12-2012

Detection of Soybean Amino Acid QTLs and Seed Yield QTLs Using Selective Genotyping

Benjamin David Fallen
bfallen@utk.edu

To the Graduate Council:

I am submitting herewith a dissertation written by Benjamin David Fallen entitled "Detection of Soybean Amino Acid QTLs and Seed Yield QTLs Using Selective Genotyping." I have examined the final electronic copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Plant Sciences.

Vincent Pantalone, Major Professor

We have read this dissertation and recommend its acceptance:

Fred L. Allen, Dean A. Kopsell, Arnold Saxton

Accepted for the Council:
Carolyn R. Hodges

Vice Provost and Dean of the Graduate School

(Original signatures are on file with official student records.)

Detection of Soybean Amino Acid QTLs and Seed Yield QTLs Using Selective Genotyping

A DISSERTATION

Presented For The

DOCTOR OF PHILOSOPHY

Degree

THE UNIVERSITY OF TENNESSEE, KNOXVILLE

BENJAMIN DAVID FALLEN

December 2012

Acknowledgments

I would like to extend all my appreciation and thanks to all those who have made this dissertation possible. For without their kind support, hard work and dedication none of this would have been possible.

I would like to start by thanking my family and friends, for without them I would not be who or where I am today. My wife, Heather Renee Fallen, whose love and encouragement allowed me to finish this journey. To my mom Cindy Fallen and my dad David Fallen, I am thankful every day to have such kind and caring parents. I don't know how they were able to raise a child who is as stubborn and determined as I am, but somehow they did. To my "little bro" Jonathan Fallen and "big sis" Bridgett Fallen, they were right there with me growing up in the tobacco field (well maybe not every day); it means the world to me to have such great siblings.

I am also thankful for the trenchant critiques, the probing questions and the remarkable patience of my advisor- Dr. Vincent Pantalone. I cannot thank him enough. I am also grateful for the continued guidance of my committee members, Dr. Fred Allen, Dr. Dean Kopsell and Dr. Saxton. I would like to especially thank Dr. Saxton for his prodigious efforts in helping me with SAS code and computing.

I would also like to express a big thanks to the Beam Team: Jeneen Abrams, Jeffrey Boehm, Deborah Ellis, Beth Meyers, Chris Smallwood and Nicole Tacey for their continued support, even though at times I'm sure it was not easy. Thanks to Scott McIntyre, Jim Klein, Melissa Woolard and Sanbao Wang for overseeing my research plots and collecting data for me at Ohio State University, Southern Illinois University, University of Missouri and North Carolina State University, respectively. Dr. David Hyten for the tremendous effort needed to genotype the Essex by Williams82 population used in this study. Dr. Karl Broman for helping me with the construction of my genetic map and using R/qtl for QTL analysis on the very large data sets in this study.

Support provided by the Tennessee Agricultural Experiment Station of the University of Tennessee, the Tennessee Soybean Promotion Board and United Soybean Promotion Board that made this research possible is greatly appreciated.

"Reach for the stars. Although you will never touch them, if you reach hard enough, you will find that you get a little star dust on you in the process."

- Norman Borlaug

"Some sat in darkness and the deepest gloom, prisoners suffering in iron chains, for they had rebelled against the words of God and despised the counsel of the Most High…Then they cried to the LORD in their trouble and he saved them from their distress. He brought them out of darkness and the deepest gloom and broke away their chains." – Psalm 107:10-14

Abstract

The U.S. Census Bureau projects the world's population will top more than nine billion by 2050. Today, soybeans account for 56 % of the world oilseed production and 68 % of the world protein meal consumption, with U.S. soybean production accounting for 33 % of the world soybean production. So, to meet the demand of the world's growing population and of the livestock industry improvements in both the composition and the yield of soybean is essential.

The primary objective of this project was to use molecular markers to identify genomic regions associated with amino acid composition and yield in soybean. For amino acid quantitative trait loci (QTL) detection 282 $F_{5:9}$ recombinant inbred lines (RIL) developed from a cross between Essex and Williams 82 were used. The Universal Soy Linkage Panel (USLP) 1.0 of 1536 single nucleotide polymorphic markers (SNPs) was used to identify 480 polymorphic molecular genetic markers and to genotype the 282 RILs. A total of ten QTL were detected on chromosomes 5, 7, 9, 10, 13 and 20 that explained 5 to 14 % of the total phenotypic variation for a particular amino acid.

To detect yield QTL 875 $F_{5:9}$ RIL developed from a cross between Essex and Williams 82 were used. The 875 RILs were divided into four groups based on maturity and each group was grown in Knoxville, TN and one other location of adaptability. Each RIL was genotyped with >50,000 SNPs of which 17,232 were polymorphic across the population. A total of forty-six yield QTLs were detected in this study, explaining 4.5 % to 11.9% of the phenotypic variation for yield. In addition, marker assisted selections (MAS) were made using only additive effects and using a yield prediction model (YPM) in each environment and across environments for each group. By including additive by additive effects in addition to additive effects into the YPM, more top yielding lines were selected than by just using only additive effects. This study

provides new information concerning amino acid research in soybean and may offer some important insights into using an YPM that includes epistasis in soybean.

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Chapter 1

Introduction and Literature Review

Introduction

The genus *Glycine* Wild is divided into two subgenera, *Glycine* and *Soja*. The subgenus *Soja* (Moench) includes the cultivated soybean, *Glycine max* (L.) Merrill and the wild soybean, *Glycine soja* Sieb. & Zucc. *Glycine soja* is the wild ancestor of *Glycine max* and grows in China, Japan, Korea, Taiwan and Russia. *Glycine Soja* is an annual, weed-like, climbing pioneer of secondary seccessions whose pods shatter at maturity and contain black seeds (Chung, et. al, 2008).

The taxonomic classification of the soybean is as follows (USDA Plants Database):

Kingdom Plantae

Division Magnoliophyta

Class Magnoliopsida

Order Fabales

Family Fabaceae

Genus and species *Glycine max* (L.) Merrill

The soybean [*Glycine max* (L.) Merrill] was first cultivated over 3,000 years ago in China. However, soybean didn't come to America until almost 2,800 years later. Today more soybean are grown in the United States than anywhere else in the world. In 2011, 30.3 million hectares of soybean were planted in the United States, producing 83.2 million metric tons. The total value of the crop exceeded US$ 35.7 billion. In 2011, worldwide soybean production reached 251.5 million metric tons. Soybeans represented 68 % of 2011 world meal consumption, with 177.2 million metric tons. An estimated 35.6 million metric tons of soybean meal was produced in the United States in 2011 at an average price of $336 per ton (Soy Stats, 2011).

Literature Review

Plant biotechnology has largely been acknowledged as a key strategy for improving crop production in the United States. Today the biotechnology toolbox available to plant breeders offers several new possibilities for increasing productivity, crop diversification and production, while developing a more sustainable agriculture. One of the promising techniques used in modern crop improvement programs is molecular markers. Molecular markers have already played a major role in the genetic characterization and improvement of many crop species. Substantial progress has been made in recent years in mapping, tagging and isolating many agriculturally important genes using molecular markers due in large part to improvements in the techniques that have been developed to help find markers of interest. The first generation of molecular markers, Restriction Fragment Length Polymorphism (RFLPs) was based on DNA-DNA hybridization and was slow and expensive. The invention of the polymerase chain reaction (PCR) to amplify short segments of DNA gave rise to a second generation of faster and less expensive PCR-based markers. These included Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPDs), Sequence Characterized Amplified Regions (SCARs) or Sequence Tagged Sites (STS), Simple Sequence Repeats (SSRs) and most recently Single Nucleotide Polymorphisms (SNPs). A brief history of some of these molecular marker systems is described below.

RFLP

Restriction fragment length polymorphism (RFLP) is defined as different fragment lengths of restriction endonuclease digested DNA detected by a defined probe between individuals (Iqbal and Lightfoot, 2005). The different fragments of DNA are produced by restriction enzymes that recognize and cleave the DNA at specific sequences of nucleotides.

Each fragment length is considered an allele and can be used in genetic analysis. By digesting total DNA with specific restriction enzymes, an unlimited number of RFLPs can be generated. RFLPs are relatively small in size and are co-dominant in nature. If two individuals differ by as little as a single nucleotide in the restriction site, the restriction enzyme will cut the DNA of one but not the other. Restriction fragments of different lengths are thus generated.

In 1980, Botstein et al. proposed the construction of a genetic linkage map in humans based on RFLP. A few years later genetic linkage maps based on RFLP were constructed in numerous plant and animal species. The markers on these maps had broad applications, ranging from the localization of genetic loci controlling human disease to the improvement of plant cultivars by plant breeders. While not always the case, RFLP is often the result of the absence or presence of an endonuclease restriction site. Thus, in many instances only two alleles exist at a genetic locus. However, the likelihood that a particular molecular marker locus will be informative is positively related to the number of alleles at that locus.

The report of RFLP loci in humans with as many as eight different alleles in 1980 by Wyman and White, suggested the possibility of greatly enhanced informativeness per locus. These so-called Variable Number Tandem Repeat (VNTR) loci (Nakamura et al. 1987) consisted of sets of tandemly repeated DNA core sequences and were referred to as "minisatellite" sequences by Jeffreys et al. (1985). The core units varied in length from 11 to 60 base pairs and the repeat regions were flanked by conserved endonuclease restriction sites. These sequences could be found on many chromosomes, and often showed variations in length between individuals.

RFLP was the first marker system to be used in soybeans. In 1990, the first RFLP-based map of the soybean genome was published (Keim et al., 1990). The genetic map saw further expansion during the 1990s with the addition of more than 350 RFLP loci (Shoemaker and Olson, 1993).

However, the tetraploid origin of soybean contributed to the detection of multiple DNA fragments with all RFLP probes (Iqbal and Lightfoot, 2005). The multiplicity of RFLP loci can make the locus identity ambiguous. Other factors that prevent the use of RFLP in mapping and marker-assisted breeding are the low levels of polymorphisms observed (Shoemaker and Specht, 1995) and limitations of the automation procedure for high throughput screening.

RAPD

To complement RFLP markers, a second type of molecular marker based upon Polymerase Chain Reaction (PCR) technology was developed by Mullis et al. (1986). Williams et al. (1990) proposed the use of single arbitrary 10 base oligonucleotide PCR primers for the generation of molecular markers. These Random Amplified Polymorphic DNA (RAPD) markers could be easily developed and because they were based on PCR amplification followed by agarose gel electrophoresis they were quickly and readily detected.

Most RAPD markers are dominant and therefore, heterozygous individuals cannot be distinguished from homozygotes. This contrasts with RFLP markers which are co-dominant and therefore, distinguish among the heterozygote and homozygotes. Thus, relative to standard RFLP markers, and especially VNTR loci, RAPD markers generate less information per locus examined.

SSR

It was subsequently suggested (Jefferys, et al., 1988) that the highly informative nature of VNTR loci could be combined with the specificity and rapidity of polymerase chain reaction (PCR) technology (Mullis et al., 1986). Primers to the conserved flanking regions of VNTR loci were developed allowing amplification of the entire VNTR locus. Resulting PCR products possessed electrophoretic mobilities which differed according to the number of core units in the VNTR allele(s) present. This approach was then extended to a different type of repetitive DNA in humans (Litt and Luty, 1989; Weber and May, 1989; Tautz, 1989). Rather than repeat units in the range of 11-60 bp in length as occur in the minisatellites, these workers suggested that high levels of polymorphism exist in dinucleotide tandem repeat sequences. This type of reiterated sequence was termed a simple sequence repeat (SSR) **(**Jacob et al. 1991), or microsatellite (Litt and Luty, 1989).

Simple sequence repeat (SSR) markers are defined as any one series of very short (2-10 bp), repetitive, tandemly arranged, highly variable (hypervariable) DNA sequences dispersed throughout fungal, plant, animal and human genomes (Iqbal and Lightfoot, 2004). SSR or microsatellites represent DNA sequences of two to four base pairs that are repeated many times in a tandem fashion along the chromosome, such as-GCGTCGATATATATCCC (four repeats) or GCGTCGATATCCC (two repeats). SSRs seem to be distributed fairly randomly throughout the soybean genome, with a minimum evidence of clustering (Akkaya et al., 1995). There are about two SSRs (as defined by Akkaya et al., 1995) per 100 kbp of soybean sequence. Such a high level of allelic diversity increases the possibility of detecting polymorphism between parents of populations derived from the hybridization of adapted soybean genotypes. SSR alleles, amplified products of variable length, can be separated by gel electrophoresis and visualized by silver-staining, autoradiography (if primers are radioactively labelled) or via automation (if primers are fluorescently labeled).

In 1992, Akkaya et al. first reported the polymorphism and heritability of simple sequence repeat (SSR) markers in soybean. The development and mapping of a large set of soybean simple sequence repeat (SSR) markers were initiated in 1995 and as a result of that effort more than 600 SSR loci were developed and mapped in three mapping populations to create the first publicly available version of a soybean integrated genetic linkage map (Cregan et al., 1999). As a result, the 20-plus linkage groups derived from each of the three populations were aligned into a consensus set of 20 homologous groups correlating to the 20 pairs of soybean chromosomes. A second version of the integrated linkage map was published five years later using five mapping populations and contained a total of 1,015 SSR loci (Song et al., 2004).

