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ORIGINAL PAPER

Genetic variation at *bx1* controls DIMBOA content in maize

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Abstract The main hydroxamic acid in maize (*Zea mays* L.) is 2-4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one (DIMBOA). DIMBOA confers resistance to leaf-feeding by several corn borers. Most genes involved in the DIMBOA metabolic pathway are located on the short arm of chromosome 4, and quantitative trait loci (QTLs) involved in maize resistance to leaf-feeding by corn borers have been localized to that region. However, the low resolution of QTL linkage mapping does not allow convincing proof that genetic variation at *bx* loci was responsible for the variability for resistance. This study addressed the following objectives: to determine the QTLs involved in DIMBOA synthesis across genetically divergent maize inbreds using eight RIL families from the nested association mapping population, to check the stability of QTLs for DIMBOA content across years by evaluating two of those RIL families in 2 years, and to test the involvement of *bx1* by performing association mapping with a panel of 281 diverse inbred lines. QTLs were stable across different environments. A genetic model including eight markers explained approximately 34% of phenotypic variability across eight RIL families and the position of the largest QTL co-localizes with the majority of structural genes of the DIMBOA pathway. Candidate association analysis determined that sequence polymorphisms at *bx1* greatly affects variation of DIMBOA content in a diverse panel of maize inbreds, but the specific causal polymorphism or polymorphisms responsible for the QTL detected in the region 4.01 were not identified. This result may be because the causal polymorphism(s) were not sequenced, identity is masked by linkage disequilibrium, adjustments for population structure reduce significance of causal polymorphisms or multiple causal polymorphisms affecting *bx1* segregate among inbred lines.

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Introduction

Cyclic hydroxamic acids and their derivatives (benzoxazinoids) are major secondary metabolites among poaceous plants. These compounds have biological activity against plants, insects, fungi, and microorganisms (Niemeyer 1988; Pérez and Ormeño-Nuñez 1991) and could also be involved in detoxification of toxic inorganic molecules (Poschenrieder et al. 2005). The main hydroxamic acid in maize (*Zea mays* L.) is the 2-β-D-glucopyranosyloxy-4-hydroxy-7-methoxy-1,4-benzoxazin-3-one (DIMBOA-Glc) (Tipton et al. 1967; Cambier et al. 2000). The benzoxazinoid glucosides are stored in vacuoles as inactive phytoanticipines, while the glucosidases specific for their activation are present in the plastids (Babcock and Esen 1994; Czjzek et al. 2000). Upon exogenous or endogenous

damage to tissues, the glucoside comes in contact with the glusosidase and the toxic aglucone, DIMBOA (2-4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one), is released (Oikawa et al. 1999; von Rad et al. 2001; Park et al. 2004).

DIMBOA confers resistance to leaf-feeding by several corn borer species (Klun et al. 1967; Reid et al. 1991; Gutiérrez and Castañera 1986; Tseng 1997). DIMBOA decreases in vivo endoproteinase activity in the larval midgut of the European corn borer (*Ostrinia nubilalis*) limiting the availability of amino acids and reducing larval growth (Houseman et al. 1989, 1992). DIMBOA has also been reported to affect detoxication and hydrolysis enzymes for Asian corn borer (*O. furnacalis*) and Mediterranean stem borer (*Sesamia nonagrioides*) (Yan et al. 1995; Ortego et al. 1998) larvae. However, DIMBOA had a differential impact on two closely related leaf-feeding generalists, *Spodoptera frugiperda* and *S. exigua* (Rostas 2007). *S. frugiperda*, which is native in the New World, copes well with DIMBOA in the diet, while DIMBOA is detrimental to *S. exigua*, an Asian species. Hedin et al. (1993) demonstrated that benzoxazinoids are also toxic factors for *Diatraea grandiosella*. The protection against insect attack that DIMBOA confers to the plant is restricted to early stages of plant development because DIMBOA concentration decreases with plant age (Morse et al. 1991; Barry et al. 1994; Cambier et al. 2000). Benzoxazinoids are considered as constitutive compounds, but their biosynthesis seems to be increased after insect damage or treatments with methyl jasmonate, a signal molecule of herbivore damage (Gutiérrez et al. 1988; Morse et al. 1991; Huang et al. 2006; Wang et al. 2007). Richardson and Bacon (1993) suggested that growth-limiting conditions, such as water deficit, also increases the accumulation of benzoxazinoids. Therefore, plant age, insect damage, and certain environmental factors can alter DIMBOA levels.

In maize, the genes involved in DIMBOA's metabolic pathway have been cloned and mapped (Jonczyk et al. 2008). Seven genes (*bx1*, *bx2*, *bx3*, *bx4*, *bx5*, *bx6*, and *bx8*) map to a genomic region of approximately 6 cM on the short arm of chromosome 4, *bx7* is also in the short arm of chromosome 4 and *bx9* is localized on chromosome 1. BX1 catalyzes the formation of free indole from indole-3-glycerol phosphate, then the stepwise action of four maize cytochrome P-450-dependent monooxygenases (BX2, BX3, BX4, and BX5) convert free indole to DIBOA (2-4-dihydroxy-1,4-benzoxazin-3-one) (Frey et al. 1997; Glawischnig et al. 1999). Sequence analysis indicates that BX1 is a modified form of the tryptophan synthase alpha subunit (TSA). *bx1* is also evolutionary related to the gene *igl*, which codifies for indole-3-glycerol phosphate lyase, responsible for the formation of volatile indole (Frey et al. 2000; Gierl and Frey 2001). *bx1* is expressed constitutively in young seedlings, while *igl* is induced in more advanced stages of plant development and contributes to the blend of odors that attract beneficial parasitoids. Therefore, duplications of the *TSA* gene involved in the primary metabolism have played an important role in augmenting the plant chemical-defense capacity against insect attack.

The next step in the metabolic pathway is the conversion of DIBOA to DIBOA-glc by the action of specific glucosyltransferases. Two gluocosyltransferases are responsible for the glucosylation of DIBOA, BX8, and BX9 (von Rad et al. 2001). The conversion of DIBOA-glc to DIMBOA-glc requires hydroxylation and methylation. BX6 is responsible for the hydroxylation step that converts DIBOA-glc to TRIBOA-glc (2,4,7-trihydroxy-2H-1,4-benzoxazin-3(4H)-one) and this conversion likely takes place in the cytosol (Frey et al. 2003; Jonczyk et al. 2008). Methylation is catalyzed by BX7, rendering DIMBOA-glc.

Quantitative trait locus (QTL) analysis has been used to study maize resistance to leaf-feeding by European corn borer and other insect pests (Bohn et al. 2001; Jampatong et al. 2002; Brooks et al. 2005, 2007; Cardinal et al. 2006). There is only one report on the involvement of a QTL close to the *bx* gene cluster in resistance to leaf-feeding by a native American lepidopteran species (Bohn et al. 2001). These results could be the consequence of two important facts, DIMBOA may be non-toxic to most native species (Rostas 2007) and/or materials used could have low amounts of DIMBOA. On the contrary, all studies to localize QTLs involved in resistance to leaf-feeding by European corn borer have found QTLs close to the region of chromosome 4 where most *bx* genes reside (Jampatong et al. 2002; Cardinal et al. 2006). However, the low resolution of the QTL linkage mapping approach does not allow convincing proof that genetic variation at *bx* loci was responsible for the resistance found in those crosses. In contrast, association mapping is a fine mapping approach, which enables researchers to look for functional variation in a broader germplasm background (Zhu et al. 2008). Association mapping could be focused on one or few candidate genes or on the scanning of the entire genome. Although the use of whole genome scan association mapping to identify loci with major effect has been successful for some particular traits such as oleic acid content in maize kernels (Beló et al. 2008), the candidate gene approach has been favored in species with a fast decay of linkage disequilibrium (LD), such as maize. Association mapping studies with candidate genes have been successful to locate polymorphisms in maize genes *bt2*, *sh1*, and *sh2* associated to kernel composition traits, in *ae1* and *sh1* to amylose levels, in *vgt1* and *dwarf8* to flowering-time variation and in *c2* and *whp1* to maysin content in the silks (Wilson et al. 2004; Szalma et al. 2005; Camus-Kulandaivelu et al. 2006; Ducrocq et al. 2008). Recently, nested association mapping (NAM) has been proposed as a

powerful genome-wide association analysis tool to dissecting the genetic basis of quantitative traits in species with low LD (Yu et al. 2008; McMullen et al. 2009a; Buckler et al. 2009). NAM has an increased cost-effective power compared to conventional genome-wide association mapping approaches because the highly dense map obtained for the founders of the RIL's populations can be projected to the RILs by using common parent-specific markers for genotyping founders and progenies.

