

Quantitative Trait Loci for Leaf Angle, Leaf Width, Leaf Length, and Plant Height in IBM-94
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Introduction

Modern maize varieties are more productive than varieties of a few decades ago, partly due to higher population densities and adaptations that permit vigorous growth at high densities. Plant forms that enable efficient light interception at high population densities will increase yield production under modern field conditions. Leaf angle has been shown to affect yield especially at high densities. To determine the QTL affecting leaf traits and plant height in maize I experimented with IBM-94, a B73 x Mo17 recombinant inbred line (RIL) population developed by other researchers for genetic studies (Lee et al 2002, Coe et al 2002, Cone et al 2002).

Materials and Methods

Seed for the 93 RIL constituting IBM-94 was obtained from the Maize Genetics Cooperative Stock Center (<http://maizecoop.cropsci.uiuc.edu>). In year 2006 the original seed was grown and plants were self-pollinated to produce enough RIL seed to plant replicated experimental plots at Sioux Falls, SD, USA. In years 2007, 2008, and 2009 the 93 RIL were grown in randomized complete blocks with three replicates each year. Space was limited, so each plot included four plants spaced 279 mm apart in rows 76 mm apart. There were no extra spaces between plots in rows. At anthesis or soon after, the total plant height to the tassle tip and the leaf at the uppermost ear shoot were measured on the two center plants in each plot. Leaf measurements included the leaf angle from vertical, maximum leaf width, and distance from the ligule to the tip of the straightened leaf.

Statistical analysis, including analysis of variance and heritability was performed with PLABSTAT (University of Hohenheim, Germany, <https://plant-breeding.uni-hohenheim.de/~ipspwww/soft.html>). Genetic map distances of markers and molecular marker genotypes of each RIL was obtained from the Maize Genetics and Genomics Database (MaizeGDB) (<http://www.maizegdb.org>). Phenotype data for the RILs was combined with marker genotypic information and map distances from the MaizeGDB IBM2 map to analyze for QTL using PLABMQTL (University of Hohenheim, Germany, <https://plant-breeding.uni-hohenheim.de/~ipspwww/soft.html>).

Results

There was significant variation among genotypes (Table 1) and 1 to 3 QTL identified for each of the measured traits (Table 2). Larger plots and the larger IBM-302 population might have improved precision and enabled detection of more QTL. The total area taken up by nursery rows and experimental plots was about 50 by 75 feet, illustrating that even with limited resources the IBM-94 population and MaizeGDB data can be used for QTL mapping.

References

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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					
Mean †	26 ± 2.6		91.0 ± 2.95		764.6 ± 20.76		2231.3 ± 101.24
se among RILs ‡	9 to 53		71.2 to 114.5		641.7 to 907.0		1323.2 to 2796.8
<u>ANOVA</u>							
	MS, F						
Source of Variation							
Replicates	623.8	10.49**	576.6	7.24**	26374	6.80**	362149
Genotypes	1026.0	9.54*	990.6	3.31	582080	35.41**	18780568
Genotype × Year	59.5	1.68**	79.6	1.52**	3878	1.86**	92242
Replicates in Years	107.5	3.04**	299.2	5.72**	16436	7.87**	263924
Residual	35.3		52.3		2089		21617
<u>Variance Components and H²</u>							
Genetic	62.7 ± 10.13		55.2 ± 9.40		2500 ± 429.8		29990 ± 5965.4
Environmental	3.3 ± 2.61		2.5 ± 2.57		2027 ± 1475.5		66368 ± 47600.4
Genotype × Environment	8.1 ± 2.19		9.1 ± 2.96		596 ± 141.2		23542 ± 3226.4
Residual	0.8 ± 0.58		2.7 ± 1.61		154 ± 88.4		2605 ± 1419.0
Genetic + Environmental	35.3 ± 2.14		52.3 ± 3.16		2089 ± 126.2		1617 ± 1304.8
Genetic + Environmental + Genotype × Environment	90.47		86.20		85.30		74.53
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

2. Regression models with QTL for leaf angle, leaf width, leaf length, and plant height in IBM94 RILs. The QTL were detected in regression models if LOD values in scans were greater than the LOD threshold corresponding to $\alpha = 0.05$, 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 ²	Effect [¶]	R ² _{adj} [#]
<u>Leaf Angle</u>								
-1.05	umc1603–uaz273	1/480	59.8%	465–495	4.27			
-5.05	csu308–umc1482	5/375	44.6	345–390	4.80	13.9		
-9.01	umc1867–lim343	9/30	62.9	15–45	4.76	10.4		
<u>Leaf Width</u>								
-2.04	umc2088–umc2250	2/320	86.5	300–340	5.20	21.6	4.076	25.0
-8.03	umc1735–php20714	8/280	85.9	260–300	5.28	15.2		
<u>Leaf Length</u>								
-2.09	bnlg1893–	2/660	54.4	640–680	4.08	11.1		9.1
<u>Plant Height</u>								
-4.06	umc2027–	4/350	40.3	330–360	4.01	10.4	-26.64	8.4

[†] $\alpha = 0.05$ or 0.01 , respectively, for the probability that this QTL affected the trait independently of other QTL. [‡] where the flanking markers are located and positions are the coordinate values on the MaizeGDB IBM2 map (www.maizegdb.org). [§] frequency of detection within a 1-LOD support interval in 1000 CV runs with families randomly divided for detection and permutation. [¶] value with LOD scores within 1 LOD of the QTL peak. [#] effects were determined in a simultaneous multiple regression that included factors with LODs \geq the $\alpha = 0.05$ threshold. ^{††} adjusted for the number of terms in the multiple regression models. ^{†††} proportion of genotypic variance explained by all QTL in the models.

