

1 ***Genome-wide SNP genotyping of DNA pools identifies untapped***
2 ***landraces and genomic regions that could enrich the maize***
3 ***breeding pool***

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17 **ABSTRACT**

18 Maize landraces preserved in genebanks have a large genetic diversity that is still
19 poorly characterized and underexploited in modern breeding programs. Here, we genotyped
20 DNA pools from 156 American and European landraces with a 50K SNP Illumina array to
21 study the effect of both human selection and environmental adaptation on the genome-wide
22 diversity of maize landraces. Genomic diversity of landraces varied strongly in different parts
23 of the genome and with geographic origin. We detected selective footprints between landraces
24 of different geographic origin in genes involved in the starch pathway (*Su1*, *Waxy1*),
25 flowering time (*Zcn8*, *Vgt3*, *ZmCCT9*) and tolerance to abiotic and biotic stress (*ZmASR*, *NAC*
26 and *dkg* genes). Landrace diversity was compared to that of (i) 327 inbred lines representing
27 American and European diversity (“CK lines) and (ii) 103 new lines derived directly from
28 landraces (“DH-SSD lines”). We observed limited diversity loss or selective sweep between
29 landraces and CK lines, except in peri-centromeric regions. However, analysis of modified
30 Roger’s distance between landraces and the CK lines showed that most landraces were not
31 closely related to CK lines. Assignment of CK lines to landraces using supervised analysis
32 showed that only a few landraces, such as Reid’s Yellow Dent, Lancaster Surecrop and
33 Lacaune, strongly contributed to modern European and American breeding pools. Haplotype
34 diversity of CK lines was more enriched by DH-SSD lines that derived from the landraces
35 with no related lines and the lowest contribution to CK lines. Our approach opens an avenue
36 for the identification of promising landraces for pre-breeding.

37 Keywords: *Zea mays*, gene banks, Landraces, Pre-breeding, DNA pooling, Genetic
38 diversity, Selective footprints, Allelotyping

39

40 ***SIGNIFICANCE STATEMENTS***

41 Maize landraces are a valuable source of genetic diversity for addressing the challenges of
42 climate change and the requirements of low input agriculture as they have been long selected
43 to be well adapted to local agro-climatic conditions and human uses. However, they are
44 underutilized in modern breeding programs because they are poorly characterized, genetically
45 heterogeneous and exhibit poor agronomic performance compared to elite hybrid material. In
46 this study, we developed a high-throughput approach to identify landraces that could
47 potentially enlarge the genetic diversity of modern breeding pools. We genotyped DNA pools
48 from landraces using 50K array technology, which is widely used by breeders to characterize
49 the genetic diversity of inbred lines. To identify landraces that could enrich the modern maize
50 germplasm, we estimated their contribution to inbred lines using supervised analysis and a
51 new measurement of genetic distance.

52

53 **INTRODUCTION**

54 Plant genetic resources are the basic raw material for future genetic progress (1–4). Maize
55 landraces are an interesting source of genetic diversity for addressing the challenges of
56 climate change and the requirements of low input agriculture, as they have been long selected
57 to be well adapted to local agro-climatic conditions and human uses (4–7). During the early
58 twentieth century, landraces were used as parent material for the development of improved
59 hybrid varieties to meet the needs of modern agriculture. During this transition from landraces
60 to hybrids, many favorable alleles were probably lost as a result of their association with
61 unfavorable alleles and/or genetic drift (8–11). Nowadays, modern breeding programs tend to
62 focus on breeding populations that can be traced back to a few ancestral inbred lines derived
63 from landraces at the start of the hybrid era (12–15). Landraces that did not contribute to this
64 founding material may be expected to be useful for enriching modern maize diversity,
65 particularly for traits that enhance adaptation to adverse environmental conditions (7).
66 However, maize landraces are used to a very limited extent, if at all, in modern plant breeding
67 programs because they are poorly characterized, genetically heterogeneous and exhibit poor
68 agronomic performance compared to elite hybrid material (3, 6, 16–18). Therefore,
69 understanding the genetic diversity of maize landraces and their relation to the maize elite
70 pool is essential for better management of genetic resources and for genetic improvement
71 through genome-wide association studies, genomic selection and the dissection of quantitative
72 traits (2, 6, 7).

73 Maize was domesticated in the highlands of Central Mexico approximately 9,000 years
74 ago (19, 20). It then diffused to South and North America (21, 22) and spread rapidly out
75 from America (23). It is now cultivated in highly diverse climate zones ranging from 40°S to
76 50°N. In Europe, the presently accepted hypothesis is that maize was first introduced through
77 Spain by Columbus, although other sources of maize that were pre-adapted to temperate
78 climates have been important for adapting to northern European conditions (22, 24–29). After
79 being introduced in different parts of the world, maize landraces were then selected by
80 farmers to improve their adaptation to specific environments, leading to changes in flowering
81 behavior, yield, nutritive value and resistance to biotic and abiotic stress, resulting in
82 subsequent differentiation of the material (7, 27, 30).

83 In recent years, the genetic diversity of maize landraces, which are conserved *ex situ*, has
84 been studied extensively using various types of molecular markers such as restriction
85 fragment length polymorphisms (RFLPs) (8, 25–28, 31–34) and simple sequence repeats

86 (SSRs) (8, 23, 35, 36). Single nucleotide polymorphisms (SNPs) are now the marker of choice
87 for various crop species such as maize (37), rice (38) and barley (39). They are the most
88 abundant class of sequence variation in the genome, are co-dominantly inherited, genetically
89 stable, easily automated and, thus, suitable for high-throughput automated analysis (40).
90 Unlike SSRs, allele coding can be easily standardized across laboratories and the cost of
91 genotyping is very low, which is a major advantage for characterizing genetic resources. A
92 maize array with approx. 50,000 SNP markers has been available since 2010 (37). It has been
93 successfully used to analyze the diversity of inbred lines and landraces by genotyping a low
94 number of plants per accession (13, 16, 41–44).

95 However, due to high within-accession diversity, the characterization of maize landraces
96 should be carried out on a representative set of individuals (45). Despite recent technical
97 advances, genotyping large numbers of individuals remains very expensive in the context of
98 genetic characterization. As a result, DNA pooling (or allelotyping) has been actively
99 developed as a valuable alternative strategy for collecting information on allele frequency
100 from a group of individuals while significantly reducing the effort required for population
101 studies using DNA markers (46, 47). In maize, DNA pooling has been successfully used to
102 decipher the global genetic diversity of landraces using RFLP (32) and SSR markers (23, 27,
103 28, 48, 49). The recent development of SNP arrays in maize (37, 50), combined with DNA
104 pooling, could be useful for characterizing the genetic diversity of maize landraces at a fine
105 genomic scale. In a previous study, we developed a new method for predicting the allelic
106 frequency of each SNP from a maize Illumina 50K array within DNA pools based on the
107 fluorescence intensity of the two alleles at each SNP (51). This new method accurately
108 predicts allelic frequency, safeguards against the false detection of alleles and leads to little
109 ascertainment bias for deciphering global genetic diversity (51).

110 In the present study, we applied this new method on a pilot scale to: i) investigate the
111 genome-wide diversity and genetic structure of 156 maize landraces that are representative of
112 European and American diversity; ii) compare the diversity of these landraces to that of a
113 panel of 327 inbred lines that represent the diversity presently used in North-American and
114 European breeding, the “CK lines” (27) and 103 new inbred lines derived from landraces, the
115 “DH-SSD lines”; and iii) identify the landraces that could potentially broaden the genetic
116 diversity of the CK lines.

117 **RESULTS**

118 ***Genetic diversity within maize landraces***

119 Only 25 SNPs out of 23,412 were monomorphic in the landrace panel. The average total
120 diversity (HT) was 0.338 ± 0.001 . The distribution of minor allelic frequency (MAF) showed
121 a deficit in rare alleles (MAF<0.05) compared to other frequency classes (Fig. S1).

122 In order to compare the genetic diversity of populations from different regions, we
123 classified the 156 landraces into five geographic groups: Europe (EUR), North America
124 (NAM), Central America and Mexico (CAM), the Caribbean (CAR) and South America
125 (SAM) (Table 1, Fig. S2, Table S1). All five geographic groups displayed both alleles for
126 nearly all loci, with the exception of CAR which was monomorphic at 1,227 loci out of
127 23,387 (Fig. S3). The lowest and highest within-group HT was found in CAR (0.301) and
128 CAM (0.328), respectively. Note that there was an excess of rare alleles in EUR, CAR and
129 NAM but not in SAM and CAM (Fig. S1).

130 The average number of alleles per locus and per landrace within the entire landrace panel
131 was 1.629 ± 0.003 and ranged from 1.098 (Ger8) to 1.882 (Sp11). Gene diversity within
132 landraces (Hs) was on average 0.192 ± 0.001 , (Table 1) and varied between 0.03 (Ger8 and
133 Ger9) and 0.28 (Sp11) (Table S1). The CAM group displayed on average the highest diversity
134 (0.219 ± 0.008), while the EUR group displayed the lowest (0.177 ± 0.002).

135 Genetic differentiation between landraces (FST) was 0.428 on average. FST within a
136 geographic group varied between 0.314 (CAR) and 0.434 (EUR) (Table 1). Overall genetic
137 differentiation between geographic groups was low (FST=0.05). FST between pairs of
138 geographic groups varied between 0.016 (EUR and NAM) and 0.083 (NAM and CAR) (Table
139 S2).

140 ***Relationship between maize landraces and population structure***

141 The average modified Roger's distance (MRD) between landraces was 0.379. The lowest
142 MRD between landraces was 0.158 (Chi12 and Chi9). It is slightly higher than the distance
143 between two pools of independent individuals from a same population (0.092-0.120, (51)).
144 The highest MRD was 0.552 (Ant1 and Ger8). The average MRD between populations from a
145 same geographic group ranged from 0.320 (CAR) to 0.367 (EUR) (Table 1). The average
146 MRD between populations belonging to two different geographic groups varied between
147 0.354 (CAM vs CAR) and 0.420 (NAM vs CAR) (Table S2).

