QTL Correspondence in Diverse Sorghum Populations: Statistically Significant Overlap of Tiller Height and Testa Factor QTLs

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INTRODUCTION

Sorghum is an important cereal in arid and semi-arid regions, and approximately 100,000 mt were produced in 39 countries in 1998 (1). Many agronomically important quantitative traits have been mapped in sorghum and other grasses as quantitative trait loci (QTL), chromatin segments explaining a portion of the phenotypic variation. These QTLs are highly relevant in the cross and environment in which they were mapped. However, correspondence of QTLs across populations, taxa, and environments all contribute evidence regarding the importance of that chromatin region in contributing to the phenotype under varied evolutionary and environmental conditions.

We have compared genetic marker and QTL locations between two sorghum populations which share one common parent, BTx623 (*S. bicolor*; 2N=2X=20), but differ by morphologically and evolutionarily-different parents, specifically *S. bicolor* accession IS3620C, and *S. propinquum* (SP; 2N=2X=20). Several QTLs have been published for the BTx623/IS3620C cross(2), and QTLs associated with tillering/rhizomatousness(3), plant height/maturity(4), seed size and shattering(5) were previously identified in the BTx623/SP population. Using phenotype and recombination data, we evaluated correspondence of QTLs between the two mapping populations.

RESULTS

Genetic maps were reconstructed using MAPMAKER/EXP(6) and QTLs were detected using MAPMAKER/QTL(7). The BTx623/IS3620C cross consisted of 137 F6-8 RILs mapped with a subset of 145 SSR/RFLP markers out of a 470 marker 'superset' (8). Eighty-five QTLs (LOD>2.5) representing twenty-nine measured traits were detected in the BTx623/IS3620C cross. Similarly, the markers used in QTL mapping for the BTx623/SP cross are a subset of markers (96/2514 RFLP) mapped in 370 F2 individuals, drawn from a denser genetic map (Bowers et al, submitted). Fifty-six QTLs representing 14 traits were mapped in BTx623/SP. Common markers from the two 'superset' maps were used to join the two 'subset' maps using Genomepixelizer(9), and QTL LOD-intervals were mapped (Fig. 1). Both genetic maps consisted of 10 linkage groups (LG) that contained enough common markers with consistent order to confidently compare 9/10 LG for QTL correspondence.

Twelve traits were analogous in both studies, and the overlap of comparable QTLs derived from these traits was determined (BTx623/IS3620C = 31 QTLs; BTx623/*S. propinquum* = 39 QTLs). The hypergeometric probability distribution(10) was employed to generate a formal measure that QTL overlap was not due to chance (Fig. 2A). Of thirteen QTLs found to overlap, four QTLs representing two traits corresponded more than would be expected by chance (Fig. 2B; p<0.05). These traits include <u>tiller height</u> (2 QTLs; p=0.014) and <u>testa presence and color</u> (2 QTLs; p=0.007). Eleven orthologous QTLs explaining partial phenotypic variance for five other traits were found, but these correlations could be due to chance (prange 0.07 ↔ 0.81). Figure 3 lists all 70 QTLs that were tested for correspondence.

DISCUSSION

Although the two crosses shared a common parent (BTx623), the experimental conditions were quite different: 1) F6-8 RILs vs. F2 individuals 2) evolutionarily-divergent parents 3) multiple environments. Thus, the presence of orthologous QTLs provide strong evidence for their legitimacy. However, only 8/70 QTLs examined overlapped more than would be expected by chance. It is likely that some traits segregate for QTLs at different locations due to the tremendous divergence between the two different parents, specifically *S. bicolor* IS3620C and a morphologically distinct wild relative, *S. propinquum*. The correspondence of QTLs for testa development (P=.007) tiller height (p=0.014) and possibly maturity (p=0.068) suggests that the genetic control mechanisms for these phenotypes may be similar between the divergent species. Conversely, the absence of QTL correspondence for traits such as leaf width (p=0.408) and leaf length (p=.807) implies that leaf development controls may have diverged. The inclusion of QTLs from future intrageneric sorghum crosses is necessary to test these notions.

