

Variables factor map (PCA)

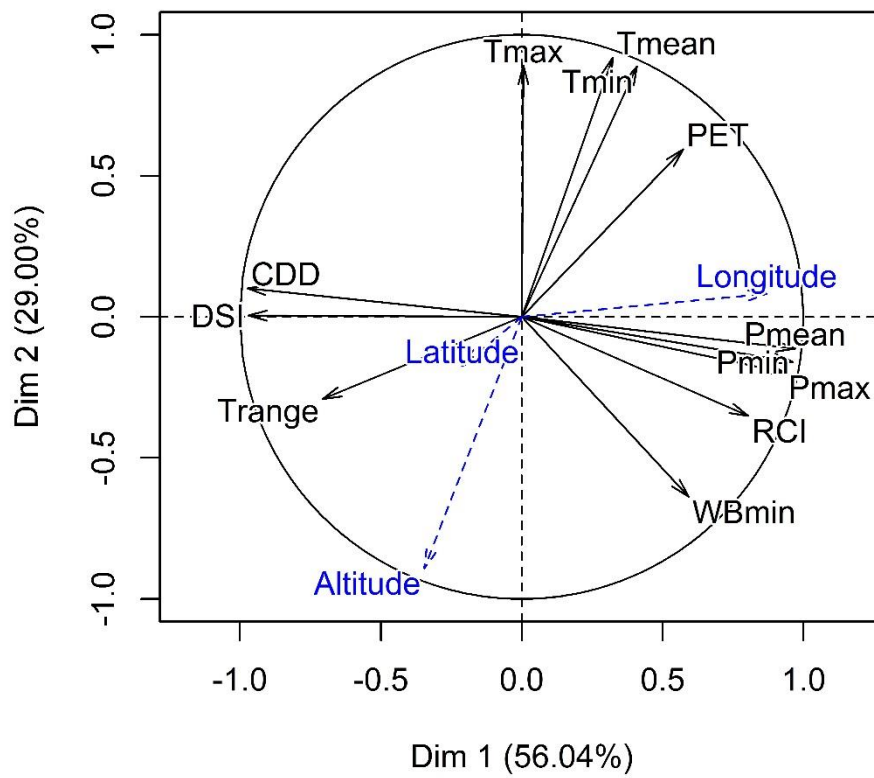


Figure S1. PCA results for the 12 climatic variables. Longitude, Latitude and Altitude were set as illustrative factors. Percentage of explained variance of each axis is given in parentheses.