148 We investigated the relationship between maize landraces using Principal Coordinate
149 Analysis (PcoA) and Ward hierarchical clustering based on MRD (Fig. 1). For both PcoA and
150 Ward hierarchical clustering analysis, landraces mostly clustered according to their
151 geographic proximity (Fig. 1, Fig. S4, Fig. S5). The first axis (PC1, 18.4% of the total
152 variation) discriminated (i) temperate landraces belonging to the Northern Flint cluster (from
153 northern Europe and North America) from (ii) tropical and subtropical landraces (from the
154 Caribbean and South and Central America) (Fig. 1A). The second axis (PC2, 5% of the total
155 variation) discriminated (i) North American (Corn Belt Dent cluster), Central American and
156 Mexican populations (Mexican cluster) from (ii) Italian (Italian Flint cluster), and Spanish and
157 French populations (Pyrenean-Galician cluster). Ward hierarchical clustering showed that at
158 the highest level (k=2, Fig. 1B), 62 of the 83 European landraces clustered together (European
159 cluster) while 70 of the 83 American landraces clustered together (American cluster). At a
160 deeper level (k=7), we distinguished 4 clusters of American or European landraces, each
161 originating from a geographic area with homogeneous agro-climatic conditions (cluster a, b, e
162 and f in Fig. 1B, Fig. S4). Cluster “a” grouped 15 landraces that originated mainly in Mexico
163 and southwestern USA. Cluster “b” comprised 10 South American landraces that originated
164 along the Andean Mountains. Cluster “e” grouped 31 European landraces that originated
165 either along the Pyrenean Mountains or in Central Eastern Europe. Cluster “f” grouped
166 mainly Italian Flint landraces. Three clusters grouped together American and European
167 landraces (cluster c, d and g on Fig. S4). Cluster “c” comprised 14 dent landraces that
168 originated mainly from Eastern European landraces and the US Corn Belt. Cluster “d”
169 grouped 65 landraces mostly from southern Spain (latitude <40°N), southwestern France and
170 from the Caribbean Islands and countries bordering the Caribbean Sea (d1, d2 and d3 on Fig.
171 S4). Cluster “g” comprised 12 North American flint landraces from higher latitudes (>40°N)
172 and 18 northeastern European landraces mainly from Germany (g on Fig. S4). Using a
173 pairwise Mantel test for each geographic area, we observed a low but significant correlation
174 between the genetic distance and geographic distance matrices for EUR ($r^2 = 0.05$, $P < 0.001$,
175 Fig. S6A), NAM ($r^2 = 0.12$, $P < 0.001$, Fig. S6B) and CAM ($r^2 = 0.0858$, $P = 0.02$, Fig. S6C).

176 We analyzed the genetic structure of 156 landraces using the ADMIXTURE program.
177 Likelihood analysis indicated that the optimal number of genetic groups was K=2, K=3 and
178 K=7 (Fig. S7). We considered K=7 as the reference, as this value was consistent with the one
179 obtained with 24 SSRs by Camus- Kulandaivelu et al. (27). Landraces from different
180 geographic regions were assigned to different genetic groups, with a clear trend along latitude

181 and longitude. Fig. 2). Assignment to these groups was also highly consistent with PcoA and
182 hierarchical clustering (Fig. 1, Fig. 2, Fig. S4, Fig. S5). The genetic structure obtained with
183 SNP markers was highly consistent with that obtained with the 17 SSR markers; indeed, 72%
184 (K=7) to 100% (K=3) of landraces were assigned to the same group by both types of markers
185 (Table S3). The main differences between the SSR and SNP results at K=7 were that the
186 Northern Flint landrace group obtained with SNPs is split in two with SSRs and the separate
187 Pyrenean-Galician and Italian groups found with SNPs form a single group with SSRs.

188 ***Scanning the maize landrace genomes for regions under selection***

189 Using a sliding window approach, we identified 14 regions with windows containing at
190 least two SNPs with extremely low genetic diversity ($\overline{HT}_l < 0.069$) across the entire landrace
191 panel (Fig. 3A, Table S4). These regions were mainly located in the centromeric region of
192 chromosomes 5 and 7. Genomic regions showing low diversity within geographic groups
193 were most abundant in CAR (67), followed by EUR (56), CAM (39), SAM (36) and NAM
194 (26) (Fig. 3E to 3I, Table S4). These regions were mostly located close to the centromeres but
195 varied between geographic groups. In the centromeric region of chromosome 1, we observed
196 (i) no loss of diversity for CAR and NAM and (ii) a depletion in genetic diversity for CAM,
197 EUR and SAM. Conversely, we observed a strong depletion on chromosomes 3 and 4 in CAR
198 landraces that was not observed in other geographic groups.

199 Outlier analysis of FST values among individual landraces identified 20 and 17 genomic
200 regions displaying high differentiation ($\overline{FST}_l > 0.568$) and low differentiation ($\overline{FST}_l < 0.235$)
201 between landraces, respectively (Fig. 3L, Table S4). Genetic differentiation was highest
202 upstream of chromosome 6 (Sp10 in Table S5), in two regions upstream of chromosome 4
203 (Sp6 and Sp7 in Table 2) and in one region on chromosome 3 (Sp3 in Table 2).

204 Outlier FST analysis between geographic groups identified 26 regions with high
205 differentiation ($\overline{FST}_g > 0.150$) and 8 regions with low differentiation ($\overline{FST}_g < 0.007$) (Fig. 3J,
206 Table S4); BAYESCAN identified 379 loci under divergent selection (Fig. 3J, Table S6 and
207 S7, Fig. S8). The five genomic regions that were previously identified as being highly
208 differentiated between landraces by outlier FST analysis were also detected by both FST
209 outlier and BAYESCAN analyses between geographic groups. (Table 2). Only one highly
210 differentiated genomic region was identified between landraces but not between all five
211 geographic groups (Sp10 in Table S5) whereas 6 genomic regions were identified exclusively
212 between the five geographic groups (Sg6, 7, 13, 15, 17, 18 and 20 in Table S5). These regions

213 displayed contrasted allelic patterns across geographic groups. Sp10 (11.7 Mbp – 15.3 Mbp
214 on chromosome 6, $\overline{FST_g} = 0.08$ and $\overline{FST_l} = 0.65$) had 9 SNPs that were close to fixation in
215 CAM (HT<0.1), but were segregating in NAM (~0.4) and also to a lesser extent in EUR,
216 CAR and SAM (HT~0.2). Sg2-Sp3 (84-85 Mbp on chromosome 3, $\overline{FST_g} = 0.18$ and $\overline{FST_l} =$
217 0.63) had 3 SNPs showing a continuous allelic frequency gradient between tropical and
218 temperate landraces with one allele largely predominant in NAM and EU (~70%), minor in
219 CAM (~30%) and absent in CAR (~0%). Sg4-Sp6 (40.3-41.8Mbp on chromosome 4, $\overline{FST_g} =$
220 0.27 and $\overline{FST_l} = 0.63$) had 4 SNPs that were nearly fixed in temperate landraces (NAM, EUR)
221 and displaying intermediate frequencies in CAM. By contrast, the Sg5-Sp7 region
222 ($\overline{FST_g}=0.16$, $\overline{FST_l}=0.63$) displayed higher diversity in temperate (HT_{NAM} and HT_{EUR}~0.4)
223 than in tropical landraces (HT_{CAM}~0.2 and HT_{CAR}~0.05) (Fig. 3 D, E, F, G, H). The outlier
224 loci displaying the highest FST values within this region were located up to 10 kbp upstream
225 of the *Su1* gene which is involved in the starch pathway.

226 Outlier FST analysis between pairs of geographic groups identified 214 and 41 regions
227 displaying high and low differentiation, respectively (Fig. S9). BAYESCAN analysis
228 identified 363 SNPs under selection between pair of geographic groups, including 167 new
229 SNPs that were not previously identified between all five geographic groups (Table S8). The
230 new highly differentiated regions identified by BAYESCAN were mostly specific to a single
231 pair of geographic groups (Fig. S9, Fig. S10). Putative functions could be assigned to 272 of
232 the 536 (50.7%) outlier loci identified by BAYESCAN analysis of all five and pairs of
233 geographic groups. These included known genes involved in adaptation to abiotic stress,
234 flowering time or human uses (Table S8 and S9).

235 ***Genome-wide comparison of diversity between landraces and inbred***
236 ***lines***

237 The panel of CK lines contained more monomorphic SNPs than landraces (263 vs 25) but
238 still captured 99% of the alleles present within the landrace panel. HT was slightly higher in
239 inbred lines than in landraces (0.353 vs 0.338). Allelic frequency of loci and HT values in
240 inbred lines and landraces were strongly correlated ($r^2=0.89$ and $r^2=0.80$, respectively, Fig.
241 S11). Overall genetic differentiation between landraces and inbred lines was limited ($0.010 \pm$
242 0.066). Some regions were more diverse in landraces than in inbred lines, notably the peri-
243 centromeric region of chromosomes 3 and 7, while the opposite was found in centromeric
244 regions of chromosomes 1, 3, 4, 5 and 6 (Fig. 3B).

245 Comparison of landraces and inbred lines using the outlier FST approach identified 128
246 highly differentiated genomic regions ($FST > 0.04$) and 32 regions with an excess of similarity
247 ($FST < 4.21e-05$). While highly differentiated regions were mainly located on chromosomes 3,
248 4, 8, 9 and 10, weakly differentiated regions were mainly located on chromosomes 3, 5 and 9
249 (Fig. 3K). BAYESCAN analysis of landraces *vs* inbred lines identified 61 loci (0.3%) that
250 were significantly more differentiated than expected under the drift model (Fig. 3K, Table
251 S10).