SNP

Single nucleotide polymorphism (SNP) is defined as any polymorphism between individuals, created by a single nucleotide exchange, small deletion or insertion (Iqbal and Lightfoot, 2004). Like SSR markers, SNP is a new marker technology originally developed in humans. Various scientific endeavors were in progress even before the completion of the first human genome reference sequence to identify unique genetic differences between individuals. Syvanen (2001) reported that 99.9% of one individual’s DNA sequences will be identical to that of another person and that of the 0.1% difference, over 80% are thought to be single nucleotide polymorphisms (SNPs).

In soybean, SNPs occur about twice as often in noncoding compared to coding DNA. The SNP frequency in coding and noncoding DNA are approximately 1.98/kbp and 4.68/kbp, respectively, as estimated from the analysis of 25 soybean genomes (Zhu et al., 2003). In coding DNA, about one quarter to one half of SNPs alter amino acid sequence depending on the genes examined (Meksem et al. 2001; Zhu et al. 2003).

SNPs have two main advantages over other molecular markers; they are the most abundant form of genetic variation within genomes (Zhu et al., 2003), and a wide array of technologies have now been developed for high throughput SNP analysis (Fan et al., 2006). Despite being the most abundant source of DNA polymorphisms in soybean, the SNP frequency is relatively low compared to other cultivated crop species (Hyten et al., 2006; Zhu et al., 2003). The relatively low sequence variation in *Glycine max* can be attributed to domestication which reduced variation by 50% and the low sequence variation in the wild ancestor of soybean, *Glycine soja* (Hyten et al., 2006).

Choi et al. (2007) successfully discovered 5,551 SNPs (including 4,712 single base changes and 839 indels) in 2,032 transcripts and mapped at least one SNP from 1,141 of those transcripts to create what is now called the version three soybean integrated linkage map. SNPs were discovered via the re-sequencing of sequence tagged sites (STS) developed from EST sequence. Of the 1,141 genes, 291 mapped to 72 of the 112 gaps of 5 to 10 cM in the pre-existing SSR-based map, while 111 genes mapped in 19 of the 26 gaps larger than 10 cM.

The addition of 1,141 sequence-based genetic markers to the soybean genome map will provide an important resource to soybean geneticists, as well as soybean breeders who increasingly depend upon marker assisted selection in cultivar improvement. However, despite the current availability of over 2,000 PCR based markers on the version three map, the marker density is likely to be inadequate to allow a thorough scan of the genome for purposes of quantitative trait locus (QTL) discovery and map-based cloning.

GoldenGate Assay

While molecular markers have become extremely important in helping to improve crops such as soybean because they can be used to determine the position of genes that lead to genetic improvements, methods for testing large numbers of molecular markers, such as SNPs, simultaneously in soybean have remained untested. Recently, a new method called the

GoldenGate assay was evaluated to determine how successful this method could be in helping to accelerate molecular marker analysis in soybean. The GoldenGate assay is capable of testing up to 1536 SNPs in 192 DNA samples over a three day period. The GoldenGate assay was designed specifically for multiplexing to high levels while retaining the flexibility to choose any SNPs of interest to assay. The process uses a high specificity extension and ligation assay that allows the simultaneous analysis of over 1500 loci in a single reaction and uses the Universal Sentrix arrays by incorporating into the reaction products a unique address sequence for each locus being interrogated that is matched to a specific bead type's illumiCode. The illumiCode is a specific address sequence assigned to each SNP. Each of these addresses is complementary to a unique capture sequence represented by one of the bead types in the array. This universal address system, allows for the separation of the assay products in solution onto a solid surface for individual SNP genotype readout. This type of readout can be performed with the IScan system or BeadArray Reader. Both the iScan and the BeadArray Reader are cutting-edge array scanners that support rapid, sensitive and accurate imaging of Illumina's array-based genetic analysis products.

The GoldenGate assay performs allelic discrimination directly on genomic DNA, generates a synthetic allele-specific PCR template afterward, and then performs PCR on the artificial template. Conventional SNP genotyping assays typically use PCR to amplify a SNP of interest, allelic discrimination is then carried out on the PCR product. This difference allows the GoldenGate assay to use only three universal primers for PCR and eliminates primer sequence-related differences in amplification rates between SNPs. Once assay oligonucleotides targeted to specific SNPs of interest are annealed to the genomic DNA, two allele-specific oligonucleotides (ASOs) and one locus-specific oglionucleotide (LSO) are designed for each SNP.

The two ASOs have a sequence region that is a perfect complement to the genomic region directly adjacent to the target SNP site, but differ in their 3' base such that they only match one of the two alleles at the site. A second region acts as a universal primer site for the subsequent amplification reaction. The LSO consists of three parts: at the 5' end is a SNP locus-specific sequence that hybridizes 1 to 20 bases downstream of the target SNP site; in the middle is a unique illumiCode sequence that perfectly matches an illumiCode oligonucleotide on an array bead and at the 3' end is a universal PCR priming site. After oligonucleotide hybridization, a polymerase with high specificity for 3' mismatch is added and only extends the ASO(s) that perfectly match the target sequence at the SNP site. This employs DNA polymerase to extend ASOs if their 3' base is complementary to their cognate SNP in the genomic DNA template. At this time DNA ligase joins the extended ASOs to their corresponding LSOs, to create PCR templates. Requiring the joining of the two fragments to create a PCR template provides an additional level of genomic specificity. After the high specificity extension and ligation reaction any ASO that matches a SNP will be incorporated into a super structure that is a perfect substrate for universal amplification. Amplification for all loci is completed with the addition of only three more primers. One universal primer labeled with Cy3 that hybridizes to Universal PCR Sequence 1, another universal primer labeled with Cy5 that hybridizes to Universal PCR Sequence 2, and a third unlabeled primer for PCR Sequence 3. Only those ASOs that match the SNP and were extended form the super-structure and are amplified, confirming the alleles present at all sites. After amplification the products are hybridized to the Sentrix array for detection. The internal IllumiCode that is specific for each locus binds only to its complementary bead. Therefore, the products of the 1,152 assays hybridize to different bead types in the array, allowing all 1,152 genotypes to be read out simultaneously (Fan et al., 2003).

In an initial trial of 384 soybean SNPs using the GoldenGate assay, successful assays were obtained for 90% of the SNPs tested in soybean genetic mapping populations (Hyten et al., 2008). The high success rate of the GoldenGate assay indicates that it is a useful technique for quickly assaying large numbers of SNPs in soybean. The information developed by those scientists will be used by crop researchers, crop breeders and seed companies to increase the efficiency of SNP analysis for gene discovery and soybean improvement.

Marker-Assisted Selection (MAS) for Targeted Genes/Traits

Marker-assisted selection is a process where genetic markers have been associated with traits or QTL, which allows plant breeders to select the desired phenotype by selecting for the desired DNA marker(s). Marker assisted selection essentially has three major steps: (1) development of the genomic linkage map, (2) pinpointing on the linkage map were markers are located (QTL position) that co-segregate with the trait (phenotype) and (3) selection during the breeding process of molecular markers linked to those QTL (Sleper, 2006).

Soybean importance in U.S. agriculture has played a significant role in the generation of large number of markers for qualitative and quantitative traits, both by the public and private sector. Marker-assisted selection can improve upon the efficiency of plant breeding by reducing the time to develop a new improved cultivar and by eliminating linkage drag. Soybean is one of the best examples where MAS is playing a significant role in new and improved variety development.

One such example of MAS in soybean is selection for resistance to soybean cyst nematode (SCN). Soybean cyst nematode *(Heterodera glycines*) is a small plant-parasitic roundworm that attacks the roots of soybeans and causes significant crop losses in the infected fields. Two QTL significantly contributing to soybean resistance to *H. glycines*, *Rhg*1 and *Rhg*4 have been mapped on chromosomes 18 and 8. Furthermore, six genes associated with resistance to sudden death syndrome in soybeans (SDS) have been identified and three of those are clustered with SCN resistance *Rhg*1 (Meksem et al., 1999, Iqbal et al., 2001).

In 1994, Pioneer patented a process using MAS to select soybean varieties with resistance to SCN (Webb, 1994). The specific claim of this patent was to introduce: 1) what SCN resistance lines are used in a breeding program; 2) what kinds of molecular markers are used; and 3) which QTL are used, where these QTL are mapped on a soybean chromosome and their associated markers. Pioneer has since released other patents related to SCN resistance. Patent 6,162,967 introduces a method of positional cloning of SCN resistance genes (Webb, 1997). Patent 6.538,175 introduces a method of identifying a QTL associated with SCN resistance (Webb, 2003). In a review of the QTL identified for SCN resistance in soybean by Concibido et al. (2004), six QTL were found under patent 6,538,175 (Webb, 2003). Webb (2003) found QTL effective against multiple races of SCN on chromosomes 8, 11, 4, 18, 16, and 7 in PI 437654. In addition, Nguyen et al. (2011) also identified several QTL that are genetically linked to resistance to SCN. Eleven total QTL were identified from four sources: PI 437654, PI467312, PI 438489B and PI 567516C. These QTL were mapped to genomic regions on chromosomes 18, 8, 11, 20, 10 and 4.

QTL Controlling Seed Yield in Soybean

Over the years a considerable amount of work has been done to identify QTL associated with seed yield in soybean. Orf et al. (1999a) studied F_7 derived RILs from two populations 'Minsoy' x 'Archer' and 'Noir 1' x 'Archer.' These lines were evaluated in three environments and screened with more than 400 molecular markers. From that study a pair of interacting yield QTL were identified whose effect was independent of environment as well as a pair of loci whose interaction was environment specific. Reyna and Sneller (2001) reported the value of incorporating three seed yield QTL identified in Archer by Orf et al. (1999b) into southern environments and genetic background. But they found that none of the marker effects were significant for any of the three QTL for any trait. The results suggested that the Archer alleles were not superior to the southern alleles when tested in southern environments. This led the authors to hypothesize it may be difficult to successfully exploit beneficial alleles for complex traits in genetic backgrounds that are different than where they were originally mapped. Yuan et al. (2002) conducted a study to test if molecular markers linked to QTL can be used to combine traits of low heritability, such as yield, with disease resistance. Two RIL populations were used that segregated for SCN resistance genes (*rhg1* and *Rhg4*). 100 RILs from the cross 'Essex' x 'Forrest' and a population of 94 RILs from the cross 'Flyer' x 'Hartwig' were evaluated in four environments over four years. A total of 134 polymorphic SSR markers were used to screen the Essex x Forest population and 33 polymorphic SSR markers were used to screen the Flyer x Hartwig population. Four markers were found to be significantly associated with seed yield in the Essex x Forrest population and two markers were significantly associated with seed yield in the Flyer x Hartwig population.

In more recent years, studies have focused on detecting QTL from both *Glycine max* and *Glycine soja* plant introductions. Plant introductions often carry undesirable alleles that can be detrimental to breeding programs. However, the availability of molecular markers makes it possible to isolate specific genomic regions and transfer them into commercial cultivars with minimal linkage drag. Concibido et al. (2003) identified a yield-enhancing QTL from *Glycine soja* PI 407305. The study was conducted in three locations in 1996 and seven locations in 1997. The lines carrying the yield-enhancing allele from PI 407305 showed an average 9.4% seed yield increase across years and locations. Wang et al. (2004) conducted a study to map QTL from *Glycine soja* that could be incorporated into elite soybean cultivars. Five populations of BC_2F_4-derived lines were developed using 'IA2008' as a recurrent parent and PI 468916 as a donor parent. The field testing was done over two years and at two locations each year. Each line was screened for 302 polymorphic SSR markers and QTL were mapped by composite interval mapping (CIM). Four seed yield QTL were identified, each derived from IA2008. The authors commented that CIM was unable to detect significant seed yield QTL from PI 468916, which was most likely due to the lack of QTL alleles from PI 468916 that could increase yield of IA2008. Guzman et al. (2007) mapped QTL for yield and other agronomic traits in three backcross populations. In the development of the three backcross populations, lines were developed and tested for seed yield and only those lines with the greatest seed yield were crossed back to the recurrent parent. The populations were developed using PI 68658, PI 297544, and PI 68658 as donor parents and 'Beeson 80', 'Kenwood', and 'Lawrence' as recurrent parents, respectively. Lines from each population were evaluated with 45, 84, and 30 polymorphic SSR markers, respectively. A total of 13 QTL significant for seed yield were identified, as well as 19 QTL for three other agronomic traits. Eight of the 13 QTL were derived from the PI parents (PI 68658, PI 297544, and PI 68658) and all 13 QTL were mapped to regions that seed yield QTL were previously reported.

Unfortunately, limited progress has been made in improving elite populations through the use of mapped QTL controlling seed yield (Reyna and Sneller, 2001). So, Sebastian et al. (2010) proposed a method for implementing the use of seed yield QTL within elite populations. The authors use a method known as Context-Specific Marker Assisted Selection (CSMAS) for improved grain yield. CSMAS is an effective method for interpreting complex DNA fingerprints.

