

Supplementary Materials for

The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange

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The PDF file includes:

Figs. S1 to S8
Tables S1 to S4

Other Supplementary Material for this manuscript includes the following:

Files S1 to S7

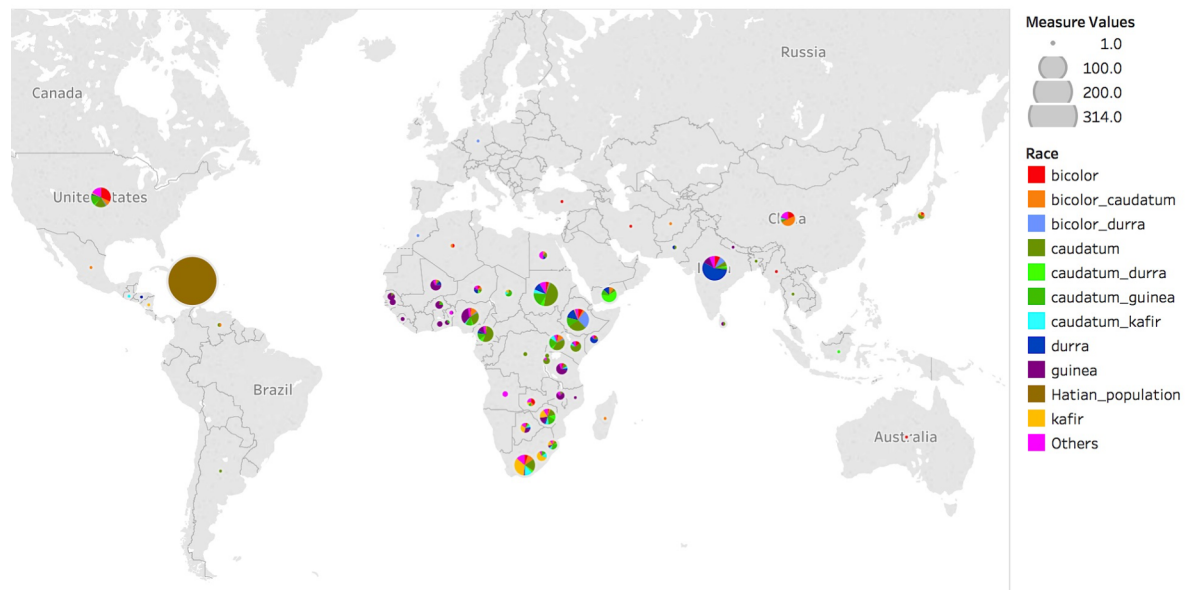


Figure S1: Global diversity panel used to study population genomics of Haitian breeding population. The size of each circle is proportional to the number of accessions and the botanical type is noted with color-coding.

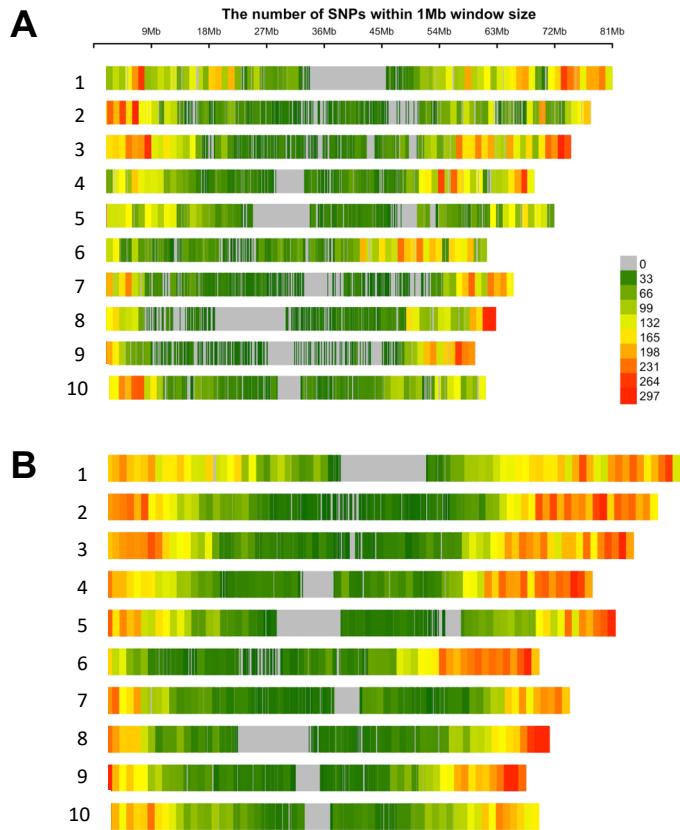


Figure S2: Marker density of genome-wide single-nucleotide polymorphism data set. The number of single-nucleotide polymorphism (SNP) within 1 Mb windows for the Haitian breeding population (A) and global diversity panel (B) on the ten chromosomes of sorghum.