252 ***Relationship between inbred lines and landrace populations: genetic***
253 ***distances and supervised analysis***

254 The average MRD between landraces and CK lines was $0.499 (\pm 0.034)$, which is greater
255 than between landraces (0.379 ± 0.059) and less than between lines (0.590 ± 0.024). The
256 distribution of MRD genetic distances between a given landrace and CK lines (MRD_{LI}) is
257 displayed as a series of boxplots (Fig. 4A) listed in ascending order of landrace expected
258 heterozygosity (H_s) (Fig. 4B). Landraces with a low genetic diversity generally showed a
259 higher median and a wider range for MRD_{LI} , with some notable exceptions (*e.g.* Chi5, Per10,
260 Par2, Par1, Bra4, Ecu17, Vir4 and Svt1 in Fig. 4). Accordingly, the median MRD_{LI} and the
261 within landrace genetic diversity H_s were strongly negatively correlated ($r = -0.978$, $t = -$
262 61.314 , p -value $< 2.2e-16$) and displayed a linear relationship (Fig. S12). Considering a
263 similar level of genetic diversity, some landraces were closely related to certain inbred lines,
264 whereas other landraces were not (Fig. 4A and Fig. S12).

265 In order to identify the source material of modern varieties, and *a contrario* the landraces
266 that did not contribute much to these varieties, we quantitatively assigned 442 inbred lines to
267 166 landraces using a supervised analysis (Table S11). The 234 first cycle inbred lines (*i.e.*
268 directly derived from a single landrace) were assigned to a total of 60 landraces. Among these
269 landraces, 47 had at least one inbred line assigned with a probability $> 60\%$. For first cycle
270 inbred lines of known pedigree and whose ancestral landrace is included in our study (a total
271 of 121 lines and 50 landraces), we noted a very good match between pedigree and main
272 assignment (71.9% of cases). Among these 121 lines, DH-SSD lines, which were derived
273 recently from landraces, were more frequently assigned to their population of origin than lines
274 from the diversity panel (77.6% *vs* 58.3%, p -value=0.04). For the 208 inbred lines from more
275 advanced breeding cycles, we identified a total of 66 landraces as the main assignment of at
276 least one inbred line. Among these, temperate inbred lines were frequently assigned to Reid's

277 Yellow Dent and Lancaster Surecrop. Chandelle (one of the few tropical landraces in our
278 study) was identified as the most likely source for many tropical lines.

279 A few landraces contributed strongly to the whole diversity panel, with the 10 first
280 landraces cumulating half of the total contributions (Fig. 4C, Fig. S13A). 80% of lines were
281 assigned to these 10 landraces with a $> 60\%$ probability (Fig. S13B). Interestingly, the mean
282 contribution of landraces differed strongly between first cycle lines and more advanced lines
283 with a strong decrease ($> 1\%$) for 15 landraces and a strong increase ($> 1\%$) for 8 landraces
284 (Fig. S13C).

285 We tested whether the mean contribution of landraces and the MRD_{LI} distance
286 “normalized” by within landraces genetic diversity could be used as a criterion to identify
287 untapped sources of genetic diversity that could enrich the CK line panel. First, we selected
288 66 DH-SSD lines that were correctly assigned to 33 landraces from the landrace panel. We
289 then classified these 33 landraces according to: (i) their average contribution to CK lines (Fig.
290 5A) and (ii) the normalized MRD distance from their closest lines (Fig. 5C). For each class,
291 we estimated with 979 haplotype markers the average number of new haplotypes discovered
292 in the 66 DH-SSD lines compared to those existing in the CK lines. We discovered 66 new
293 haplotypes in the DH-SSD lines compared to 4,355 different haplotypes in the CK lines. The
294 number of new haplotypes discovered in DH-SSD lines ranged from 0 (Bul3) to 11 (Arg8).
295 The average number of new haplotypes was significantly higher for lines derived from
296 landraces with a low contribution than those with a high contribution (p -value = 0.008, Fig.
297 5B). It was also higher for landraces that were not close to any of the CK lines than for those
298 that were close to certain lines (p -value = 0.0004, Fig. 5D).

299 **DISCUSSION**

300 ***Patterns of genetic diversity and population structure within landraces***

301 The total expected heterozygosity observed in our study based on SNPs (0.338) was lower
302 than the values reported previously for landraces of comparable origin that were analyzed
303 with SSR markers (0.58 in (26), 0.63 in (27), 0.62 in (28)) but comparable to those observed
304 with SNPs in diversity inbred line panels (42, 43). These differences can be primarily
305 explained by the fact that SNP markers are typically bi-allelic, whereas SSR markers are
306 multi-allelic, which has the potential to increase gene diversity (43, 52). Trends in the
307 partition of genetic diversity within and between landraces, and within and between
308 geographic groups were similar to previous findings. The diversity of individual landraces
309 represented on average 57% of the total genetic diversity, which was slightly lower than for
310 RFLP markers (~66% in (23, 26)). This difference may be due to the counter-selection of
311 SNP markers with low MAF during the design of 50K Illumina array (37), which may
312 increase total diversity more than within diversity (53, 54). On the other hand, genetic
313 structure analyses based on SNPs and 17 SSRs were highly congruent, which indicates that
314 the ascertainment bias of prefixed PZE SNPs from the 50K Illumina chip used to study
315 landraces is negligible (43, 51).

316 Each geographic group contained most of the overall landrace genetic diversity, ranging
317 from 89% (CAR) to 97% (CAM). Central American and Mexican landraces displayed the
318 highest diversity, which is consistent with their proximity to the center of maize
319 domestication (13, 20). This confirms that genetic diversity was lost during the spread of
320 maize away from its domestication center due to successive bottlenecks related to climatic
321 adaptation and isolation by distance (7, 21, 22, 29, 55). This loss of genetic diversity is
322 consistent with the scenario of maize diffusion with (i) less genetic diversity in European
323 than in North and South American landraces, and (ii) more diversity in South America than in
324 North America, where maize was introduced more recently (21, 23, 29, 35). Our results
325 nevertheless confirm that the bottleneck during the introduction of maize in Europe was
326 certainly limited, as also shown by Brandebourg *et al.*, (29) with whole genome sequencing
327 of 67 inbred lines from Europe and America. Some northern European landraces originating
328 from Germany and Austria have extremely low genetic diversity ($H_s < 0.10$), with more than
329 70% of loci being fixed, suggesting a strong bottleneck. The fact that some of these landraces

330 have been cultivated mostly in gardens may have decreased their effective population size
331 (26). The genetic load could have been more or less purged depending on the severity and the
332 duration of the bottleneck. This could explain the strong variation in success rate observed for
333 deriving inbred lines from European Flint landraces by haplodiploidization (56, 57).

334 Genetic distance, Ward hierarchical clustering (Fig. 1B), principal component (Fig. 1A)
335 and population structure (Fig. 2) analyses showed major trends in population structure. We
336 confirmed the central position of Mexican and Caribbean landraces and a clear differentiation
337 between North and South American landraces (Fig. 1 and 2). This is consistent with the
338 domestication of maize in Mexico followed by southwards and northwards dispersion (22,
339 55). The similarity between landraces from southern Spain and the Caribbean confirms the
340 historical data on the introduction of maize in the south of Spain by Columbus in 1493 after
341 his first trip to the Caribbean (Fig. 1B, cluster d). Strong similarities between groups of
342 northeastern American and northeastern European landraces (mostly from Germany, Poland
343 and Austria) (Fig. 1B, cluster g) also supports an independent introduction of North American
344 material that was pre-adapted to the northern European climate (21, 22, 26, 28, 29, 58). Some
345 landraces from northern Spain and southwestern France, located along the Pyrenean
346 Mountains, were admixed either with Caribbean or Northern Flint. This result supports the
347 hypothesis that new Pyrenean-Galicia Flint groups originated from hybridization between
348 Caribbean and Northern Flint material that were introduced in southern Spain and northern
349 Europe, respectively. (27, 29, 59). Interestingly, some southwestern Spanish landraces have
350 elevated admixture with Italian Flint groups and are closely related to Italian landraces on the
351 NJ tree (Fig. S5), while northern Spanish landraces (latitude >42°N) do not. These results
352 support the hypothesis that Italian landraces are probably derived from an ancestor from
353 southern Spain (29, 60). Our results also highlighted a new putative hybridization event in
354 Central Eastern Europe. Central Eastern European landraces were close to Italian Flint
355 landraces on the Ward cluster tree and one northern Italian Flint landrace (Nostrano
356 Quarantino) was admixed with Italian Flint (~30-40%) and Northern Flint (~30-50%). This
357 suggests that Italian Flint landraces certainly spread in Central Eastern Europe, where they
358 intermated with Northern Flint landraces.

359 Differentiation of landraces was greater in Europe than in Central America and the
360 Caribbean, indicating that gene flow is lower in the latter two. Genetic and geographic
361 distances were significantly correlated in NAM, EUR and CAM but not in SAM and CAR
362 (Fig. S6), suggesting that isolation by distance played a role in shaping the genetic structure of

363 maize landraces in these regions, albeit to a variable degree. In the case of CAM, the effect of
364 isolation by distance is partially blurred by variation in altitude producing major gradients in
365 environmental conditions (temperature, rainfall) (7, 30, 61). Indeed, Mexican landraces
366 clustered according to both altitude and distance (Fig. 1B, Table S1) suggesting
367 environmental adaptation (7, 30).