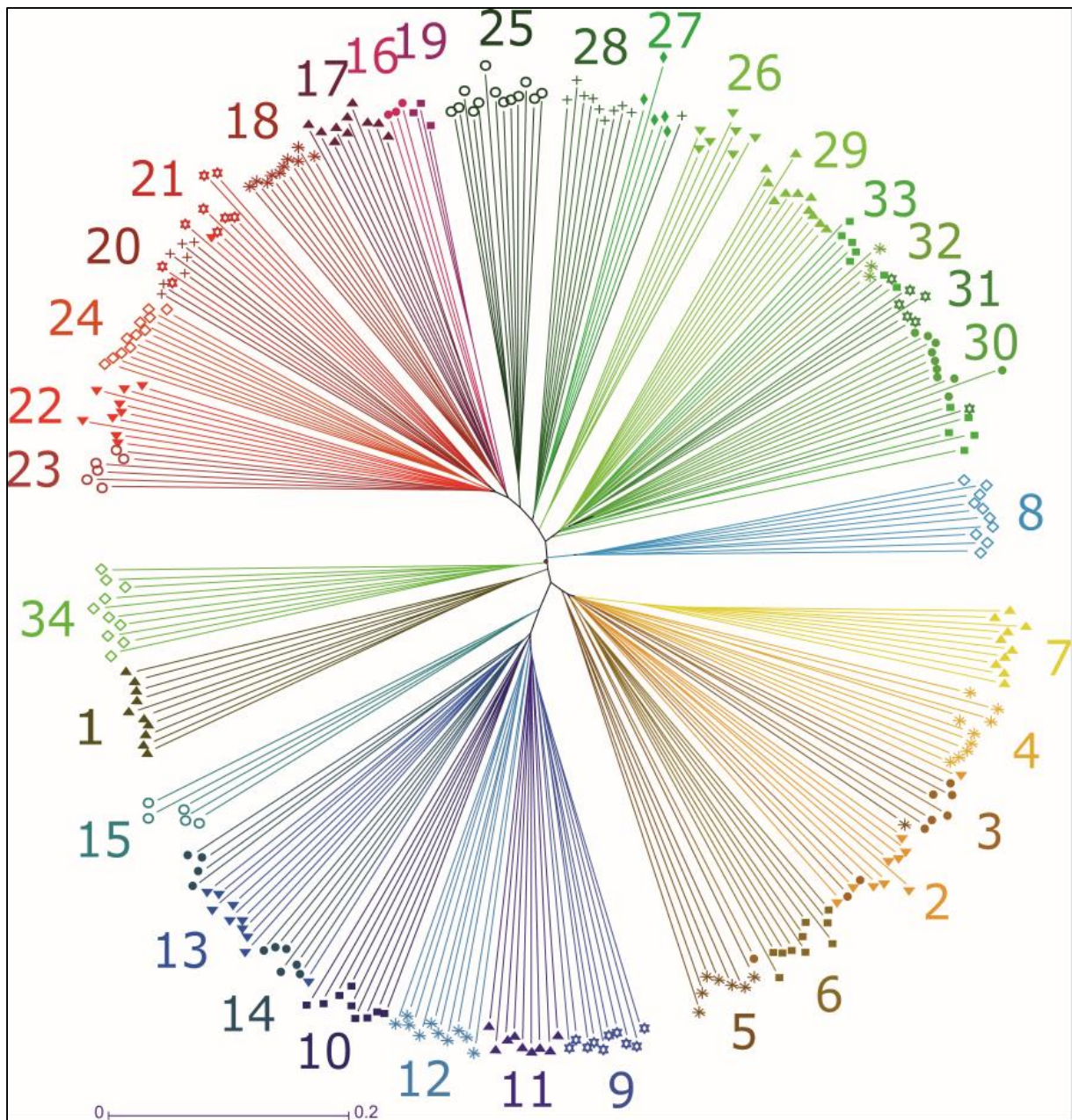


Figure S2. Unweighted NJ tree based on Jaccard's distances estimated from 1860 filtered SilicoDArT markers among 296 *C. mauritiana* (individuals < 5% NA) samples originating from 34 source populations in Reunion Island. Source population codes are given in Table 1. Colors distinguish the main geographical regions of sampling.