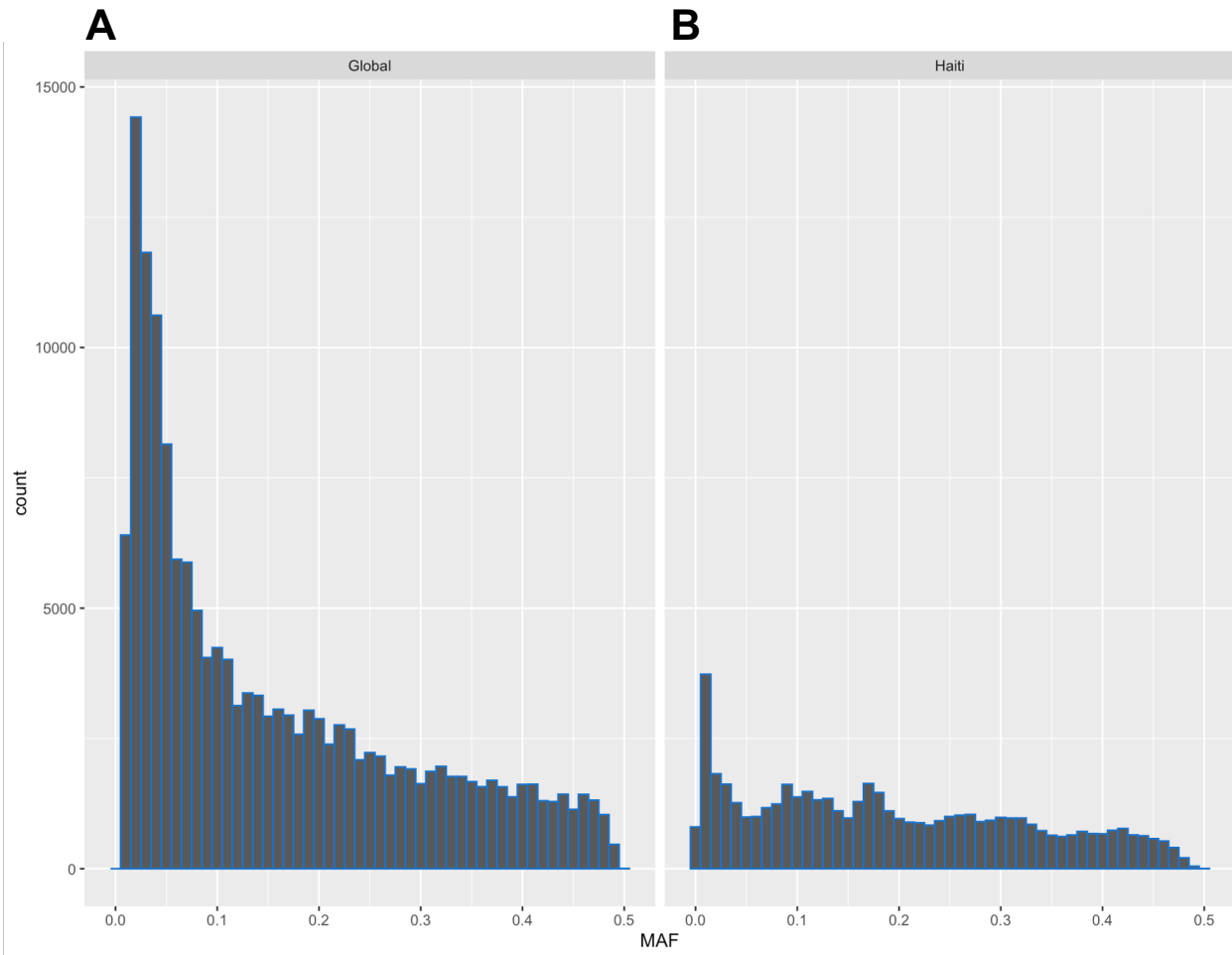


Figure S3: Minor allele frequency (MAF) distribution in genome-wide single-nucleotide polymorphism data set. MAF for the global diversity panel (A) and the Haitian breeding population (B).

