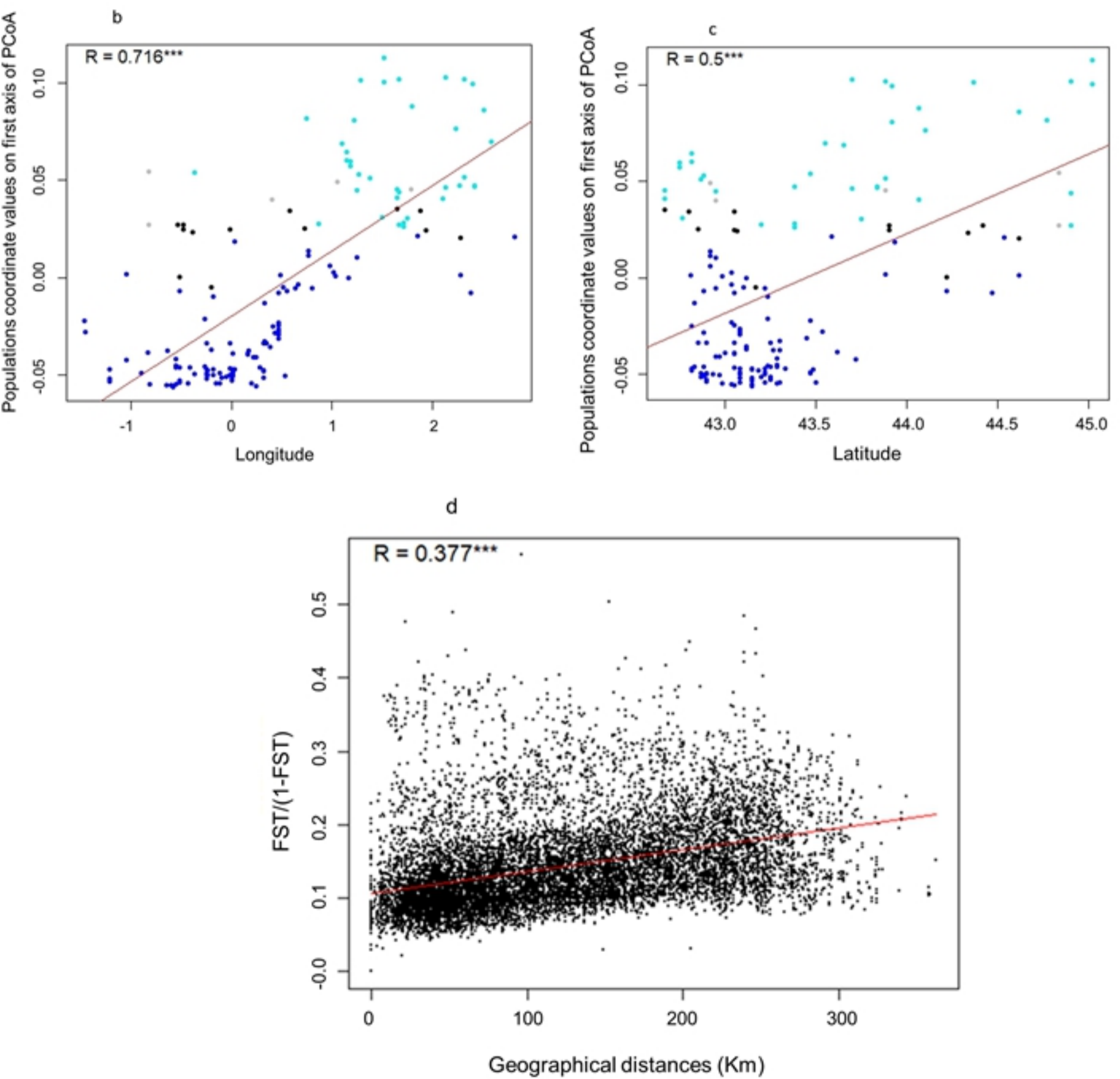


Fig3

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