Supplementary Figures

Figure S1 . Population structure analysis of 326 cultivars, 403 seed born individual west Mediterranean and 15 wild east genotypes

Figure S2 . Population structure analysis of 142 truly WW.

Figure S3 . Principal component analysis for complexity reduction of the soil variables extracted for the 403 sampled location from SoilGrid 250.

Table S2: Variance inflation factor (VIF) for all selected environmental variable including five bioclimatic variables and four soil variables.

Figure S4. Environmental Niche Modelling (ENM)

Figure S5. Redundancy analysis (RDA) biplot based on 142 truly-wild individuals.

Figure S6. Spatial genomic offset (GO) of wild genotypes at the northernmost and southernmost extremes of the sampled area

Figure S7. Scaled cultivar genomic offset.

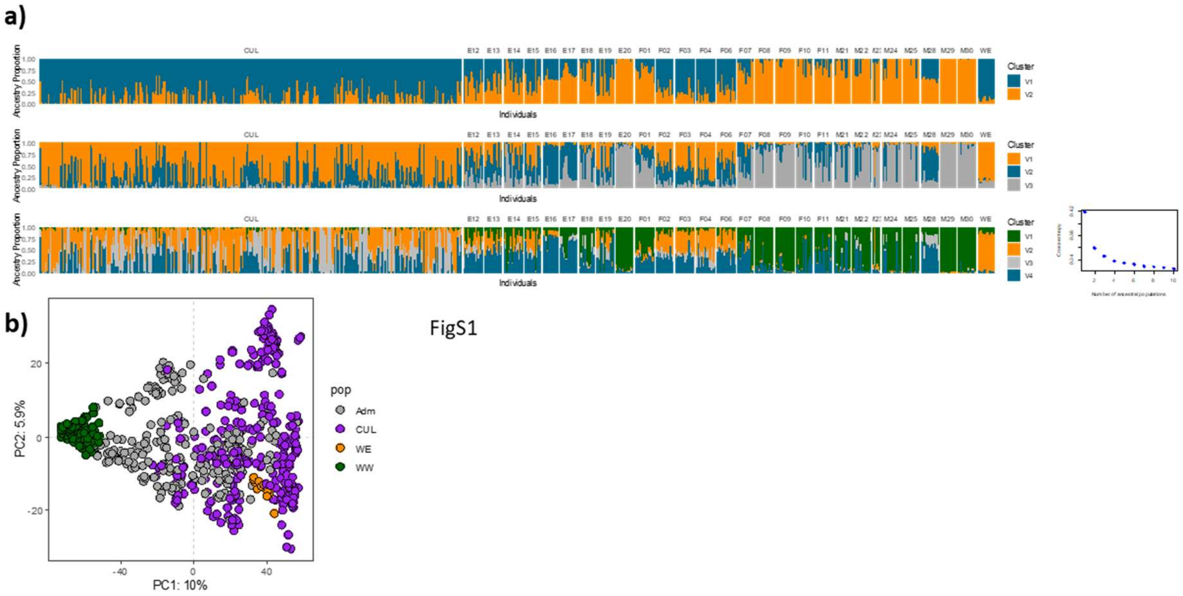


Figure S1 . Population structure analysis of 326 cultivars, 403 seed born individual from western Mediterranean and 15 wild east genotypes **(a)** ancestry bar plot inferred by sNMF, each horizontal bar indicates individuals assignment to a genetic cluster with K being the number of genetic cluster (from 2 to 4) **(b)** genomic PCA, where 142 truly wild-West (WW) individuals are colored in green, 15 wild-East (WE) individuals colored in orange, admixed seed-born genotypes are shown in grey, and cultivated genotypes from the WOGBM collection are shown in purple.