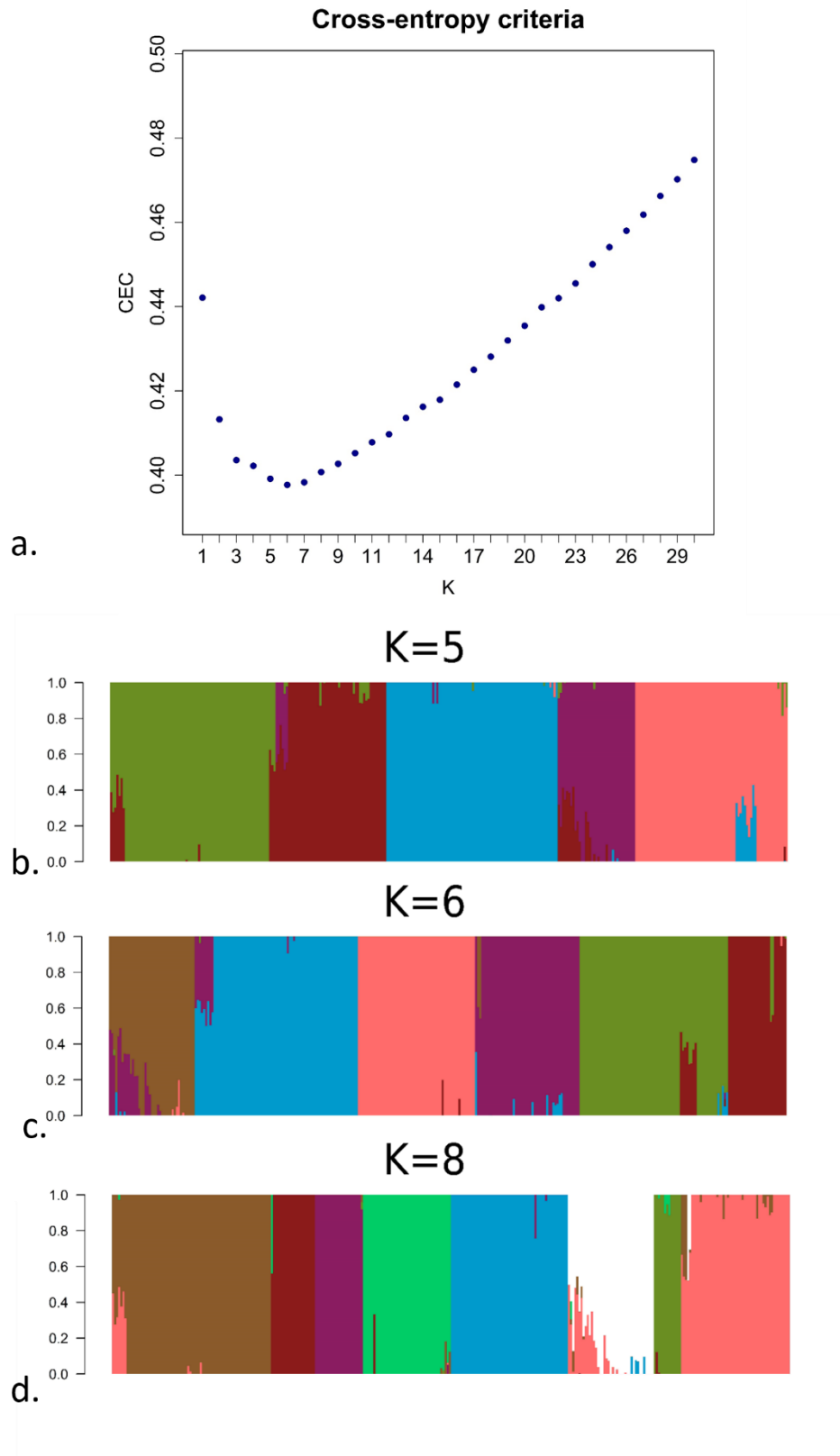


Figure S3. Inference of spatial genetic structure using sNMF. **(a)** Values of cross-entropy criteria (CEC) estimated for each putative number of genetic clusters (K). The best CEC value is displayed for each putative K value. **(b)** Group assignment at K=5. **(c)** Group assignment at K=6. **(d)** Group assignment at K=8.

