Supporting Information

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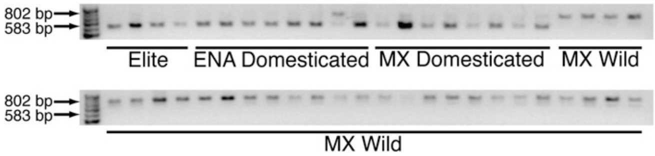

Fig. S1. Sample of restriction digest genotyping of *FLOWERING LOCUS T* homologue *HaFT1* PCR products. The frameshift mutation in the domesticated allele introduces a BstEII restriction site. No Mexican (MX) wild populations contained the frameshift, and their undigested PCR products ran at 802 bp. All improved, elite crop lines, all MX early domesticates, and all but one of the eastern North American (ENA) early domesticates included in this sample were homozygous for the domesticated allele (longer digestion product at 583 bp). One ENA early domesticate (seventh from left) shown is heterozygous for wild and domesticated alleles. All MX wild individuals were genotyped by restriction digest. All MX landrace genotypes were confirmed additionally by cloning and sequencing of PCR products.

Table S1. American and Canadian diversity panel

Species	Type	GRIN ID	Line name or population location
Helianthus argophyllus	Wild	PI 494571	Corpus Christi, TX
		PI 494572	North Padre Island, TX
		PI 494573	Port Aransas, TX
		PI 494580	Rachal, TX
		PI 494576	Skidmore, TX
		PI 494582	Victoria, TX
Helianthus annuus	Improved	PI 552943	RHA280
		PI 599984	HA821
		PI 534655	HA369
		PI 599768	RHA801
		PI 600000	RHA417
		PI 552937	HA292
		PI 578872	HA383
		PI 578873	HA384
		PI 607505	HA414
		PI 633744	HA434
		PI 599773	HA89
		PI 599759	RHA274
		PI 560141	RHA373
		PI 560145	RHA377
		PI 633746	RHA436
		PI 633748	RHA438
		PI 340790	USSR VNIIMK 8931 '66
		PI 650650	Ames7574, Mennonite
	Domesticated	PI 369357	Arikara
		PI 369360	Seneca
		PI 600717	Mandan #1
		PI 600718	Mandan #2
		PI 600719	Mandan #3
		PI 600720	Hidatsa #1
		PI 600721	Hidatsa #2
		PI 432504	Hopi dye
		PI 432505	Hopi
		PI 432507	Hopi dye
		PI 432508	Hopi dye
		PI 432509	Hopi dye
		PI 369358	Havasupai
		PI 369359	Hopi
		PI 432510	Hopi dye, possible hybrid w/Mammoth
		PI 432515	Zuni
		PI 432516	Pueblo

Table S1. Cont.

Species	Type	GRIN ID	Line name or population location
		PI 432521	Anzac Pueblo
		PI 432522	Laguna Pueblo
	Wild	PI 659440	Ann1238, Cedar Point Biological Station, NE
		PI 613750	Dickinson, ND
		PI 592325	Carievale, Saskatchewan
		PI 592316	Keeler, Saskatchewan
		PI 435434	Riviera, TX
		PI 435619	Tulsa, OK
		PI 494567	Skidmore, TX, Ann1811
		PI 468439	Colfax, ND
		PI 586879	Norden, NE
		PI 586872	Axtell, NE
		PI 435616	Topaz, MO
		PI 586869	Silver Creek, NE
		PI 586856	Great Bend, KS
		PI 586849	Colby, KS
		PI 613751	Minot, ND
		PI 613723	Crete, ND
		PI 613722	Onida, SD
		PI 613720	Garden City, KS
		PI 613711	Woonsocket, SD
		PI 592326	Boissevain, Manitoba
		PI 435505	McLoud, OK
		PI 468475	Childress, TX
		PI 597890	Yankton, SD

GRIN ID, US Department of Agriculture Germplasm Resources Information Network (http://www.ars-grin.gov/npgs/) identification number.