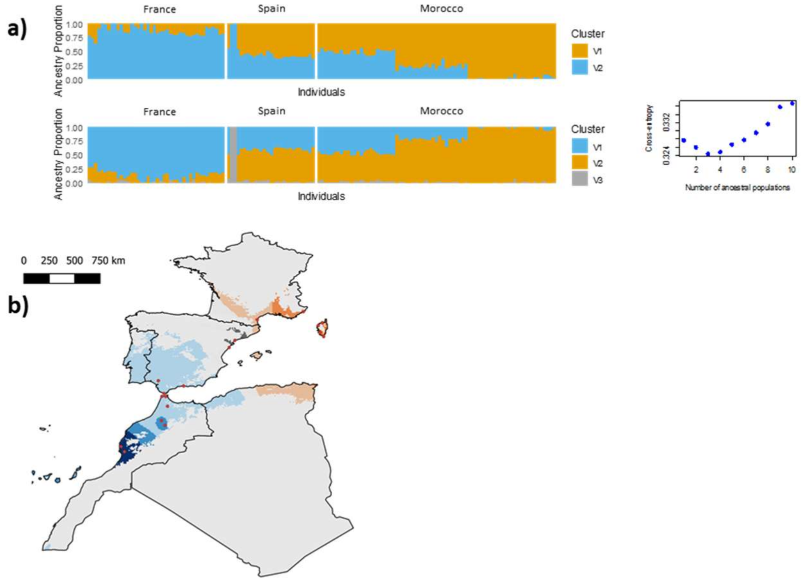


Figure S2 . Population structure analysis of 142 truly WW. **(a)** ancestry bar plot inferred by sNMF, each horizontal bar indicates individuals assignment to a genetic cluster with K being the number of genetic cluster (from 2 to 3) **(b)** spatial Kriging interpolation of ancestry values at K=3

