

## Supplementary Tables

**Supplementary Table S1.** Summary of QTL mapping studies for bioenergy traits involving sweet sorghum.

Reference	Population/Parents <sup>1</sup>	Population size and generation	Number of trials (trial names)	Number of markers (technology <sup>2</sup> )	Number of groups (total length, in cM)	QTL mapping <sup>3</sup> (software)
Murray <i>et al.</i> (2008a, 2008b)	Rio (S) × BTx623 (G)	176 F <sub>4:5</sub>	3 (WE05, CS05, CS06)	259 (SSR, AFLP)	10 (1,836.0)	SMA, IM and CIM (WinQTLCart)
Ritter <i>et al.</i> (2008)	R9188 (S) × R9403463-2-1 (G)	184 F <sub>6</sub>	2 (RB1-2)	228 (AFLP, SSR)	16 (2,012.9)	SMA, CIM (WinQTLCart)
Murray <i>et al.</i> (2009)	Diverse panel	125 lines	3 (CS06, CS07, ITH07)	469 (SSR, SNP)	-	GWAS (TASSEL)
Shiringani <i>et al.</i> (2010) and Shiringani and Friedt (2011)	M71 (G) × SS79 (S)	188 F <sub>5:6</sub>	4 (GG1-2, RH1-2)	157 (AFLP, SSR, EST-SSR)	11 (1,028.3)	CIM (PLABQTL)
Guan <i>et al.</i> (2011)	Shihong137 (G) × L-Tian (S)	186 F <sub>2</sub> , 186 F <sub>2:3</sub>	4 (E1-4)	118 (SSR)	15 (1,884.6)	CIM (WinQTLCart)
Felderhoff <i>et al.</i> (2012)	Rio (S) × BTx623 (G)	185 F <sub>3:4</sub>	4 (CS09.1, CS09.2, CS10, WE10)	381 (SNP)	10 (3,359.0)	SMA, IM, CIM (WinQTLCart)
Lv <i>et al.</i> (2013)	Diverse panel (43 S + 76 G)	119 lines	4 (S10-11, H10-11)	51 (SSR)	-	GWAS (TASSEL)
Burks <i>et al.</i> (2015)	Diverse panel	252 lines	3 (13EF, 14EF, 13 DS)	42,926 (SNP)	-	GWAS (GAPIT)
Harris-Shultz <i>et al.</i> (2015)	Honey Drip (S) × Collier (S)	130 F <sub>2</sub> (map), 92 F <sub>2</sub> (QTL)	1 greenhouse trial	4,547 polymorphic, 353 mapped (SNP)	19 (not available)	SMA, CIM (JMP Genomics)
Mocoeur <i>et al.</i> (2015)	E-Tian (S) × Ji2731 (G)	209 F <sub>2</sub> , 196 F <sub>2:3</sub> , 175 F <sub>2:5</sub>	5 (CN1, DK1, DK2, CN2, CN3)	374 (PAV, SSR)	10 (1,430.3)	SMA, IM, CIM (MapQTL)
Wang <i>et al.</i> (2016)	Shihong137 (G) × L-Tian (S)	181 F <sub>7</sub>	4 (E1-4)	181 (SSR)	10 (2,415.3)	CIM (WinQTLCart), Q × E (QTLNet)
Bai <i>et al.</i> (2017)	Rio (S) × BTx623 (G)	189 F <sub>6-8</sub>	3 (2013-5)	126 (SSR, INDEL)	10 (1,418.7)	ICIM (IciMapping)
Disasa <i>et al.</i> (2018)	Sorcoll 163 (G) × Gambella (S)	192 F <sub>2:3</sub>	2 (MARC, Dhera)	76 (SSR)	10 (2,531.3)	SMA, IM, ICIM (IciMapping)
Brenton <i>et al.</i> (2016, 2020)	Diverse panel (132 S + 20 G + 238 B)	390 lines	3 (2013-5)	232,303 (SNP)	-	GWAS (GAPIT)
This study	Brandes (S) × Wray (S)	272 F <sub>2:6</sub> (map), 223 F <sub>2:6</sub> (QTL)	3 (T1-3)	3,767 (SNP)	10 (1,368.8)	MIM, MT-MIM (OneQTL)

<sup>1</sup> S: sweet sorghum, G: grain sorghum, B: biomass sorghum; <sup>2</sup> SSR: simple sequence repeats, AFLP: amplified fragment length polymorphism, EST: expressed sequence tag, SNP: single nucleotide polymorphism, PAV: presence-absence variation, INDEL: insertion-deletion; <sup>3</sup> GWAS: genome-wide association study, SMA: single markers analysis, IM: interval mapping, CIM: composite interval mapping, Q × E: QTL by environment interaction, ICIM: inclusive CIM, MIM: multiple interval mapping, MT-MIM: multi-trait MIM

**Supplementary Table S2.** Soil analysis of the experimental areas, located at Embrapa Milho e Sorgo, Sete Lagoas, MG, Brazil. Area 1 was used for Trials 1 and 2, and Area 2 for Trial 3.