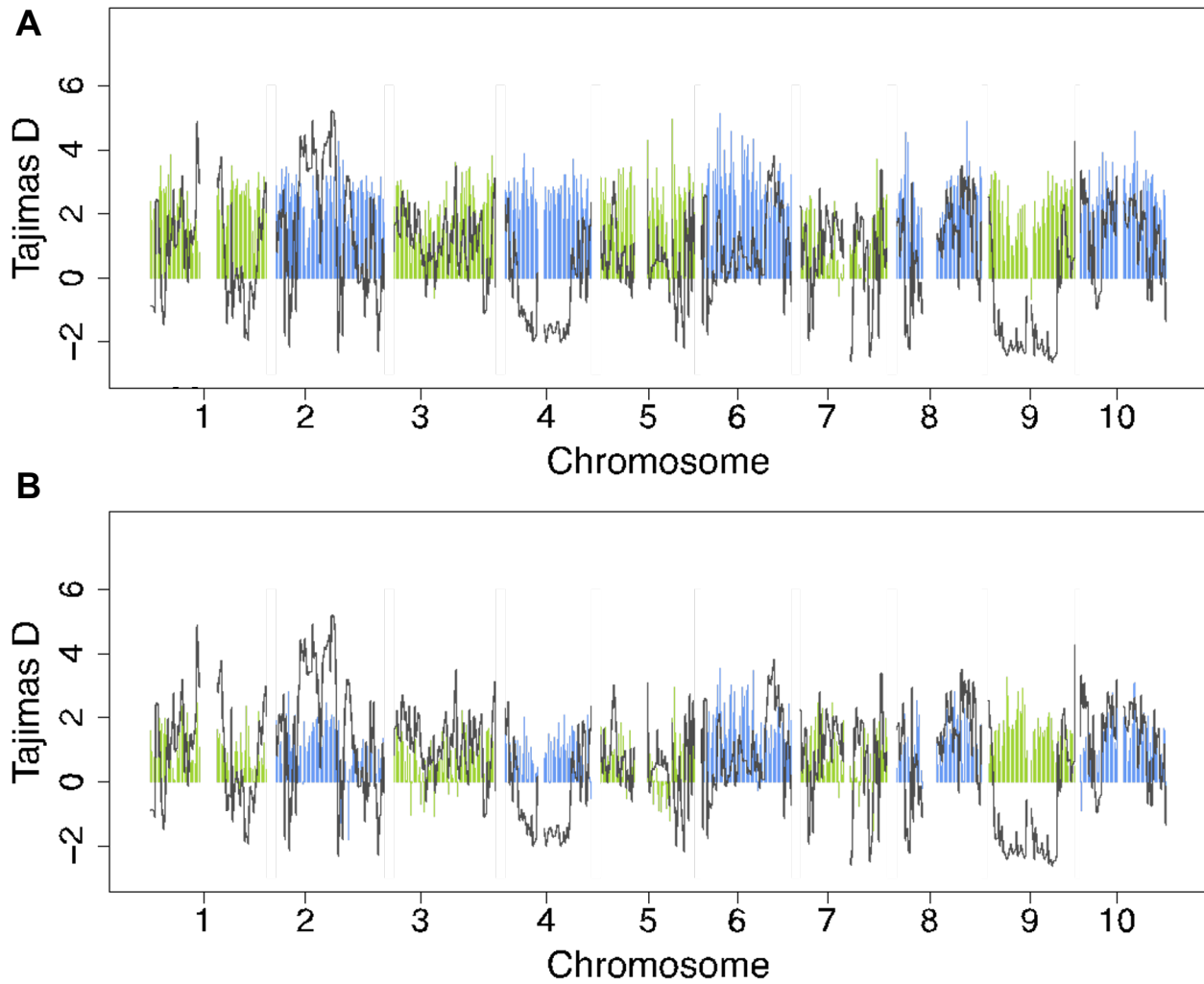


Figure S4: Comparative genome-wide patterns of Tajima's D for non-overlapping sliding windows of 1 Mbp across the genome. Tajima's D test statistic between HBP (black lines) versus (A) East African Caudatum (EAC) (colored bars) or (B) Texas A&M University publicly-available prebreeding lines (colored bars).