It allows scientist to identify genetically superior crop cultivars during the very first phase of yield testing by reducing the confounding effects of environmental variation and individual plot measurement errors. In the study conducted by Sebastian et al. (2010) $F_{7:8}$ lines derived from elite cultivars were grown as plant-row yield trials within a limited set of environments to model a target genotype and to select subline haplotypes that comprise the target genotype. Analysis was done using a mixed linear model and at statistically significant loci, the allele associated with the highest yield mean was considered the favorable allele for the purpose of selecting higher-yielding lines. The yield potential, of the selected subline haplotypes were then compared to their respective mother lines across multiple environments and years. The seed yields of the reselected lines were greater than the original five elite cultivars by an average of 3.1% and yield gains of up to 5.8% were confirmed in some of the selected sublines. Two of the improved sublines were released as improved cultivars.

Neus et al. (2010) conducted a study to determine whether a method of MAS for seed yield in elite soybean lines would be applicable to selection in soybean plant-row yield trials (PRYTs). Two single cross populations were developed in 2006 by Pioneer Hi-Bred International by crossing pairs of elite Pioneer cultivars possessing desirable agronomic traits. The first population was tested with 53 SNPs and the second population with 26 SNPs. Lines from each population were selected from 2008 PRYTs to form five groups from each population: high and low seed yield phenotypes, high and low seed yield genotypes and random genotypes. The five groups from each population were planted in eight diverse locations in 2009. In one population, the mean of the genotypic high group was not statistically different than the phenotypic high group. In the other population, the mean of the genotypic high group was within 90 kg ha^{-1} of the mean of the phenotypic high group and was superior to the random group for seed yield. They concluded even with limited marker coverage, the genotypic selection method successfully identified lines in a PRYT that would not have been selected due to poor seed yield performance in 2008.

Amino Acids

The amino acid requirements for poultry and swine are reasonably well elucidated. Using this information and the digestible amino acid profile of corn (the major energy feedstuff used in poultry and swine diets), the ideal amino acid profile of soybean protein can be targeted. When designing the optimum amino acid profile for soybean meal, consideration should also be given to market dynamics of alternative amino acid sources. In other words, there is more value in targeting breeding strategies for increased concentrations of amino acids that are higher priced than those that are lower priced. Specific amino acids that should be targeted are tryptophan (Trp), leucine (Leu), threonine (Thr), methionine (Met), and valine (Val) for swine diets (Boisen, 2003), and the amino acids lyseine (Lys), tryptophan (Trp), arginine (Arg), threonine (Thr), and valine (Val) for poultry diets (Baker, 2003).

Improvement in protein digestibility would also enhance the value of soybean meal. Soybean meal protein digestibility is approximately 85% (Woodworth et al., 2001), ranging between 82% and 94% for individual amino acid digestibility. Improving intestinal availability of the amino acids to 95% or greater concomitantly with modifications of the amino acid profile would substantially improve the value of soybean meal protein for animal feed use.

There are a few papers regarding genomic regions controlling amino acid biosynthesis in maize. Wang and Larkins (2001) investigated the basis for almost double the content of lysine in *opaque*-2 maize, by characterizing amino acid accumulation during endosperm development of several wild-type and *opaque*-2 inbreds. Through quantitative trait locus mapping they were able to identify four significant loci that accounted for about 46% of the phenotypic variance in lysine content. Wang et al. (2001) identified QTL associated with the maize Oh545*o2* inbred line, which is able to accumulate high levels of free amino acids lysine, threonine, methionine, and iso-leucine. The results indicated that the Lys-sensitive Asp kinase 2, rather than the Thr-sensitive Asp kinase (AK)-homoserine dehydrogenase (HSDH) 2, is the best candidate gene for the quantitative trait locus affecting free amino acid content in Oh545*o2*.

There are very few papers on genetic analysis of amino acid composition in soybean or improvements being made to the amino acid profile. Panthee et al. (2006a) identified genomic regions controlling essential and non-essential amino acid composition in soybean seed. A total of 94 polymorphic simple sequence repeat (SSR) molecular genetic markers were screened in DNA from 101 F_6 recombinant inbred lines developed from a cross between N87-984 x TN93-99. Using this population at least one QTL for each amino acid was detected; QTL linked to molecular markers Satt143, Satt168, Satt203, Satt274 and Satt495 were associated with most of the amino acids. The heritability estimates for the amino acids were low to moderately high, a reflection of genetic variation. Essential amino acids Thr, Met, Leu, Ile, Phe, Trp and Val had medium to high levels of heritability. Non-essential amino acids Asp, Glu, Pro, Arg, and Tyr had moderately high heritability estimates, whereas the remaining amino acids had low to medium estimates. They authors concluded that detecting genomic regions for amino acids may provide a means for selection or manipulation, but it may be difficult to change the concentration of only one amino acid because many amino acids have a common biosynthesis pathway. Also, Panthee et al. (2006b) conducted a study on QTL controlling sulfur containing amino acids, methionine and cysteine, on the same population. The RIL differed for both Met and Cys concentrations, with a range of 5.1-7.3 g kg^{-1} seed dry weight for Cys and 4.4-8.8 g kg^{-1} seed dry weight for Met. The RIL were screened with a total of 94 polymorphic SSR markers. Four QTL were found linked to Satt235, Satt252, Satt427 and Satt436 on chromosomes 1, 13 and 18 that were associated with Cys. Three QTL were found linked to Satt252, Satt564, and Satt590 on chromosomes 13, 18 and 7 that were associated with Met (Panthee et al., 2006b).

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Chapter 2

Detection of Amino Acid QTL in Soybean Using the Universal Soy Linkage Panel 1.0 of 1536 SNPs

Abstract

Soybean [*Glycine max* (L.) Merr.] is an integral component of the U.S. agriculture industry and the use of soybean in animal feed is important to the viability of the agriculture industry. Soybean meal is the largest source of protein in animal feed because of its amino acid profile. However, few studies have been conducted to evaluate genomic regions controlling amino acid composition is soybean. Designing soybean seed compositions that will benefit animal production is essential. The objective of this study was to identify genomic regions controlling essential and non-essential amino acid composition in soybean seed. To achieve this objective, 282 $F_{5:9}$ recombinant inbred lines (RIL) developed from a cross of Essex x Williams 82 were used. Ground soybean seed samples were analyzed for amino acids and a significant difference ($p < 0.05$) was found among genotypes in the population for all amino acid concentrations. The Universal Soy Linkage Panel (USLP) 1.0 of 1536 SNPs was used to identify 480 polymorphic molecular genetic markers and to genotype the 282 RILs. The software R/qtl was used to identify candidate quantitative trait loci (QTL), which were validated using R/MQM. A total of ten QTL were detected on chromosomes 5, 7, 9, 10, 13 and 20 that explained 5 to 14 % of the total phenotypic variation for a particular amino acid. Using SNPs from the USLP 1.0 to detect QTL for amino acids in soybean provides additional information to the limited literature for this important component of soybean meal.

Introduction

Animal feed is the primary user of the meal component of soybeans. Breeding and gene modification strategies have been successfully employed to alter the seed composition of soybeans in a manner that enhances their use in animal feeds. The majority of soybean meal is used to provide amino acids to poultry and swine. Typically, soybean meal is used to meet the animal's requirement for limiting amino acids, because soybean meal is usually the most cost-effective source of amino acids. Soybean meal is also one of the best protein sources for complementing the limiting amino acid profile of corn meal. However, the use of soybean meal in a corn-based diet results in the overfeeding of nonlimiting amino acids. The amino acids overfed are metabolized by the animal to carbon dioxide and urea, with the urea contributing to nitrogen excretion. Thus, the economics of soybean meal use in animal diets has changed from the original requirement of the lowest cost source of amino acid. To adjust to market economics, the primary structure of soybean protein needs to be altered and its digestibility needs to be improved.

Twenty standard amino acids are classified into two groups: essential amino acids and nonessential amino acids. An essential amino acid or indispensable amino acid cannot be made by the body and must be supplied by food. These include isoleucine, leucine, lysine, methionine, phenylalanine, threonine, trytophan, and valine for humans (Ufaz and Galili, 2008). Another amino acid, histidine is considered semi-essential because the body does not always require dietary sources. The nonessential amino acids are arginine, alanine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, proline, serine, and tyrosine (Ufaz and Galili, 2008). The classification of an amino acid as essential or nonessential does not reflect its importance, because all 20 amino acids are necessary for human health. In addition, classification also depends on the organism because an essential amino acid cannot be synthesized by the organism. For example, there are 10 essential amino acids for swine: phenylalanine, valine, threonine, methionine, arginine, tryptophan, histidine, isoleucine, leucine and lysine (Boisen, 2003). Failure to obtain an adequate quantity of even a single essential amino acid leads to degradation of the body's proteins to obtain the deficient amino acid. Unlike fat and starch, the body does not store excess amino acids for later use. Therefore, the amino acids must be obtained from food every day.

Objectives

In order to efficiently develop soybean cultivars with improved amino acid profiles, the genetic basis of amino acid composition should be explored thereby allowing for marker assisted selection (MAS) of desired amino acids for improved protein quality. The objective of this study was to use the USLP 1.0 to identify genomic regions controlling essential and non-essential amino acid composition in soybean seed.

Materials and Methods

Population Development

The initial crosses for the 'Essex' x 'Williams 82' population were made at the East Tennessee Research and Extension Center (ETREC) in Knoxville, TN in the summer of 2005. Essex originated from the cross Lee x S5-7075 at the Virginia Agricultural Experiment Station and was released in 1972 (Smith and Camper, 1973). Essex is characterized as having purple flowers, gray pubescence, a group V maturity, average protein, oil, height and yield and is susceptible to SDS. Williams 82 was developed by the USDA-ARS and the Illinois Agricultural Experiment Station through a series of backcrosses to Williams to transfer the Rps_1 gene (Bernard and Cremeens, 1988). The Rps_1 gene confers resistances to certain races of phytophthora rot. Williams 82 is characterized as having white flowers, tawny pubescence, a group III maturity, average protein and oil, resistance to phytophthora rot and mild resistance to sudden death syndrome (SDS). Williams 82 has contributed to the genetic background of many northern U.S. cultivars and Essex has contributed to the genetic background of many southern U. S. cultivars and elite breeding lines (Sneller, 2004; Gizlice et al., 1996). A population formed from these diverse parents reflects a broad measure of the range of amino acids available in elite U.S. soybean cultivars. Therefore, QTL detected in this population could be used in other populations in different breeding programs.

Experimental Design

In the fall of 2005, the F_1 seeds obtained from the Essex x Williams 82 cross were harvested and grown in Puerto Rico at the Tropical Agricultural Research Station (TARS). The population was advanced from the F_2 to the F_5 generation through single seed descent (Brim, 1966). At the East Tennessee Research and Extension Center (ETREC) in Knoxville, TN the F_2 generation was grown in 2006 and the F_3 generation was grown in 2007. The F_4 and F_5 generations were grown at the TARS location in the winter of 2007/2008 and the spring of 2008, respectively. In the summer of 2008, 284 individual $F_{5:6}$ RILs were planted in 3.1 m single plant rows at ETREC. From each row, leaf tissue was collected for DNA extraction and agronomic data was recorded. In 2009, yield trials were conducted using the $F_{5:7}$ recombinant inbred lines. Three population subsets: early (94 genotypes, four checks and the two parents), mid (94 genotypes, four checks and the two parents) and late (94 genotypes, four checks and the two parents) were planted in two 6.1m row plots in a randomized complete block design replicated three times in Knoxville, TN, Harrisburg, IL and Fayetteville, AR. Checks were assigned by maturity group. In the early test ‘IA4004’, LD00-2817P, LD00-3309 and ‘Macon’ were used as checks. In the mid test TN05-4008, TN06-189, TN06-196 and ‘5002T’ were used as checks. In the late test JTN-5203, ‘Osage’, ‘5002T’ and ‘5601T’ were used as checks.

Experimental Field Procedures

After planting, all the plots were evaluated for agronomic traits. Flower color (purple, white or segregating) was recorded when 95 % of the plants had bloomed. At maturity, plant height was taken as an estimation of the distance from the soil surface to the tip of the main stem in cm. Lodging was scored on a scale from 1-5; with 1 being all the plants in the plot were erect and 5 being all the plants in a plot were prostrate. Maturity was recorded as the date, according to the Julian calendar, when 95 % of the pods achieved their mature color. At that time pubescence color was also recorded. Seed yield was estimated after the plots had been end trimmed to 4.88 m in length. Seed yield was obtained by an onboard seed spectrometer (Almaco, IA) and was reported in kg ha^{-1} at 13 % maturity basis. Seed size was taken as the weight in g from a random 100 seed sample.

Laboratory Procedures

Sample Preparation for Amino Acid Composition via NIR Analysis

Approximately 20 g of soybean seed collected from plot samples were ground in a water-cooled Knifetec 1095 Sample Mill (FOSS Tecator, S-26321, Hogana, Sweden) for 20 s. This produced soybean flour that is uniform in particle size. The samples were analyzed using a FOSS 6500 near infrared spectrometer (NIR). A dehumidifier was used throughout the analysis to reduce the humidity to 40 %, and room temperature was maintained at approximately 20ºC. Initially the NIR was warmed up for 2 h after turning on the lamp. Auto diagnostics were run for instrument response, wavelength accuracy and NIR repeatability. Ground soybean samples were scanned to get the predicted concentrations of oil and protein (g kg^{-1}), and 18 amino acids alanine (Ala), arginine (Arg), asparagine (Asp), cysteine (Cys), glutamine (Glu), glycine (Gly), histidine (His), isoleucine (Ile), leucine (Leu), lysine (Lys), methionine (Met), phenylalanine

(Phe), proline (Pro), serine (Ser), threonine (Thr), tryptophan (Trp), tyrosine (Tyr), valine (Val) using ISIscan (System II version 2.80 software (FOSS, State College, PA). The instrument was left on for the whole period of analyses, and diagnostics was performed every day until the scanning was finished. Each amino acid sample was corrected as a percentage of overall crude protein content to report values as g of the amino acid per kg of crude protein.

