Supporting Information

Doust et al. 10.1073/pnas.1308940110

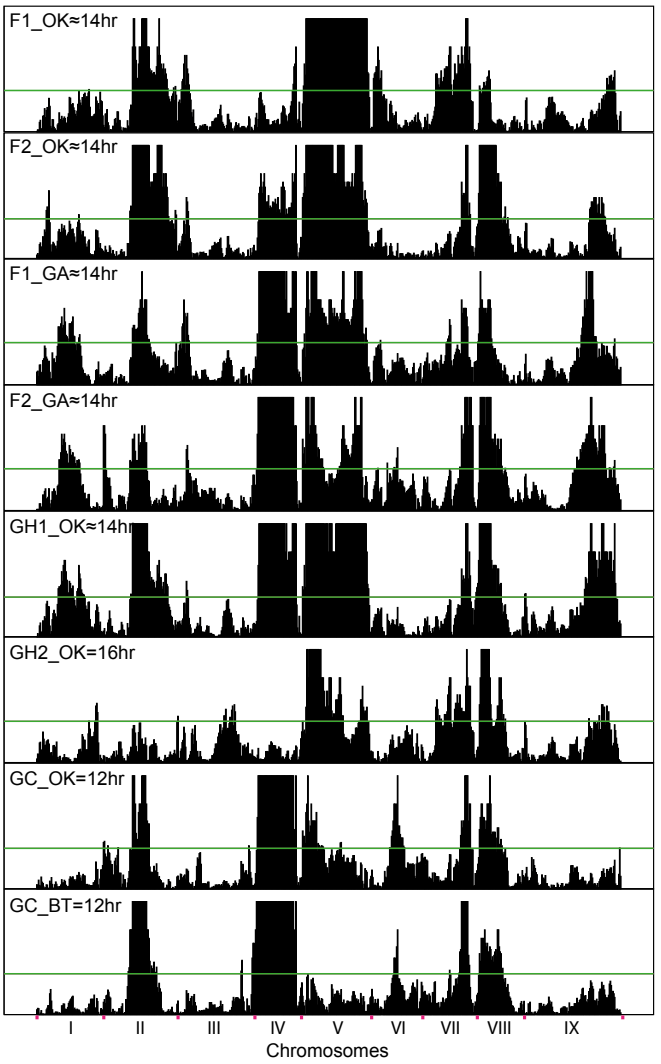

Fig. S1. Quantitative Trait Loci (QTL) plots for flowering time in eight trials. QTL plots (black) are derived from single-marker analysis on 684 markers spread throughout the genome, with chromosomes delineated on the bottom axis. QTL positions are very close to those derived through composite interval analysis (1). Trials varied in photoperiod, with five trials having daylengths of ~14 h, one trial with a daylength of 16 h, and two trials with daylengths of 12 h. Trials also differed in other variables, including growth conditions, temperature, and locality. Peaks above the green horizontal line in each case represent QTL declared significant at a liberal genome-wide level of $P = 0.0014$. This was done to ensure comparability between QTL and biallelic epistasis results (Fig. S2). F, field; GH, greenhouse; GC, growth chamber; OK, Oklahoma; GA, Georgia; BT, Boyce Thompson Institute, New York.

1. Mauro-Herrera M, et al. (2013) Genetic control and comparative genomic analysis of flowering time in Setaria (Poaceae). *G3* 3(2):283–295.