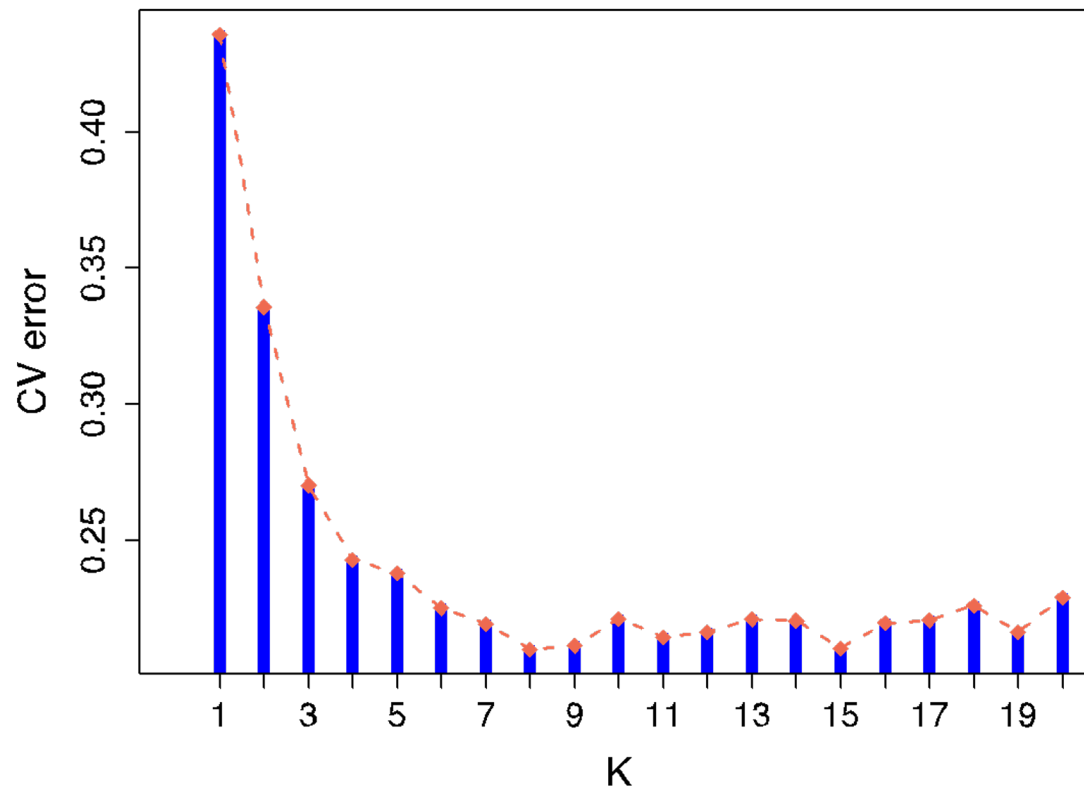


Figure S5: Cross-validation for ADMIXTURE population structure analysis. Ten-fold cross-validation (CV) error rates for $K = 1$ to 20 determined in ADMIXTURE analysis.