Genotypic Data

Each RIL was genotyped with 480 SNPs using the Illumina GoldenGate Assay (Hyten et al., 2008). DNA was extracted from a 10 leaf sample and processed to contain 50 μl of DNA at a 200 ng/μl concentration. The samples were then sent to the Soybean Genomics Laboratory at the USDA Beltsville Agricultural Research Center (USDA-ARS) in Beltsville, MD, where a total of 1,536 SNP markers were assayed on each RIL genotype using the Universal Soybean Linkage Panel 1.0 (USLP 1.0) (Hyten et al., 2010), using the GoldenGate® assay and analyzed on the Illumina BeadStation 500G (Illumina, San Diego, CA) (Hyten et al., 2008).

Experimental Analysis

Analysis of variance and LSD mean separation was conducted in SAS using PROC MIXED (SAS ver. 9.1.3, Cary, NC) to test for significant genotype differences among RIL for amino acid concentrations. Location and replication were considered as two random blocking factors in the model and genotypes were considered fixed effects. Relationships among the 18 amino acids were analyzed using PROC CORR and principal component analysis was performed using PRINCOMP in SAS version 9.1.3 (SAS Institute, 2003). Restricted maximum likelihood analysis (REML) was used to estimate variance components for calculating heritability estimates. The REML estimation was performed by including METHOD=REML as an option in the PROC MIXED Statement. Heritability was estimated to determine the fraction of phenotypic variation among individuals that was due to genetic differences. A broad sense estimate of heritability of the trait in the population was calculated on an entry mean basis (Nyquist 1991) as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \left(\frac{\sigma_{ge}^2}{e}\right) + \left(\frac{\sigma^2}{re}\right)}$$

where, h^2 represents the heritability, σ_g^2 is genotypic variance, σ_{ge}^2 is genotype x environment variance, σ^2 is error variance, r is number of replications and e is number of environments. This estimate primarily includes additive effects because inbred lines ($F_{5:9}$) were used. Thus, the estimate functionally provides a narrow sense heritability estimate.

Marker order, position and composite interval mapping were completed using R/qtl (Broman and Sen, 2009). In addition, Multiple-QTL Mapping (MQM) was used to confirm QTL found by R/qtl (Broman and Sen, 2009). 1,000 permutations were performed on each amino acid for all chromosomes to establish empirical LOD thresholds at the 5% probability level.

Results and Discussion

There were differences ($p<0.001$) among the RIL for all essential and non-essential amino acids tested in this study, but most of the differences were small **(Table 2.1)**. There was also very little variation in amino acid concentrations across environments and maturity groups **(Table 2.2)**. A major limitation of soy proteins is their deficiency in sulfur-containing amino acids, Met and Cys (Ufaz and Galili, 2008). In this study the difference between the mean and max for Cys was 2.4 g kg^{-1} crude protein, a 15 % increase and 1.5 g kg^{-1} crude protein for Met, a 10 % increase **(Table 2.1)**. For Cys the variation across environments and maturity groups was 1.4 g kg^{-1} crude protein and for Met the variation across environments and maturity groups ranged from 0.8 to 1.7 g kg^{-1} crude protein **(Table 2.2)**. The modest amount of variation and the stability of the amino acid concentrations among the RILs across environments and maturity groups suggest that modest genetic gains can be made in soybean, including genetic gains for Cys and Met. For Cys and Met only a slight increase (~0.5 g kg^{-1} crude protein) can lead to significant improvements in poultry and swine diets (Baker, 2003; Boisen, 2003).

The heritability estimates for most amino acids were moderate to high (31-74 %) (**Table 2.1**). Gly, His, and Lys, had moderately low heritability estimates of 47 %, 31 %, and 39 %, respectively. Ala, Asp, Cys, Glu, Leu, Met, Pro, Ser, Thr, and Val had moderately high heritability estimates of 55 %, 69 %, 63 %, 64 %, 65 %, 67 %, 68 %, 61 %, 63 %, and 63 %, respectively. Arg, Ile, Phe, Trp, and Tyr had high heritability estimates of 72 %, 72 %, 74 %, 71 % and 70 %, respectively. Panthee et al. (2006a) reported the heritability for amino acids in soybean were low to moderately high (12.7-66.6%) in their population (N87-984-16 x TN93-99). They reported Asp, Glu, Pro, Val, Arg, Ile, Leu, Tyr, Trp and Met had moderately high heritability estimates of 57 %, 52 %, 55 %, 63 %, 54 %, 57 %, 60 %, 67 %, 50 % and 57 %, respectively. The moderate to high heritability estimates reported in this study along with the low to moderately high heritability estimates reported by Panthee et al. (2006a) suggest genetic improvements could be attainable. However, there are very few papers on the genetic analysis of amino acid composition in soybean and how genetic improvements for amino acid composition can be made in soybean.

To examine the relationship among 18 amino acids in soybean, phenotypic correlations were determined using PROC CORR in SAS version 9.1.3 (SAS Institute, 2003). Almost all the amino acids were positively correlated (r = 0.33 to 0.97) (**Table 2.3**). However, Lys was shown to have a weak to moderately negative correlation with twelve amino acids and a weak to moderately positive correlation with three amino acids. Lys had a weak negative correlation with Asp (r = -0.11), Cys (r = -0.23), Ile (r = -0.05), Met (r = -0.29), Pro(r = -0.27), Trp (r = -0.16) and Tyr (r = -0.30). Lys had a moderately negative correlation with Gly (r = -0.53), His (r = -0.61), Ser (r = -0.43), Thr (r = -0.39) and Val (r = -0.32). In addition, Lys had a weak positive relationship with Leu (r = 0.17) and a moderately positive relationship with Ala (r = 0.41) and Glu (r = 0.31). Panthee et al (2006a) reported weak to moderately negative correlations between Lys and eight of the same amino acids reported in that study and weak negative correlation between Lys and total protein. Panthee et al. (2006a) reported Lys had a weak negative relationship with His (r = -0.02) and Trp (r = -0.07) and a moderately negative with Gly (r = -0.56), Pro (r = -0.29), Ser (r = -0.36), Thr (r = -0.46), Tyr (r = -0.52) and Val (r = -0.55). Lys is essential in the swine and poultry diet, as well as many other animal diets (Baker, 2003; Boisen, 2003). Breeding for increased Lys may be difficult due to the inverse relationship with total protein and other essential amino acids.

As mentioned earlier, a major limitation of soy proteins is their deficiency of sulfur-containing amino acids, Met and Cys. Because of this deficiency, either synthetic or natural supplementary ingredients are utilized to fulfill the requirement of Met in soy based animal feed. However, Met supplementation has possible problems such as leaching during processing and bacterial degradation leading to formation of undesirable volatile sulfides (George and de Lumen 1991). In this study a strong positive correlation was seen between Met and Cys (r = 0.76). A moderate to strong positive correlation was also seen between Met, Cys and all other amino acids reported in this study (r = 0.45 to 0.92) except for a weak positive correlation between Cys and Trp (r = 0.05) and a weak negative correlation between Lys and Cys (r = -0.23) and Lys and Met (r = -0.29). Panthee et al. (2006b) reported a moderate positive correlation between Cys and Met (r = 0.41). A moderate to positive correlation was reported in their study between Cys, Arg, Phe, His, Trp, Thr and Ser and a moderate correlation was reported between Met, Arg, Pro, Phe, His, and Trp. The only amino acid they found in both the swine and poultry diet that had a negative correlation with Cys and Met was Val (r = -0.22 and r = -0.05, respectively) (Panthee et al., 2006b). These results suggest increasing Cys and Met content in soybean will not adversely affect other amino acids concentrations needed in swine and poultry diets.

Though the metabolic pathways for the biosynthesis of amino acids are well understood, literature regarding the elucidation of genetic control of variation of amino acid content in soybean is limited. To further understand the relationship of amino acids in soybean, a principal component analysis (PCA) was conducted on all 18 amino acids. Using PCA, 18 amino acids were reduced to 3 principal components that explained 88.2% of the observed phenotypic variation (**Tables 2.4, 2.5**). Almost all amino acid concentrations contributed to PC1, basically averaging all variables and was not very informative. Glu, Lys and Leu concentrations mainly contributed to PC2 and Cys and Trp concentrations mainly contributed to PC3.

Based on chemical similarities and only a few starting compounds, all amino acids can be regarded as members of five families: the serine-glycine family (which also includes cysteine) derived from 3-phosphoglycerate, the family of aromatic amino acids (which includes tyrosine phenylalanine and tryptophan) derived from phosphoenolpyruvate, the alanine-valine-leucine family derived from pyruvate, the aspartate family (which includes threonine, lysine, methionine and isoleucine) derived from oxaloacetate, and the glutamate family (which includes glutamine, proline, arginine and histidine) derived from alpha-ketoglutarate (Taiz and Zeiger 2006). PC2 contained one amino acid from each of the last three families and PC3 contained one amino acid from each of the first two families. Although the analysis did not provide a mechanism or demonstrate causality, it does provide a quantitative measure of relatedness of variables to one another that can be suggestive of the underlying processes controlling the variability among amino acid concentrations in soybean. An improved understanding of plant amino acid pathways would make it possible to engineer increased amino acid content not only using classical plant breeding, but also transgenic approaches. The potential of using PCA has been shown to be a useful tool for exploring multiple trait data and multitrait selection because trait associations and trait profiles of the genotypes can be displayed in a table or graphically using biplots. Yan et al. (2008) demonstrated how PCA can be used for selecting potential cultivars and for parent selection in plant breeding programs. Also, Yan et al. (2005) demonstrated how PCA can be used for QTL identification and marker-based selection.

So far, classical genetic approaches for improved amino acid content have resulted in relatively limited success. The success of genetic approaches has been mostly restricted mostly to maize by generating maize cultivars, which are enriched in Lys and to some extent with enriched Trp in their seeds (Ufaz and Galili, 2008). The only commercially available transgenic plant with elevated amino acid content is high-lysine maize (Frizzi et al., 2008; Ufaz and Galili, 2008). In soybean the feasibility of increasing Trp content has been demonstrated by Inaba et al. (2007) and Falco et al. (1995) who were able to increase the Lys content in soybean seed by as much as 5-fold. The transgenic insertion of a Brazil nut gene to soybean for increased methionine concentration was abandoned by Pioneer Hi-Bred International in the early 1990s because of the common human allergy to some protein in Brazil nut (Streit, et al., 2001). In addition, QTL have been identified for amino acids in soybean. QTL have been found for beta conglycinin and glycinin storage proteins (Panthee et al. 2004), for other various essential and nonessential amino acids (Panthee et al. 2006a) and for the sulfur containing amino acids cysteine and methionine (Panthee et al., 2006b). From the genetic mapping population used by Panthee et al. (2004, 2006a, 2006b) TN04-5321 was developed and released as a soybean germplasm line with significantly elevated sulfur containing amino acid levels (Panthee and Pantalone, 2006). This is the first soybean line registered specifically for improved amino acid concentration (Pantalone, 2011).

In our study R/qtl was used to determine genetic linkage and distance between markers to compose a genetic map. When the map was constructed chromosome 13 had a 966.85 cm gap in the middle resulting in a chromosome length >1000 cm. So, chromosome 13 was split into two chromosomes. QTL were identified using composite interval mapping (CIM) and multiple QTL mapping (MQM) using R/qtl (Broman and Sen, 2009). Only markers that were found to be significant using both MQM and CIM are reported (**Table 2.6**).

Initially, twelve QTL were detected. However, maturity of the population varied from a maturity group (MG) III to a MG V, and a maturity gene (*E1*) was mapped on chromosome 6 (110 cM) in the same area as one of the amino acid QTLs detected in this study. The gene for maturity (*E1*) has previously been reported to be located at 114 cM on chromosome 6 (Hyten et al., 2004). In addition, the locus for growth habit segregates in the Essex (determinate) by Williams 82 (indeterminate) cross and a gene for growth habit (Dt1) was mapped on LG L (75 cM) in the same area as another one of the amino acid QTLs detected in this study. The gene for growth habit (Dt1) is located at 89.1 cM on the integrated soybean genetic linkage map (Song et al., 2004). Hyten et al. (2004) conducted a study to identify modifier FA QTL in an Essex x Williams population. They found a single marker interval on chromosome 19 and chromosome 6 contained the largest QTL for palmitic, oleic, linoleic and linolenic acids. Some of the FA QTL mapped at chromosome 6 were determined to be a consequence of the maturity QTL on chromosome 6 and some of the FA QTL mapped at chromosome 19 were determined to be a consequence of the growth habit QTL on chromosome 19. However, several QTL were found in our study that did not coincide with these factors. To determine which QTL were significant for an amino acid and not maturity or growth habit a 1.5-LOD support interval was estimated for chromosomes 6 and 19 (Broman and Saunak, 2009). In total ten QTL outside of the likely interval for the Dt1 and E1 loci were reported that each explained 5%-14 % of the total phenotypic variation (R^2) for a particular amino acid (**Table 2.6**).

