

Table 1. Characterization of IBM-94 RIL grown at Sioux Falls, SD, in 2007, 2008, and 2009.

	Leaf Angle		Leaf Width		Leaf Length		Plant Height	
	Degrees		mm					
RIL Mean †	26 ± 2.6		91.0 ± 2.95		764.6 ± 20.76		2231.3 ± 101.24	
Range among RILs ‡	9 to 53		71.2 to 114.5		641.7 to 907.0		1323.2 to 2796.8	
ANOVA								
Source of Variation	MS, F							
Genotypes	623.8	10.49**	576.6	7.24**	26374	6.80**	362149	3.93**
Years	1026.0	9.54*	990.6	3.31	582080	35.41**	18780568	71.16**
Genotype × Year	59.5	1.68**	79.6	1.52**	3878	1.86**	92242	4.27**
Replications in Years	107.5	3.04**	299.2	5.72**	16436	7.87**	263924	12.21**
Error	35.3		52.3		2089		21617	
Variance Components and H <sup>2</sup>								
σ <sup>2g</sup>	62.7 ± 10.13		55.2 ± 9.40		2500 ± 429.8		29990 ± 5965.4	
σ <sup>2e</sup>	3.3 ± 2.61		2.5 ± 2.57		2027 ± 1475.5		66368 ± 47600.4	
σ <sup>2ge</sup>	8.1 ± 2.19		9.1 ± 2.96		596 ± 141.2		23542 ± 3226.4	
σ <sup>2rep(e)</sup>	0.8 ± 0.58		2.7 ± 1.61		154 ± 88.4		2605 ± 1419.0	
σ <sup>2error</sup>	35.3 ± 2.14		52.3 ± 3.16		2089 ± 126.2		1617 ± 1304.8	
H <sup>2</sup> , %	90.47		86.20		85.30		74.53	
H <sup>2</sup> , 90% confidence int.	86.24, 93.26		80.08, 90.23		78.78, 89.59		63.25, 81.97	

\*,\*\* Significant at α = 0.05, 0.01, respectively.

† ± Standard error

Table 2. Regression models with QTL for leaf angle, leaf width, leaf length, and plant height in IBM94 RILs. The QTL were detected and included in regression models if LOD values in scans were greater than the LOD threshold corresponding to α = 0.05, by permutation test. Effects that are positive in sign are favored by the Mo17 allele.

Bin†	Marker interval	Chrom. and position	CV‡	Support Interval§	LOD	Partial R <sup>2</sup>	Effect¶	R <sup>2</sup> # <sub>adj</sub>	ˆp ††
Leaf Angle									
1.05–1.05	umc1603–uaz273	1/480	59.8%	465–495	4.27	16.4%	-3.802	27.1%	32.5%
5.04–5.05	csu308–umc1482	5/375	44.6	345–390	4.80	13.9	3.084		
9.01–9.01	umc1867–lim343	9/30	62.9	15–45	4.76	10.4	-2.760		
Leaf Width									
2.04–2.04	umc2088–umc2250	2/320	86.5	300–340	5.20	21.6	4.076	25.0	31.2
8.03–8.03	umc1735–php20714	8/280	85.9	260–300	5.28	15.2	-3.080		
Leaf Length									
2.09–2.09	bnlg1893–AY110389	2/660	54.4	640–680	4.08	11.1	-21.531	9.1	11.9
Plant Height									
4.06–4.06	umc2027–AY110310	4/350	40.3	330–360	4.01	10.4	-26.64	8.4	32.1

\*, \*\* α = 0.05 or 0.01, respectively, for the probability that this QTL affected the trait independently of other QTL.

† Bins where the flanking markers are located and positions are the coordinate values on the MaizeGDB IBM2 map (<http://www.maizegdb.org>).

‡ Frequency of detection within a 1-LOD support interval in 1000 CV runs with families randomly divided for detection and validation.

§ Interval with LOD scores within 1 LOD of the QTL peak

¶ Effects were determined in a simultaneous multiple regression that included factors with LODs ≥ the α = 0.05 threshold.

# R<sup>2</sup> adjusted for the number of terms in the multiple regression models.

††The proportion of genotypic variance explained by all QTL in the models.