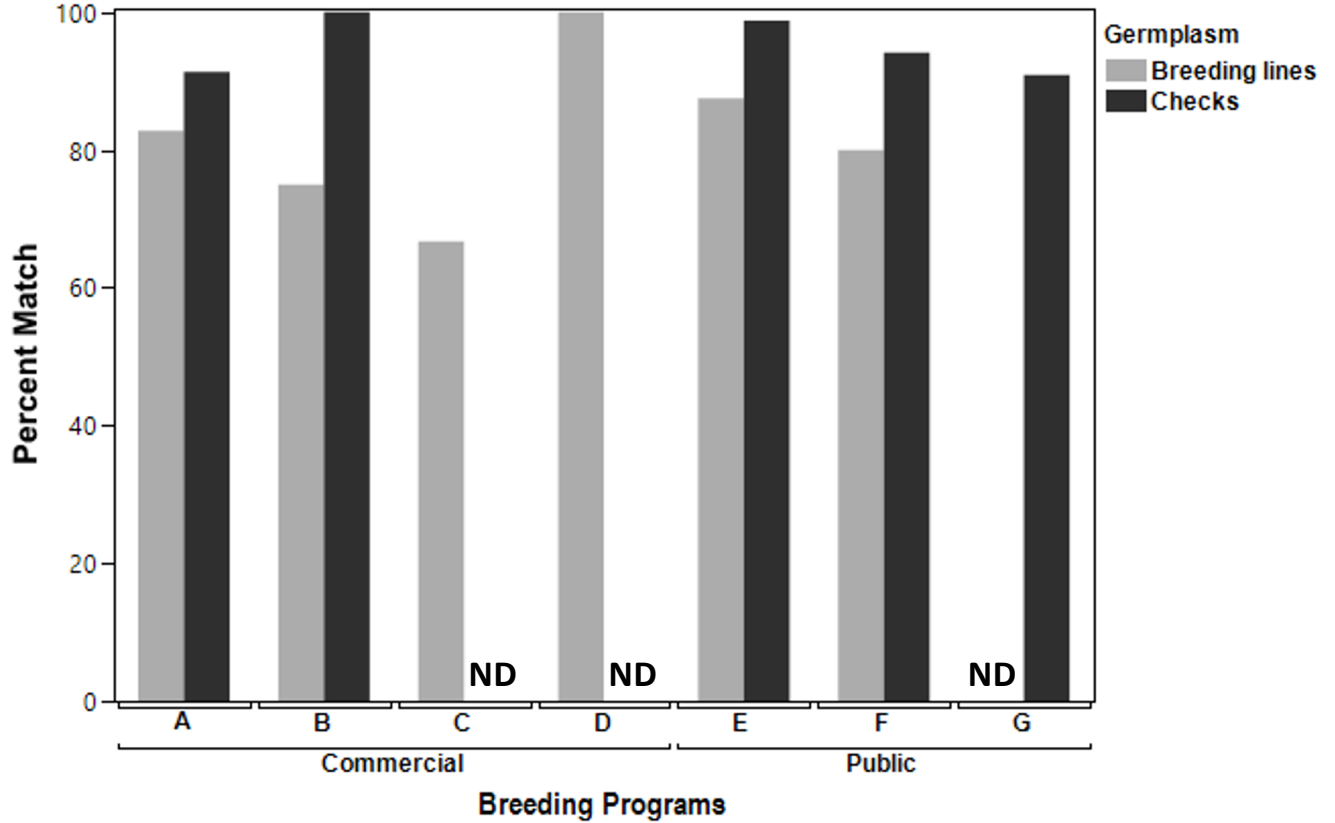


Figure S6: Evaluation of the molecular marker at SNP 06_02892438 in seven US breeding programs, with only unique genotypes counted. No biological or technical replication of genotypes included. Percent match of KASP marker genotyping prediction with breeder-provided SCA resistance classification for five commercial breeding programs and three public breeding programs. ND = Not determined.