One QTL was detected on chromosome 5. The QTL on chromosome 5 was associated with Ala and Val and was linked to molecular marker ss107923612, which explained 5.5 and 6.0 % of the total phenotypic variation (R^2), for those two amino acids, respectively. A QTL linked to molecular markers ss107928831 and ss107926274 on chromosome 7 was detected for Asp (R^2=5.5). Two QTL for Asp and Leu were detected on chromosome 9. Marker ss107912627 (R^2 = 10.5) on chromosome 9 was found to be linked to a major QTL (R^2 > 10%) for Leu. Three molecular markers (ss107920438/ss107912744/ss107919004) were linked to a QTL associated with His and Tyr on chromosome 10, explaining 7.4 and 5.7% of the phenotypic variation, respectively. Three QTL were detected on chromosome 13 that were associated with 12 amino acids, explaining 5-9.5% of the total phenotypic variation. On chromosome 19 ss107917837 was linked to a QTL associated with Glu that had an R^2 of 13.8 %. A QTL linked to ss107929220 and ss107914151 was associated with Cys (R^2 = 6.0%) on chromosome 20.

Lys, Thr, Met, and Trp are the most important amino acids in swine diets (Boisen, 2003), whereas for young poultry Lys, Trp, Arg, Thr, and Val are the most important (Baker, 2003). Four of the minor QTL reported in this study are associated with amino acids that are essential to chicken diets and two minor QTL are essential to swine diets. Today, there are very few papers on the genetic analysis of amino acid composition in soybean. Panthee et al. (2006a) detected between one and four QTLs for each amino acid using 94 polymorphic simple sequence repeat (SSR) molecular genetic markers. Panthee et al. (2006a) reported a QTL for Gly and Thr linked to Satt518 (46.4 cM) roughly 20 cM from a QTL we detected on chromosome 9 near marker ss107913002 (62.54 cM), which was linked to Asp and Leu.

In a study conducted by Warrington (2011) 421 polymorphic markers (98 SSRs and 323 SNPs) were used to investigate the inheritance of QTL associated with protein and amino acid concentrations. Warrington (2011) detected a QTL associated with Thr linked to BARC-048619 (79.06 cM) and Met linked to BARC-042449 (77.4 cM) on chromosome 9. These are within ~10 cM of the two markers reported in this study on chromosome 9 (86.91 cM) associated with Asp and Leu.

Another QTL detected by Warrington (2011) associated with Met linked to Satt592 on chromosome 10 (91.4 cM) was within 20 cM of the QTL linked to markers ss107920438, ss107912744 and ss107919004 on chromosome 10 (110.18 cM) in this study. In addition, Panthee et al. (2006a) reported a QTL on chromosome 13 linked to Satt252 (16.0 cM) only 5 cM away from markers ss107912657 and ss107913658 (21.51 cM). Satt252 was associated with Cys, Ile, Met and Val (Panthee et al., 2006a). In this study marker ss107912657 and ss107913658 were associated with Arg, Iso, Phe, Pro, Ser, Tyr and Val.

It is well documented that in the biochemical pathway of Met biosynthesis, Cys is the intermediate product in the process of assimilating sulfur (Matthews, 1999; Saito, 1999). It is also known methionine occupies a central position in cellular metabolism in which the process of protein synthesis, methyl group transfer, polyamine and ethylene syntheses are interconnected

(Ravanel et al., 1998). Among these pathways, the synthesis of proteins is the only pathway consuming the entire Met molecule.

Met is the initiating amino acid in the synthesis of virtually all eukaryotic proteins. Cys plays a crucial role in protein structure and in protein-folding pathways because of its ability to form disulfide bonds (Brosnan and Brosnan, 2006). So, an increase in either Cys or Met or both Met and Cys may require an increase in total protein content. In this study one QTL was reported to be associated with Cys and one QTL was associated with Met. The QTL, linked to marker ss107917837, associated with Met was located on chromosome 13 and associated with eleven other amino acids. Reinprecht et al. (2006) detected a seed protein QTL associated with marker Satt569 (2.35 cM) on chromosome 13 only ~2 cM upstream from marker ss107917837 (4.86 cM). Brummer et al. (1997) detected a QTL associated with seed protein linked to marker K002_1 (46.3 cM) on chromosome 13. This marker was ~6 cm from markers ss107920654 and ss107924336 (40.69 cM) reported in this study linked to a QTL associated with ten amino acids.

The proximity of the markers reported in this study and in previous studies indicates that some of the same QTL may have been detected in all studies. However, most QTLs were associated with different amino acids than the ones reported in this study. This may be due to the strong to moderate positive correlation seen between most amino acids. So, selection of only a few QTL may greatly enhance genetic gains. In addition, three genomic regions on chromosome 13 (4.89, 21.51, 40.69 cM) were found to control multiple amino acids. Two of these regions were very close to previously reported QTL associated with seed protein content. This suggests some of the QTLs reported for seed protein content in soybean may also be involved in determining protein quality.

Also, in this study new QTLs for improving amino acid composition in soybean were discovered that do not coincide with any previously found QTLs. Through selection of these new amino acid QTLs and the previously reported QTL, improved amino acid profiles could be developed in soybean lines by breeders to help meet industry demands. The results from this study are intended to provide a basis for future research in soybean amino acid composition using SNPs, which could provide valuable benefits to the animal feed industry.

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Appendix A:

Chapter 2 Tables

Table 2.1 Descriptive statistics (g kg^{-1} crude protein) of essential and non-essential amino acid concentration in soybean seed from 282 $F_{5:9}$-derived RILs of Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

Trait	Min	Mean	Max	$LSD_{0.05}$	h^2 (%)
	(g kg^{-1} crude protein)				
Essential amino acids					
Leu	67.3	71.3	79.9	1.7	65.2
Lys	51.9	56.6	60.4	2.4	39.7
Ile	44.3	46.7	47.2	0.7	72.5
Met	14.5	15.6	17.1	0.2	67.7
Phe	47.2	50.2	55.7	0.9	74.2
Thr	40.3	42.9	45.7	0.9	63.3
Trp	9.7	10.7	12.1	0.2	71.3
Tyr	35.5	39.8	42.7	0.7	70.9
Val	50.9	57.8	65.4	1.7	63.7
His	28.7	33.9	45.5	1.7	31.2
Non-essential amino acids					
Ala	45.5	49.3	53.8	1.2	55.3
Arg	64.7	74.6	82.0	1.7	72.1
Asp	106.6	114.2	129.9	2.1	69.8
Cys	14.2	15.6	18.0	0.5	63.2
Glu	151.4	162.1	179.4	4.7	64.7
Gly	49.8	58.5	65.2	2.6	47.8
Pro	48.8	53.8	58.3	1.2	68.4
Ser	48.1	55.7	61.4	2.1	61.5

Table 2.2 Descriptive statistics of mean amino acid concentration (g kg^{-1} crude protein) of 282 $F_{5:9}$-derived RILs from Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

Mat	Loc	†Ala	†Arg	†Asp	†Cys	†Glu	†Gly	†His	†Pro	†Ser	‡Leu	‡Lys	‡Ile	‡Met	‡Phe	‡Thr	‡Trp	‡Tyr	‡Val
		g kg^{-1} crude protein																	
Early	AR	52.1	80.6	120.9	16.6	168.2	64.0	37.9	56.9	61.6	73.5	54.5	49.8	16.6	52.1	45.0	11.8	42.7	61.6
	IL	47.5	73.2	109.7	15.2	158.3	54.9	30.1	52.0	53.0	69.2	58.1	45.6	14.9	48.8	42.1	10.6	38.8	55.4
	TN	49.9	75.7	115.7	15.6	163.1	59.9	34.3	54.3	56.7	71.5	56.0	47.2	15.7	50.9	43.4	11.2	40.2	58.8
Mid	AR	50.7	75.5	118.1	16.4	166.0	60.8	36.6	55.3	57.1	73.6	56.5	47.8	15.9	51.9	43.9	10.8	40.9	59.7
	IL	47.2	72.4	108.4	15.0	156.1	54.6	30.9	51.5	52.6	68.7	57.4	45.0	14.8	48.2	41.9	10.3	38.5	55.0
	TN	49.6	74.0	113.9	15.7	159.8	59.8	33.8	53.9	56.5	70.6	55.5	46.3	15.6	49.9	43.3	11.2	39.5	58.1
Late	AR	49.8	74.8	117.7	16.5	167.5	58.2	35.6	54.4	55.9	73.8	57.6	47.3	15.8	51.7	43.1	10.4	40.2	58.2
	IL	47.7	74.7	110.8	15.1	159.1	55.1	31.2	52.2	53.3	70.1	58.7	46.1	15.0	49.4	42.4	10.4	39.2	56.2
	TN	50.1	74.4	114.6	15.7	162.1	60.2	35.8	53.9	56.6	71.3	55.3	46.6	15.7	50.3	43.4	11.0	39.9	58.7

†Essential amino acids

‡Non-essential amino acids

Table 2.3 Simple phenotypic correlation coefficients between amino acids in soybean seed in 282 $F_{5:9}$-derived RILs of Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

	Ala	Arg	Asp	Cys	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr
Arg	0.78																
Asp	0.85	0.82															
Cys	0.63	0.42	0.77														
Glu	0.41	0.63	0.76	0.49													
Gly	0.96	0.69	0.72	0.52	0.20												
His	0.84	0.57	0.79	0.70	0.43	0.78											
Iso	0.85	0.92	0.94	0.59	0.73	0.72	0.73										
Leu	0.57	0.71	0.88	0.63	0.95	0.37	0.59	0.84									
Lys	0.41	ns	-0.11	-0.23	0.31	-0.53	-0.61	-0.05	0.17								
Met	0.92	0.78	0.88	0.76	0.45	0.86	0.79	0.84	0.63	-0.29							
Phe	0.80	0.86	0.97	0.67	0.80	0.66	0.72	0.96	0.90	ns	0.88						
Pro	0.96	0.87	0.87	0.59	0.49	0.91	0.77	0.91	0.63	-0.27	0.91	0.86					
Ser	0.93	0.74	0.72	0.52	0.21	0.96	0.72	0.73	0.38	-0.43	0.89	0.67	0.92				
Thr	0.93	0.75	0.73	0.55	0.21	0.93	0.74	0.77	0.39	-0.39	0.88	0.70	0.91	0.93			
Trp	0.51	0.54	0.41	0.05	0.37	0.51	0.39	0.51	0.33	-0.16	0.41	0.44	0.53	0.47	0.42		
Tyr	0.92	0.81	0.79	0.52	0.36	0.89	0.75	0.85	0.53	-0.30	0.86	0.80	0.93	0.89	0.94	0.45	
Val	0.97	0.84	0.86	0.59	0.43	0.92	0.80	0.89	0.59	-0.32	0.91	0.84	0.97	0.90	0.94	0.50	0.94

All values were significant at $p < 0.01$

Table 2.4 Principal components obtained using amino acid concentrations in soybean seed of 282 $F_{5:9}$-derived RILs of Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

Principal Component	Eigenvalue	Difference	Proportion	Cumulative
1	12.7	10.25	0.6733	0.6733
2	2.53	1.09	0.133	0.8066
3	1.43	0.60	0.606	0.8821

Table 2.5 Eigenvectors for principal components obtained using amino acid concentrations of soybean seed in 282 $F_{5:9}$-derived RILs of Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

Amino Acid	Principal Component 1	Principal Component 2	Principal Component 3
Tyr	0.25	-0.11	0.03
Val	0.27	-0.09	0.04
Asp	0.26	0.17	-0.08
Cys‡	0.19	0.08	-0.43‡
Glu†	0.16	0.47†	0.05
Gly	0.24	-0.26	0.04
His	0.23	-0.11	-0.19
Iso	0.26	0.15	0.08
Leu†	0.20	0.40†	-0.05
Lys†	-0.07	0.49†	0.18
Met	0.26	-0.05	-0.09
Ohe	0.25	0.22	-0.01
Pro	0.27	-0.05	0.06
Ser	0.24	-0.22	0.03
Thr	0.25	-0.21	0.01
Trp‡	0.14	-0.02	0.50‡
Ala	0.27	-0.13	0.01
Arg	0.24	0.12	0.24

† Signifies the amino acids that compose principal component 2
‡ Signifies the amino acids that compose principal component 3

Table 2.6 Quantitative trait loci identified using R/qtl and R/MQM located on various molecular chromosomes associated with essential and non-essential amino acid concentration in soybean seed in 282 $F_{5:9}$-derived RILs of Essex 86-15-1 x Williams 82-11-43-1 grown in Knoxville, TN, Fayetteville, AR, and Harrisburg, IL in 2009.