Both linkage mapping and association approaches could be complementary when used to study maize functional variation for DIMBOA content. First, NAM is used to localize QTLs for DIMBOA content across different RIL families. Then, if QTLs for DIMBOA content variation are identified in the proximity of *bx* genes, the candidate gene approach will be used with *bx1*, which is the committal step into the DIMBOA pathway and, consequently, it is the prime candidate for affecting total DIMBOA accumulation. Association mapping will also be performed with sequences from genes *bx2*, *bx3*, *bx4*, *bx5,* and *bx8* to check whether significant associations between *bx1* polymorphisms and DIMBOA content could be consequence of LD between *bx1* and the other *bx* genes located in the same contig. *bx6* has been mapped near to *bx4* (Jonczyk et al. 2008), but AY104457/PCO086194, which matches by BLAST to AF540907 (cDNA sequence for *bx6*) maps in chromosome 2 rather than in 4.01. Therefore, no amplicons could be obtained for *bx6* because there is not a reliable genomic sequence for that gene. This study addressed the following objectives: to determine the QTLs involved in DIMBOA synthesis across genetically divergent maize inbreds using eight RIL populations from the NAM, to check the stability of QTLs for DIMBOA content across years by evaluating two of those RIL populations in 2 years, and to study the involvement of *bx1* by performing association mapping with a panel of 281 diverse inbreds.

Materials and methods

QTLs for DIMBOA across NAM families

Plant material

RIL families derived from B73 × Il14H and B73 × CML322 were evaluated in 2007 and 2008 for determining QTL stability. Eight RIL families derived from crosses between the inbred line B73 and inbreds CML52, CML322, IL14H, M37W, MS71, NC350, Oh43, and Tx303 were used to determine the QTLs involved in DIMBOA synthesis across genetically divergent maize inbreds.

In summer of 2007, two RIL families of the NAM population, derived from crosses B73 × Il14H and B73 × CML322, were evaluated for DIMBOA, DIMBOA-glc, and the sum of the two which we designate as DIMBOA-(T) for total DIMBOA. Fifteen kernels per row were planted in 3.6 m rows, 0.9 m aisles, and 0.9 m between rows on May 18 at the Agronomy Research Center near Columbia, MO, USA. An augmented design was used for each RIL family in which both parental lines were used as common testers across blocks of 20 RILs. Therefore, the inbred B73 was also a common tester across RIL families. On June 25, 38 days after planting, two representative plants per row were selected and a 5-cm section of whorl tissue centered at the highest ligule was collected. After discarding the outside leaf, the whorl sections from the two plants per row were bulked, lyophilized, ground, and maintained at −20°C until chemical analyses.

In 2008, eight RIL families derived from crosses between the inbred line B73 and inbreds CML52, CML322, IL14H, M37W, MS71, NC350, Oh43, and Tx303 were evaluated for DIMBOA, DIMBOA-glc, and DIMBOA-T. These eight RIL families are all part of the NAM population (Yu et al. 2008; McMullen et al. 2009a) and include the two families evaluated in 2007. These plants were grown at Hinkson Bottoms within Columbia, MO, USA. The kernels were planted on June 10 and whorl tissue collected on July 11, 32 days after planting. Planting conditions and tissue handling were as in 2007.

In 2008, the day before tissue collection, the number of emerged leaves per plant was recorded on the two plants per plot which were going to be collected. The fifth leaves had previously been marked 22 days after planting to assure a proper leaf count.

Chemical analyses

Chemical determinations of the amount of DIMBOA and DIMBOA-Glc molecules were performed using high-performance liquid chromatography (HPLC) using a modification of the procedure of Nakagawa et al. (1995). Purified DIMBOA was a gift from Dr. Monika Frey, Technische Universität München, Freising, Germany. DIMBOA-Glc was isolated from corn leaves and identified by its enzyme hydrolysis products. All other reagents were ACS grade or better and purchased from Thermo-Fisher (St. Louis, MO, USA). As a DIMBOA-Glc standard was not commercially available, DIMBOA-Glc concentration in samples was calculated based on DIMBOA standards and adjusted for differences in molecular weights.

One hundred milligrams of freeze-dried ground whorl tissue was weighed into screw capped 15 mL polypropylene Falcon tubes and 5 mL of HPLC grade methanol and 50 μL of acetic acid were added to each tube. The tubes were vortexed and placed in a sonicator water bath for

60 min at 60°C. The supernatant (0.5 mL) was combined with 0.5 mL distilled water in a microcentrifuge tube, vortexed, and centrifuged for 5 min at 13,000 rpm. The supernatants were transferred into auto-sample vials for analysis by HPLC. The HPLC system consisted of a Hitachi Model L-7100 pump with a Hitachi Model L-7400 UV detector (280 nm), Hitachi Model L-7200 autosampler with Hitachi D-7000 data acquisition interface and CertChrom software on a microcomputer. The column was a 100 × 4.6 mm reversed-phase Luna 3 µm C18 BDS analytical column (Phenomenex) fitted with a C_{18} ODS SecurityGuard 4.0 × 3.0 mm guard column (Phenomenex) with a mobile phase consisting of metahnol:1% acetic acid in water (20:80) run at a flow rate of 1 mL min.

Statistical analyses

To check the stability and precision of QTLs detected for DIMBOA content, linkage mapping was done independently for each of the RIL families derived from B73 × CML322 and B73 × IL14H in each year (2007 and 2008) and across years. Original linkage maps for each population had more than 700 SNP markers (www.panzea.org); but QTL analyses were performed using linkage maps with an average distance between loci of about 10 cM, yielding a final set of 183 and 178 markers for the 185 and 194 RILs obtained from crosses B73 × CML322 and B73 × Il14H, respectively. QTL Cartographer (Basten et al. 2005) was used for cofactor selection using a p value for the partial F statistic of 0.01. A LOD threshold of 3.0 was chosen for declaring the putative QTL significant using composite interval mapping. The LOD of 3.00 is slightly above the score value obtained by the permutation test method (Churchill and Doerge 1994) yielding an experiment wise error rate of 25%. PLABQTL (Utz and Melchinger 2003) was used to obtain a final simultaneous fit using as covariates those loci detected by QTL Cartographer. In addition, all putative QTLs were examined for QTL × environment interaction. The proportion of phenotypic variance explained by all QTLs was determined by the adjusted coefficient of determination of regression (R^2_{adj}) fitting a model including all detected QTLs. The proportion of genotypic variance explained by all QTL for one trait (p) was calculated as $p =$ (genetic variance explained by QTL effects/genetic variance) × 100.

Fivefold cross-validation (CV/G) of QTLs was performed following the procedures described by Utz et al. (2000). The whole data set was randomly split into $k = 5$ data subsets. Four of these subsets were combined to form the estimation set (ES) and the remaining subset formed the test set (TS) in which predictions derived from ES were tested for their validity by correlating predicted and observed data. We used 1,000 replicate CV/G runs. Estimates of medians and percentiles and frequency of QTL detection in ES and TS were calculated over all replicated CV/G runs. The PLABQTL (Utz and Melchinger 2003) software package was used for all calculations.

To assess the allelic effects of QTLs shared across families, QTL analyses for DIMBOA-(T) content were made across the eight NAM RIL families (1,524 RILs) from 2008 using a multiple regression approach with 1,106 loci (Buckler et al. 2009). The NAM map used can be found at www.panzea.org. The PROC GLMSELECT procedure of SAS Institute Inc (2000) was used to choose cofactors using a probability level of 0.00001 for entering and deleting factors (Buckler et al. 2009). Regression analysis was performed with those cofactors and the best fit model for DIMBOA-(T) content was obtained by using the PROC GLM procedure of SAS.

Diversity analysis of the *bx* candidate genes

Two hundred and eighty-one genetically diverse inbreds were evaluated in 2008 (see list at http://www.panzea.org/lit/Basic281Inbreds_20081210.xls). The experimental design was a complete random block design with two replications. The experimental plot was the same as for RIL evaluations. Thirty-five days after planting, 5 cm of whorl tissue were collected from two plants per plot, bulked, lyophilized, ground, and maintained at −20°C until performing chemical analyses.

The DNA was extracted using standard protocols (Saghai-Maroof et al. 1984) with minor modifications. The genomic DNA sequence X76713 (http://www.ncbi.nlm.nih.gov), corresponding to *bx1* was BLASTed against the B73 sequence database (http://www.maizesequence.org/index.html) and an evidence-gene sequence, AC200309.3: 82911-85155 bp (GRMZM2G085381), was identified. PCR primers to amplify four amplicons of 500–800 bp (Supplemental Table 1) covering the evidence-gene from 36 bp downstream of the 5′ end to 148 bp upstream of 3′ end were designed using the Primer3 program (http://frodo.wi.mit.edu/). Similarly, evidence-gene sequences for *bx1*-adjacent *bx* genes (*bx2*, AC200309.3:87362-89517 (GRMZM2G085661); *bx3*, AC193441.3:7574-10352 (GRMZM2G167549); *bx4*, AC213878.3:11418-114239 (GRMZM2G172491); *bx5*, AC213878.3:49953-52529 (GRMZM2G063756), and *bx8*, AC200309.3:36796-38707 (GRMZM2G085054) were identified and PCR primer pairs were designed to generate amplicons for each sequence. Touchdown PCR was performed using Promega or Phire Taq in a DNA Engine Tetrad thermocycler (MJ Research). The PCR program consisted of one cycle of 1 min at 94°C, 1 min at 65°C, and 1 min 30 s at 72°C; the same cycle was repeated with 1°C decrement in annealing temperature per cycle until annealing temperature is 55°C; then, 34 cycles of 1 min at

94°C, 1 min at 55°C, and 1 min 30 s at 72°C are performed. Following PCR amplification, unincorporated primers and deoxynucleotide triphosphates were removed by ethanol precipitation prior to sequencing. For each amplicon, the PCR products were sequenced with forward and reverse primers using BigDye terminator version 3.1 terminator cycle sequencing kit (Applied Biosystems, Carlsbad, CA, USA) and analyzed on an ABI 3700 sequencer (Applied Biosystems).