368 ***Genomic pattern of nucleotide variation in landraces***

369 FST outlier and BAYESCAN analyses identified 13 genomic regions that showed high
370 levels of differentiation between geographic groups and/or landraces (Table S5). The four
371 highly differentiated genomic regions between landraces displayed contrasted patterns of
372 allelic frequencies between geographic groups (Table 2, Table S5), suggesting different types
373 of selection. The Sp10 region was found to be highly differentiated between landraces but not
374 between the five geographical groups. It suggests that there was strong selection in some
375 specific geographic areas but not across all geographic groups. This region contains genes
376 associated with tolerance to high temperature and evaporative demand (62). The second
377 genomic region (Sg4-Sp6: 7.8 Mbp – 9.3 Mbp on chromosome 4) was nearly fixed in
378 temperate landraces (NAM, EUR) whereas it showed intermediate frequencies in CAM,
379 suggesting a strong directional selection effect during the spread from Mexico to North
380 America. This results is in agreement with Romero-Navaro et al. (55), who identified 5 SNPs
381 in this region with allelic frequencies varying significantly with latitude in American
382 landraces, and Brandenburg et al., (29), who identified two highly differentiated regions
383 between Corn Belt Dent and Tropical first cycle lines. By contrast, the third genomic region
384 (Sp5-Sg7; 40-41.9 Mbp on chromosome 4) displayed higher genetic diversity in temperate
385 landraces (NAM, EUR) than in tropical landraces (CAM, CAR) suggesting strong
386 diversifying selection in EU and NAM. This region included the *Su1* gene, which is involved
387 in the starch pathway and is known to be under strong selective pressure (63–66). Romero-
388 Navaro et al., (55) also found an association between allelic frequency variation at the *Su1*
389 locus and both latitude and longitude. Furthermore, Brandenburg et al., (29) identified a strong
390 selective sweep between Corn Belt Dent/Tropical and Northern Flint first cycle lines in the
391 *Su1* gene. The fourth region (Sg2-Sp3; 84-85 Mbp on chromosome 3) showed a continuous
392 gradient of allelic frequencies between tropical and temperate landraces suggesting strong
393 directional selection for adaptation either to temperate or tropical climates. In agreement with
394 this finding, Romero-Navaro et al., (55) identified in this region 22 and 4 SNPs with allelic

395 frequencies varying significantly with altitude and latitude, respectively. This region also
396 carries a large 6 Mbp inversion that is putatively involved in flowering time variation (55).

397 BAYESCAN analysis between geographic groups identified several regions that were not
398 identified by outlier FST analysis (Table S8 and S9). Notably, we identified several loci under
399 strong selection that were close to genes known to be involved in flowering time variation: (i)
400 PZE-108070380 on chromosome 8 (123.5 Mbp) localized 5 kbp upstream of *Zcn8* (42, 67,
401 68); (ii) PZE-109070904 on chromosome 9 (115.7 Mbp) in *ZmCCT9* (69); (iii) two loci on
402 chromosome 3 (PZE-103098664 (158.9 Mbp) and PZE-103098863 (159.17 Mbp) close to
403 *Vgt3*, a major loci that is strongly associated with flowering time variation in temperate maize
404 (62, 70). We also identified several genes/genomic regions that are putatively involved in
405 adaptation to abiotic stress: (i) PZE-102108435 on chromosome 10 that is 10 kbp upstream of
406 *ZmASR2* which is involved in abscisic stress ripening (71); (ii) PZE-104128228 on
407 chromosome 4 in the *nactf125* gene (within Sg6 in table S5), PZE-102051809 in the *nactf36*
408 gene (chromosome 1) and PZE-107058109 in the *nactf14* gene (chromosome 7), all of which
409 belong to the NAC protein family, which encodes plant transcription factors involved in biotic
410 and abiotic stress responses (72); (iii) two diacylglycerol kinases (*dgk2* and *dgk3*) that exhibit
411 differential expression patterns in response to abiotic stress including cold, salinity and
412 drought and are upregulated in cold conditions (73). Finally, we identified several genomic
413 regions carrying genes involved in the hormonal systems regulating growth, cell division and
414 proliferation such as giberellin2-oxydase9 (*ZmGA2ox9*, GRMZM2G152354), phytosulfakine
415 (GRMZM2G031317) or in the starch pathway (*Su1*, *waxy1*, *dull endosperm1*).

416 The detection of genomic regions and loci under selection have therefore allowed the
417 identification of genes that underlie the adaption of maize to diverse agro-climatic conditions
418 and/or human uses during the spread of landraces from America (7, 22, 23, 29, 55, 74). These
419 genomic regions could be useful for mining new alleles from landraces, retrieving some of the
420 genetic diversity that was lost by genetic drag linked to genes close to those under selection
421 (7, 41, 74), or creating new genetic diversity by targeted mutation (7).

422 ***Identification of promising landraces to enlarge the modern genetic
423 pool***

424 Intensive selection to enhance agronomic performance can considerably reduce genetic
425 diversity in crops (1). However, we found little difference in genetic diversity between
426 landraces and inbred lines, which is consistent with the low genetic differentiation we

427 observed between landraces and inbred lines. This suggests that the genomic diversity
428 (inferred from SNPs) present in landraces was retained in our panel of CK lines and that
429 selection during maize improvement has not altered allele diversity over a very broad
430 geographic scale. This observation is similar to findings in soybean (75) and wheat (76),
431 which also showed a minor effect of crop improvement on diversity, suggesting that landraces
432 have been and still are extensively used in the development of modern inbred lines in these
433 crops. It is important to note however that our line panel included many old lines that have
434 made only a limited contribution, if any, to commercial F1 hybrids or recent breeding pools.
435 Our panel therefore certainly overestimates the genetic diversity present in the germplasm of
436 modern breeding inbred lines (57).

437 Several factors could be responsible for the low genetic erosion accompanying the
438 transition from landraces to inbred lines. A first hypothesis is that selection during modern
439 maize breeding targeted only a small number of genes (77) and therefore affected genetic
440 diversity and allelic frequency only in the genomic regions flanking the genes under selection.
441 Another hypothesis is that, even if only a limited number of landraces were used as parents of
442 first cycle lines, i.e. the initial modern inbred line breeding pools, selection of genetically
443 diverse and complementary heterotic groups may have mitigated the loss of diversity (78).
444 Furthermore, SNPs from 50K arrays were previously identified in 27 lines (79). These SNPs
445 may not reflect well the total genetic diversity of landraces, as certain specific landrace
446 haplotypes may not have been transmitted to first cycle lines due to their deleterious effect at
447 the homozygous state (inbreeding depression) or gamete sampling (drift) (57).

448 Despite the limited differences in overall diversity between landraces and inbred lines,
449 two different approaches highlighted that the majority of landraces had made a limited
450 contribution to recent breeding. We identified a number of landraces with a high median H_s
451 value and a small MRD_{LI} distance range reflecting a lack of similarity similarity to any inbred
452 line. These landraces probably did not contribute to the modern maize germplasm. Indeed,
453 supervised analysis showed that inbred lines from our diversity panel could be traced back to
454 a few landraces and that the first 10 landraces cumulated half of the total contribution to the
455 diversity panel. Most of these landraces (Reid's Yellow Dent, Lancaster Surecrop and Krug
456 Yellow Dent for the dent genetic group, Lacaune and Gaspe Flint for the flint genetic group
457 and Chandelle for Tropical lines) were previously identified as the source of the modern
458 maize breeding germplasm (12, 13, 55). Interestingly, we observed a large increase or
459 decrease in the contribution of landraces between first cycle lines and more advanced lines

460 (Fig. S13C). This can be explained by the fact that some lines were extensively used to derive
461 more advanced lines whereas others were not (12, 14, 15). Interestingly, DH-SSD lines that
462 were recently derived from landraces were assigned more frequently (and with higher
463 probability) to their population of origin than older lines that were maintained for a long time
464 in gene banks. This suggests that some landraces could have evolved since contributing to
465 inbred lines from the diversity panel or that the pedigree of these lines was erroneous. Our
466 results suggest that we could use supervised analyses to curate the landrace collection and the
467 pedigree of first cycle lines.

468 In order to identify landraces that differ the most from inbred lines, we developed an
469 indicator of genetic distance from inbred lines which was normalized by their genetic
470 diversity (Fig. S12). By classifying landraces according to (i) this normalized distance and (ii)
471 their average contribution to reference inbred lines, we were able to identify landraces that
472 have the greatest potential to broaden the genetic diversity of these lines (Fig.5). By
473 combining closely located SNPs, we were able to identify novel haplotypes in the DH-SSD
474 lines, which were absent in the CK panel, even though both alleles were present in landraces
475 and the inbred line panel. The number of new haplotypes was significantly higher for DH-
476 SSD lines created from landraces classified as genetically distant from the modern germplasm
477 according to the criteria described previously, which confirms their relevance when choosing
478 landraces for diversity enhancement. This strategy to identify untapped landraces in modern
479 breeding germplasm can be easily extended to other plant species, other material (hybrids,
480 private germplasm), and other technologies (sequencing). Additionally, this strategy can be
481 focused on some genomic region to identify new alleles of interest. Our strategy opens an
482 avenue to identify valuable landraces and genomic regions for prebreeding.

483 **MATERIALS AND METHODS**

484 ***Plant material***

485 ***Landraces***

486 A total of 156 different landrace populations (Table S1) were sampled from a panel of 413
487 landraces (Supplementary Information 1). These 156 landraces captured a large proportion of
488 European and American diversity and have been analyzed in previous studies using RFLP
489 (25, 31–34) and SSR markers (23, 27, 28). Each population was represented by either one or

490 two sets of 15 individual plants (for 146 and 10 populations, respectively), pooled equally as
491 described in Reif *et al.* (48) and Dubreuil *et al.* (28). The 166 DNA samples corresponding
492 to the 156 landrace accessions were classified into five geographic groups (Table S1): Europe
493 (EUR), North America (NAM), Central America and Mexico (CAM), the Caribbean (CAR)
494 and South America (SAM).

495 ***Inbred lines***

496 We analyzed 234 inbred lines that were derived directly by single seed descent or by
497 haplodiploidization of landraces, referred to as “first cycle lines”, and 208 lines that were
498 derived from a more advanced cycle of breeding, referred to as “advanced lines” (Table S11).
499 These 442 lines were partitioned into three sets (the “Panel” column in Table S11):

- 500 1. “CK lines”: a panel of 120 first cycle and 207 advanced lines (327 lines in total)
501 representing American and European diversity (27, 42) including some key founders
502 of modern breeding programs (*e.g.* F2, B73, C103).
- 503 2. “Parent Controlled Pools”: a set of 12 lines used to build 4 series of 8 controlled DNA
504 pools (see below).
- 505 3. “DH-SSD lines”: a set of 45 single seed descent (SSD) and 58 double haploid (DH)
506 lines derived recently from 48 landraces (first cycle lines).