MARKER(S)	TRAIT	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT†
ss107923612	Ala	5	A1	145.5	3.21	5.5	0.02 (E)
ss107917837	Ala	13b	Fb	4.86	3.96	6.9	-0.03 (W)
ss107920654/ss107924336	Ala	13b	Fb	40.69	3.81	6.6	-0.02 (W)
ss107917837	Arg	13b	Fb	4.86	3.14	5.7	-0.05 (W)
ss107912633/ss107918763	Arg	13b	Fb	21.51	3.46	6.1	-0.06 (W)
ss107920654/ss107924336	Arg	13b	Fb	40.69	4.49	7.9	-0.06 (W)
ss107928831/ss107926274	Asp	7	M	71.31	2.97	5.5	-0.06 (W)
ss107913002	Asp	9	K	62.54	3.75	5	0.07 (E)
ss107912627	Asp	9	K	86.91	2.92	7.4	0.06 (E)
ss107917837	Asp	13b	Fb	4.86	3.07	5.5	-0.07 (W)
ss107920654/ss107924336	Asp	13b	Fb	40.69	3.46	6.1	-0.07 (W)
ss107929220/ss107914151	Cys	20	I	133.42	2.94	6	-0.01 (W)
ss107924237	Glu	19	L	116.09	3.32	13.8	0.08 (E)
ss107917837	Gly	13b	Fb	4.86	3.72	6.4	-0.05 (W)
ss107920654/ss107924336	Gly	13b	Fb	40.69	2.95	5	-0.05 (W)
ss107920438/ss107912744/ ss107919004	His	10	O	110.18	3.98	7.4	0.04 (E)
ss107917837	Iso	13b	Fb	4.86	3.57	6.3	-0.03 (W)
ss107912633/ss107918763	Iso	13b	Fb	21.51	3.18	5.4	-0.02 (W)
ss107920654/ss107924336	Iso	13b	Fb	40.69	5.01	8.9	-0.04 (W)
ss107913002	Leu	9	K	62.54	5.57	5.7	0.04 (E)
ss107912627	Leu	9	K	86.91	4.08	10.7	0.03 (E)
ss107917837	Met	13b	Fb	4.86	2.97	5.2	-0.01 (W)
ss107917837	Phe	13b	Fb	4.86	3.16	5.7	-0.03 (W)
ss107912633/ss107918763	Phe	13b	Fb	21.51	3.33	5.7	-0.03 (W)
ss107920654/ss107924336	Phe	13b	Fb	40.69	4.23	7.5	-0.03 (W)
ss107917837	Pro	13b	Fb	4.86	3.9	7	-0.04 (W)
ss107912633/ss107918763	Pro	13b	Fb	21.51	3.52	6	-0.03 (W)
ss107920654/ss107924336	Pro	13b	Fb	40.69	5.42	9.5	-0.04 (W)

Table 2.6 Continued.

MARKER(S)	TRAIT	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT†
ss107917837	Ser	13b	Fb	4.86	3.67	6.5	-0.04 (W)
ss107912657/ss107913658	Ser	13b	Fb	21.51	3.27	5.6	-0.04 (W)
ss107920654/ss107924336	Ser	13b	Fb	40.69	3.07	5.2	-0.04 (W)
ss107917837	Thr	13b	Fb	4.86	3.72	6.6	-0.02 (W)
ss107920654/ss107924336	Trp	13b	Fb	40.69	3.81	6.5	-0.02 (W)
ss107920438/ss107912744/ ss107919004	Tyr	10	O	110.18	3.1	5.7	0.02 (E)
ss107917837	Tyr	13b	Fb	4.86	3.75	6.7	-0.02 (W)
ss107912657/ss107913658	Tyr	13b	Fb	21.51	3.02	5	-0.02 (W)
ss107920654/ss107924336	Tyr	13b	Fb	40.69	3.46	6	-0.02 (W)
ss107923612	Val	5	A1	145.5	3.38	6	0.05 (E)
ss107917837	Val	13b	Fb	4.86	4.18	7.4	-0.05 (W)
ss107912633/ss107918763	Val	13b	Fb	21.51	2.97	5	-0.04 (W)
ss107920654/ss107924336	Val	13b	Fb	40.69	4.5	7.9	-0.05 (W)

†Additive effect refers to the quantitative change in amino acid composition that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Chapter 3

Selective Genotyping for Marker Assisted Selection Strategies for Soybean Yield Improvement

Abstract

Molecular markers have already played a major role in the genetic characterization and improvement of many crop species. The location of major loci is now known for disease resistance, tolerance to abiotic stresses and quality traits. However, although many quantitative trait loci (QTL) have been identified for quantitative traits, few previously reported QTLs have been confirmed in subsequent studies and even fewer reports have utilized them for marker assisted selection (MAS). Most yield QTLs are population specific and the genetic variation found in the specific bi-parental population might not be shared in other genetic populations. The major objective in breeding soybean is to develop cultivars with the potential for high seed yield. Unfortunately, yield is also a complex trait to characterize from both a phenotypic and genotypic perspective. The objective of this study was to identify QTL associated with soybean seed yield in preliminary yield trials and evaluate their effective use for MAS in different environments. To achieve this objective, 875 $F_{5:9}$ recombinant inbred lines (RIL) from a population developed from a cross between two prominent ancestors of the North American soybean (Essex and Williams 82) were used. The 875 RILs and check cultivars were divided into four groups based on maturity and each group was grown in Knoxville, TN and one other location of adaptability. Each RIL was genotyped with >50,000 single nucleotide polymorphic markers (SNPs) of which 17,232 were polymorphic across the population. Yield QTL were detected using single factor ANOVA and composite interval mapping (CIM). Based on CIM, 23 yield QTLs were identified. Twenty-one additional QTL were detected using single factor ANOVA. Individually, these QTLs explained from 4.5 % to 11.9% of the phenotypic variation for yield. QTLs were identified on all 20 chromosomes and five of the 46 QTLs have not been

previously reported. Some of these new loci may be attractive candidate regions for further understanding the genetic basis of soybean yield.

In addition, MAS were made using two methods in each environment and across environments for each group. One method including using only additive effects and the other method included using a yield prediction model (YPM). The yield prediction model included mean yield, additive and additive by additive effects. By including additive by additive effects in addition to additive effects into the YPM, more top yielding lines were selected than by just using only additive effects. For example, from the lines selected using only the additive effects for the favorable alleles for the three QTLs identified in Wooster, OH in 2011, eight lines were selected in the top yielding 10 % of all RILs averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011. From the lines selected using additive and additive by additive effects in the YPM for the nine QTLs shown to have a significant interaction with the three QTLs identified in Wooster, OH in 2011, 16 lines were selected in the top yielding 10 % of all RILs averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011. This study provides new information concerning yield QTL in soybean and may offer important insights into MAS strategies for soybean.

Introduction

Without cultivar improvements in yield potential, the soybean would not have become the most important source of vegetable protein and oil in the world and the second most important crop in the U.S. In 2011, the estimated seed yield of soybean in the U.S. was 83.2 million metric tons harvested from 30.3 million hectares of land (Soy Stats, 2012). However, yield increases in soybean may seem moderate when compared to other crops, such as corn (*Zea mays* L.). The annual rate of genetic gain from 1924 to 2011 in the U.S. was 25.7 kg/hectare in soybean; whereas corn yields increased by 115.3 kg/hectare annually. From 1990 to 2011 the annual rate of gain was slightly lower in soybeans with 23.5 kg/hectare, whereas corn yields increased by 153.8 kg/hectare annually (Hao et al., 2012; Orf et al., 2004). There are several possible explanations for this slow progress and the declining efficiency in soybean yield improvement compared with corn. Many of these have to do with the basic differences in the physiology of these crop plants. For example, in the seeds of soybean the major storage is in protein (38-42%) and oil (18-22%), whereas in corn the major storage is in starch. It is also important to consider that corn produces higher yields and therefore gains in yield can occur on a larger scale than in soybean. Nevertheless, the genetic gain is still only about 1 % a year in soybean, compared to about 2 % in corn (Hao et al., 2012).

Another reason proposed by Sebastian (2005) and Hyten et al. (2006) is that current selection procedures are not efficient in exploiting the available genetic diversity. MAS for yield could greatly improve our understanding of the genetic mechanisms of seed yield and increase breeding efficiency dramatically. Yet, despite economic incentives and scientific interest, very few yield QTL in soybean have been validated across a wide range of environments and populations. Bernado (2008) concluded that because estimated QTL effects for traits such as grain yield are limited to the set of segregating progeny from a single cross, QTL mapping for such traits will likely have to be repeated for each breeding population. Sebastian et al (2010) used context-specific MAS (CSM) to detect yield QTL in elite soybean cultivars. Selected subline haplotypes were compared to their respective mother lines in highly replicated yield trials across multiple locations and years. From the selected sublines, significant yield gains of up to 5.8% were confirmed and two of the improved sublines were released as improved cultivars.

Further, building statistical models that can handle data sets consisting of a massive number of markers that well exceed the number of observations can be very statistically challenging. Traditionally, a subset of predictors in a regression model are obtained by forward selection, backward elimination and stepwise selection (Li et al., 2011), but these approaches are impossible to use when the number of predictors (SNPs) far exceed the number of observations. Long et al. (2011) conducted a study to evaluate two dimension reduction methods, supervised principal component regression (PCR) and sparse principal least-square regression (PLS), for predicting genomic breeding values (BV) of dairy bulls for milk yield using SNPs. PCR and PLS reduce model dimension and overcome multicollinearity problems by transforming the large number of original variables into a relatively small number of orthogonal latent components and then regress the response variable on those latent components. In their study supervised PCR was used to preselect SNPs based on strength of association of each SNP with the phenotype. Two types of supervised PCR were used: method I was based on single-SNP analyses and method II was based on multiple-SNP analyses. Then the Bayesian Lasso (a statistical technique) was used to estimate the regression coefficients of the principal components and these regression coefficients were used to rank and select SNPs. They concluded PCR II was the best method for dimension reduction and variable selection for predicting genomic BVs. Li et al. (2011) also proposed a two stage procedure for multi-SNP modeling and analysis in genome wide association studies (GWASs), by first producing a 'preconditioned' response variable using a supervised principle component analysis and then formulating Bayesian Lasso to select a subset of significant SNPs. Using simulation data they demonstrated that when the number of markers greatly exceeds the number of observations 'preconditioned' or specialized PCA can successfully identify almost all SNPs with true genetic effects. Other studies have also used

PCR and PLS for genome-assisted prediction of breeding values (Solberg et al., 2009; Macciotta et al., 2010). However, these methods can be very challenging to use and require extensive computing technology and time. Some studies have shown single factor ANOVA and CIM can identify significant QTL for MAS (Primomo et al., 2005; Palomeque et al., 2010).

To identify and characterize QTL affecting yield, a large recombinant inbred line (RIL) population was derived from a cross between Essex 86-15-1 and Williams 82-11-43-1, where the numbers 86-15-1 and 11-43-1 designate specific reselections of 'Essex' and 'Williams82', respectively. The population will be hereafter referred to as Essex x Williams82. The two cultivars Essex (Smith and Camper, 1973) and Williams (Bernard and Lindahl, 1972) have contributed prominently to the genetic background of many southern and northern cultivars and elite breeding lines, respectively in the U.S. (Sneller, 1994; Gizlice et al. 1996). The diversity created by the Essex x Williams cross is credited for producing the widely grown cultivar Asgrow A3127 which served as a genetic bridge between the northern and southern U.S. germplasm pool (Sneller, 1994; Hyten et al., 2004).

Objectives

The objectives of this study were to test whether: 1) MAS for haplotypes accumulating the top 5% of loci positive for yield differ significantly than the population mean when grown in different environments and thus are considered favorable for selecting high yielding lines; 2) MAS for haplotypes can distinguish low yielding vs. high yielding lines; and 3) phenotypic selections for yield differ from genotypic SNP selections for yield.

Materials and Methods

Population Development

The initial crosses for the Essex x Williams 82 population were made at the East Tennessee Research and Extension Center (ETREC) in Knoxville, TN in the summer of 2005. In the fall of 2005 the F_1 seeds obtained were harvested and grown in Puerto Rico at the USDA Tropical Agricultural Research Station (TARS). The population was advanced from the F_2 to the F_5 generation through single seed descent (Brim, 1966): The F_2 generation was grown in 2006 at ETREC and the F_3 generation was grown in 2007 at ETREC. The F_4 and F_5 generations were grown at the TARS location in the winter of 2007 and the spring of 2008, respectively. In Beltsville, MD in the summer of 2009, F_5 plants were grown in a greenhouse and leaf tissue was collected from each plant individually. A total of 977 individually tagged F_5 plants were harvested and planted as $F_{5:6}$ plant rows in Homestead, FL in the fall of 2009. The $F_{5:6}$ rows were harvested individually and in 2010 the $F_{5:7}$ recombinant inbred lines were planted in Knoxville, TN.