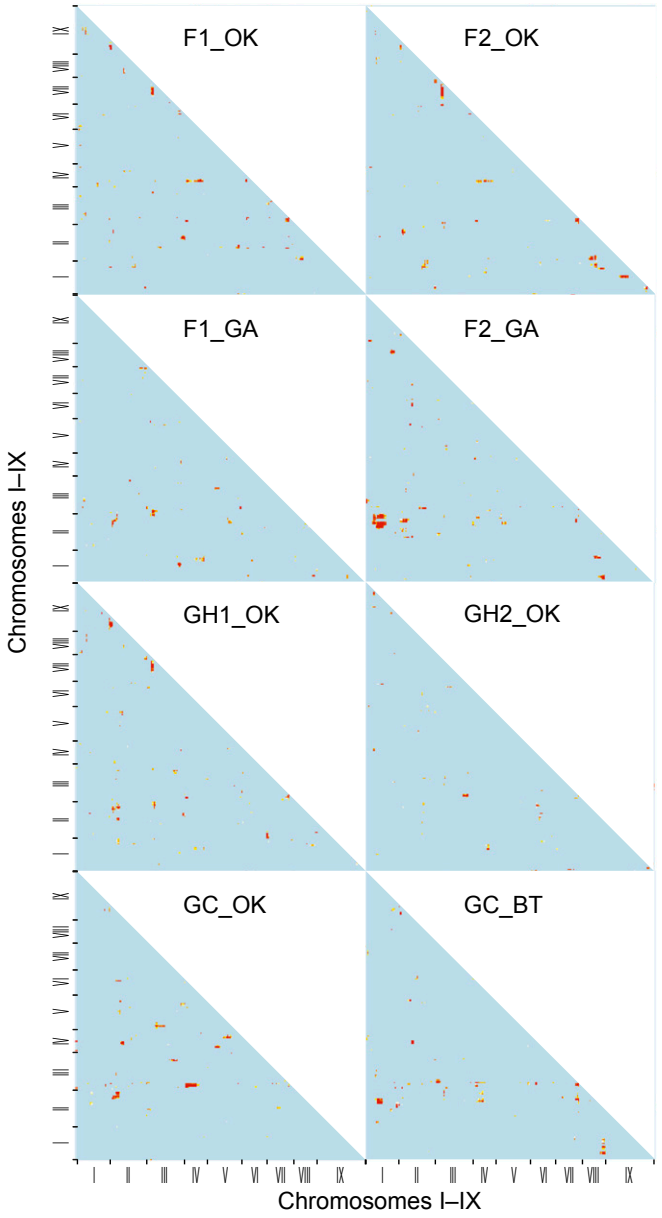

Fig. S2. Biallelic epistasis plots for eight trials of flowering time. Each plot has a blue background of points (biallelic interactions) that are not significant, superimposed with yellow to red points of varying significance (yellow, $P = 0.0014–0.0001$; orange, $P = 0.0001–0.00001$; red, $P < 0.00001$). The bottom and side axes contain the same set of markers, but data were binned in marker groups of three to make interactions visible; thus, there are 228 positions on each axis. All epistasis plots have the same set of markers, allowing direct comparison between them.