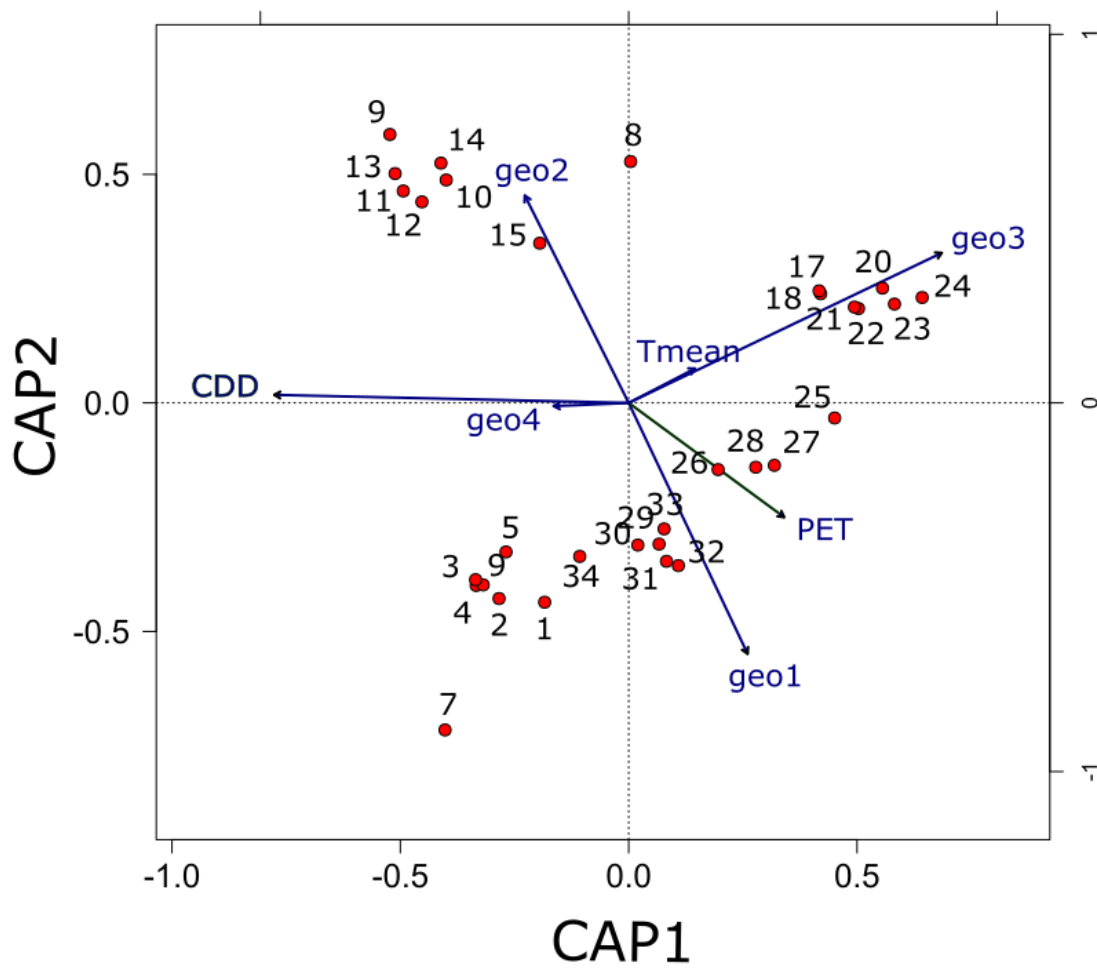


Figure S4. Biplot of RDA analysis. Information on source populations is given in table 1. Eigenvalues for constrained axes: CAP1=34.37%; CAP2=10.09%. Tmean: average daily temperature; CDD: mean number of consecutive dry days; PET: average monthly potential evapotranspiration; geo1, geo2, geo3: uncorrelated descriptors of geographic distances

Table S1. Species sampled for DArTseq experiment

Species	Origin	Acc. Code*	Biogeographic group
<i>C. mauritiana</i>	Reunion Island	1 to 326	Mascarenes
<i>C. mauritiana</i>	Mauritius	RM-CF-00599	Mascarenes
<i>C. macrocarpa</i>	Mauritius	RM-CF-00615	Mascarenes
<i>C. bernardiniana</i>	Mauritius	RM-CF-00638	Mascarenes
<i>C. bernardiniana</i>	Mauritius	RM-CF-00655	Mascarenes
<i>C. bernardiniana</i>	Mauritius	MPL-B	Mascarenes
<i>C. myrtifolia</i>	Mauritius	MPL-M	Mascarenes
<i>C. myrtifolia</i>	Mauritius	RM-CF-00662	Mascarenes
<i>C. myrtifolia</i>	Mauritius	RM-CF-00658	Mascarenes
<i>C. bertrandii</i>	Madagascar	RM-CF-00515	Madagascar
<i>C. perrieri</i>	Madagascar	RM-CF-00513	Madagascar
<i>C. tsirananae</i>	Madagascar	RM-CF-00514	Madagascar
<i>C. dolichophylla</i>	Madagascar	MPL-D	Madagascar
<i>C. sessiliflora</i>	Kenya	RM-CF-00487	East Africa
<i>C. pseudozanguebariae</i>	Kenya	RM-CF-00471	East Africa
<i>C. eugenioides</i>	Kenya	RM-CF-00422	East Africa
<i>C. canephora</i>	D.R. Congo	MPL-HD200-94	West and central Africa
<i>C. liberica</i>	Central African R.	RM-CF-00207	West and central Africa

* Accession numbers of either the IRD *Coffea* field genebank (RM-CF, www.intertrop.antilles.inra.fr/Portail/) or the greenhouse collection (MPL) are given.