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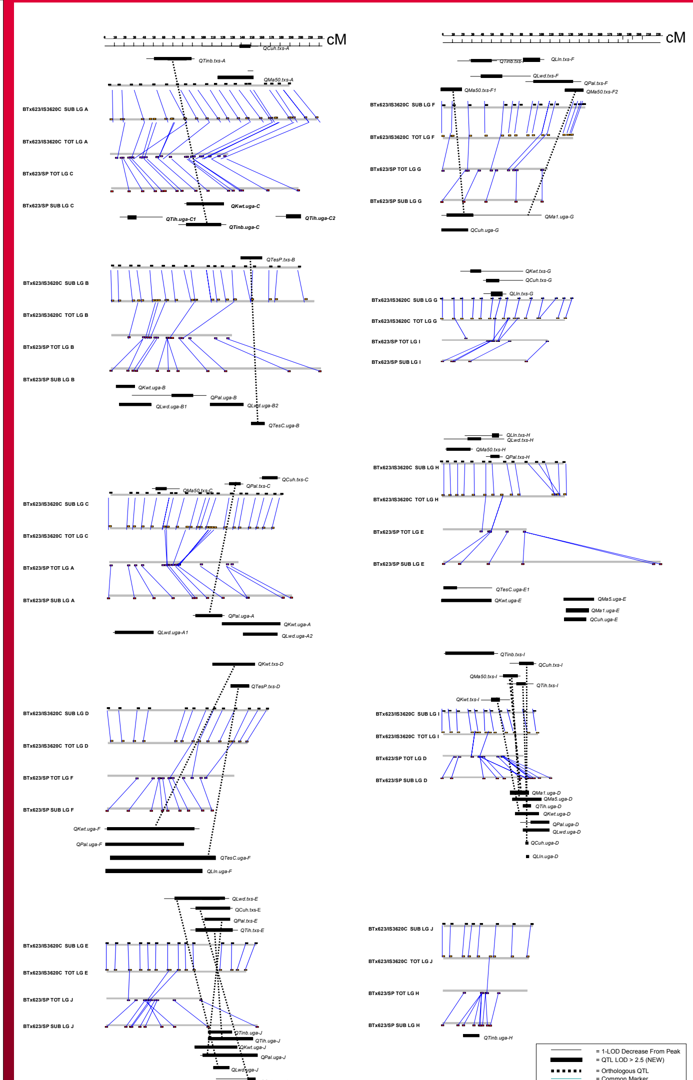

FIG. 1 Alignment of two sorghum genetic maps and QTLS

Genetic maps were constructed for both BTx623/IS3620C and BTx623/*S. propinquum* crosses and QTLs for twelve traits are shown. These maps contain a subset (i.e. SUB LG) of genetic markers from a more extensive map (i.e. TOT LG). Genetic markers common to both 'superset' maps were used to align the two sub maps, and the maps were constructed with Genomepixelizer (http://www.atgc.org/). A dotted line was drawn between QTLs if their 1-LOD interval overlapped between the two maps. Note that differing LG nomenclature was used between the two previous maps.

A

$$p = \frac{\binom{l}{m}\binom{n-l}{s-m}}{\binom{n}{s}}$$

B

Trait	QTL Symbol	l	s	m	p-value
Testa color/presence	*QTes(C/P)*	3	2	2	0.007
Tiller Height	*QTih*	4	2	2	0.014
Maturity*	*QMa(50/1/5)*	6	6	3	0.068
Panicle Length	*QPal*	4	4	2	0.109
Culm Height	*QCuh*	5	4	2	0.109
Kernal Weight	*QKwt*	7	3	2	0.119
Tiller Number	*QTinb*	3	3	1	0.259
Leaf Width	*QLwd*	6	3	1	0.408
Leaf Length	*QLln*	3	2	0	0.807

*Ma50: Days to Flower; Ma1/5: Days to (culm)/(culm + 4 Tillers)