507 ***Controlled DNA Pools***

508 To prepare the controlled DNA pools, two sets of three inbred lines were considered:
509 EP1 – F2 – LO3 (European Flint inbred lines) and NYS302– EA1433 – M37W (Tropical
510 inbred lines). For each set of parental lines, nine controlled pools were prepared by varying
511 the proportion of each line in the mix, quantified by the number of leaf disks of equal size as
512 *per* Dubreuil *et al.*, (32). The genotype of each line and the proportion of parental lines in
513 each pool were used to estimate allelic frequencies in the nine pools, and subsequently to
514 calibrate the model for predicting allelic frequency (see (51) for more detail).

515 ***Genotyping and prediction of allelic frequencies in DNA pools***

516 We used the 50K Illumina Infinium HD array (37) to genotype (i) landraces, (ii)
517 controlled DNA pools, (iii) the DH-SSD inbred lines and (iv) the parental lines of the
518 controlled DNA pools (Table S1 and S11). For CK lines, we used the 50K genotyping data
519 from Bouchet *et al.* (2013). 23,412 SNPs were filtered based on their suitability for diversity

520 analysis and their quality for predicting allelic frequency in DNA pools (Supplementary
521 Information 2).

522 Allelic frequency of selected SNPs in DNA pools was estimated using the two-step
523 procedure described in (51) based on the fluorescence intensity ratio (FIR) of alleles A and B
524 for each SNP. First, we tested whether SNPs were monomorphic or polymorphic. For SNPs
525 that were considered to be polymorphic, we then estimated the allelic frequency of the B
526 allele using a generalized linear model calibrated on FIR data from 1,000 SNPs from 2 series
527 of controlled pools (see (51) for more detail and equation 2 for the model).

528 We also used the genotyping data from 17 SSRs from 145 and 11 landraces obtained by
529 Camus-Kulandaivelu et al. (27) and Mir et al. (23), respectively.

530 ***Diversity analyses***

531 ***Estimation of genetic diversity parameters***

532 For each landrace, each geographic group, all landraces combined and the panel of inbred
533 lines, we determined for each locus: the mean allele number (A), the Minor Allele Frequency
534 (MAF) and the expected heterozygosity (H) (80, 81).

535 Genetic differentiation (FST) was estimated between: individual landraces (FST_i),
536 between the five landrace geographic groups (FST_g), between 10 pairs of geographic groups
537 ($FST_{EUR-NAM}$, $FST_{EUR-CAM}$, $FST_{EUR-CAR}$, $FST_{EUR-SAM}$, $FST_{NAM-CAM}$, $FST_{NAM-CAR}$, $FST_{NAM-SAM}$,
538 $FST_{CAM-CAR}$, $FST_{CAM-SAM}$, $FST_{CAR-SAM}$) and between landraces and inbred lines (FST_i). FST
539 was estimated at each locus and across all loci as *per* (81, 82) (Supplementary Information 3).

540 ***Genome-wide diversity analysis and scans for identifying selection signatures***

541 We used a sliding window of 1 Mbp, shifting by 500 kbp at each step along the genome,
542 to analyze the genome-wide variation in genetic diversity and differentiation between
543 landraces, between geographic groups, and between landraces and inbred lines. The maize
544 genome was divided into 4,095 overlapping windows containing an average of 11.3 ± 5.2
545 SNPs. We computed the average value for the parameters described above for all loci in a
546 given window. Outlier regions for H and FST were identified based on the distribution of
547 these parameters for individual loci over the entire genome using the 5th and 95th percentile
548 (below 5% and above 95%) as thresholds (Table S4). All statistics were computed using *ad*
549 *hoc* scripts in the R language v 3.0.3 (83).

550 Genomic scans were carried out to detect the genomic signature of selection between
551 landraces, between the five geographic groups and between landraces and inbred lines using
552 two approaches: (i) the detection of 1 Mbp regions that were outliers for FST, referred to as
553 “Outlier FST analysis” (ii) the detection of loci under selection using the drift model
554 implemented in the BAYESCAN software (84) (Supplementary Information 4).

555 ***Genetic structure and relationship between landraces***

556 We estimated the genetic distance between all landraces using modified Roger’s distance
557 (MRD) (85) based on the allelic frequencies of 23,412 prefixed PZE SNPs. MRD was then
558 averaged within and between geographic groups (Table 1, Table S2). We analyzed the
559 relationship between genetic and geographic distances within each geographic group by
560 plotting MRD against geographic distances. We tested this correlation using the Mantel test
561 (86). Geographic distances were calculated using the latitude and longitude of each sampling
562 site using the geosphere R package v. 1.5-10 (87).

563 To decipher the structure of genetic diversity within our panel of landraces from 23,412
564 filtered SNPs, we used two approaches:

- 565 1) A distance-based approach in which MRDs between the 166 landraces were used to
566 perform (i) a principal coordinate analysis (PCoA) (88), (ii) hierarchical clustering using
567 either Ward or Neighbor-Joining algorithms implemented in the “hc” and “bionj”
568 functions of the “ape” R package v 5.0 (89), respectively.
- 569 2) A Bayesian multi-locus approach, implemented in the ADMIXTURE software, to assign
570 probabilistically each landrace to K ancestral populations assumed to be in Hardy-
571 Weinberg Equilibrium (90). Different methods were used to identify the most appropriate
572 number of ancestral populations (K): Cross-validation error or difference between
573 successive cross-validations (90) and Evanno’s graphical methods (91). Since
574 ADMIXTURE requires multi-locus genotypes of individual plants, we simulated the
575 genotype of five individuals for each population for a subset of 2,500 independent SNPs
576 to avoid artifacts of linkage disequilibrium (Supplementary Information 5).

577 ***Contribution of populations to inbred lines using supervised analysis
578 and modified Roger’s distance***

579 To analyze the contribution of landraces to the modern breeding germplasm, we used two
580 different approaches:

581 1) A distance-based approach in which we estimated the modified Roger's distance
582 between each landrace and the 327 CK lines (MDRLI) in order to determine whether they
583 are related or not.

584 2) A Bayesian supervised approach implemented in ADMIXTURE in which the 442
585 inbred lines were assigned probabilistically to the 166 landrace populations in order to
586 identify the most likely source population of each inbred line (Table S11). For each
587 landrace, we estimated (i) its average contribution to CK lines by averaging the
588 assignment probability over 327 lines and (ii) the number of inbred lines mainly assigned
589 to this landrace, with an assignment probability > 60%. We also analyzed the evolution of
590 the contribution of landraces across breeding cycles by comparing contributions to (i) first
591 cycle lines and (ii) advanced lines from the CK line panel. To check the accuracy of the
592 assignment method, we estimated the percentage of first cycle lines that were correctly
593 assigned to their parental landrace as known from their pedigree and analyzed in our study
594 (121 of the 234 first cycle lines, known to be derived from 50 landraces). We tested if this
595 percentage was different between CK lines and DH-SSD lines using a Kruskal-Wallis chi-
596 squared test. To represent each landrace, we used the same five simulated individuals as in
597 the structure analysis.

598 Identification of landraces that could enrich the modern breeding germplasm We assessed
599 whether the mean contribution of landraces and their MRD_{LI} distribution parameters could be
600 used as criteria to identify landraces that could enrich the modern breeding germplasm. To
601 this end, allelic diversity was estimated in the two inbred panels (DH-SSD and CK lines) for
602 979 haplotypes. These haplotype markers were defined by genotyping triplets of adjacent
603 SNPs from 50K arrays that were less than 2 kbp apart. We estimated the average number of
604 new haplotypes discovered in the DH-SSD lines compared to those in the 327 CK lines. To
605 avoid noise due to seedlot error during DH-SSD line production, we selected 66 DH-SSD
606 lines that were correctly assigned to 33 landraces analyzed from this study.

607 To analyze the effect of mean contribution, we classified these 33 landraces into three
608 classes: low, intermediate, and high contribution based on the 30th and 90th percentile of the
609 distribution of mean landrace contribution to CK lines.

610 To analyze the usefulness of MRD_{LI} , we took into account the negative correlation
611 between MRD_{LI} and within-gene diversity of landraces (H_s), which could strongly bias
612 against landraces with the lowest within diversity. For each landrace, we defined a
613 “normalized” MRD distance (MRD_{norm}) based on the absolute difference between (i) the

614 median MRD_{LI} between a landrace and lines of CK panel (MRD_{med}) and (ii) the MRD_{LI} from
615 the closest lines (MRD_q) defined by the 5th (MRD_{05}) and 10th (MRD_{10}) percentile of
616 MRD_{LI} , corresponding to the 5 and 10% closest lines. In order to correct the bias due to Hs,
617 we used the linear regression coefficient “a” between MRD_{med} and Hs. We defined MRD_{norm}
618 as the orthogonal deviation of MRD_q (with $q = 5\%$ or 10% for MRD_{05} and MRD_{10} ,
619 respectively) from the linear regression:

620
$$MRD_{norm} = (MRD_{med} - MRD_q) \times \sin(\tan^{-1}(a)) \quad (1)$$

621 We used MRD_{norm} based on MRD_{10} to categorize the 33 landraces into three classes based
622 on the percentile distribution of MRD_{norm} . Landraces with MRD_{norm} below 30%, between 30%
623 and 70% quantile and above 70% were considered to have none, few or many derived lines,
624 respectively.

625 Finally, we performed a variance analysis to test the effect of mean contribution and
626 MRD_{norm} on the number of new haplotypes discovered in the DH-SSD lines.

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641 ***Author contributions***

642 S.D.N, A.C and B.G designed and supervised the study and selected the plant material; M.A,
643 S.D.N, A.C, B.G drafted and corrected the manuscript; D.M, V.C and M-C.L-P extracted
644 DNA and managed the genotyping of landraces and inbred lines; C.B, B.G and A.C collected
645 and maintained the collection of landraces and inbred lines; S.D.N, M.A, A.C and T.M-H
646 developed the statistical methods for predicting allelic frequency from fluorescence data;
647 M.A, B.G and S.D.N analyzed the genetic diversity of the landrace panel; M.A and S.D.N
648 analyzed the selective sweep; M.A, S.D.N and A.C investigated the relationship between
649 landraces and inbred lines; S.D.N developed the normalized distance measure and performed
650 the analysis of diversity enrichment.