Table S2. Mexican accessions used in this study

Type	*N*	Population ID number	Culture or line	Location	Latitude	Longitude
Landrace	2	33655	Tarahumara	Chihuahua	26.84509	−106.93494
	2	34177	Nahua	Guerrero	17.92778	−99.52629
	2	34111	Nahua	Guerrero	17.92372	−99.51938
	2	34285	Tzeltal	Chiapas	16.90928	−92.09041
	2	34055	Nahua	Guerrero	17.92528	−99.52958
	2	34112	Nahua	Guerrero	17.92372	−99.51938
	2	34282	Tzeltal	Chiapas	16.90928	−92.09041
	1	34324	Mixe	Oaxaca	16.9601	−95.84218
	2	Ames 6859/PI 650646	Maiz de Tejas			
	2	34120	Nahua	Guerrero	17.9248	−99.33792
	2	34110	Nahua	Guerrero	17.92372	−99.51938
	2	34102	Nahua	Guerrero	17.92098	−99.52727
	2	34109	Nahua	Guerrero	17.92372	−99.51938
	2	33724	Mennonite	Chihuahua	28.3095	−106.10909
	2	34107	Nahua	Guerrero	17.9236	−99.53328
	2	Ames 19070/PI 650761	Maiz negro			
Wild	9	28280		Tamaulipas	22.86712	−99.10377
	6	28321		Nuevo Leon	24.11155	−99.82345
	11	28353		Zacatecas	22.78198	−103.5582
	7	28315		San Luis Potosi	22.30028	−100.837
	6	28339		Nuevo Leon	27.27295	−100.18203
	9	28395		Sinaloa	24.75317	−107.49903
	5	28392		Sinaloa	26.30297	−109.03337
	14	28376		Chihuahua	27.14178	−104.92337
	8	28307		Tamaulipas	23.00933	−99.69512
	8	28366		Zacatecas	24.71628	−101.3117
	12	28381		Chihuahua	28.57192	−105.95682
	10	28390		Sonora	27.5891	−109.92963
	7	28385		Sonora	30.20812	−111.09735
	4	PI 413123		Mayo Experimental Station		
	4	PI 413067		North of España		

Numbers with a "PI" (GRIN ID) were obtained from the US Department of Agriculture. Other accessions were collected by R.A.B. and D.L.L. from 2001 to 2005. All wild collections retrieved by R.A.B. and D.L.L. displayed the wild- type morphology with small heads, thin pedicels, and multiple flowering stalks per plant.

Table S3. Distribution of diversity at 12 microsatellite loci in domesticated and wild *H. annuus* from eastern North America (ENA) and Mexico (MX)

	ORS005	ORS008	ORS059	ORS078	ORS176	ORS229	ORS297	ORS337	ORS398	ORS399	ORS534	ORS596
Either/both wild only	16	6	23	2	16	6	15	8	30	15	20	8
Both wild + either/both domesticated	6 *68.83/ 88.00*	7 *99.67/ 99.30*	6	3 *80.13/ 59.59*	7 *88.22/ 88.67*	8 *90.74/ 100.00*	7	11	9	5	10 *99.39/ 99.29*	5
ENA wild + both domesticated	1 *17.59/ 12.00*	1 *0.33/ 0.70*										
ENA wild + ENA domesticated	2 *13.58/ 0.00*					1 *9.26/ 0.00*					1 *0.61/ 0.00*	
ENA wild + MX domesticated												
MX wild + both domesticated												
MX wild + ENA domesticated												
MX wild + MX domesticated											1 *0.00/ 0.71*	
Both domesticated only				1 *19.87/ 40.41*	1 *11.78/ 11.33*							
Total	25	14	29	6	24	15	22	19	39	20	32	13

Numbers are allele counts per locus in each distribution class. Class allele frequencies for ENA domesticated/MX domesticated accessions are listed in italics for loci where alleles (*i*) were present only in domesticated accessions or (*ii*) were present in either ENA or MX domesticated but were found in in wild populations in only one region. The average sample sizes per locus were as follows: ENA wild, 233 individuals; MX wild, 190 individuals; ENA domesticated, 158 individuals; MX domesticated, 74 individuals.