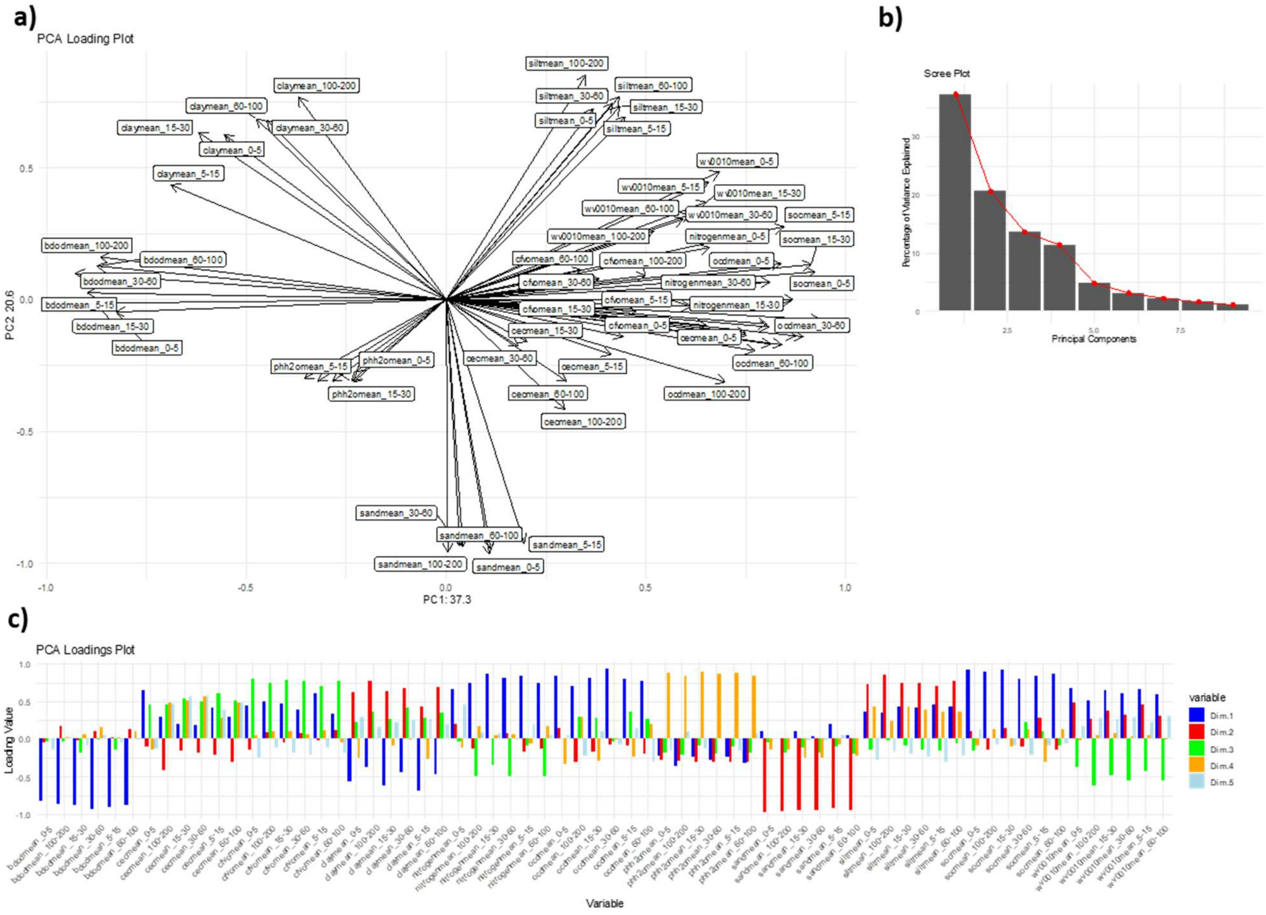


Figure S3 . Principal component analysis for complexity reduction of the soil variables extracted for the 403 sampled location from SoilGrid 250. **(a)** PCA loading plot of the entire set of soil variables. **(b)** Scree plot representing the relative percentage of explained variance for each PCs. **(c)** Loading values of each explanatory variable across the four main PCs **(d)** Variance inflation factor (VIF) for all selected environmental variable including five bioclimatic variables and four soil variables.

Table S2: Variance inflation factor (VIF) for all selected environmental variable including five bioclimatic variables and four soil variables.

Variable	*VIF Value*	*Type*
bio2 (Mean Diurnal Range)	3.733	Bioclimatic
bio10 (Mean Temp. of Warmest Quarter)	1.969	Bioclimatic
bio11 (Mean Temp. of Coldest Quarter)	3.875	Bioclimatic
bio15 (Precipitation Seasonality)	4.200	Bioclimatic
bio18 (Precipitation of Warmest Quarter)	2.594	Bioclimatic
bio19 (Precipitation of Coldest Quarter)	2.328	Bioclimatic
Clay (%)	3.055	Soil
Nitrogen (N)	2.588	Soil
Soil pH	1.480	Soil
Sand (%)	2.885	Soil