651 ***Data availability***

652 Fluorescence Intensity Data from 166 DNA samples of landraces used for predicting allelic
653 frequency and modified Roger's distance matrix are available at
654 <https://doi.org/10.15454/D4JTKB>. To predict allelic frequency in 166 DNA pools, we
655 calibrated our two-step model with fluorescence intensity data of 327 inbred lines (for
656 calibrating the fixation test) and two series of controlled pools (for calibrating logistic
657 regression) with R script that are available at the following address:
658 <https://doi.org/10.15454/GANJ7J>. Note that data will be available at the two web links below
659 upon the publication will have been accepted in a journal.

660 ***Conflicts of interest***

661 No

662

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Table 1: Genetic diversity within the five geographic groups of landraces, the entire landrace panel and the CK line panel.

	Europe (EUR) mean \pm s.d.	North America (NAM) mean \pm s.d.	Central America and Mexico (CAM) mean \pm s.d.	Caribbean (CAR) mean \pm s.d.	South America (SAM) mean \pm s.d.	Landrace Panel (LP) mean \pm s.d.	CK line Panel (IL) mean \pm s.d.
Number of populations / inbred lines	83	22	25	14	22	166	327
Allele Number (A) <i>group level</i>	1.996 \pm 0.001	1.989 \pm 0.005	1.990 \pm 0.004	1.947 \pm 0.017	1.992 \pm 0.004	1.999 \pm 0.000	1.989 \pm 0.001
Allele Number (A) <i>average within pop / line</i>	1.584 \pm 0.005	1.649 \pm 0.021	1.701 \pm 0.018	1.662 \pm 0.034	1.671 \pm 0.021	1.629 \pm 0.003	1.004 \pm 0.000
Minor Allele Frequency (MAF) <i>group level</i>	0.235 \pm 0.001	0.235 \pm 0.006	0.244 \pm 0.006	0.223 \pm 0.011	0.240 \pm 0.007	0.253 \pm 0.001	0.265 \pm 0.001
Minor Allele Frequency (MAF) <i>average within pop / line</i>	0.128 \pm 0.001	0.141 \pm 0.002	0.159 \pm 0.001	0.150 \pm 0.001	0.149 \pm 0.001	0.139 \pm 0.000	0.002 \pm 0.000
Total expected heterozygosity across groups (HT)	0.314 \pm 0.002	0.317 \pm 0.007	0.328 \pm 0.006	0.301 \pm 0.012	0.323 \pm 0.007	0.338 \pm 0.001	0.353 \pm 0.001
Expected heterozygosity (Hs) <i>average of within pop / line</i>	0.177 \pm 0.002	0.195 \pm 0.009	0.219 \pm 0.008	0.206 \pm 0.014	0.205 \pm 0.009	0.0192 \pm 0.001	0.002 \pm 0.000
Modified Roger's Distance between landraces / inbred lines (MRD)	0.367 \pm 0.061	0.351 \pm 0.063	0.336 \pm 0.033	0.320 \pm 0.026	0.346 \pm 0.068	0.379 \pm 0.059	0.580 \pm 0.024
Differentiation between landraces (F_{ST}) and between inbred lines (F_{ST})	0.393 \pm 0.001	0.341 \pm 0.001	0.303 \pm 0.001	0.275 \pm 0.001	0.334 \pm 0.001	0.405 \pm 0.002	0.994

Table 2: Genomic regions identified as being highly differentiated between landraces and geographic groups. Only SNPs that were detected by BAYESCAN with decisive evidence of selection and Outlier FST windows carrying at least two SNPs are listed.

Outlier FST windows							Bayescan hits (Decisive) – Geographical						Frequency of allele B						
Name *	Chr	Start - Stop (Mbp)	SNP _w	FST _g	FST ₁	HT ₁	Hs	SNP _b	Marker name	Pos. (Mbp)	FST _b	Closest Gene	Dist. from gene (kbp)	Functionnal annotation	EUR	NAM	CAM	CAR	SAM
Sg1, Sp2	3	77.5 - 79	4	0.15	0.54	0.39	0.15	4	PZE-103058385	78.2	0.26	GRMZM2G584078	4		0.76	0.73	0.39	0.00	0
									PZE-103058429	78.5	0.30	AC202959.3_FG001	0		0.30	0.34	0.72	1.00	0
Sg2, Sp3	3	84 - 85	3	0.18	0.63	0.50	0.19	3	PZE-107023081	84.9	0.29	GRMZM2G112579	5.6	Pectin lyase-like superfamily protein	0.69	0.65	0.32	0.00	0
									PZE-107023082	84.9	0.29		5.7		0.31	0.35	0.64	1.00	0
Sg4, Sp6	4	7.8 - 9.4	7	0.27	0.63	0.23	0.07	6	PZE-104010709	8.8	0.30	GRMZM2G119698	0	pectinesterase	0.06	0.06	0.79	0.29	0
									PZE-104010719	8.8	0.28	GRMZM2G702341	0.2		0.98	0.95	0.34	0.95	0
Sg5, Sp7	4	40.9 - 41.9	7	0.16	0.63	0.44	0.16	4	PZE-104033199	41.2	0.26	GRMZM5G889780	13.7	Thioredoxin superfamily protein	0.43	0.28	0.90	1.00	0
									PZE-104033229	41.4	0.28	GRMZM2G138198	0		0.49	0.66	0.06	0.00	0
Sg9, Sp11	6	134.3 - 135.3	15	0.16	0.58	0.41	0.17	6	PZE-104033340	41.7	0.27	GRMZM2G174149	0	RNA pseudouridine synthase 3 mitochondrial	0.54	0.39	0.94	1.00	0
									PZE-106078726	134.5	0.25	GRMZM2G055678	0		0.51	0.34	0.96	0.99	0
								6	PZE-106078990	134.8	0.24	GRMZM2G170646	0	GDSL esterase/lipase	0.50	0.63	0.07	0.01	0
									PZE-106079041	134.8	0.28	GRMZM2G162702	0.6		0.55	0.44	0.97	1.00	0
								6	PZE-106079060	134.9	0.25		0	Probable receptor-like protein kinase	0.57	0.49	0.96	1.00	0
									PZE-106079065	134.9	0.27		0		0.57	0.49	0.98	1.00	0
								6	PZE-106079127	135.0	0.29	GRMZM2G307720	0	TATA box-binding protein	0.49	0.31	0.92	1.00	0

* Sg and Sp indicate highly differentiated genomic regions between geographic groups and landraces, respectively; SNP_w and SNP_b indicate the number of SNPs within Outlier FST windows and detected as being under selection by Bayescan, respectively; FST_g and FST₁ indicate the average FST across all loci in the window, and between geographic groups and landraces, respectively. FST_b indicates the FST estimated by Bayescan for markers under selection between geographic groups. Distance from gene (“Dist. from gene”) was based on the closest start or stop codon of the gene, 0 indicates that the SNP is within the gene. Functional annotation was retrieved from Gramene (<https://www.gramene.org/>).