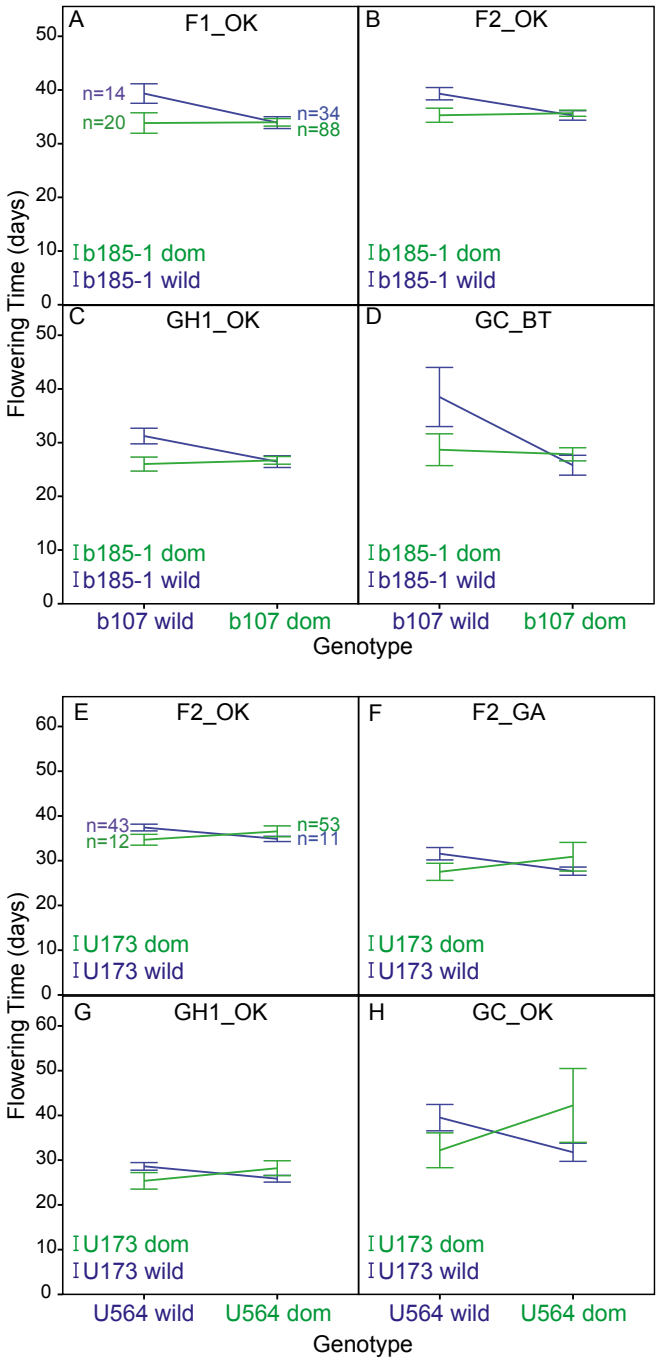

Fig. S3. Epistatic interactions between loci for flowering time in a cross between foxtail millet and green millet. (*A–D*) The epistatic interaction between loci b107 and b185-1 across the four trials in which this interaction is significant (Table S2). In all four cases the pattern of interaction is the same, although the absolute values shift between trials. (*E–H*) The epistatic interaction between U564 and U173 across the four trials in which it is significant. In *A–D* the domestication allele is less sensitive than the wild allele, whereas in *E–H* both alleles are equally sensitive.

Table S1. Markers associated with QTL peaks for flowering time in a foxtail by green millet cross

QTL	QTL marker	Locus 2	Chromosome for locus 2
II-1	U162	U200	II
III-1	U857	U827	III
IV-1	U912	–	–
V-1	U288	–	–
V-2	U364	–	–
V-3	U387	–	–
VII-1	b107	b185-1	VII
VIII-1	U513	U781	III

Roman numerals for QTL name signify chromosome for that QTL. The column labeled "QTL marker" lists the marker closest to the peak value of the QTL, while the column labeled "Locus 2" is the marker associated with a significant interaction for each QTL (if any).

Table S2. Percentage variation explained for shared epistatic interactions for flowering time in an F7 mapping population of a foxtail millet by green millet cross

Locus 1	Locus 2	F1_OK	F2_OK	F1_GA	F2_GA	GH1_OK	GH2_OK	GC_OK	GC_BT
B112	U578				12.4	8.5			10.1
U162	U189	9.9				9.8			
U200	U162					11.3			9.5
U212	U163	8.6				10.3			
U223	U699							13.2	9.8
U827	U867	9.5	11.4			9.4			
U827	U861	8.2	9.1						
U827	U857	8.6	9.6						
U785	U867		8.7			8.7			
U781	U518					8.2			9.3
U806	U762					8.8		11.5	
C562	U774	8.3				8.1		10.0	
B107	B185_1	8.5	9.2			9.5			11.5
U532	U118				9.3			11.5	
U564	U173		8.5		8.3	9.2		13.0	

Only significant interactions at the $P < 0.0014$ level are shown. Locus names shaded in green are those that have significant main effects (i.e., were detected as additive QTL). Cells shaded in blue for five loci pairs show multiple trials sharing these significant interactions between loci. Locus names beginning with U refer to UGSF markers as detailed in Bennetzen et al. (1). F1_OK and F2_OK, field trials 1 and 2, Oklahoma; GH1_OK and GH2_OK, greenhouse trials 1 and 2, Oklahoma; GC_OK, growth chamber trial, Oklahoma; F1_GA and F2_GA, field trials 1 and 2, Georgia; GC_BT, growth chamber trial, Boyce Thompson Institute, New York.

1. Bennetzen JL, et al. (2012) Reference genome sequence of the model plant Setaria. *Nat Biotechnol* 30(6):555–561.