Base calling, quality assessment, and trimming of trace files were conducted with PHRED (Ewing and Green 1998; Ewing et al. 1998), and sequence assembly was performed by PHRAP. The multiple sequences for each gene were aligned with DNAAlignEditor (Sanchez-Villeda et al. 2008) and edited manually. All sequences are available from GenBank with accessions GF098181-GF099430 and GF100745-GF101806 and association mapping and LD analyses were performed using TASSEL version 2.1 (Bradbury et al. 2007). Polymorphisms with low allele frequency (<5%) were removed. Association analyses were performed by using generalized linear (GLM) and mixed linear (MLM) regression models accounting for population structure (GLM and MLM) and relatedness among individuals (MLM). Population Structure and familial relatedness were controlled using both the (Q) and kinship (K) matrixes as reported by Flint-García et al. (2005) and Yu et al. (2006), respectively.

Results

Mapping of QTLs across years

Linkage mapping of RIL families derived from B73 × CML322 and B73 × IL14H for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) content was performed across years (2007 and 2008). The parents of the (B73 × CML322) RIL family differed for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) content in 2007, but not in 2008 (Table 1). Similarly, the parents of the (B73 × Il14H) RIL family differed for the three fractions in 2007, but only for DIMBOA content in 2008. Heritabilities for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) contents were high in both RIL families (Table 1).

QTLs affecting DIMBOA, DIMBOA-Glc, and DIMBOA-(T) contents across years were detected in both RIL families (Tables 2, 3). In general, QTLs detected for DIMBOA-(T) co-localized with QTLs detected for either DIMBOA and/or DIMBOA-Glc. Five QTLs were found for DIMBOA-(T) in the RILs derived from B73 × CML322 (Table 2). The largest QTL was detected on the short arm of chromosome 4, explaining the 42.5% of the phenotypic variance for DIMBOA-(T). The favorable allele was supplied by the inbred B73. Two other major QTLs on chromosomes 1 and 8, explained 18.4 and 13.7% of the phenotypic variability, respectively. Favorable alleles for these two QTL were also contributed by B73. Favorable alleles for minor QTLs situated in chromosomes 3 and 7 were inherited from the parental inbred with low DIMBOA-(T) content, CML322. The final model explained 55.3% of genetic variance. In cross-validation analysis, the median QTL effect for the QTL on chromosome 4 calculated from CV/G was similar to the value calculated from the full data set. However, for the other QTLs, the ratio between CV/G and full data set varied from 0.80 to 2.40. QTLs located on chromosomes 1, 3, 4, 7, and 8 were detected in 97.2, 79.0, 100.0, 82.1, and 62.0% of all cross-validations runs, and explained almost 50% of the genetic variance.

Table 1 LSMeans of the parents and RILs, RIL range and heritability (H) for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) content (ppm) evaluated in 2007 and 2008

Year		Genotype	B73 × CML322			B73 × IL14H		
			DIMBOA	DIMBOA-Glc	DIMBOA-(T)c	DIMBOA	DIMBOA-Glc	DIMBOA-(T)
2007	Mean	P1	1,211.39 a	1,800.66 a	3,012.05 a	613.21 b	2,482.40 b	3,095.61 b
		P2	36.87 b	1,013.38 b	1,050.24 b	1,527.12 a	4,310.23 a	5,837.35 a
		RILs	583.81	1,544.43	2,128.23	1,385.59	3,107.88	4,493.47
2008	Mean	P1	602.97 a	1,644.00 a	2,246.97 a	410.16 b	1,490.43 a	1,900.59 a
		P2	603.88 a	1,699.75 a	2,303.63 a	796.23 a	1,451.71 a	2,247.94 a
		RILs	229.21	985.68	1,213.97	594.30	1,680.83	2,261.00
Across	Mean	P1	907.19 a	1,722.33 a	2,629.51 a	511.69 b	1,986.41 b	2,498.10 b
		P2	320.38 b	1,356.56 a	1,676.93 b	1,161.68 a	2,880.97 a	4,042.64 a
		RILs	405.21	1,259.53	1,664.25	999.99	2,378.21	3,371.34
	Range	RILs	0–2,240	0–4,120	0–6,112	0–4,343	0–6,918	365–10,927
	H (%)	RILs	63.2	82.4	87.4	82.9	68.7	79.8

Parent means followed by the same letter did not differ at the 0.05 probability level

Table 2 Summary of QTLs affecting DIMBOA (D), DIMBOA–Glc (D_g), and DIMBOA-(T) (D_t) across years in a maize RIL family derived from the cross B73 × CML322, with their respective additive effects determined using the whole data set ($\hat{a}$) or 200 fivefold cross-validation runs ($\hat{a}_{TS.ES}$)

Trait	Chr[a]	Position (cM)	Confidence interval (cM)	LOD score	Left flanking marker	$\hat{a}$[b]	R^2_{adj}[c]	% σ^{2d}_g	Cross-validation $\hat{a}_{TS.ES}$[e]			
									Median	(10; 90) Percentile	Freq %	R^{2f}_{adj}
D	1[g]	78	74–82	10.03	L00776	−143.9 ± 21.9[h]	19.6		−131.3	(−108.4; −154.8)	97.3	
	4[g]	0	0–2	17.13	L00959	−190.7 ± 21.1[h]	31.5		−209.1	(−183.8; −236.7)	99.9	
	8	102	94–110	3.19	L00489	−66.5 ± 21.1[h]	5.3		−84.3	(−72.3; −102.9)	42.2	
							43.4	47.1				30.7
D_g	1[i]	78	70–82	3.07	L00776	−188.4 ± 40.4[h]	11.1		−165.2	(−141.3; −210.7)	47.5	
	3	118	112–122	5.46	L00286c	137.0 ± 38.8	6.6		251.5	(158.2; 330.7)	92.7	
	4[i]	0	0–2	18.04	L00959	−400.4 ± 38.9[h]	37.4		−376.2	(−330.6; −421.9)	100.0	
	8[i]	82	76–86	5.21	L00534	−208.5 ± 38.8[h]	14.1		−193.2	(−154.1; −240.8)	80.5	
							48.9	63.4				40.0
D_t	1[i]	78	74–82	6.69	L00776	−334.9 ± 53.1[h]	18.4		−261.5	(−211.5; −325.7)	97.2	
	3	118	114–126	3.43	L00286c	174.7 ± 51.7	6.2		242.4	(186.8; 382.6)	79.0	
	4[i]	4	0–2	23.57	L00959	−585.7 ± 51.3[h]	42.5		−592.0	(−532.1; −660.2)	100.0	
	7	7	60–68	4.71	L00545	149.2 ± 51.6[h]	4.5		363.9	(257.3; 496.8)	82.1	
	8[i]	100	94–108	7.40	L00489	−289.4 ± 54.8[h]	13.7		−229.8	(−192.6; −290.3)	62.0	
							51.9	55.3				49.1

[a] Chromosome where the QTL is located

[b] Mean additive effect ± standard deviation based on whole data, negative effects mean that the allele for higher amount came from B73

[c] Proportion of phenotypic variance explained

[d] Proportion of the genotypic variance explained by detected QTL after adjusting for QTL × environment interactions

[e] Median, percentiles, and frequency of QTL detection were calculated based on 200 fivefold CV/G runs

[f] Proportion of phenotypic variance explained by detected QTLs calculated in 200 cross-validations runs

[g] QTL × environment effect was significant

[h] Additive effects were significant in each individual environment

[i] QTL × environment effect was not significant

Three QTLs were found for DIMBOA-(T) content in the RIL family obtained from B73 × Il14H (Table 3). The most important QTL was again localized at the beginning of chromosome 4 and explained approximately the 9.5% of phenotypic variability. The favorable allele for this QTL was derived from the inbred Il14H. The two other QTLs were located in chromosomes 1 and 6. B73 supplied the favorable allele for the QTL in chromosome 1 and Il14H for the QTL in chromosome 6. In this particular RIL family, QTL × environment effects were very important, and the QTL detected only explained 5.4% of genetic variability. Again, the median QTL effect for the QTL in chromosome 4 calculated from CV/G runs approximated the value calculated from the full data set. The ratio between CV/G and full data set for QTLs in chromosomes 1 and 6 varied from 1.20 to 1.40. QTLs in chromosomes 4 and 6 were detected in 76.5 and 80.4% of CV/G runs, but the QTL on chromosome 1 was only detected in 26.7% of CV/G runs. The analysis of 2 years data for two RIL families indicated that shared QTLs are present on chromosomes 1 and 4. The results also suggest that an allelic series exists for the chromosome 4 QTL with Il14H > B73 > CML322.