Experimental Design

In 2010, 973 recombinant inbred lines were planted in Knoxville, TN. Each line was planted in one rep as a two row plot 6 m in length, with 76 cm spacing between rows. The lines were divided into four groups based on the maturity date recorded on a single plant in Beltsville, MD in 2009. The lines were again divided into four groups based on the maturity date recorded in 2010. In 2011, the four groups containing a total of 875 recombinant inbred lines and 12 commercial checks (for overall agronomic comparisons) were planted in Knoxville, TN. The four groups were designated as: Group A, Group B, Group C and Group D. In Group A there were 218 RILs and three checks: ‘IA3024’, ‘IA3023’, and LD00-3309. The maturity ranged from an early maturity group (MG) III to a late MG III. In Group B there were 221 RILs and three checks: ‘IA4005’, LD00-3309 and LD00-2817P. The maturity ranged from a late MG III to an early MG IV. In Group C there were 216 RILs and three checks: LD00-2817P, TN09-008 and ‘5002T’. The maturity ranged from an early MG IV to a late MG IV. Check LD00-2817P was not included in the final mean seed yield comparison in Groups B and C because of poor germination and plant stand. In Group D there were 220 RILs and three checks: ‘5002T’, ‘5601T’ and ‘Osage’. The maturity ranged from an early MG V to a late MG V. A randomized complete block design was used and each line was planted in two reps of a two row plot 3.5 m in length, with 76 cm spacing between rows. In addition, Group A was planted in Wooster, OH in two reps of a two row plot 4.9 m in length, with 76 cm spacing between rows. Group B was planted in Belleville, IL in two reps of a two row plot 4.5 m in length, with 76 cm spacing between rows. Group C was planted in Portageville, MO in two reps of a two row plot 3.5 m in length, with 76 cm spacing between rows. Group D was planted in Plymouth, NC in two reps of a two row plot 5 m in length, with 76 cm spacing between rows. This allowed all groups to be planted in the same location (Knoxville, TN) and for each group to be planted in another environment where it was expected to be well adapted.

Experimental Procedures

Phenotypic Data

After planting, all the plots were evaluated for agronomic traits. At maturity, plant height was measured as an estimation of the distance from the soil surface to the tip of the main stem. Lodging was scored on a scale from 1-5; with 1 being all the plants in the plot were erect and 5 being all the plants in a plot were prostrate. Maturity was recorded as the date, according to the

Julian calendar, when 95 % of the pods achieved their mature color. At that time pubescence color was also recorded. At ETREC seed yield was estimated from two rows after the plots had been end trimmed to 4.88 m in length. In Wooster, OH, Belleville, IL and Portageville, MO seed yield was estimated from harvesting two rows at 4.9 m, 4.5 m and 3.5 m length rows, respectively. In Plymouth, NC seed yield was estimated from harvesting two rows after the plots had been trimmed to 3.5 m in length. All yields were adjusted to 13 % moisture.

Genotyping

DNA was extracted from each F_5 greenhouse plant grown at the Soybean Genomics Laboratory at the USDA Beltsville Agricultural Research Center (USDA-ARS) in Beltsville, MD. Each DNA sample was processed to contain 50 µl of DNA at a 200 ng/µl concentration. The samples were then assayed using >50,000 SNP markers using the GoldenGate® assay and analyzed on the Illumina BeadStation 500G (Illumina, San Diego, CA) (Hyten et al., 2008). A total of 17,232 polymorphic SNP markers were found in the population.

Experimental Analysis

Marker order, position and composite interval mapping were conducted using R/qtl (Broman and Sen, 2009). A total of 1,000 permutations were performed for all chromosomes to establish an empirical LOD threshold at the 5 % probability level. Of the 17, 232 polymorphic SNP markers 15, 448 were assigned to 20 chromosomes; the remaining 1,784 markers were unlinked. The estimated map length was 2072 cM with an average distance between markers of 0.2 cM.

Single factor analysis of variance was also used for QTL analysis (P<0.01) using SAS (PROC MIXED, SAS ver. 9.1.s, Cary, NC). Each marker was considered a factor with two levels: “A” designating the Essex allele type and “B” designating the Williams82 allele type and the phenotype (yield) as the dependent variable. Heterozygotes were not included for QTL analysis using R/qtl or single factor ANOVA.

An additive effect for each QTL was determined using the software in which the QTL was detected (R/qtl or SAS). Additive effects were determined separately for each environment and across environments within each group. Next, the lines were sorted by the number of favorable alleles for seed yield that each line contained and only the top 10 % were selected. Then, the top 10 % MAS using only additive effects were compared to the lines yielding in the top 10 % (based on kg ha^{-1}) for each environment and across environments. The bottom 10 % of lines containing the unfavorable alleles were also compared to the lines yielding in the bottom 10 % (based on kg ha^{-1}) for each environment and across environments.

Prediction models for yield in each group were made based on 2010 QTL data; from QTL data for each 2011 environment; and using QTL data combined over 2010 and 2011 environments. Yield was predicted using the following: (a) the overall mean yield of each genotype, (b) the additive effect of the markers identified using single factor ANOVA in SAS or (c) R/qtl and the additive by additive epistatic effects ($P<0.01$) of those markers. Additive by additive epistatic effects were determined separately for each group for each environment and across environments at $P<0.01$ using the Epistacy macro, version 2.0 in SAS (Holland, 1998).

Results

Group A: Agronomic Traits

The effect and contribution of each source of variation to yield was evaluated through a combined analysis of variance (ANOVA) over all environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) (**Table 3.1**), in Knoxville, TN in 2011 (**Table 3.2**) and in

Wooster, OH in 2011 (**Table 3.3**). The environmental effect ($P<0.0001$) explained the greatest amount of variation in the model when all environments were evaluated and genotypes were also highly significant ($P<0.0001$) (**Table 3.1**). At the individual environments, genotypes were significant at Knoxville, TN in 2011 ($P<0.05$) and highly significant at Wooster, OH in 2011 (**Table 3.2; Table 3.3**). The highly significant genotype effect in Wooster, OH in 2011 may be due to the highly adapted maturity of Group A for that environment (Sleper, 2006). The maturity ranged from an early MG III to a late MG III, which is more adapted to be grown in Wooster, OH than Knoxville, TN (Sleper, 2006). The Group A mean yield (kg ha^{-1}) was greater at Wooster, OH than at Knoxville, TN, allowing for better statistical separation of genotype effects.

In Group A, Wooster, OH had an average yield (3339 kg ha^{-1}) that was significantly ($p<0.01$) higher than the average yield in Knoxville, TN in 2010 (1740 kg ha^{-1}) and 2011 (1486 kg ha^{-1}) **(Table 3.4).** Average lodging and height were not significantly different across locations. Average maturity was significantly different across all locations. The average maturity date was 260 for Knoxville, TN in 2010, 250 for Knoxville, TN in 2011 and 270 for Wooster, OH in 2011 **(Table 3.4).**

Group A:

MAS Using Only Additive Effects

R/qtl

In 2010 in Knoxville, TN three QTLs were identified for yield using R/qtl **(Table 3.5)**. Using MAS to select lines with the favorable allele for these QTLs, six lines were selected that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those six lines two were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.6)**. Conversely when MAS was conducted to target reduced yield to demonstrate allele effectiveness; eight lines selected by MAS using the unfavorable allele for the same three QTLs were in the bottom yielding 10 % of RILs grown in Knoxville, TN in 2010 and three of those lines were in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.7)**. Line 800 was among the lines selected using MAS in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 and was the 3rd lowest yielding line.

In 2011 in Wooster, OH three QTLs were identified for yield using R/qtl **(Table 3.5)**. Using MAS to select lines with the favorable allele for these QTLs seven lines were selected that were in the top yielding 10 % of RILs grown in Wooster, OH in 2011 and of those seven lines five were in the top yielding 5 % of RILs grown in Wooster, OH in 2011 **(Table 3.6)**. Lines 814 and 689 were among the top yielding 5 % in that environment selected using MAS and ranked 1st and 3rd in yield, respectively. Using MAS to select lines with the unfavorable allele for the same three QTLs, nine lines were selected in the bottom yielding 10 % of RILs grown in Wooster, OH in 2011and seven of those lines were in the bottom yielding 5 % of RILs grown in Wooster, OH in 2011 **(Table 3.7)**. Lines 931, 724 and 800 were among the bottom yielding 5 % grown in that environment selected using MAS and were the 2nd, 3rd, and 5th lowest yielding lines, respectively.

From data combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011 three QTLs were identified for yield using R/qtl **(Table 3.5)**. Using MAS to select lines with the favorable allele for these QTLs, nine lines were selected that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Wooster, OH in 2011) and of those nine lines five were in the top yielding 5 % of RILs combined over three environments **(Table 3.6)**. Lines 481, 833 and 144 were among the top yielding 5 % of RILs combined over three environments selected by MAS and ranked 1st, 2nd and 5th in yield, respectively. Using MAS to select lines with the unfavorable allele for the same three QTLs, twelve lines were selected in the bottom yielding 10 % of RILs combined over three environments and seven of those lines were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.7)**. Lines 202 and 1015 were among the bottom yielding 5 % of RILs combined over three environments selected using MAS and were the 3rd and 5th lowest yielding lines, respectively.

From the lines selected with the favorable allele for the three QTLs identified in Knoxville, TN in 2010 using MAS, five lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Wooster, OH in 2011) and of those two were in the top yielding 5 % of RILs combined over three environments **(Table 3.8)**. The two lines selected by MAS in the top yielding 5 % of RILs combined over three environments were 481 and 144 and ranked 1st and 5th in yield, respectively. Further credibility of yield QTL was demonstrated when five lines selected by MAS with the unfavorable alleles for the three QTLs identified in Knoxville, TN in 2010 were in the bottom yielding 10 % of RILs combined over three environments and three of those five were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.9)**. Lines 202 and 1015 were among the lines selected using MAS in the bottom yielding 5 % of RILs combined over three environments and were the 3rd and 5th lowest yielding lines, respectively.

From the lines selected with the favorable alleles for the three QTLs identified in Wooster, OH in 2011 using MAS, eight lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Wooster, OH in 2011) and six of those lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.8)**. Lines 481, 689 and 144 were among the lines selected in the top yielding 5 % of RILs combined over three environments and ranked 1st, 4th and 5th in yield, respectively. Elven lines selected by MAS with the unfavorable alleles for the three QTLs identified in Wooster, OH in 2011 were in the bottom yielding 10 % of RILs combined over three environments and six of those were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.9)**.

SAS

In 2010 in Knoxville, TN four QTLs were identified for yield using SAS **(Table 3.10)**. Using MAS to select lines with the favorable allele for these QTLs, five lines were selected that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those five lines only one was in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.11)**. Seven lines selected by MAS using the unfavorable allele for the same four QTLs were in the bottom yielding 10% of RILs grown in Knoxville, TN in 2010 and three of those lines were in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.12)**. The three lines selected in the bottom yielding 5 % were the three lowest yielding lines in Group A in Knoxville, TN in 2010.

In 2011 in Wooster, OH four QTLs were identified for yield for yield using SAS **(Table 3.10)**. Using MAS to select lines with the favorable allele for these QTLs six lines were selected that were in the top yielding 10 % of RILs grown in Wooster, OH in 2011 and of those six lines three were in the top yielding 5% of RILs grown in Wooster, OH in 2011 **(Table 3.11)**. Six lines selected by MAS using the unfavorable allele for the same four QTLs were in the bottom yielding 10 % of RILs grown in Wooster, OH in 2011and five of those lines were in the bottom yielding 5 % of RILs grown in Wooster, OH in 2011 **(Table 3.12)**.

From data combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 seven QTLs were identified for yield using SAS **(Table 3.10)**. Using MAS to select lines with the favorable allele for these QTLs, three lines were selected that were in the top yielding 5 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) **(Table 3.11)**. Using MAS to select lines with the unfavorable allele for the same seven QTLs, five lines were selected in the bottom yielding 10% of RILs combined over three environments and four of those lines were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.12)**.

From the top lines selected using MAS with the favorable allele for the four QTLs identified in Knoxville, TN in 2010 using MAS, five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Wooster, OH in 2011) and three of those five were in the top yielding 5 % of RILs combined over three environments **(Table 3.13)**. Using MAS to select lines with the unfavorable allele for the same four QTLs identified in Knoxville, TN in 2010, seven lines were selected in the bottom yielding 10 % of RILs combined over three environments and five of those seven were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.14)**. Lines 372 and 200 were among the five lines selected using MAS in the bottom yielding 5 % of RILs combined over three environments and were the lowest and 3rd lowest in yield, respectively.

From the lines selected with the favorable alleles for the four QTLs identified in Wooster, OH in 2011 using MAS, five lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Wooster, OH in 2011) and only one of those five was in the top yielding 5 % of RILs combined over three environments **(Table 3.13)**. Nine of the bottom lines selected by MAS with the unfavorable alleles for the four QTLs identified in Wooster, OH in 2011 were in the bottom yielding 10 % of RILs combined over three environments and six of those nine were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.14)**. Lines 372 and 615 were among the five lines selected in the bottom yielding 5 % of RILs combined over three environments and were the two lowest yielding lines.

When comparing MAS made in the individual environments of Wooster, OH in 2011 and Knoxville, TN in 2010 using SAS, more top yielding lines were selected using MAS in Wooster, OH in 2011 **(Table 3.11).** This was also true when using R/qtl (**Table 3.6**). These results suggest that MAS using R/qtl or SAS can be successful using data collected from a single environment, but better results are seen when the environment is well adapted for the maturity group of the soybean.

In total six QTLs were identified using R/qtl on five chromosomes (2, 3, 4, 5 and 19) and eleven QTLs using SAS on eleven chromosomes (2, 3, 9, 10, 11, 13, 14, 15 and 19). A yield QTL was identified with marker Gm02_47790307_C_T from data averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011 using R/qtl (150.38 cM) and in Knoxville, TN in 2010 using SAS (121.66 cM) **(Tables 3.5, 3.10)**. Gm19_44937486_T_C was associated with a yield QTL in Knoxville, TN in 2010 using SAS at 76.71 cM and R/qtl at 70.65 cM **(Tables 3.8, 3.13)**. Gm02_49126947_T_C (127.25 cM) was associated with a yield QTL in Wooster, OH in 2011 and from data averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011 using SAS **(Table 3.10)**. Although, fewer QTLs were identified using R/qtl more top yielding or bottom yielding lines were selected in individual environments and averaged over all environments. And using R/qtl more lines were selected among the top 5 yielding lines in individual environments and averaged over all environments. These results suggest that MAS is better using R/qtl than SAS in an early MG III to a late MG III soybean. To further improve upon the results we found using only additive effects, we developed a yield prediction model (YPM) which included additive and additive by additive effects.