Area	1		2	
	0-20	20-40	0-20	20-40
Sampling depth (cm)				
pH (H <sub>2</sub> O)	4.00	4.90	6.00	6.10
H <sup>+</sup> Al (cmol <sub>c</sub> · dm <sup>-3</sup> )	10.99	8.55	7.39	7.36
O. M. (g · kg <sup>-1</sup> )	4.32	3.84	5.28	4.63
C (Total)	2.51	2.23	3.07	2.69
SC (cmol <sub>c</sub> · dm <sup>-3</sup> )	2.34	1.70	10.58	10.30
CEC (cmol <sub>c</sub> · dm <sup>-3</sup> )	12.62	10.25	17.97	17.66
V (%)	18.55	16.55	58.88	58.32
Al Sat. (%)	32.36	32.06	0.38	0.48

H<sup>+</sup>Al: potential acidity; O. M.: organic matter; C: organic carbon; SC: sum of cations (Ca<sup>2+</sup> + Mg<sup>2+</sup> + K<sup>+</sup>); CEC: cation exchange capacity; V: cation saturation ratio; Al Sat.: aluminum saturation indicator.

**Supplementary Table S3.** Akaike (AIC) and Bayesian (BIC) information criteria for selecting genetic variance-covariance structures  $G_L$  ( $L = 3$  trials). The smallest values are in bold and represent the most likely structure per trait according to each criterion.

Matrix	Description	#parameters	Criterion	FLW	HGH	FBY	JUC	BRX	SUC	RSU	FIB
ID	Diagonal with identical variances	1	AIC	13360.29	18405.91	15348.41	10804.37	8379.86	8324.38	2005.42	7498.52
			BIC	13377.09	18422.70	15365.18	10821.15	8396.64	8341.15	2022.20	7515.29
DIAG	Diagonal with heterogeneous variances	$L = 3$	AIC	13129.82	18393.70	15262.75	10767.95	8380.52	8326.04	1918.04	7393.47
			BIC	13157.81	18421.69	15290.71	10795.91	8408.49	8354.00	1946.01	7421.43
CS	Compound symmetry with identical variances	2	AIC	13193.50	18193.94	15283.09	10761.62	8234.04	<b>8170.12</b>	1969.28	7449.13
			BIC	13215.89	18216.32	15305.45	10783.99	8256.42	<b>8192.50</b>	1991.65	7471.51
CS <sub>Het</sub>	Compound symmetry with heterogeneous variances	$L + 1 = 4$	AIC	12897.62	<b>18170.27</b>	15188.97	10724.35	<b>8233.85</b>	8170.92	NC	7331.68
			BIC	12931.21	<b>18203.85</b>	15222.52	10757.90	<b>8267.41</b>	8204.48	NC	7365.23
AR1	First-order autoregressive with identical variances	2	AIC	13179.60	18206.80	15266.22	10760.11	8247.86	8180.86	1971.80	7443.29
			BIC	13201.99	18229.18	15288.58	10782.48	8270.23	8203.23	1994.17	7465.67
AR1 <sub>Het</sub>	First-order autoregressive with heterogenous variances	$L + 1 = 4$	AIC	12899.61	18179.41	15180.77	10719.39	8246.78	8180.39	NC	<b>7326.68</b>
			BIC	12933.19	18212.99	15214.32	<b>10752.94</b>	8280.34	8213.95	NC	<b>7360.24</b>
UNST	Unstructured	$L(L + 1)/2 = 6$	AIC	<b>12868.72</b>	18173.50	<b>15161.20</b>	<b>10717.16</b>	8234.93	8174.64	<b>1876.25</b>	7327.04
			BIC	<b>12913.50</b>	18218.27	<b>15205.93</b>	10761.90	8279.68	8219.38	<b>1921.00</b>	7371.78

Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in  $t \cdot ha^{-1}$ ), juice extraction yield (JUC, in %), total soluble solids (BRX, in °Brix), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %). NC = model did not converge.

**Supplementary Table S4.** Summary of raw data, physical map (imputed and filtered markers), and genetic maps from GBS-derived markers relative to the *Sorghum bicolor* chromosomes (v2.1).

Chromosome	Number of markers			Genetic map	
	Raw	Physical map	Genetic map	Length (cM)	Density (SNPs/cM)
1	71,878	8,109	594	207.67	2.86
2	59,518	9,489	512	181.19	2.83
3	59,958	8,382	414	111.88	3.70
4	51,905	7,206	396	145.88	2.71
5	33,491	5,826	308	128.00	2.41
6	40,664	6,975	364	123.03	2.96
7	33,905	4,893	327	132.16	2.47
8	31,969	2,790	212	102.28	2.07
9	38,524	5,964	330	120.77	2.73
10	39,429	6,373	310	115.97	2.67
Total	461,241	66,007	3,767	1,368.83	2.75