Mapping of QTLs across RIL families

To further test for shared QTL and the presence of allelic series for DIMBOA QTL eight RIL families were evaluated in 2008 (Table 4). Mean values for each genotype were not adjusted by the block effect because there were not significant differences among blocks for DIMBOA-(T) content in any experiment (data not shown). Differences for DIMBOA-(T) were significant between the parents of the RILs derived from B73 × CML52, B73 × MS71, and B73 × NC350. The mean of the DIMBOA-(T) amounts of RILs within a family, varied from approximately the value of the high parent, intermediate between both parents or similar to the parent with the low amount (Supplemental Table 2). The average of the RIL family derived from B73 × CML322 for DIMBOA-(T) content was significantly lower than the mean of either parent.

Table 3 Summary of QTLs affecting DIMBOA (D), DIMBOA-Glc (D_g), and DIMBOA-(T) (D_t) across years in a maize RIL family derived from the cross B73 × IL14H, with their respective additive effects determined using the whole data set ($\hat{a}$) or 200 fivefold cross-validation runs ($\hat{a}_{TS.ES}$)

Trait	Chr[a]	Position (cM)	Confidence interval (cM)	LOD score	Left flanking marker	$\hat{a}$[b]	R^{2c}_{adj}	% σ^{2d}_g	Cross validation $\hat{a}_{TS.ES}$[e]			R^{2}_{adj}[f]
									Median	(10;90) Percentile	Freq %	
D	1[g]	144	140–148	5.31	L01175	215.5 ± 48.2[h]	10.1		219.3	(187.4; 274.0)	86.2	
	6[g]	6	0–16	4.70	L00743	195.7 ± 51.3[h]	7.6		228.2	(192.8; 270.6)	86.3	
	6[g]	82	78–86	3.25	L00448	175.7 ± 47.2[h]	7.3		201.4	(174.3; 363.7)	42.9	
							19.1	21.2				6.6
D_g	4[g]	10	4–16	4.11	L00074	397.8 ± 95.4[h]	8.8		409.8	(350.9; 487.5)	67.3	
							7.8	4.5				2.7
D_t	1	62	50–66	3.06	L00116	−369.2 ± 130.0[h]	4.3		−513.4	(−452.8; −605.9)	26.7	
	4[g]	10	6–16	5.05	L00074	554.0 ± 128.1[h]	9.4		578.1	(491.1; 678.5)	76.5	
	6[g]	6	0–16	4.52	L00743	465.1 ± 130.7[h]	6.6		562.9	(481.8; 671.9)	80.4	
							16.1	5.4				4.5

[a] Chromosome where the QTL is located

[b] Mean additive effect ± standard deviation based on whole data, negative effects mean that the allele for higher amount came from B73

[c] Proportion of phenotypic variance explained

[d] Proportion of the genotypic variance explained by detected QTL after adjusting for QTL × Environment interactions

[e] Median, percentiles, and frequency of QTL detection were calculated based on 200 fivefold CV/G runs

[f] Proportion of phenotypic variance explained by detected QTLs calculated in 200 cross-validations runs

[g] QTL × environment effect was not significant

[h] Additive effects were significant in each individual environment

From the GLMSELECT analysis across the eight families, QTLs with significant effects for DIMBOA-(T) content were found on chromosomes 1, 2, 4, 5, 6, and 8 (Table 4). After accounting for the variability explained by differences among families (family as a term in the model), the closest marker to the major QTL detected in chromosome 4 explained more than 15% of phenotypic variation across the eight families. Each of the closest markers to QTLs in chromosomes 2 and 5 explained more than 3% of phenotypic variability and each of the remaining markers explained from 1.6 to 2.8% of the phenotypic variability across all families. The final model explained approximately 34% of intra-population phenotypic variability across the eight families.

For DIMBOA-(T), significant effects of markers PZA03189 (chromosome 1, at bin 1.04), PHM1184 (chromosome 4, at bin 4.01), PZA01527 (chromosome 6, at bin 6.01), and PZA00473 (chromosome 6, at bin 6.05), displayed both positive (favorable allele came from the non-B73 parent) or negative (favorable allele came from B73) effects, depending on the specific RIL family (Table 4). Significant effects of the markers PZA00635 (chromosome 2, at bin 2.04) and PZA02746 (chromosome 8, at bin 8.06) were always negative, while significant additive effects of markers PZA02002 (chromosome 4, at bin 4.04) and PZA00980 (chromosome 5, at bin 5.07) were always positive. The effects of the marker PHM1184.26 were significant in seven out of the eight RIL families, PZA03189.4 in six, PZA00473 and PZA02746 in five, PZA00635 in four, PZA00980 and PZA01527 in three, and PZA02002 in two. The additive genetic effect of the marker PHM1184 was more than 1,000 ppm in two families, while genetic effects of markers PZA03189 (chromosome 1, at bin 1.04), PZA00635 (chromosome 2, at bin 2.04), PZA00980 (chromosome 5, at bin 5.07) reached 600 ppm in specific families (Table 4).

As DIMBOA content declines with plant age, faster growing plants may have a lower DIMBOA content by dilution of DIMBOA with greater plant mass. To determine if plant growth is a confounding factor for any of the QTL reported above we determined the correlation of leaf number with DIMBOA levels and mapped QTL for leaf number present at time of tissue collection. The number of leaves was significantly and negatively correlated with DIMBOA-(T) content across populations ($r = -0.19$, $p < 0.0001$), and within the RIL families derived from the crosses B73 × CML52, B73 × M37W, B73 × MS71, and B73 × Oh43, although correlation coefficients were low (Supplemental Table 2).

As a significant relationship was found between DIMBOA-(T) content and number of leaves per plant, QTL analyses for leaf number were performed. Three minor

Table 4 Position, and effects of markers identified as significant for DIMBOA-(T) (ppm) content in the GLM model

Marker	Chrom[a]	Position[b]	Contig	Parameter[c]	CML322	CML52	IL14H	M37W	MS71	NC350	Oh43	Tx303	R^2
DIMBOA-(T)													
PZA03189	1	73.3	ctg14	Effect	**−213.9**[d]	**−328.0**[d]	−163.6	**−227.3**	**295.7**	**−635.4**[d]	**−235.0**	−98.5	2.80[e]
				p	0.049	0.002	0.169	0.048	0.004	<0.001	0.031	0.356	
PZA00635	2	73.5	ctg80	Effect	−55.1	**−252.5**	−85.0	**−637.6**[d]	**−379.6**[d]	−84.5	**−222.2**	−53.5	3.41
				p	0.609	0.024	0.454	<0.001	<0.001	0.430	0.033	0.616	
PHM1184	4	7.2	ctg155	Effect	**−489.8**[d]	**−1,061.9**[d]	**300.2**	**325.1**	**435.4**[d]	**−338.7**	**1,042.8**[d]	47.0	15.74
				p	<0.001	<0.001	0.020	0.001	<0.001	0.001	<0.001	0.660	
PZA02002	4	49.4	ctg163	Effect	−39.5	49.5	99.1	**498.9**	**420.1**	153.5	205.8	−36.3	2.44
				p	0.725	0.641	0.496	<0.001	<0.001	0.156	0.053	0.731	
PZA00980	5	114.3	ctg251	Effect	−6.8	**333.6**	200.8	**675.2**[d]	122.5	189.0	**320.0**	195.3	3.34
				p	0.963	0.006	0.080	<0.001	0.263	0.080	0.002	0.061	
PZA01527	6	8.8	ctg265	Effect	97.2	**332.4**	226.7	22.4	**487.1**[d]	27.8	**−410.1**	122.5	2.40
				p	0.368	0.001	0.056	0.828	<0.001	0.801	<0.001	0.245	
PZA00473	6	45.9	–	Effect	127.6	**−215.1**[d]	**262.5**	**268.8**	**255.2**	−134.2	**427.7**	23.0	1.61
				p	0.253	0.036	0.026	0.012	0.028	0.242	<0.001	0.844	
PZA02746	8	94.1	ctg362	Effect	**−262.9**[d]	−108.5	−262.9	**−389.5**	−137.4	**−409.5**	**−262.1**	−24.2	2.26
				p	0.017	0.317	0.023	<0.001	0.190	<0.001	0.014	0.827	

Significant effects are in bold

[a] Chromosome where the QTL is located

[b] Position of the marker in cM

[c] Mean additive effect of the marker in each RIL family with its corresponding probability level, positive effects negative effects mean that the allele for higher amount came from B73

[d] The QTL identified by individual analysis of the specific RIL family was less than 5 cM apart from the marker identified as associated to DIMBOA-(T) content across populations

[e] Proportion of intra-population phenotypic variance explained

QTLs were detected explaining approximately the 9% of variability for number of leaves. Those markers were PZA0300.2 located in chromosome 1 at bin 1.05, PZA00485.2 located in chromosome 2 at bin 2.05, and PZB02044.1 in chromosome 3 at bin 3.05.