FIG. 2 Evaluating correspondence between groups of QTLs

A) Hypergeometric probability distribution. n = the number of <u>intervals</u> which can be compared. (defined as 30 cM, approximating a QTL likelihood interval); m = the number of 'matches' declared between QTLs (when 1-LOD likelihood intervals for two taxa overlapped);l = the total number of QTLs found in the larger sample; s = the number of QTLs found in the smaller sample

B) QTL correspondence p-value for comparable QTLs

Trait	LG	QTL	LOD_{high}	$\%V_a$	n	e	INTERVAL
Culm Ht.	A	*QCuh.txs.A*†	2.5	12.6	1	1	Xumc104-Xumc167
	C	*QCuh.txs.C*†	3.0	10.7	2	1	Xumc124.1-Xumc121
	E	*QCuh.txs.E*†	8.1	24.3	4	2	Xtxp92-Xtxs1579
	G	*QCuh.txs.G*†	3.6	10.4	3	2	Xumc109.2-Xumc21
	I	*QCuh.txs.I*	3.3	12.2	2	1	Xcdo718-Xtxp6
	J	*QCuh.uga.J*	7.2	10.5	1	1	pSB164-pSB815
	G	*QCuh.uga.G*	4.5	7.3	1	1	pSB416-pSB445
	E	*QCuh.uga.E*†	18.4	77.0	1	1	pSB047-pSB343
	D	*QCuh.uga.D*	47.4	50.4	1	1	pSB189-pSB188x
Kernal Wt	D	*QKwt.txs.D*†	4.2	16.2	1	1	Xtxp51-Xcdo516.1
	G	*QKwt.txs.G*	2.5	8.7	1	1	Xisu136.2-Xcdo516.2
	I	*QKwt.txs.I*	2.8	9.2	1	1	Xtxs1030-Xisu138
	C	*QKwt.uga.C*	4.1	7.3	1	1	SHO68-pSB062
	B	*QKwt.uga.B*	3.3	4.8	1	1	pSB077-pSB643x
	A	*QKwt.uga.A*	5.8	10.3	1	1	pSB443c-pSB109
	F	*QKwt.uga.F*	3.2	5.5	1	1	pSB341ab-pSB637b
	J	*QKwt.uga.J*	3.8	6.9	1	1	pSB637a-pSB164
	E	*QKwt.uga.E*	4.7	9.0	1	1	pSB504-pSB200
	D	*QKwt.uga.D*	6.7	10.1	1	1	pSB521a-pSB428a
Leaf Length	F	*QLln.txs.F*	2.7	11	1	1	Xtxs3000-Xtxp67
	G	*QLln.txs.G*	3.4	10.6	2	1	Xumc109.2-Xumc21
	H	*QLln.txs.H*	2.8	8.9	2	1	Xcdo459-Xtxs645.2
	F	*QLln.uga.F*	3.9	5.2	1	1	pSB201-pSB193
	D	*QLln.uga.D*	17.2	20.6	1	1	pSB189-pSB188x
Leaf Width	E	*QLwd.txs.E*	3.4	14.0	2	1	Xtxp92-Xtxs1579
	F	*QLwd.txs.F*	2.7	12.8	1	1	Xtxp339-Xbcd454.2
	H	*QLwd.txs.H*	2.6	9.4	1	1	Xtxs1220-Xcdo459
	A	*QLwd.uga.A1*	3.7	9.4	1	1	pSB443a-pSB379
	A	*QLwd.uga.A2*	4.2	5.5	1	1	pSB109-pSB243
	B	*QLwd.uga.B1*	9.7	15.8	1	1	pSB075-pSB500
	B	*QLwd.uga.B2*	14.7	22	1	1	pSB080-pSB495
	J	*QLwd.uga.J*	8.2	11.1	1	1	pSB164-pSB815
	D	*QLwd.uga.D*	7.3	9.4	1	1	pSB188x-pSB580
Maturity	A	*QMa50.txs.A*	3.6	16.9	1	1	Xumc128-Xumc167
	C	*QMa50.txs.C*	2.5	10.7	1	1	Xtxs422-Xumc16
	F1	*QMa50.txs.F1*†	7.7	19.5	2	1	Xisu140-Xcdo393