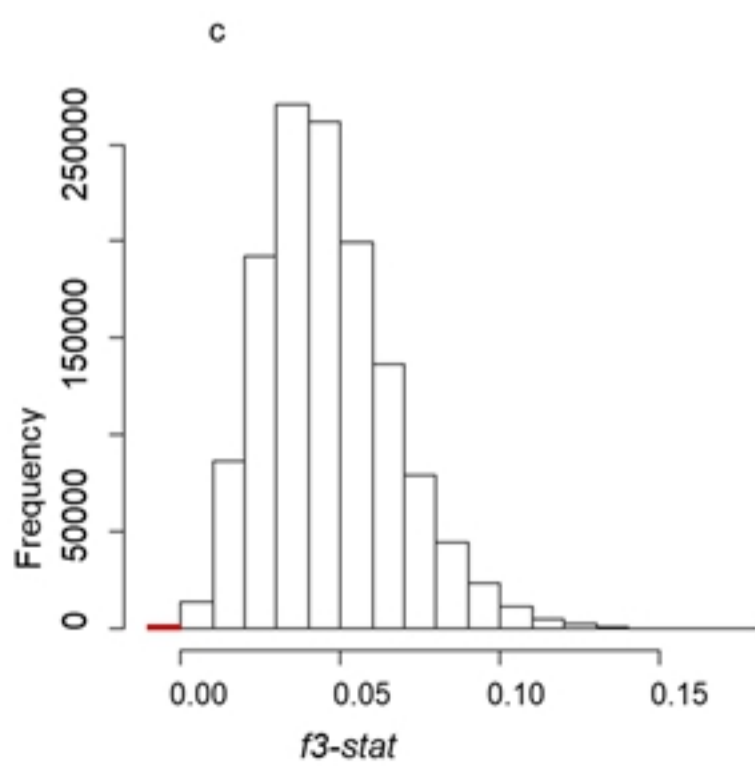
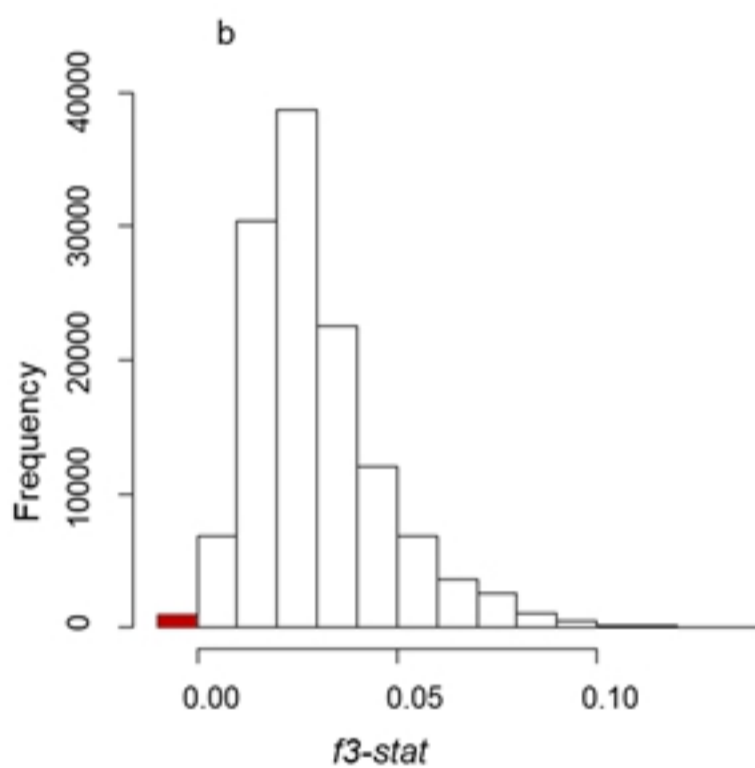
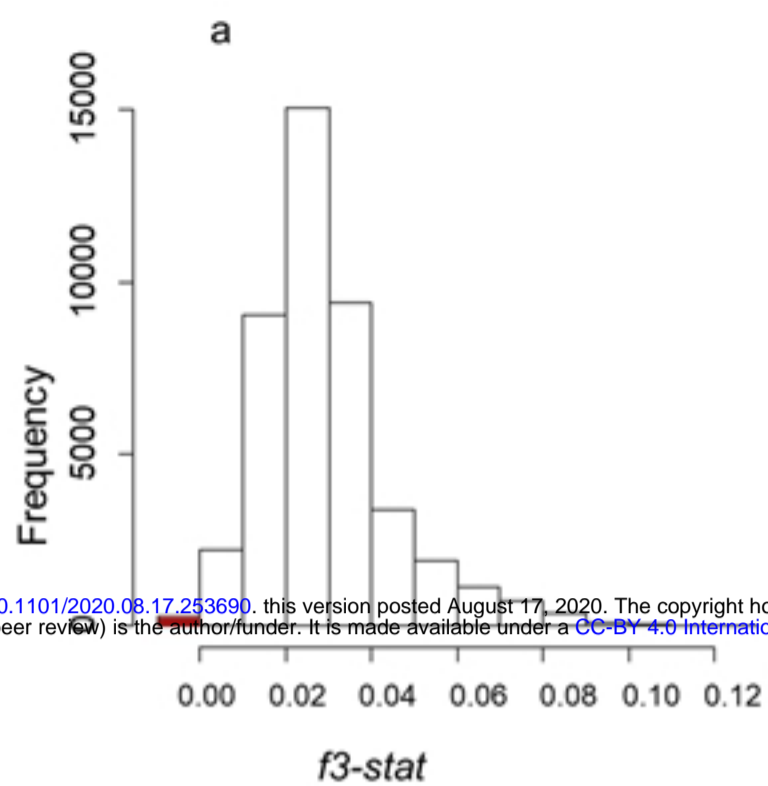