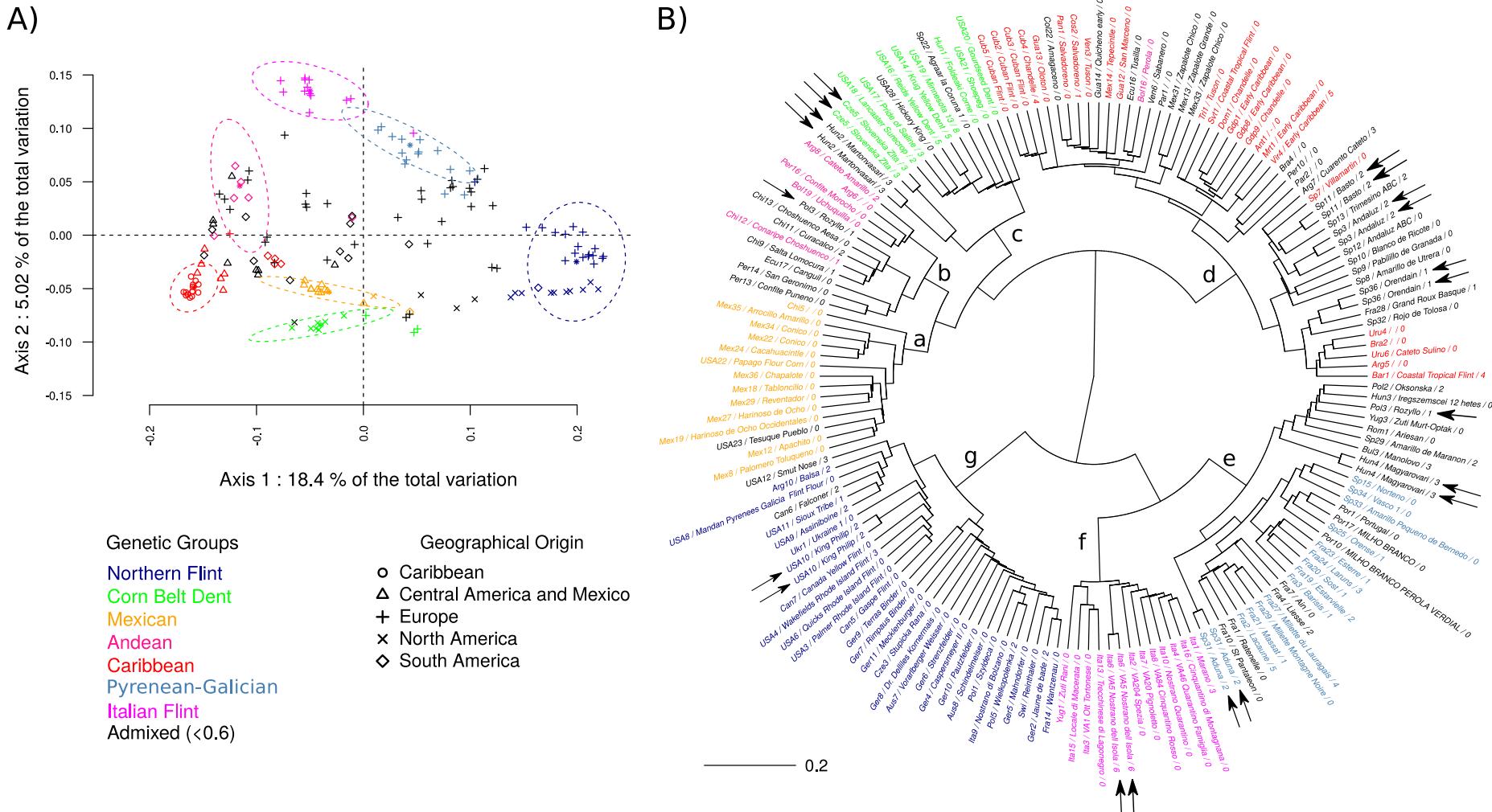


Fig. 1: Genetic relationship between 156 maize landraces based on their modified Roger's distance (MRD). A) Projection of the 166 DNA samples on the first two axes of the Principal Coordinate Analysis. Symbols indicate the geographic origin of landraces. B) Dendrogram obtained by Hierarchical clustering, using Ward's algorithm. Labels indicate for each landrace their abbreviation code, common names and number of first cycle inbred lines they contributed to, respectively. Black arrows indicate the 10 landraces with duplicated DNA samples. Colors indicate the assignment of landraces to the seven genetic groups defined by ADMIXTURE. Landraces with an assignment probability below 0.6 were considered admixed and colored in black.

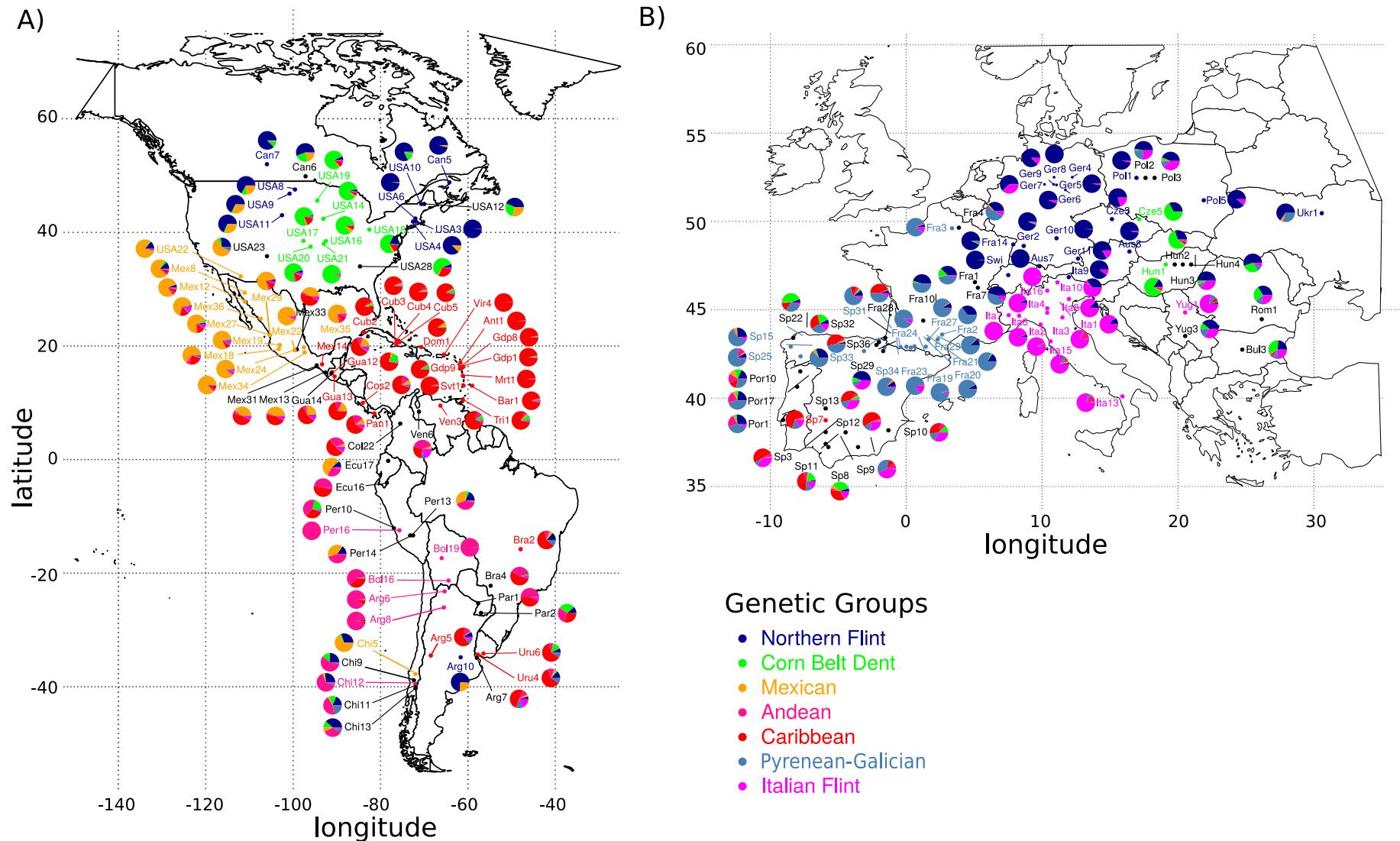


Fig. 2: Spatial genetic structure of American (A) and European (B) maize landraces. Population structure is based on ADMIXTURE analysis with $K = 7$. Each population is represented by a pie diagram whose composition indicates admixture coefficients. Population labels are colored according to their main assignment (>0.6), and are black if the landrace is admixed.

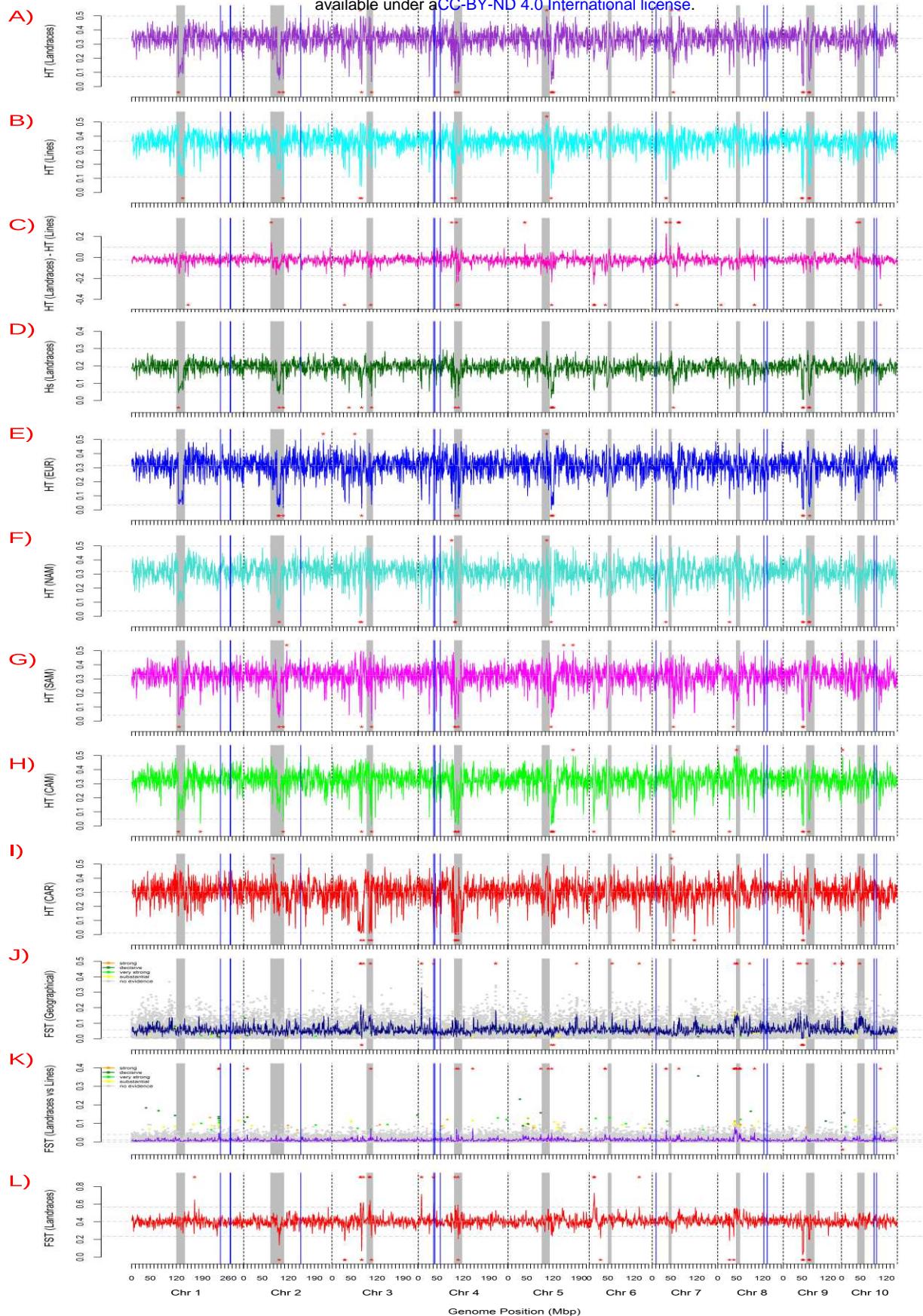


Fig. 3: Variation in genetic diversity and differentiation along the maize genome. A) Total expected heterozygosity across landraces: HT (Landraces); B) total expected heterozygosity (HT) across inbred lines: HT (Lines); C) difference between the total expected heterozygosity across landraces and across inbred lines: HT (Landraces) – HT (Lines); D) mean expected heterozygosity within landraces: Hs (Landraces); total expected heterozygosity across landraces from E) Europe: HT (EUR), F) North America: HT (NAM), G) South America: HT (SAM); H) Central America and Mexico: HT (CAM), I) the Caribbean: HT (CAR), J) FST between geographic groups of landraces: FST (Geographic); K) FST between landraces and inbred lines: FST (Landraces vs. Inbred lines); L) FST between landraces: FST (Landraces). Loci with decisive, very strong, strong, substantial, no evidence of selection using bayescan are colored in orange, dark green, light green, yellow and blue (J, K, L). Vertical gray bars correspond to centromere limits. Chromosome boundaries are indicated by vertical dashed lines. Horizontal dashed lines correspond to the mean, 5th and 95th percentile of each parameter. Outlier regions are indicated by red asterisks (>95% at the top, <5% at the bottom). Vertical blue lines indicate the location of the genes *ID1*, *tb1*, *pbf1*, *su1*, *tga1*, *bt2*, *o2*, *pebp8*, *vgt1*, *nac1* and *Zmcc*