Diversity analysis of the bx candidate genes

We identified 45 INDELs and 44 SNPs across the four amplicons in *bx1*, 6 INDELs and 11 SNPs in one amplicon for *bx2*, 3 INDELs, and 19 SNPs in one amplicon for *bx3*, 7 INDELs, and 2 SNPs in two amplicons for *bx4*, 10 INDELs, and 35 SNPs across the three amplicons in *bx5*, and no polymorphisms of greater than 5% frequency for *bx8*. Twenty-eight polymorphisms across *bx1* and one polymorphism in *bx2* were significantly associated ($p < 0.001$) with DIMBOA-(T) content in analysis using both Q + K matrix (Yu et al. 2006) (Fig. 1). The most strongly associated polymorphism was an SNP (A/G) at 620 bp in amplicon X76713.5 (X76713.5_620) of the gene *bx1*, genetic variation at that polymorphism explained 4% of the phenotypic variation not accounted for by population structure and familial relatedness using MLM. Considering all polymorphisms in *bx1* significantly associated to DIMBOA-(T), more than 50 different haplotypes were identified for *bx1* (Supplemental Table 3). Therefore, in order to fit a multilocus model, we performed three-way ANOVA analyses including as sources of variation: groups (Stiff Stalk, Non Stiff Stalk and Tropical–equivalent to Q), the X76713.5_620 polymorphism (as being the most significantly associated to DIMBOA-(T) content) and then test all other significant polymorphism. The model including the polymorphisms in exons 5 and 6 at sites X76713.5_620 and bx1_1.9_143 (3 bp INDEL at 143 bp in amplicon bx1_1.9), respectively, and variation among groups was the only model in which both polymorphisms remained significant. This model explained 12% of variation not accounted for by population structure and 27% of total variability among inbreds. Average DIMBOA-(T) content for each haplotype was 1,986 ± 536 ppm for the A SNP (X76713.5_620)—3 bp insertion (bx1_1.9_143), 2,890 ± 239 ppm for G SNP (X76713.5_620)—3 bp insertion (bx1_1.9_143), 1,403 ± 283 ppm for A SNP (X76713.5_620)—3 bp deletion (bx1_1.9_143), and 2,128 ± 317 ppm for G SNP (X76713.5_620)—3 bp deletion (bx1_1.9_143). Among the parental inbreds of the RILs families, B73, M37W, MS71, Oh43, and Tx303 carried the genetic variants at those points favorable for DIMBOA-(T) accumulation (G at X76713.5_620 and 3 bp insertion at bx1_1.9_143); while CML322, CML52, IL14H, and NC350 carried the unfavorable ones (A at X76713.5_620 and 3 bp deletion at bx1_1.9_143).

In general, the level of LD within the *bx1* gene rapidly decayed with distance (Fig. 2). However, LD coefficients (r^2) between the significant polymorphisms included in the ANOVA model, X76713.5_620 or bx1_1.9-143, and other polymorphisms were >0.2 up to a distance between polymorphisms of approximately 600 bp (Fig. 1). All significant polymorphisms were in significant LD ($p < 0.01$) with X76713.5_620 and/or bx1_1.9-143, except two polymorphisms located at the beginning of *bx1* and the INDEL located at X76713.5_40 (data not shown). The result that the initially significant polymorphism in *bx2* did not remained significant in the multilocus model indicates that the initial significance is due to residual LD with the polymorphisms in *bx1*.

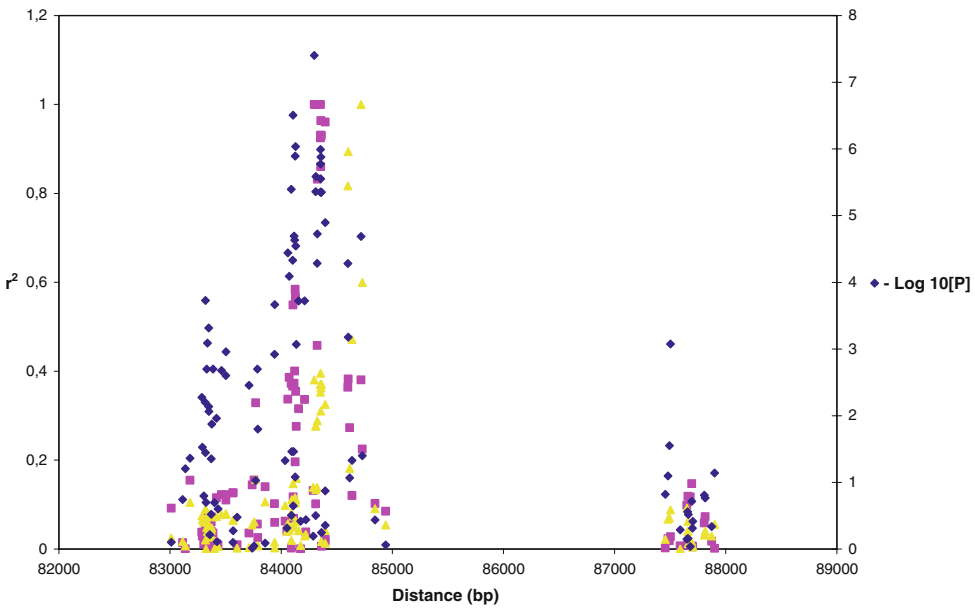

Fig. 1 Association of DNA polymorphisms with DIMBOA-(T) content across genomic portions of genes *bx1* (82,911–85,155 bp) and *bx2* (87,362–89,517 bp). The positions correspond to BAC sequence AC200309.3. *Blue diamonds* indicate association with DIMBOA content. Level of statistical association for each SNP and INDEL is expressed as −Log 10[*P*]. *Pink squares* indicate r^2 LD scores for all marker pairs involving X76713.5_620 and *yellow triangles* r^2 LD scores for all marker pairs involving bx1_1.9_143

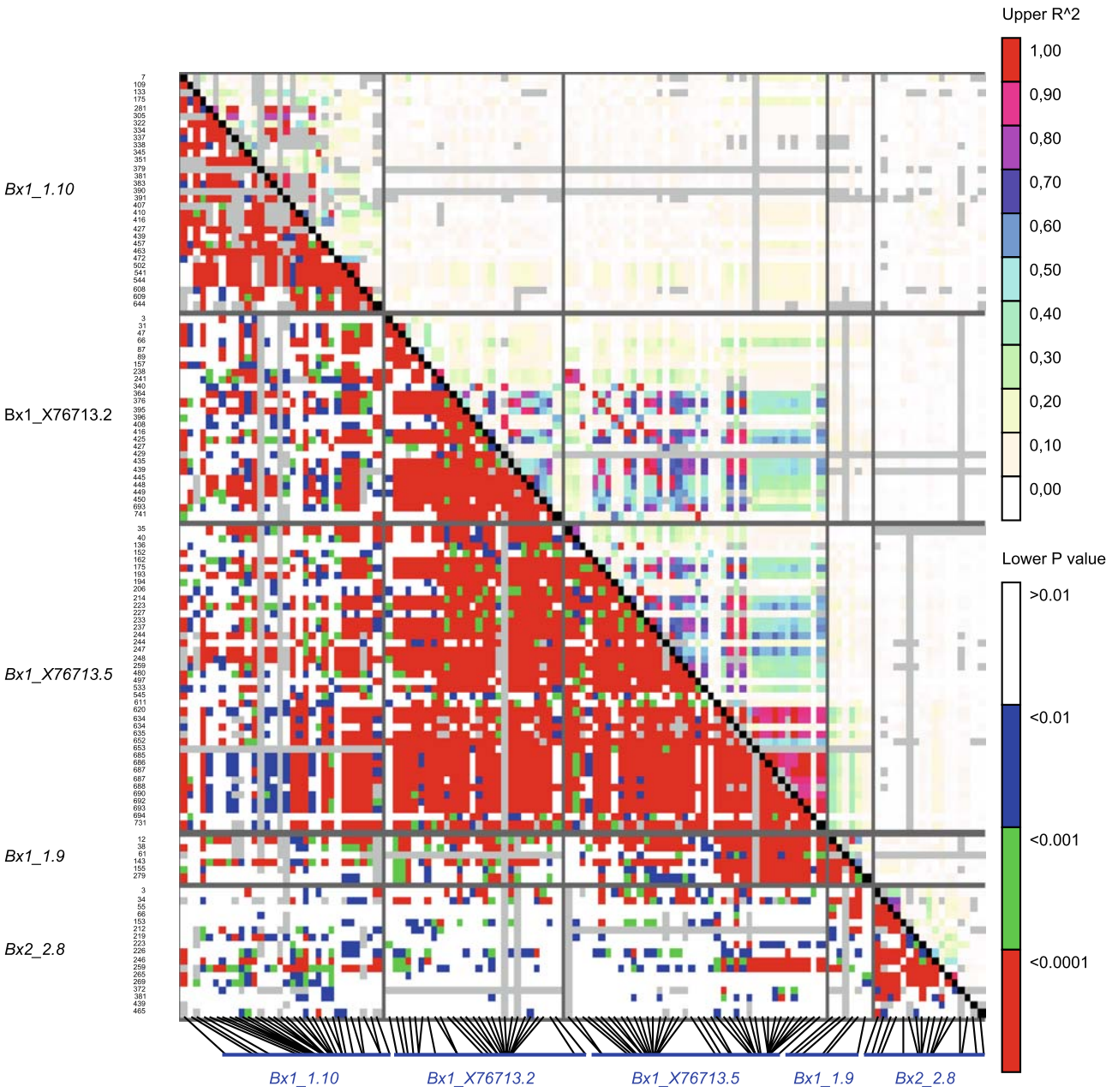

Fig. 2 Linkage disequilibrium (LD) across *bx1* and part of *bx2* genes

Discussion

Heritabilities for DIMBOA levels were high in both RIL families tested in 2 years and differences between inbred parents were significant for most traits. Therefore, QTLs with appreciable effect on DIMBOA content are expected to be found. In the B73 × CML322 family 47.1–63.4% of genetic variability for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) among RILs could be explained by the detected QTLs. This is in contrast to only 4.5–21.2% of variability for RILs derived from B73 × Il14H family. The B73 × CML322 family contrasts a moderate DIMBOA parent with a low DIMBOA parent while the B73 × Il14H family contrasts a moderate DIMBOA parent with a slightly higher DIMBOA parent. These results suggest that undetected QTLs with small effects could be responsible for unexplained differences for DIMBOA, DIMBOA-Glc, and DIMBOA-(T) contents in some backgrounds such as the B73 × Il14H family. Therefore, larger population sizes may be necessary to increase the detection power and