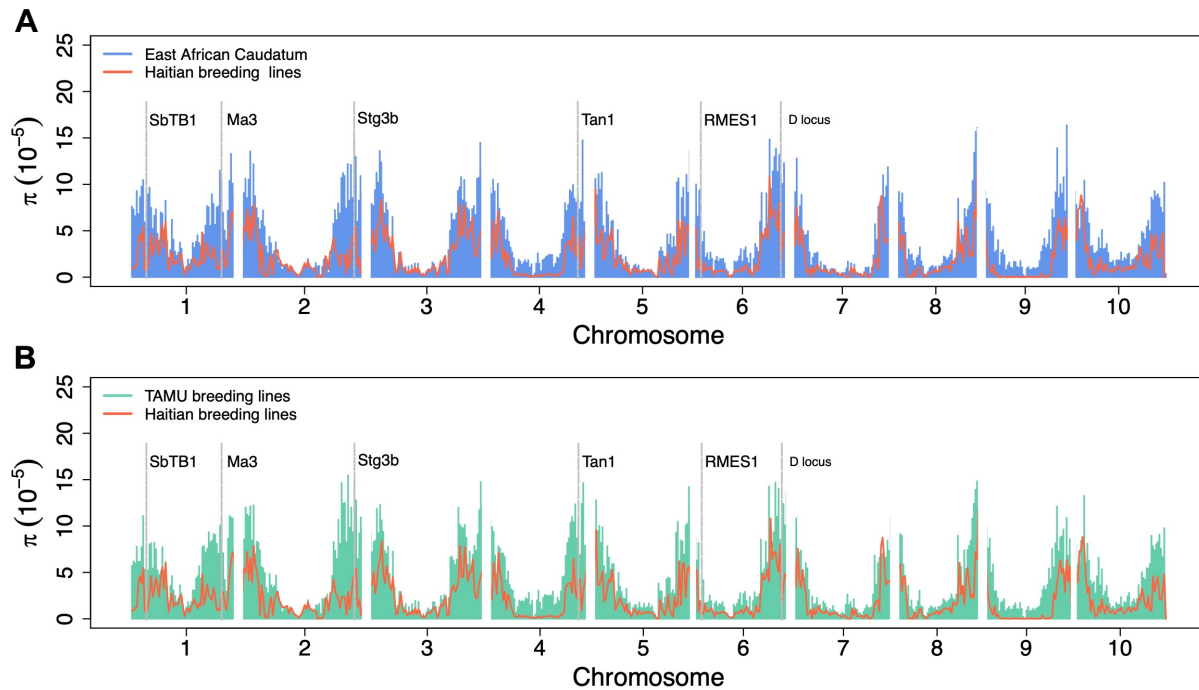
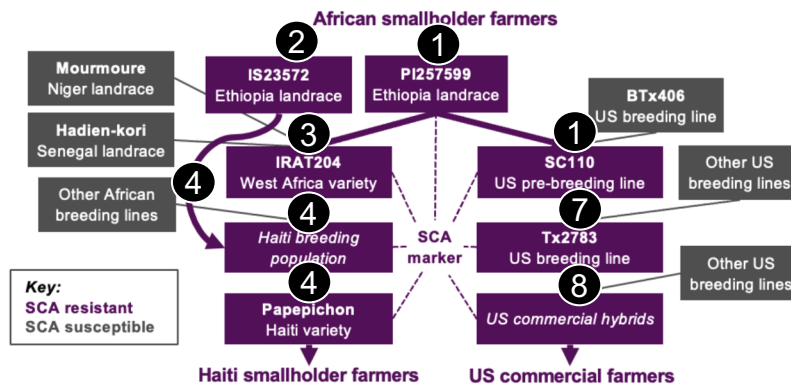
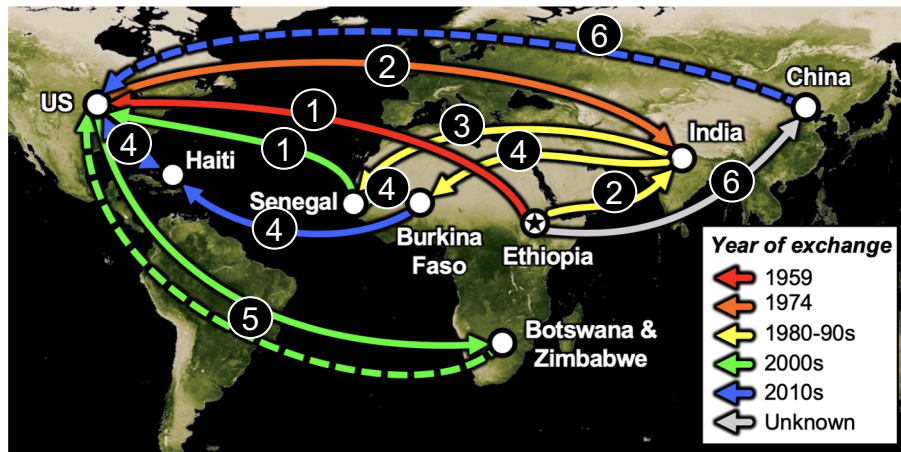


Figure S7: Genome-wide nucleotide diversity (π) in the Haitian breeding population compared to other germplasm sets. Comparison of π for the Haitian breeding population versus East African caudatum germplasm (A) and Texas A&M University (TAMU) publicly-available prebreeding germplasm (B). The grey vertical dashed lines indicate the position of previously known genes that colocalized with genomic signatures based on reduced nucleotide diversity in the Haitian breeding population compared to the global diversity. Nucleotide diversity was calculated for a non-overlapping sliding window of 1 Mbp across the genome.