Fig4

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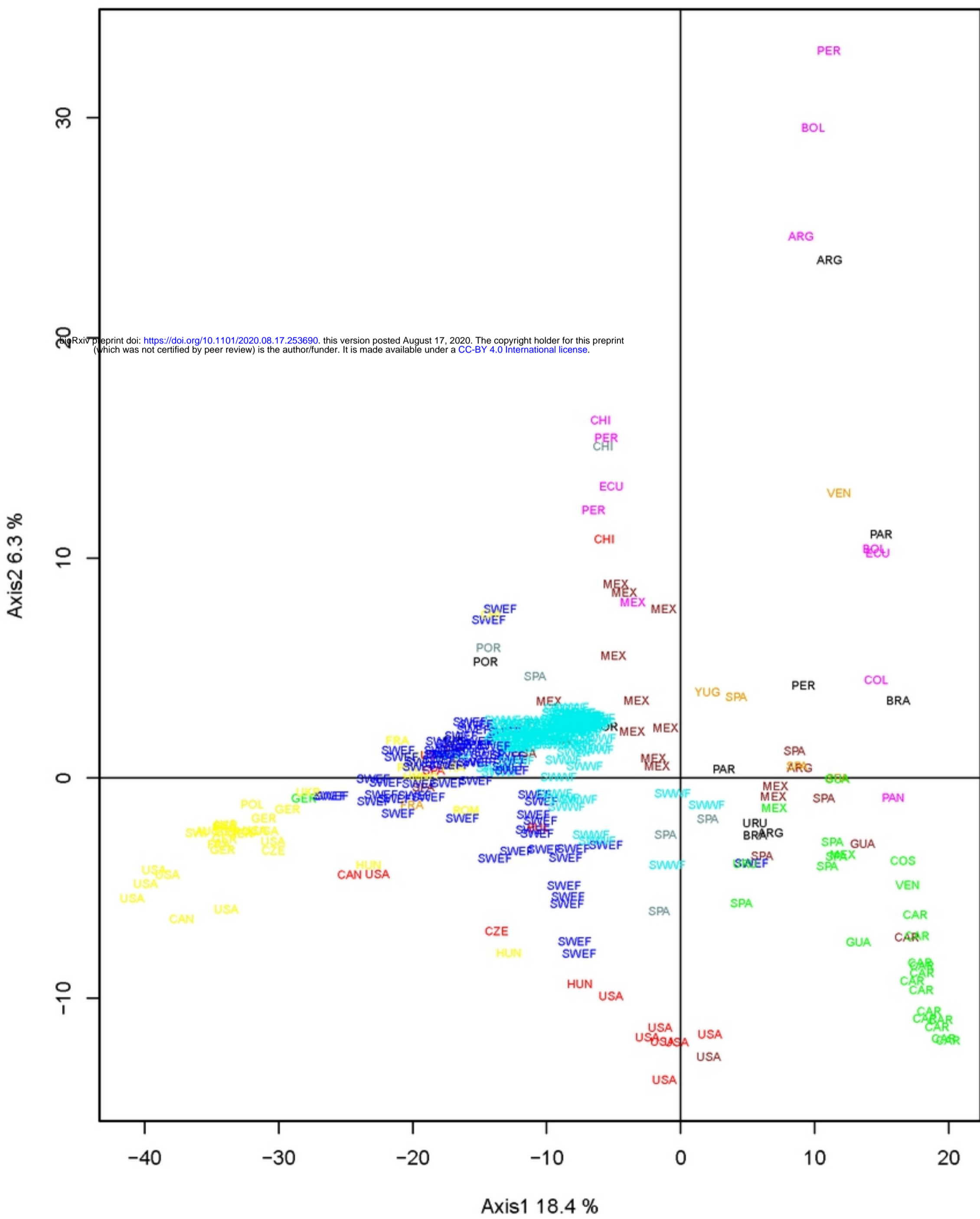


Fig5