uncover where those genes lie. The NAM population could provide that increase in power if those genes with minor effect are segregating in multiple RIL families.

The use of two environments for evaluations and cross-validation allowed tests of the consistency of the results (Bohn et al. 2001). Cross-validations provide more reliable estimates of R^2_{adj} and $\hat{a}$ by avoiding bias causing model selection (Beavis 1998). Most QTLs found in both populations were reliable because the additive effects computed with the CV/G data were significant and similar to those computed with the full data set. In addition, most QTLs were found in more than 75% of CV/G runs. Therefore, the precision of QTL positions is adequate to use markers close to them in MAS-assisted selection (Utz et al. 2000).

As QTLs for DIMBOA-(T) were, in general, the sum of QTLs detected for DIMBOA and DIMBOA-Glc, we will focus discussion on DIMBOA-(T) content. Although the additive effects for the QTL were higher among RILs derived from B73 × CML322 and accounted for a much higher percentage of genetic variability, two QTLs, located in chromosomes 1 and 4, were involved in the DIMBOA pathway in both populations. The QTL on chromosome 4 was located in both populations on the short arm of chromosome 4 where the *bx1*, *bx2*, *bx3*, *bx4*, *bx5*, *bx6*, and *bx8* genes are located (http://www.maizesequence.org/index.html). Therefore, polymorphisms for one or more of these structural genes of the DIMBOA pathway (Jonczyk et al. 2008) could be responsible for most of the variance among (B73 × CML322) RILs and for almost 10% of phenotypic variability among (B73 × Il14H) RILs. Bohn et al. (2001), Jampatong et al. (2002), and Cardinal et al. (2006) have reported QTLs for leaf-feeding damage by lepidopterous species in the same genomic area, on chromosome 4 (bin 4.01). No significant QTLs were found in the proximity of genes *bx7* (contig 160) and *bx9* (contig 37). In addition to the region of structural genes, the involvement of other genomic regions (bins 1.03–1.04, 3.08, 6.01, 7.02, and 8.06) may reveal the position of unknown regulatory genes (McMullen et al. 2009b). Regions in chromosomes 1 (1.04), 3 (3.08), 6 (6.01), and 7 (7.02), and 8 (8.06) had already been identified as involved in resistance to leaf-feeding by *D. grandiosella* and *O. nubilalis* (Bohn et al. 1997; Groh et al. 1998; Jampatong et al. 2002; Brooks et al. 2005, 2007; Cardinal et al. 2006). Therefore, there is a convergence of loci for DIMBOA levels with loci detected in insect resistance QTL experiments.

To extend the results from the two families of RIL to a broader range of germplasm, to determine the degree of shared QTL across parents, and to test for allelic series at QTL for DIMBOA, eight families from the NAM population were evaluated in 2008. The values for DIMBOA-(T) of each RIL family and its inbred parents only differed for crosses B73 × CML322, B73 × CML52, M73 × MS71, and B73 × NC350. In general, the mean of RIL families did not approximate the mid-parent value for DIMBOA-(T) content, but exhibited DIMBOA levels closer to the high or low parent or even showed less amount for DIMBOA-(T) content than both parents. These data suggest that epistatic effects may play an important role in the inheritance of DIMBOA-(T) content. However, a model including only additive effects explained approximately 34% of phenotypic variability within RIL families for DIMBOA-(T). As in the individual family analysis, the largest QTL in the across family analysis was located on chromosome 4. The position of the significant marker, PHM1184, is on BAC contig 155, and co-localises with the majority of structural genes of the DIMBOA pathway (www.maizesequence.org). In addition, seven other genomic regions (located in chromosomes 1, 2, 4, 5, 6, and 8) explained as much variability as likely explained by polymorphisms at structural genes. Previous supporting evidence of the potential involvement of some of these genomic regions in DIMBOA synthesis comes from studies of QTLs for resistance to the first generation of *O. nubilalis* (Jampatong et al. 2002; Cardinal et al. 2006) since resistance to the first generation of this insect in temperate material is largely associated to mid-whorl DIMBOA levels (Barry et al. 1994). Agreeing with those previous studies, we have found QTLs for DIMBOA-(T) at bins 4.01, 4.04, 6.01, and 8.06. However, marker polymorphisms at bins 1.04, 2.04, 5.07, and 6.05 were not previously associated with phenotypic variation for resistance to the first generation of *O. nubilalis*. The lack of prior report of these QTL for first generation resistance could be due to either a low effect level of these loci or genetic heterogeneity as positive alleles at these loci only occurred in a subset of the RIL families. All QTLs for DIMBOA content, except those located at 2.04, 4.04 and 5.07, were in regions where QTL for resistance to leaf-feeding by *D. grandiosella* and *D. saccharalis* were previously detected (Groh et al. 1998; Khairallah et al. 1998; Bohn et al. 2001; Brooks et al. 2005, 2007).

Most QTLs detected when computing QTL analyses of individual RIL families were also included in the fit model for the eight families, except those QTLs that explained less than 10% of variability within unique RIL families or were located on the same chromosome as another detected QTL (data not shown). Therefore, the procedure of searching for QTLs across individual RILs families could miss those QTLs with significant effects in unique families, mostly when they are located in close proximity of other QTLs with significant effects across populations. Yu et al. (2008) estimated the average power of NAM under different trait complexity schemes using different number of RILs and determined that the average power could be approximately 0.6 when the number of QTLs was 20, $h^2 = 0.7$, and the number of RILs = 1,500. Consequently,

it is not surprising that QTLs with low or moderate additive effects in unique populations are not identified using NAM analysis, but the decrease in power of detection when performing NAM analysis compared to conventional linkage analysis seemed to be low. Moreover, due to the increased resolution, additive effects for markers detected by the NAM approach were highly significant ($p < 0.001$) for particular RIL families in which no QTLs were found near to the marker using conventional linkage mapping (data not shown).

The tropical lines used in this study, CML322, CML52, and NC350, supplied alleles for the QTL at 4.01 with significant negative effects for DIMBOA-(T) concentration. This would explain why most studies conducted to locate QTLs for resistance to leaf-feeding by native American lepidopterous insects among tropical and subtropical inbreds did not report QTLs close to the *bx* region (Bohn et al. 2001; Brooks et al. 2005, 2007). This result also agrees with the concept that different mechanisms from DIMBOA antibiosis are present in resistant tropical maize. Bohn et al. (2001) found QTLs for resistance to leaf-feeding by *D. grandiosella* at chromosome positions 4.01 and 6.01, where QTLs for DIMBOA-(T) have been located, but the favorable alleles for resistance to the pest came from the susceptible tropical inbred (Ki3), and not from the resistance source.

The additive effects of the marker PZA00635 (at bin position 2.04) were significant in four RIL families, this maker is located in contig 80, close to the position of a gene that codes for a specific glucosidase (*β-glu2* in contig 84). It is unclear how variability for a specific glucosidase for DIMBOA-Glc, whose activity renders DIMBOA from DIMBOA-Glc (Morant et al. 2008), could affect variability for DIMBOA-(T) content.

For markers in chromosomes 1 at bin 1.04, 4 at bin 4.01, and 6 at bins 6.01 and 6.05, there were at least three different alleles because non-B73 parents supplied alleles with increased and decreased additive effects for DIMBOA-(T) content compared to B73. Therefore, although no more than two alleles were segregating in each RIL family, allowing a high detection power, the additive effects of more than two allelic variants per loci could be simultaneously estimated using the multiple family approach of NAM.

Previous studies showed that DIMBOA concentration decreases with plant age (Morse et al. 1991; Barry et al. 1994; Cambier et al. 2000). We demonstrated a significant, negative association between DIMBOA-(T) content and plant growth measured as number of leaves per plant. Therefore, we reasoned that factors regulating growth could also appear as QTL for DIMBOA synthesis. Three QTLs involved in differences for number of leaves were found and markers linked to those QTLs explained approximately the 9% of phenotypic variation for number of leaves, but none of these markers were co-localized to markers associated with variation for DIMBOA-(T) content. Therefore, none of the QTL identified for DIMBOA synthesis are genetically correlated to growth loci. The apparent negative correlation of leaf number with DIMBOA-(T) must involve small genetic effects not detected as significant QTL.