- 1. Pedigree records, USDA GRIN (PI 257599, PI 533794, PI 656031)**
https://www.ars-grin.gov/npgs/pi_books/scans/167/pi167_143.pdf
<https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=1428730>
<https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=1795270>
- 2. Pedigree records, Genesys (IS 12610, IS 23572)**
<https://www.genesys-pgr.org/a/v2kg73EQGA8>
<https://www.genesys-pgr.org/a/v2rqab1dqGQ>
- 3. Pedigree records, ISRA-Senegal**
http://www.fao.org/pgafa-gpa-archive/sen/docs/senegal_varietes/Catalogue_%20varietes.htm
- 4. Pedigree records, Chibas/Gael Pressoir**
 Current study
- 5. Publication: Teetes et al. 1995 Int J Trop Ins Sci**
 DOI: 10.1017/S1742758400018336
- 6. Publication: Wang et al. 2013 Molecular Breeding**
 DOI: 10.1007/s11032-012-9832-6
- 7. Publication: Peterson et al. 1984 Crop Science**
 DOI: 10.2135/cropsci1984.0011183X002400020062x
- 8. Marker testing and discussion with industry representatives (Fig. 5)/Geoff Morris**
 Current study

Figure S8: Detailed evidence for history of germplasm and knowledge exchange presented in Figure 6. All literature citations are provided in the main text. Map: Visible Earth/NASA

Table S1: Minor allele frequency, observed and expected heterozygosity, and inbreeding coefficient for germplasm sets

Parameters	Haitian breeding population	Global diversity panel	East African Caudatum
Minor allele frequency	0.19	0.15	0.17
Observed heterozygosity	0.03	0.02	0.02
Expected heterozygosity	0.27	0.23	0.24
Inbreeding coefficient	0.87	0.91	0.92

Table S2: Chromosome-wise summary of Tajima's *D* statistics and nucleotide diversity (π)

Chr.	Tajima's <i>D</i> statistics			Nucleotide diversity		
	Texas A&M	Haitian breeding population	Global diversity	Texas A&M	Haitian breeding population	Global diversity
1	1.03	0.84	2.32	6.1E-05	2.9E-05	7.7E-05
2	1.11	1.69	2.55	4.9E-05	2.1E-05	6.3E-05
3	0.84	1.14	2.09	5.1E-05	2.9E-05	6.3E-05
4	0.99	-0.28	2.58	4.8E-05	2.2E-05	6.2E-05
5	0.86	0.62	2.46	4.4E-05	2.2E-05	5.3E-05
6	1.80	0.90	2.93	5.1E-05	2.4E-05	5.6E-05
7	0.95	0.78	1.41	3.4E-05	1.8E-05	4.0E-05
8	1.32	1.20	2.57	4.5E-05	2.3E-05	5.2E-05
9	1.54	-1.13	2.15	4.7E-05	1.7E-05	5.4E-05
10	1.30	1.38	2.66	4.6E-05	2.4E-05	5.6E-05
Average	1.17	0.71	2.37	4.76E-05	2.29E-05	5.76E-05

Table S3: Allele frequencies of high F_{ST} SNPs around *RMES1*

Population	SNPs				
	S6_2682627	S6_2892438	S6_2927739	S6_2983634	S6_2995581
HBP (n=300)	A (293)	T (289)	T (290)	T (293)	T (292)
	C (5)	C (6)	C (6)	C (5)	C (5)
	M (2)	Y (5)	Y (4)	Y (2)	Y (3)
GDP (n=965)	A (74)	T (15)	T (21)	T (18)	T (15)
	C (873)	C (950)	C (944)	C (947)	C (949)
	M (22)	Y (4)	Y (4)	Y (4)	Y (5)
Ethiopian caudatum	A (11)	T (10)	T (11)	T (11)	T (10)
	C (14)	C (15)	C (14)	C (14)	C (14)
	M (0)	Y (0)	Y (0)	Y (0)	Y (1)
PI533794 (SC110)	A	T	T	T	T
IRAT204	A	T	T	T	T
BTx623	C	C	C	C	C

Table S4: Instance of each mismatched check from the different breeding programs, and status of subsequent verification of validity of mismatch

Breeding Program	Mismatched Check	Status
A	RTx2783	Was confirmed that seed source was inaccurate, all other sources of RTx2783 from program matched expected genotype
E	B.line/RTx2783	Was confirmed to be self, not true F1
E	SC110	Was confirmed to be a planting error in the field
E	R.line/TAM428	Unsure of cause of mismatch
F	SC110	Unsure of cause of mismatch
F	R.line/IRAT204-F2	F1 material was open pollinated, deviations from expected genotype in F2 not unexpected
F	R.line/IRAT204-F2	F1 material was open pollinated, deviations from expected genotype in F2 not unexpected
F	R.line/TAM428-F2	F1 material was open pollinated, deviations from expected genotype in F2 not unexpected
F	R.line/TAM428-F2	F1 material was open pollinated, deviations from expected genotype in F2 not unexpected
G	IRAT204	Unsure of cause of mismatch