Table S2. Pearson's correlation coefficients calculated between the 12 climatic variables, elevation, longitude and latitude. Pearson's correlation coefficients are below the diagonal and p-values calculated according to Holm's method are above.

	Tmin	Tmean	Tmax	Trange	Pmin	Pmean	Pmax	RCI	CDD	DSI	PET	WBmin	Elevation	Longitude	Latitude
Tmin		<0.001	<0.001	0.03	1	1	1	1	1	1	0.005	1	<0.001	1	1
Tmean	0.98		<0.001	0.85	1	1	1	1	1	1	0.01	1	<0.001	1	1
Tmax	0.82	0.91		1	1	1	1	1	1	1	0.86	1	<0.001	1	1
Trange	-0.59	-0.43	-0.02		0.06	0.002	0.14	1	0.001	<0.001	0.14	1	0.75	0.61	<0.001
Pmin	0.24	0.17	-0.1	-0.56		<0.001	<0.001	<0.001	<0.001	<0.001	0.24	<0.001	1	1	<0.001
Pmean	0.29	0.21	-0.12	-0.67	0.92		<0.001	<0.001	<0.001	<0.001	0.45	0.03	1	1	<0.001
Pmax	0.19	0.13	-0.14	-0.53	0.89	0.97		<0.001	<0.001	<0.001	1	0.01	1	1	<0.001
RCI	0.01	-0.02	-0.16	-0.25	0.85	0.79	0.88		<0.001	<0.001	1	<0.001	1	1	0.12
CDD	-0.29	-0.2	0.12	0.68	-0.97	-0.95	-0.89	-0.76		<0.001	0.08	0.01	1	1	<0.001
DSI	-0.41	-0.31	0.02	0.74	-0.92	-0.95	-0.89	-0.71	0.95		0.23	0.03	1	1	<0.001
PET	0.65	0.63	0.43	-0.53	0.5	0.47	0.41	0.28	-0.55	-0.5		1	0.02	1	0.03
WBmin	-0.24	-0.3	-0.41	-0.15	0.71	0.6	0.63	0.74	-0.62	-0.59	-0.24		1	1	1
Elevation	-0.98	-0.99	-0.89	0.44	-0.2	-0.22	-0.14	-0.01	0.22	0.34	-0.6	0.24		1	1
Longitude	-0.18	-0.13	0.1	0.45	-0.1	-0.32	-0.22	0.09	0.22	0.23	-0.31	0.28	0.14		0.02
Latitude	0.39	0.31	-0.04	-0.75	0.8	0.89	0.8	0.54	-0.88	-0.87	0.59	0.34	-0.33	-0.6	

Table S5. Results from *f3-statistic* tests among the seven clusters defined by sNMF analysis. Only negative Z-score are shown. According to Reich *et al.* (2009), results were considered as significant when Z-score < -2. Admixt population = population tested for admixture between parent 1 and 2.

Admixt population	Parent 1	Parent 2	f3-statistic	s.e.	Z-score
SW	W	NE	-0.00109	0.000615	-1.77402
SW	W	SE	-0.00132	0.0004	-3.28951
SW	NW	SE	-7.35E-05	0.000497	-0.14774
SW	W	E	-0.00196	0.000659	-2.98648
SE	W	E	-0.00127	0.000599	-2.12336
SE	E	SW	-0.00063	0.000414	-1.51478
C	NE	NW	-0.00165	0.000845	-1.94858
C	NW	E	-0.00164	0.000948	-1.73423