As position of the largest QTL co-localizes with the majority of structural genes of the DIMBOA pathway, and *bx1* is the committal step into the DIMBOA pathway, it is the prime candidate for affecting total DIMBOA accumulation. Therefore, association analysis was used to determine if genetic variation at *bx1* affects variation of DIMBOA-(T) content. GLM and MLM revealed associations between variability for DIMBOA-(T) content and sequence polymorphisms at *bx1* locus. After adjusting for population structure, a model including two polymorphisms in *bx1* explained 12% of phenotypic variation in a population of 282 diverse lines. This is close to the 15% effect predicted by the GLMSELECT analysis for the chromosome 4 QTL across eight families of RILs. However, these polymorphisms could not explain genetic effects for DIMBOA-(T) content of the closest marker (PHM1184) to the major QTL detected in chromosome 4. For example, inbreds CML322 and IL14H carried the same genetic variants at both polymorphisms, but among RILs families obtained from crosses to B73, the allele at PHM1184 from CML322 had a negative additive effect for DIMBOA-(T) content, while the allele from IL14H had a positive effect. Therefore, the high percentage of variation explained by the model including the two polymorphisms at exons 5 and 6 in *bx1* and their significant LD with other significantly associated polymorphisms in *bx1* and *bx2* suggests that genetic variation for *bx1* is particularly important for determining DIMBOA content in a diverse panel of maize inbred lines. The rapid decay of LD and the fact that no polymorphisms in *bx2* were significant in the presence of a significant *bx1* polymorphism suggest that the main causal polymorphisms are within or near the *bx1* gene and alter DIMBOA content by affecting BX1 level. However, the specific causal polymorphism or polymorphisms responsible for the QTL detected in the region 4.01 were not identified, either because those polymorphisms were not sequenced (*bx1* was not entirely sequenced), causal polymorphism is outside the coding region, identity is masked by LD, adjustments for population structure reduce significance of causal polymorphisms or multiple causal polymorphisms affecting *bx1* segregate among inbred lines. In characterizing QTL for flowering time in maize Buckler et al. (2009) demonstrated that common QTL with uncommon, multiple alleles is the norm. It may be that *bx1* from Il14H has a distinct causal polymorphism increasing DIMBOA levels from the causal polymorphisms in LD with the significant SNP detected in this study.

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References

Babcock GD, Esen A (1994) Substrate specificity of maize *β*-glucosidase. Plant Sci 101:31–39

Barry D, Alfaro D, Darrah LL (1994) Relation of European corn borer (Lepidoptera: Pyralidae) leaf feeding resistance and DIMBOA content in maize. Environ Entomol 23:177–182

Basten CJ, Weir BS, Zheng ZB (2005) QTL cartographer, version 1.17. Department of Statistics, North Carolina State University. Raleigh, NC

Beavis WD (1998) QTL analyses: power, precision, and accuracy. In: Paterson AH (ed) Molecular dissection of complex traits. CRC Press, New York, pp 145–162

Beló A, Zheng P, Luck S, Shen B, Meyer DJ, Bailin Li, Tingey S, Rafalski A (2008) Whole genome scan detects an allelic variant of *fad2* associated with increased oleic acid levels in maize. Mol Genet Genomics 279:1–10

Bohn M, Khairallah MM, Jiang C, Gonzalez de Leon D, Hoisington DA, Utz HF, Deutsch JA, Jewell DC, Mihn JA, Melchinger AE (1997) QTL mapping in tropical maize. II. Comparison of genomic regions for resistance to Diatraea spp. Crop Sci 37:1892–1902

Bohn M, Groh S, Khairallah MM, Hoisington DA, Utz HF, Melchinger AE (2001) Re-evaluation of the prospects of marker-assisted selection for improving insect resistance against *Diatraea spp.* in tropical maize by cross validation and independent validation. Theor Appl Genet 103:6–7

Bradbury PJ, Zhang Z, Kroon DE, Casstevens TM, Ramdoss Y, Buckler ES (2007) TASSEL: software for association mapping of complex traits in diverse samples. Bioinformatics 23:2633–2635

Brooks TB, Willcox MC, Williams WP, Buckley PM (2005) Quantitative trait loci conferring resistance to fall armyworm and southwestern corn borer leaf feeding damage. Crop Sci 45:2430–2434

Brooks TD, Bushman BS, Williams WP, McMullen MD, Buckley PM (2007) Genetic basis of resistance to fall armyworm (Lepidoptera: Noctuidae) and southwestern corn borer (Lepidoptera: Crambidae) leaf-feeding damage in maize. J Econ Entomol 100:1470–1475

Buckler ES, Holland JB, Bradbury PJ, Acharya CB, Brown PJ, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Glaubitz JC, Goodman MM, Harjes C, Guill K, Kroon DE, Larsson S, Lepak NK, Li H, Mitchell SE, Pressoir G, Peiffer JA, Rosas MO, Rocheford TR, Romay MC, Romero S, Salvo S, Sanchez Villeda H, da Silva HS, Sun Q, Tian F, Upadyayula N, Ware D, Yates H, Yu J, Zhang Z, Kresovich S, McMullen MD (2009) The genetic architecture of maize flowering time. Science 325:714–718

Cambier V, Hance T, de Hoffman E (2000) Variation of DIMBOA and related compounds content in relation to the age and plant organ in maize. Phytochemistry 53:223–229

Camus-Kulandaivelu L, Vyerieras J-B, Madur D, Combes V, Fourmann M, Barraud S, Dubreuil P, Gouesnard B, Maninacci D, Charcosset A (2006) Maize adaptation to temperate climate: relationship between population structure and polymorphism in the *Dwarf8* gene. Genetics 172:2449–2463

Cardinal AJ, Lee M, Guthrie WD, Bing J, Austin DF, Leldboom LR, Senior ML (2006) Mapping of factors for resistance to leaf-blade feeding by European corn borer (*Ostrinia nubilalis*) in maize. Maydica 51:93–102

Churchill GA, Doerge RW (1994) Empirical threshold value for quantitative trait mapping. Genetics 138:963–971

Czjzek M, Cicek M, Zamboni V, Burmeister WP, Bevan DR, Henrisaat B, Esen A (2000) The mechanism of substrate (aglycone) specificity in beta-glucosidases is revealed by crystal structures of mutant maize beta-glucosidase-DIMBOA, -DIMBOAGlc, and dhurrin complexes. Proc Natl Acad Sci USA 97:13555–13560

Ducrocq S, Madur D, Veyrieras J-B, Camus-Kulandaivelu L, Kloiber-Maitz M, Presterl T, Ouzunova M, Manicacci D, Charcosset A (2008) Key impact of *Vgt1* on flowering time adaptation in maize: evidence from association mapping and ecogeographical information. Genetics 178:2433–2437

Ewing B, Green P (1998) Base-calling of automated sequencer traces using phred. II. Error probabilities. Genome Res 8:186–194

Ewing B, Hillier L, Wendl MC, Green P (1998) Base-calling of automated sequencer traces using phred. I. Accuracy assessment probabilities. Genome Res 8:175–185

Flint-García SA, Thuillet AC, Yu J, Pressoir G, Romero SM, Mitchell SE, Doebley J, Kresovich S, Goodman MM, Buckler ES (2005) Maize association population: a high-resolution platform for quantitative trait locus dissection. Plant J 44:1054–1064

Frey M, Chomet P, Glawischnig E, Stettner C, Grun S, Winklmair A, Eisenreich W, Bacher A, Meeley RB, Briggs SP, Simcox K, Gierl A (1997) Analysis of a chemical plant defense mechanism in grasses. Science 277:696–699

Frey M, Stetner C, Paré PW, Schmelz EA, Tumlinson JH, Gierl A (2000) An herbivore elicitor activates the gene for indole emission in maize. Proc Natl Acad Sci USA 19:14801–14806

Frey M, Huber K, June Park W, Sicker D, Lindberg P, Meely RB, Simmons CR, Yalpani N, Gierl A (2003) A 2-oxoglutarate-dependent dioxygenase is integrated in DIMBOA-biosynthesis. Phytochemistry 62:371–376

Gierl A, Frey M (2001) Evolution of benzoxazinone biosynthesis and indole production in maize. Planta 213:493–498

Glawischnig E, Grün S, Frey M, Gierl A (1999) Cytochrome P450 monooxygenases of DIBOA biosynthesis: specificity and conservation among grasses. Phytochemistry 50:925–930

Groh S, Gonzalez de Leon D, Khairallah MM, Jiang C, Bergvinson D, Bohn M, Hoisington DA, Melchinger AE (1998) QTL mapping in tropical maize:III. Genomic regions for resistance to Diatraea spp and associated traits in two RIL populations. Crop Sci 38:1062–1072