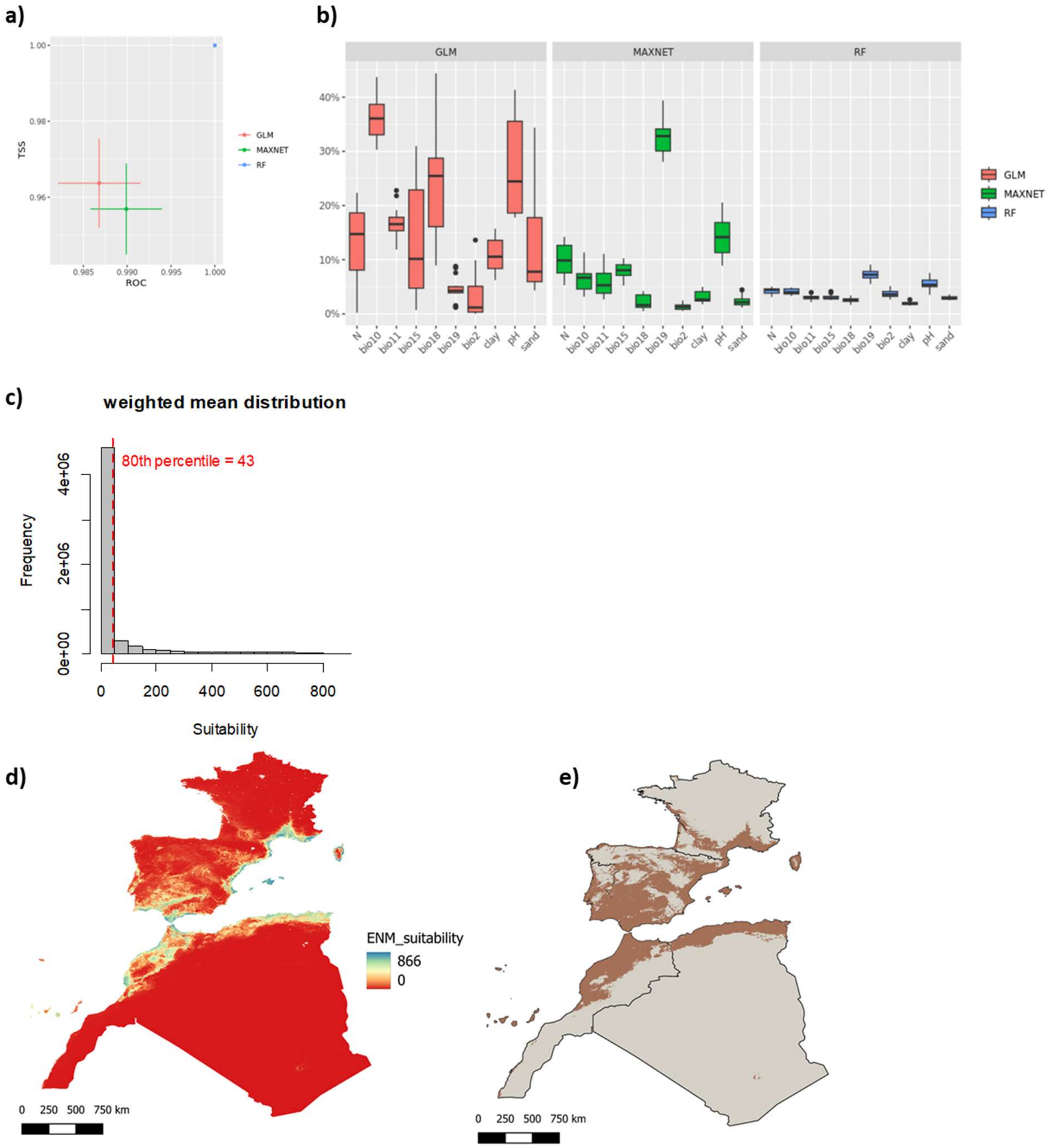


Figure S4. Environmental Niche Modelling (ENM) across the Western Mediterranean, including the countries of France, Spain, Portugal, Morocco, and Algeria.(a) Model performance scores (TSS and ROC) for the individual models (GLM, MAXENT, and RF). (b) Variable importance across the three individual algorithms. (c) Weighted ENM suitability distribution. (d) Continuous suitability map derived from an ensemble model, where individual models (GLM, MAXENT, RF) are weighted by their TSS and ROC scores. .(e)Binary ENM raster mask obtained by applying an 80th percentile threshold

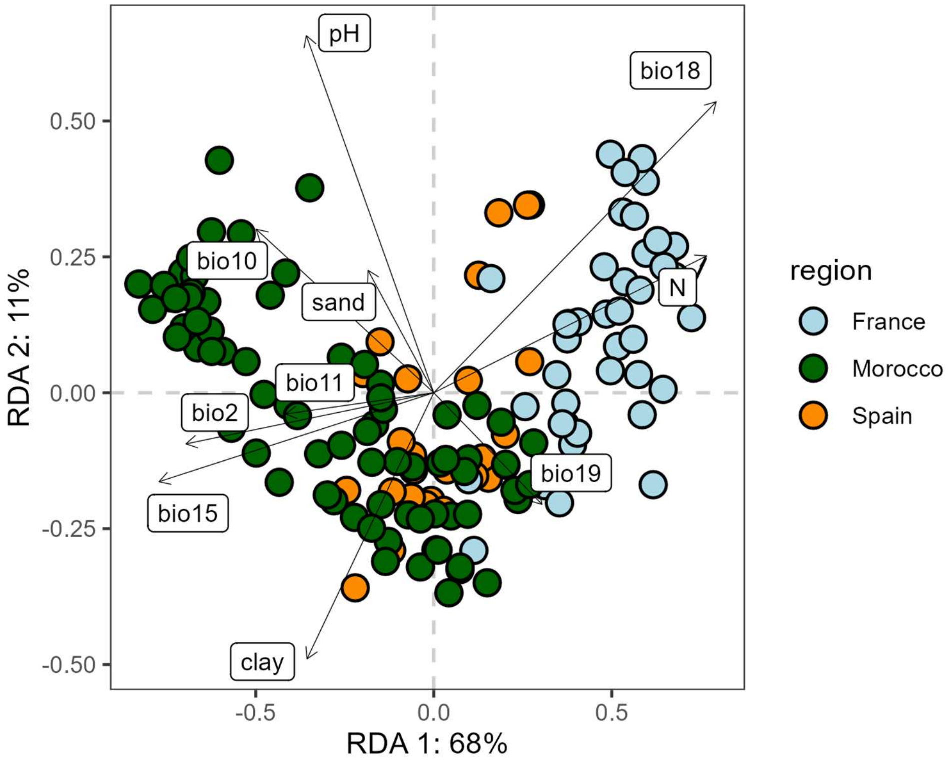


Figure S5. Redundancy analysis (RDA) biplot based on 142 truly-wild individuals. The genetic data derived from 124 LFMM-based GEA filtered for polymorphism within the cultivated population (minor allele frequency > 0.05). Arrows represent the loadings of the 10 selected climatic and soil variables. Points represent individual genotypes projected in the constrained RDA space, with colors indicating the respective country of orgin : light blue (France), orange (Spain) and green (Morocco)