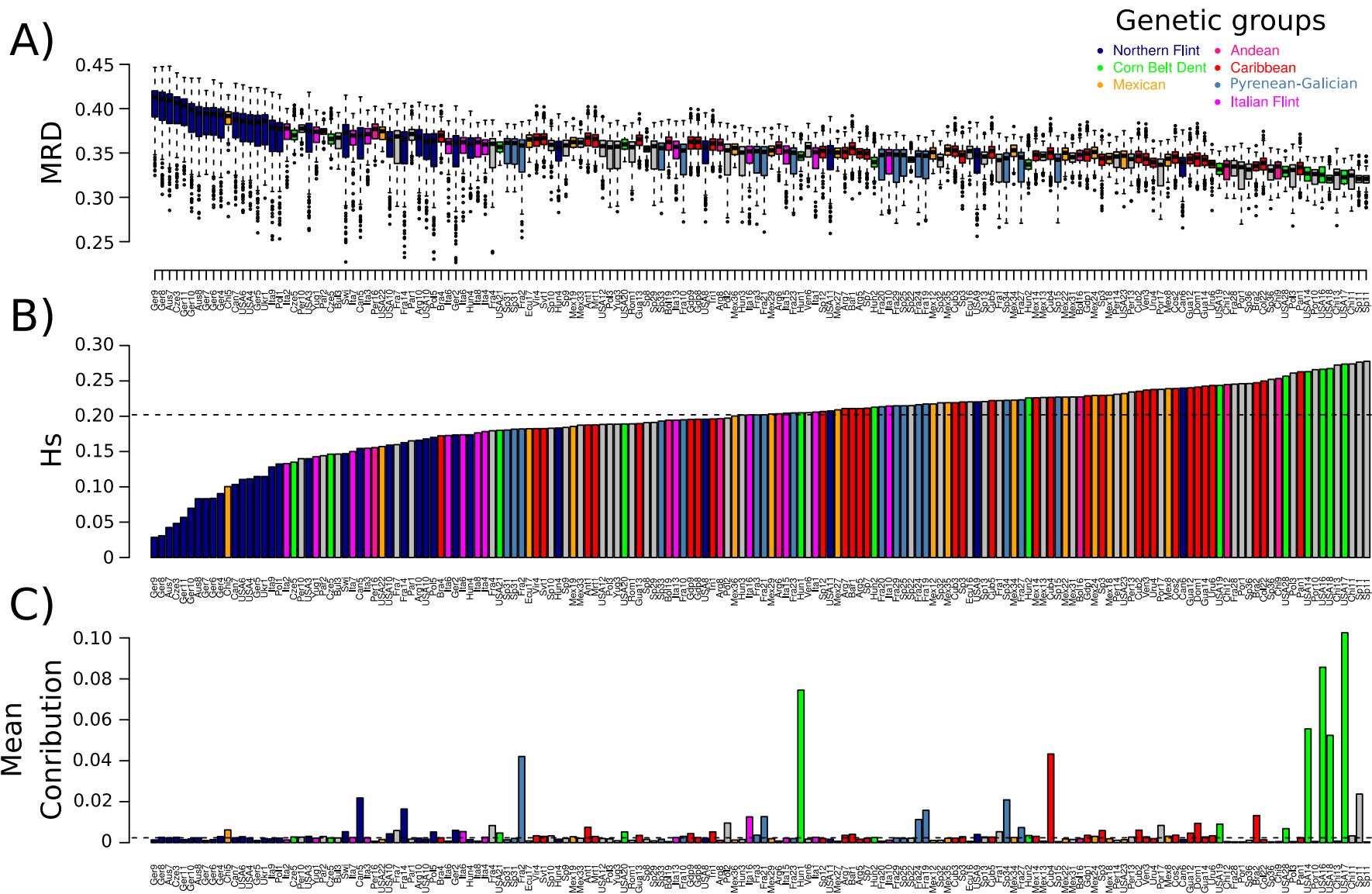


Fig. 4: Contribution of landraces to the panel of CK lines in relation to their genetic diversity. A) Box plot representation of pairwise modified Roger's distances (MRD) between individual landraces and inbred CK lines. Each box represents the interquartile range, the line within each box represents the median value and the error bars encompass 95% of values for each landrace. Circles represent outliers. B) Within population genetic diversity (Hs) C) Average contribution of the 166 landraces to the panel of CK lines estimated by supervised analysis with ADMIXTURE. Landraces are ranked in ascending order of Hs in the three figures. Boxplot and barplots are colored based on the assignment of landraces to the seven genetic groups identified by ADMIXTURE (see bottom right for colors).

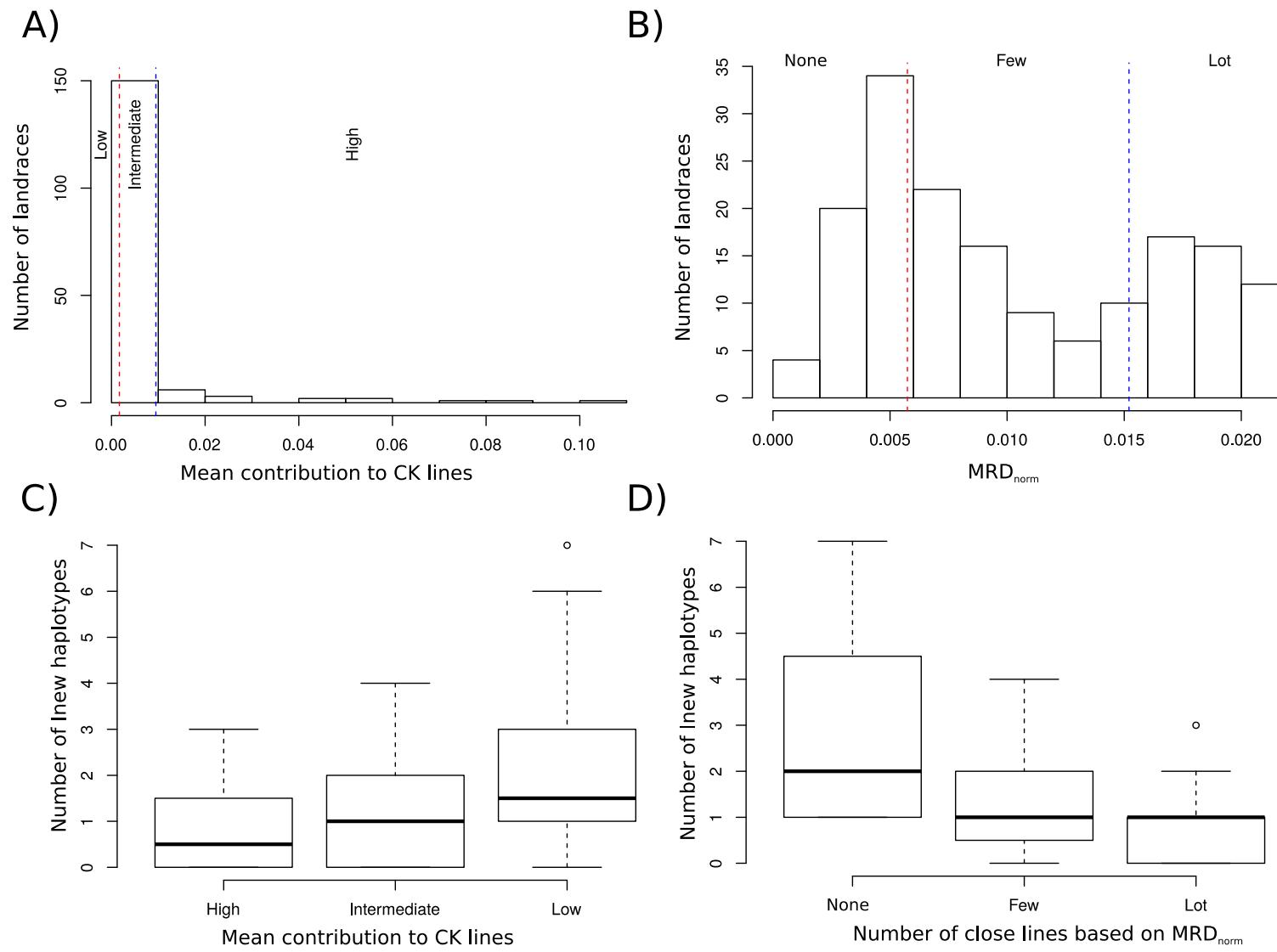


Fig. 5: Allelic enrichment of CK lines by new DH-SSD lines derived from landraces according their contribution and their genetic distance to CK lines.
 Allelic enrichment was estimated by the number of new haplotypes discovered in the 66 new DH-SSD lines derived from 33 landraces, compared to the 327 CK lines (C, D) that are classified in 3 classes according to the distribution of A) the average contribution to CK line panel using supervised analysis and B) the normalized MRD (MRD_{norm}) of the 10% closest CK lines with each landrace. Red and blue vertical dotted lines delineate the limits of three landrace classes displaying A) low, intermediate and high contribution; B) the presence of none, few and many closely related lines based on MRD_{norm} .