Gutiérrez C, Castañera P (1986) Efecto de los tejidos de maíz con alto y bajo contenido en DIMBOA sobre la biología del taladro *Sesamia nonagrioides* Lef. (Lepidoptera: Noctuidae). Investigaciones Agrarias: Producción y Protección vegetal 1:109–119

Gutiérrez C, Castañera P, Torres V (1988) Wound-induced changes in DIMBOA (2, 4 dihydroxy-7-methoxy-2H–1, 4 benzoxazin-3(4H)-one) concentration in maize plants caused by Sesamia nonagrioides (Lepidoptera: Noctuidae). Ann Appl Biol 113:447–454

Hedin PA, Davis FM, Williams WP (1993) 2-hydroxy-4, 7dimethoxy-1, 4 benzoxazin-3-one (*N-O*-ME-DIMBOA), a possible toxic

factor in corn to the southwestern corn borer. J Chem Ecol 19:531–542

Houseman JG, Philogene BJR, Downe AER (1989) Partial characterization of proteinase activity in the larval midgut of the European corn borer, *Ostrinia nubilalis* Hubner (Lepidoptera: Pyralidae). Can J Zool 67:864–868

Houseman JG, Campos F, Thie NMR, Philogene BJR, Atkinson J, Morand P, Arnason JT (1992) Effect of the maize-derived compounds DIMBOA and MBOA on growth and digestive processes of European corn borer (Lepidoptera: Pyralidae). J Econ Entomol 85:669–674

Huang CH, Wang XY, Wang RJ, Xue K, Yan FM, Xu CR (2006) Distribution and variations of three 1, 4-benzoxazin-3-ones in maize induced by the Asian corn borer, *Ostrinia furnacalis* (Guenee). C A J Bioscience 61:257–262

Jampatong C, McMullen MD, Barry BD, Darrah LL, Byrne PF, Kross H (2002) Quantitative loci for first- and second-generation European corn borer resistance derived from the maize inbred Mo47. Crop Sci 42:584–593

Jonczyk R, Schmidt H, Osterrieder A, Fiesselmann A, Schullehner K, Haslbeck M, Sicker D, Hofmann D, Yalpani N, Simmons C, Frey M, Gierl A (2008) Elucidation of the final reactions of DIMBOA-glucoside biosynthesis in maize: characterization of *Bx6* and *Bx7*. Plant Physiol 146:1053–1063

Khairallah MM, Bohn M, Jiang C, Deutsch JA, Jewell DC, Mihm JA, Melchinger AE, González-de-León D, Hoisington DA (1998) Molecular mapping of QTL for southwestern corn borer resistance, plant height and flowering in tropical maize. Plant Breed 117:309–318

Klun JA, Tipton CL, Brindley TA (1967) 2, 4-dihydroxy-7-methoxy-1, 4-benzoxazin-3–1 (DIMBOA) an active agent in resistance of maize to European corn borer. J Econ Entomol 60:1529–1533

McMullen MD, Frey M, Degenhardt J (2009a) Genetics and biochemistry of insect resistance in maize. In: Bennetzen J, Hake S (eds) Maize handbook. Springer, NY, pp 271–290

McMullen MD, Kresovich S, Sanchez Villeda H, Bradbury P, Li H, Flint-Garcia S, Thornsberry J, Acharya C, Bottoms C, Brown P, Browne C, Eller M, Guill K, Harjes C, Kroon D, Lepak N, Mitchell SE, Peterson B, Pressoir G, Romero S, Oropeza Rosas M, Salvo S, Yates H, Hanson M, Jones E, Smith S, Glaubitz JC, Goodman M, Ware D, Holland JB, Buckler ES (2009b) Genetic properties of the maize nested association mapping population. Science 325:737–740

Morant AV, Jørgensen K, Jørgensen C, Paquette SM, Sánchez-Pérez R, Linberg Møller B, Bak S (2008) β-Glucosidases as detonators of plant chemical defense. Phytochemistry 69:1795–1813

Morse S, Wratten SD, Edwards PJ, Niemeyer HM (1991) Changes in the hydroxamic acid content of maize leaves with time and after artificial damage; implications for insect attack. Ann Appl Biol 119:239–249

Nakagawa E, Amano T, Hirai N, Iwamura H (1995) Non-induced cyclic hydroxamic acids in wheat during juvenile stage of growth. Phytochemistry 38:1349–1354

Niemeyer HM (1988) Hydroxamic acids (4-hydroxy-1, 4-benzoxazin-3-ones) defense chemicals in the Gramineae. Phytochemistry 27:3349–3358

Oikawa A, Ebisui K, Sue M, Ishihara A, Iwamura H (1999) Purification and characterization of a betglucosidase specific for 2, 4-dihydroxy-7-methoxy-1, 4-benzoxazin-3-one (DIMBOA) glucoside in maize. J Bioscience 54:181–185

Ortego F, Ruiz M, Castañera P (1998) Effect of DIMBOA on growth and digestive physiology of *Sesamia nonagrioides* (Lepidoptera: Noctuidae) larvae. J Insect Physiol 44:99–101

Park WJ, Holchholdinger F, Gierl M (2004) Release of the benzoxazinoids defense molecules during lateral-and crown root emergence in *Zea mays*. J Plant Physiol 161:981–985

Pérez FJ, Ormeño-Nuñez J (1991) Difference in hydroxamic acid content in roots and root exudates of wheat (*Triticum-aestivum* L.) and rye (*Secale-cerale* L.)-Possible role in allelopathy. J Chem Ecol 17:1037–1043

Poschenrieder C, Torra RP, Barcelo J (2005) A role for cyclic hydroxamates in aluminium resistance in maize? J Inorg Biochem 99:1830–1836

Reid LM, Arnason JT, Nozzolillo C, Hamilton RI (1991) Laboratory and field resistance to the European corn borer in maize germplasm. Crop Sci 31:1496–1502

Richardson MD, Bacon CW (1993) Cyclic hydroxamic acid accumulation in corn seedling exposed to reduced water potential before, during, and after germination. J Chem Ecol 19:1613–1624

Rostas M (2007) The effect of 2, 4-hydroxy-7-methoxy-1, 4-benzoxazin-3-one on two species of Spodoptera and the growth of *Setosphaeria turcica* in vitro. J Pest Sci 80:35–41

Saghai-Maroof MA, Soliman KM, Jorgensen RA, Allard RW (1984) Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. Proc Natl Acad Sci USA 81:8014–8018

Sanchez-Villeda H, Schroeder S, Flint-Garcia S, Guill KE, Yamasaki M, McMullen D (2008) DNAAlignEditor: DNA alignment editor tool. BMC Bioinformatics 9:154

SAS Institute Inc (2000) SAS OnlineDoc, version 8. SAS Institute, Cary

Szalma SJ, Buckler ES, Snook ME, McMullen MD (2005) Association analysis of candidate genes for maysin and chlorogenic acid accumulation in maize silks. Theor Appl Genet 110:1324–1333

Tipton CL, Klun JA, Husted RR, Pierson MD (1967) Cyclic hydroxamic acids and related compounds from maize. Isolation and characterization. Biochemistry 6:2866–2870

Tseng CT (1997) The effect of DIMBOA concentration in leaf tissue at various plant growth stages on resistance to Asian corn borer in maize. In: Proceedings of an international symposium held at the international maize and wheat improvement center (CIMMYT), 27 Nov–3 Dec 1994, CIMMYT, Mexico, pp 13–20

Utz HF, Melchinger AE (2003) PLABQTL. A computer program to map QTL. Institute of plant breeding, seed science and populations genetics, University of Hohenheim, Stuttgart, Germany

Utz HF, Melchinger AE, Schön CC (2000) Bias and sampling error of the estimated proportion of genotypes variance explained by quantitative trait loci determined from experimental data in maize using cross validation with independent samples. Genetics 154:1839–1849

von Rad U, Huttl R, Lottspeich F, Gierl A, Frey M (2001) Two glucosyltransferases are involved in detoxification of benzoxazinoids in maize. Plant J 28:633–642

Wang JW, Xu T, Zhang LW, Zhong ZM, Luo SM (2007) Effects of methyl jasmonate on hydroxamic acid and phenolic acid content in maize and its allelopathic activity to *Echinochloa crusgalli* (L.). Allelopathy J 19:161–169

Wilson LM, Whitt SR, Ibáñez AM, Rocheford TR, Goodman MM, Buckler ES (2004) Dissection of maize kernel composition and starch production by candidate gene association. Plant Cell 16:2719–2733

Yan F, Xu C, Li S, Lin C, Li J (1995) Effects of DIMBOA on several enzymatic systems in Asian corn borer, *Ostrinia furnacalis* (Guenee). J Chem Ecol 21:2047–2056

Yu J, Pressoir G, Briggs WH, Bi IV, Yamasaki M, Doebley JF, McMullen MD, Gaut BS, Nielsen DM, Holland JB, Kresovich S, Buckler ES (2006) A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nat Genet 38:203–208

Yu J, Holland JB, McMullen MD, Buckler ES (2008) Genetic design and statistical power of nested association mapping in maize. Genetics 178:539–551

Zhu C, Gore M, Buckler ES, Yu J (2008) Status and prospects of association mapping in plants. Plant Genome 1:5–20