	F2	*QMa50.txs.F2*†	4.6	11.8	2	1	Xtxp358-Xrz390
	H	*QMa50.txs.H*	3.4	11.2	2	1	Xtxs1294-Xtxp105
	I	*QMa50.txs.I*	3.1	10	1	1	Xumc119-Xcdo718
	G	*QMa1.uga.G*	2.6	4	1	1	pSB416-pSB445
	E	*QMa1.uga.E*	60.6	-	1	1	pSB047-pSB343
	E	*QMa5.uga.E*	37.1	-	1	1	pSB047-pSB343
	D	*QMa1.uga.D*	96.1	-	1	1	SHO74-pSB643a
	D	*QMa5.uga.D*	72.6	-	1	1	pSB188x-pSB580
Panicle Length	C	*QPal.txs.C*	2.9	12.4	1	1	Xtxs578-Xtxs1053
	E	*QPal.txs.E*	5.4	18.4	3	2	Xtxp92-Xtxs1579
	F	*QPal.txs.F*	2.7	10.1	2	2	Xtxp67-Xtxp287
	H	*QPal.txs.H*	2.7	8.5	1	1	Xtxs645.2-Xisu54
	A	*QPal.uga.A*	3.5	4.8	1	1	pSB289-SHO65
	B	*QPal.uga.B*	2.9	3.9	1	1	pSB101-pSB080
	F	*QPal.uga.F*	5.7	9.1	1	1	pSB107-pSB201
	D	*QPal.uga.D*	3.0	4.1	1	1	pSB428a-SHO74
	J	*QPal.uga.J*	4.1	5.5	1	1	pSB164-pSB815
Testa Pres.	B	*QTesP.txs.B*	6.5	21.4	1	1	Xisu71-Xtxs1891
	D	*QTesP.txs.D*	5.0	18.6	1	1	Xtxp51-Xcdo516.1
Testa Color	B	*QTesC.uga.B*	461.0	-	1	1	pSB053-pSB174
	F	*QTesC.uga.F*	539.7	-	1	1	pSB107-pSB201
	E	*QTesC.uga.E*	477.5	-	1	1	pSB047-pSB343
Tiller #	A	*QTinb.txs.A*†	3.9	11.9	2	1	Xtxs1129-Xtxp58
	F	*QTinb.txs.F*	2.9	11.8	1	1	Xumc132-Xtxp339
	I	*QTinb.txs.I*†	4.6	13.4	3	2	Xcdo244.2-Xtxs1868
	C	*QTinb.uga.C*	3.6	5.1	1	1	SHO68-pSB062
	J	*QTinb.uga.J*†	5.5	6.9	1	1	pSB637a-pSB164
	H	*QTinB.uga.H*†	5.5	7.4	1	1	pSB510-pSB419c
Tiller Height	E	*QTih.txs.E*†	3.4	15.6	3	2	Xtxp92-Xtxs1579
	I	*QTih.txs.I*	2.5	9.1	1	1	Xcdo718-Xtxp6
	C	*QTih.uga.C1*	2.5	3.8	1	1	pSB041-pSB102
	C	*QTih.uga.C2*	3.0	6.6	1	1	pSB088-pSB508
	D	*QTih.uga.D*	6.6	7.9	1	1	pSB314-pSB189
	J	*QTih.uga.J*	9.5	12.7	1	1	pSB164-pSB815

FIG.3 QTLs tested for correspondence.

Thirty-one QTLs identified in the BTx623/IS3620C cross and 39 QTLs in the BTx623/*S. propinquum* cross are listed by trait. QTL symbols for the BTx623/IS3620C cross contain *txs* and BTx623/*S. propinquum* contain *uga*. Trait = comparable trait. LG=linkage group. QTL = Quantitative trait locus . LOD_{high} = Highest LOD score between replicate QTLs. %V=Average percent variance explained by the QTL. n = number of QTLs found in study. e = number of environments in which a QTL was found. INTERVAL = Marker interval in QTL signal was the highest. RED/YELLOW bars highlight corresponding QTLs for the given trait. †Published QTL.