Table S4. Primers

Gene	Direction	Primer
HaFT1	Forward*	GATCCTGATGCTCCCAGTCCAAGTGACCCTAA
	Reverse*	GCCCTGGTGGGAAATGATAGGAAA
	Forward†	AGAAACCCTTATCACCCAGACTCG
	Reverse†	CAAACAGTCTTTGTCGGGATCG
HaGA2ox	Forward*	TGAGAGATGGAAGCTGGATGTCTG
	Reverse*,†	GTGCTTCACTCTTTAGCAAAGGAAACAAC
	Forward†	CCACTATTTCAACCGACGGGACTT
c4973	Forward*,†	ACGSGTSAGGACAAGAACAA
	Reverse*	ATGGCGCTTGGTTTCAATGTCAGC
	Reverse†	GCCACTTTGTTCAAGTTTAGGG
HaFT2	Forward	ACATGTGGCCATCACAAGAGAAATAGTC
	Reverse	TATCTCCGTTGTCCACCAGATCCACTTTCACG
HaFT3	Forward	TCTCCGTGTCTCCTATCATTGCCC
	Reverse	CCAAGGTAGCAAGCGTTGAGCATT
ORS005	Forward	CACGACGTTGTAAAACGACATGTGGAGCAGCAAATTCAG
	Reverse	GTTTCTGCTGCCCACCATACTG
ORS008	Forward	CACGACGTTGTAAAACGACTTGGATCGATTGATGATTGTTG
	Reverse	GTTTGAATCCGTCATGTATAAAACGA
ORS059	Forward	CACGACGTTGTAAAACGACGCTTCGTAGCTTTCTTCTTCGC
	Reverse	GTTTAAGTAGCTTCGCAAGTATTCGG
ORS078	Forward	CACGACGTTGTAAAACGACGTTCGTCGAGTACATGTTCTGC
	Reverse	GTTTCCCTCTGGAAAGTTGTCA
ORS176	Forward	CACGACGTTGTAAAACGACCCCTAACTGGTTTTCTGACCC
	Reverse	GTTTAACTTTTGTTTGTTTGTCCAGG
ORS229	Forward	CACGACGTTGTAAAACGACTCCGACCCGAATCTTATGAACC
	Reverse	GTTTGACCCGAATGAGACCCAAACTG
ORS297	Forward	CACGACGTTGTAAAACGACTGCAAAGCTCACACTAACCTG
	Reverse	GTTTGTGTCTGCACGAACTGTGGT
ORS337	Forward	CACGACGTTGTAAAACGACTTGGTTCATTCATCCTTGGTC
	Reverse	GTTTGGGTTGGTGGTTAATTCGTC
ORS398	Forward	CACGACGTTGTAAAACGACCACGTCCTAAATTAAGTAGGAACGA
	Reverse	GTTTCCAAGACCTCCGTTGAGCTAT
ORS399	Forward	CACGACGTTGTAAAACGACCGTACGGTGTAGTTCTCATGGT
	Reverse	GTTTGGATCACGTGGCGTTCTATT
ORS534	Forward	CACGACGTTGTAAAACGACTCCAAACTCTCTCCCCCTCT
	Reverse	GTTTGCAGCGAAATAGGAAAAACG
ORS596	Forward	CACGACGTTGTAAAACGACTGCGATTATTCTAGGAAGGTCA
	Reverse	GTTTCATGAGGGCATTCTTGTCATT

For a subset of individuals, nested PCR was conducted to amplify the target region. Microsatellite loci start with the prefix ORS. *c4973,* chorismate synthase homolog; *HaGA2ox*, gibberellin 2-oxidase homolog.

*Primer used in first of two, nested PCR reactions.

†Primer used in second of two, nested PCR reactions.

Table S5. GenBank accession numbers for deposited sequences

Gene	Samples	GenBank accession numbers
HaGA2ox	American/Canadian panel	JF428412–JF428543
	Mexican panel	JF428388–JF428411
		JF428544–JF428719
HaFT1	American/Canadian panel	GQ884463–GQ884584
	Mexican panel	JF428724–JF428779
c4973	Chapman 2008 panel	FJ373761–FJ373782
	American landraces	JF428180–JF428353
	Mexican panel	JF428354–JF428387
PgiC (reference gene; homolog of phosphoglucose isomerase C)	American/Canadian Panel	GQ884717 –GQ884848
SCR1 (reference gene; homolog of *SCARECROW*)	American/Canadian panel	GQ884849–GQ884980
CGP41 (reference gene; homolog of *AVRPPHB SUSCEPTIBLE 1*)	American/Canadian panel	GQ884988–GQ885119
CGP53 (reference gene; homolog of *ARABIDOPSIS THALIANA BASIC LEUCINE ZIPPER 11*)	American/Canadian panel	GQ884199–GQ884330
CGP62 (reference gene; homolog of *CYCLIC NUCLEOTIDE-GATED CHANNEL 15*)	American/Canadian panel	HQ110110–HQ110241
CGP69 (reference gene; homolog of *PURPLE ACID PHOSPHATASE 17*)	American/Canadian panel	HQ110242–HQ110373
CGP112 (reference gene; homolog of *HUA1*, *ENHANCER OF AG-4 1*)	American/Canadian panel	HQ119174–HQ110505
HaFT2	Guerrero 34111	JF428720J–F428721
HaFT3	Guerrero 34111	JF428722–JF428723