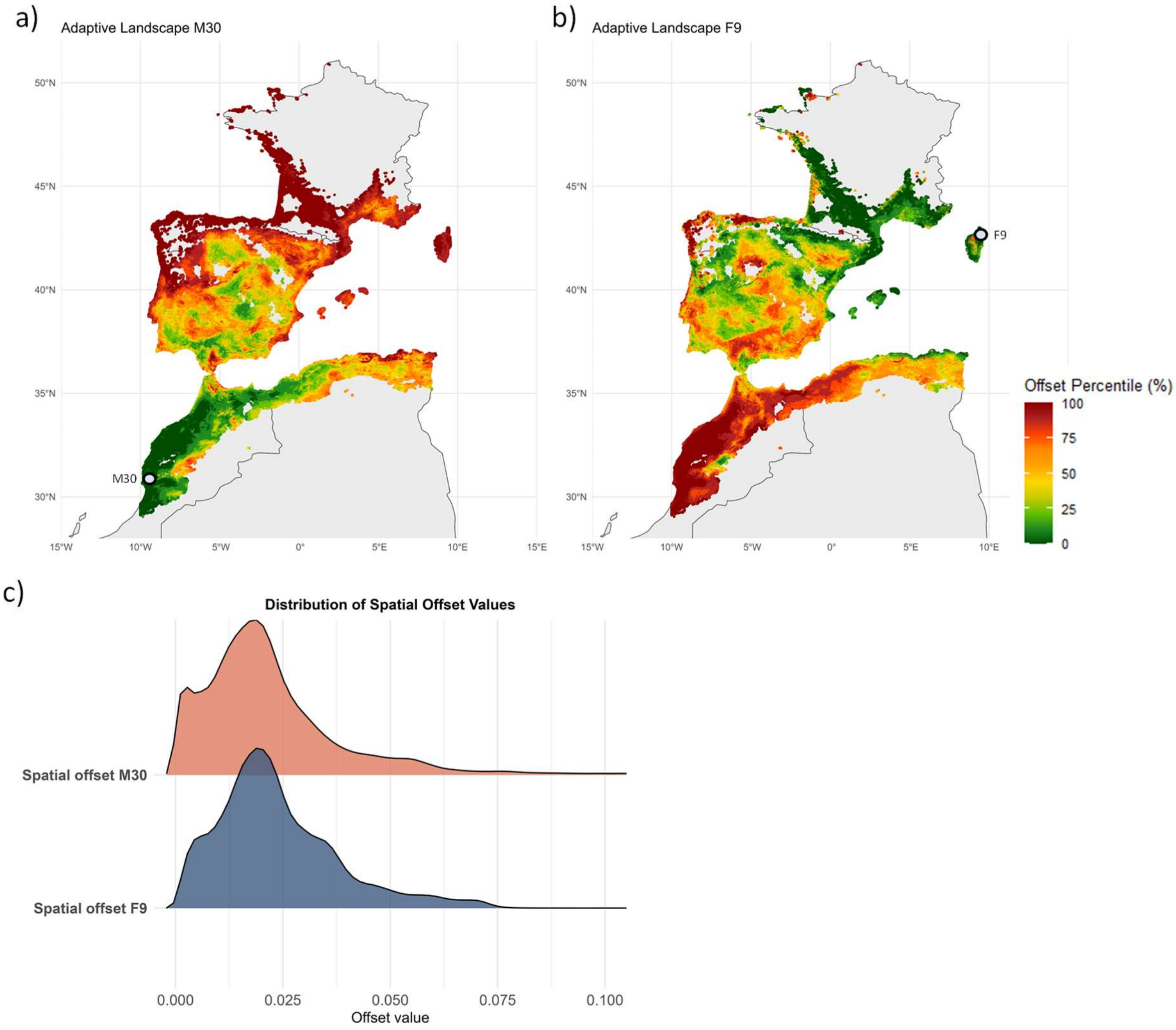
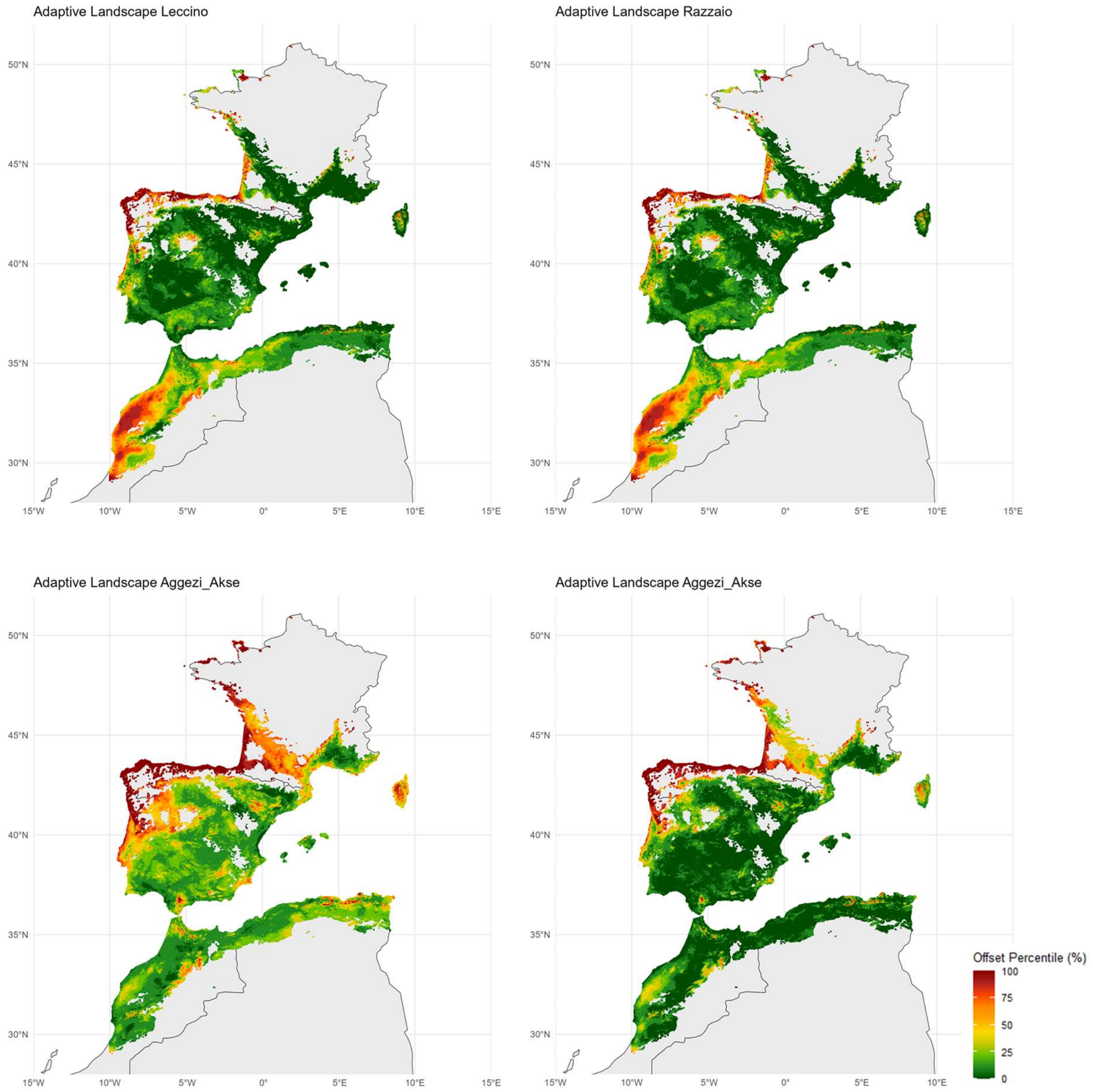


Figure S6. Spatial genomic offset (GO) of wild genotypes at the northernmost and southernmost extremes of the sampled area. **(a)** Spatial GO of one individual from the M30 wild population. **(b)** Spatial GO of one individual from the F9 wild population. **(c)** Ridge distributions represent the spatial GO values for M30 and F9, respectively.



Adaptive Landscape Leccino

Adaptive Landscape Razzaio

Adaptive Landscape Aggezi_Akse

Adaptive Landscape Aggezi_Akse

Figure S7. Scaled cultivar genomic offset.

Geographic projection of the spatial offset calculated as weighted quadratic distance (geometric offset) between the specific cultivar and all the spatial pixels.

The top two projections highlight two cultivars from the northern Mediterranean (Frantoio and Razzaio, originating from Tuscany, Italy) while the bottom two projections show two cultivars from the southern Mediterranean (Aggezi Akse from Egypt and Beladi-557 from Lebanon). Color scale of each cultivar’s GO is relative to the minimum and maximum values observed in wild sample F9 located at the northern extreme of the sampled area.