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010

R/qtl

In 2010 in Knoxville, TN five QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.15)**. This information was used to develop an YPM to select by MAS high yielding lines in subsequent years. Eleven lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, including the highest yielding line 668 **(Table 3.16)**. However, only six MAS lines from that YPM were in the top yielding 10 % of RILs when grown in Wooster, OH in 2011 and although three of those lines were in the top yielding 5 % of RILs, the MAS YPM failed to select the highest yielding line at that environment **(Table 3.16)**. Nine lines that were in the top yielding 10 % of RILs from the combined analysis of three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) were selected by MAS using an YPM and four of those lines were in the top yielding 5 % of RILs from the combined analysis of three environments, including the top two yielding lines 481 and 833 **(Table 3.16)**.

Previously when using only additive effects identified using R/qtl in Knoxville, TN in 2010 for MAS (**Table 3.8**) without using additive by additive effects in an YPM; only five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) and of those two lines were in the top yielding 5 % of RILs combined over three environments, including the top yielding line 481 (**Table 3.8**).

SAS

In 2010 in Knoxville, TN eleven QTLs were shown to have a significant interaction with three of the QTLs identified for yield using SAS **(Table 3.18)**. This information was used to develop an YPM to select by MAS the top yielding lines in subsequent years. Nine lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS and two of those lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.17)**. Five lines that were in the top yielding 10 % of RILs grown in Wooster, OH in 2011 were selected by MAS using an YPM and two of those lines were in the top yielding 5 % of RILs grown in Wooster, OH in 2011 **(Table 3.17)**. Seven lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) were selected by MAS using a YPM and five of those lines were in the top yielding 5 % of RILs combined over three environments, including the top two yielding lines 481 and 833 **(Table 3.17)**.

Earlier when MAS was conducted using only additive effects detected using SAS in Knoxville, TN in 2010 (**Table 3.13)** without the benefit of using an YPM containing epistasis; only five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) and of those three lines were in the top yielding 5 % of RILs combined over three environments (**Table 3.13**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Wooster, OH 2011

R/qtl

In 2011 in Wooster, OH seven QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.15)**. This information was used to develop an

YPM to select by MAS high yielding lines at other testing environments. Six lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those two lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.19)**. This contrasted with the fifteen lines from that YPM that were in the top yielding 10 % of RILs grown in Wooster, OH in 2011 and of those nine lines were in the top yielding 5 % of RILs grown in Wooster, OH in 2011, including the three top yielding lines 814, 292 and 689 **(Table 3.19)**. Moreover, sixteen lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) were selected by MAS using an YPM and eight of which were in the top yielding 5 % of RILs combined over three environments, including all of the top seven yielding lines **(Table 3.19)**.

Previously when using only additive effects identified using R/qtl in Wooster, OH in 2011 for MAS (**Table 3.8**) without using additive by additive effects in an YPM; only eight lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) and of those six lines were in the top yielding 5 % of RILs combined over three environments, including the top yielding line 481 (**Table 3.8**).

SAS

In 2011 in Wooster, OH nine QTLs were shown to have a significant interaction with three of the QTLs identified for yield using SAS **(Table 3.18)**. That information was used to develop an YPM to select by MAS the top yielding lines at other testing environments. Four lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected using MAS and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.20)**. Eleven lines that were in the top yielding 10 % of RILs grown in Wooster, OH in 2011 were selected using MAS and of those six lines were in the top 5 % of RILs grown in Wooster, OH in 2011, including the top four lines **(Table 3.20)**. Ten lines that were in the top yielding 10 % combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) were selected using MAS and four of those lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.20)**.

Earlier when MAS was conducted using only additive effects detected using SAS in Wooster, OH in 2011 (**Table 3.13**) without the benefit of using an YPM containing epistasis; only five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) and of those only one line was in the top yielding 5 % (**Table 3.13**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010, 2011 and Wooster, OH 2011

R/qtl

From data averaged across Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 eleven QTLs were shown to have a significant interaction with three of the QTLs identified for yield using R/qtl **(Table 3.15)**. This information was used to develop an YPM to select by MAS high yielding lines in different environments. Nine lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and five of which were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.21)**. Fourteen lines were selected by MAS using an YPM in the top yielding 10 % of RILs grown in Wooster, OH in 2011 and of those nine lines were in the top yielding 5 % of RILs grown in Wooster, OH in 2011 **(Table 3.21)**. Twelve lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown over the combined environments of Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 and of those seven lines were in the top yielding 5 % of RILs grown over the combined environments of Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011, including the top three yielding lines 481, 833 and 978 **(Table 3.21)**.

Previously when using only additive effects identified using R/qtl combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 for MAS (**Table 3.13**) without using epistatic effects in an YPM; six lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011and of those five lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011, including the top yielding line 481.

SAS

From data averaged across Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 fourteen QTLs were shown to have a significant interaction with five of the QTLs identified for yield using SAS **(Table 3.18)**. This information was used to develop an YPM to select by MAS the top yielding lines in different environments. Eight lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and five of those were in the top yielding 5 % grown in Knoxville, TN in 2011, including the top yielding lines 668 and 978 **(Table 3.22)**. Thirteen lines were selected by MAS using an YPM that were in the top 10 % of RILs grown in Wooster, OH in 2011 and of those nine lines were in the top yielding 5 % of RILs grown in Wooster, OH in 2011, including the top three lines 814, 292 and 689 **(Table 3.22)**. Thirteen lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 and eight of which were in the top yielding 5 % of RILs grown over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011, including the top five lines **(Table 3.22)**.

Previously when MAS was accomplished using only additive effects identified using SAS combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011 (**Table3.13**) without using epistatic effects in an YPM; only three lines were selected in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011.

Using the YPM more lines were selected than using only additive QTL MAS in Group A. Moreover, more top yielding lines were selected using QTLs identified by R/qtl than SAS using the Wooster, OH 2011 data and the Knoxville, TN 2010 data in the YPM. However, similar results were seen when using QTLs identified by R/qtl and SAS using the data combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011 in the YPM.

Group B: Agronomic Traits

The effect and contribution of each source of variation to yield was evaluated through a combined analysis of variance over all environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) (**Table 3.23**), in Knoxville, TN in 2011 (**Table 3.24**) and in Belleville, IL in 2011 (**Table 3.25**). The environmental effect ($P<0.0001$) explained the greatest amount of variation in the model when all environments were evaluated, just like in Group A. Genotypes were also significant ($P<0.001$) (**Table 3.23**). At individual environments, genotypes were significant at Knoxville, TN in 2011 ($P<0.05$) and highly significant at Belleville, IL in 2011 (**Table 3.24; Table 3.25**). The highly significant genotype effect in Belleville, IL in 2011 may be due to the highly adapted maturity of Group B for that environment (Sleper, 2006). The maturity of Group B ranged from a late MG III to an early MG IV, which is more adapted to be grown in Belleville, IL than Knoxville, TN, allowing for better separation of genotype effects.

In Group B, Belleville, IL had an average yield (3445 kg ha^{-1}) that was significantly (p<0.01) higher than the average yield in Knoxville, TN in 2010 (2327 kg ha^{-1}) and 2011 (1835 kg ha^{-1}) **(Table 3.26).** Average lodging and height were not significantly different across locations. Average maturity was significantly different between Belleville, IL in 2011 (289) and Knoxville, TN in 2010 and 2011 (268), but no significant difference was seen between Knoxville, TN in 2010 (269) and Knoxville, TN in 2011 (268) **(Table 3.26).**

Group B: QTL Results

R/qtl

In 2010 in Knoxville, TN two QTLs were identified for yield using R/qtl **(Table 3.27)**. Using MAS to select lines with the favorable allele for these QTLs, five lines were selected that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those two were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.28)**. To demonstrate how MAS can also be used to target reduced yield; three lines were selected in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 using the unfavorable allele for the two QTLs identified for yield using R/qtl **(Table 3.29)**.

In 2011 in Belleville, IL four QTLs were selected for yield using R/qtl **(Table 3.27)**. Using MAS to select lines with the favorable allele for these QTLs, fives lines were selected that were in the top yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.28)**. Lines 65, 550 and 826 were among the top yielding 5 % of RILs grown in that environment selected by MAS and ranked 1^{st}, 4^{th} and 5^{th} in yield, respectively. Using MAS to select lines with the unfavorable allele for the same four QTLs, eight lines were selected in the bottom yielding 10 % of RILs grown in Belleville, IL in 2011 and four of those lines were in the bottom yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.29)**. The lowest yielding line (659) was selected using MAS in Belleville, IL in 2011.

From data combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 three QTLs were identified for yield using R/qtl **(Table 3.27)**. Using MAS to select lines with the favorable allele for these QTLs, five lines were selected that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) and of those five lines three were in the top yielding 5 % of RILs combined over three environments **(Table 3.28)**. Lines 550 and 681 were among the top yielding 5 % of RILs combined over three environments selected and ranked 1^{st} and 5^{th} in yield, respectively. Using MAS to select lines with the unfavorable allele for the same three QTLs, three lines were identified in the bottom yielding 10 % of RILs combined over three environments and only one of those lines was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.29)**.

From the lines selected with the favorable allele for the two QTLs identified in Knoxville, TN in 2010 using MAS, two lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Belleville, IL in 2011) and one of those was in the top yielding 5 % of RILs combined over three environments **(Table 3.30)**. Additional credibility of yield QTL was demonstrated when four lines selected by MAS with the unfavorable alleles for the two QTLs identified in Knoxville, TN in 2010 were in the bottom yielding 10 % of RILs combined over three environments **(Table 3.31)**.

From the lines selected with the favorable alleles for the four QTLs identified in Belleville, IL in 2011 using MAS, six lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Belleville, IL in 2011) and two of those were in the top yielding 5 % of RILs combined over three environments **(Table 3.30)**. Lines 550 and 681 were the two lines selected in the top yielding 5 % of RILs combined over three environments and ranked 1st and 5th in yield, respectively. Four lines selected by MAS with the unfavorable alleles for the four QTLs identified in Belleville, IL in 2011 were in the bottom yielding 10 % of RILs combined over three environments and two of those were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.31)**. One of the two lines selected in the bottom yielding 5 % was 659 and it was the lowest yielding line averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011.

SAS

In 2010 in Knoxville, TN four QTLs were identified for yield using SAS **(Table 3.32)**. Using MAS to select lines with the favorable allele for these QTLs, three lines were selected that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and one of those three lines was in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.33)**. Using MAS to select lines with the unfavorable allele for the same four QTLs, three lines were selected in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.34)**.

In 2011 in Belleville, IL six QTLs were identified for yield using SAS **(Table 3.32)**. Using MAS to select lines with the favorable allele for these QTLs two lines were selected that were in the top yielding 5% of RILs grown in Belleville, IL in 2011 **(Table 3.33)**. Using MAS to select lines with the unfavorable allele for the same six QTLs, six lines were selected in the bottom yielding 10% of RILs grown in Belleville, IL in 2011 and five of those lines were in the bottom yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.34)**. Lines 659, 68, 398 and 132 were four of the five lines selected by MAS in the bottom yielding 5 % and were the four lowest yielding lines in Belleville, IL in 2011.

From data combined over Knoxville, TN in 2010, 2011 and Belleville, TN in 2011 eleven QTLs were identified for yield using SAS **(Table 3.32)**. Using MAS to select lines with the favorable allele for these QTLs four lines were selected in the top yielding 5 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Belleville, TN in 2011) and of which only one was in the top yielding 5 % of RILs combined over three environments **(Table 3.33)**. Using MAS to select lines with the unfavorable allele for the same elven QTLs, three lines were selected in the bottom yielding 10% of RILs combined over three environments and two of those lines were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.34)**.

From the top lines selected with the favorable allele for the four QTLs identified in Knoxville, TN in 2010 using MAS, three lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Belleville, TN in 2011) and one of those was in the top yielding 5 % of RILs combined over three environments **(Table 3.35)**. The one line selected in the top yielding 5 % was the top yielding line of RILs combined over three environments. Using MAS to select lines with the unfavorable allele for the same four QTLs identified in Knoxville, TN in 2010, four of the unfavorable allele MAS lines selected were in the bottom yielding 10 % of RILs combined over three environments and one of those was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.36)**. The one line selected in the bottom yielding 5 % was the lowest yielding line of RILs combined over three environments.

From the top lines selected with the favorable allele for the six QTLs identified in Belleville, IL in 2011 using MAS, two lines were in the top yielding 5 % of RILs combined over three environments (Knoxville, TN in 2010, 2011 and Belleville, TN in 2011) **(Table 3.35)**. Using MAS to select lines with the unfavorable allele for the same six QTLs identified in

Belleville, IL in 2011, four of the bottom lines selected were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.36)**.

In Group B an equal number of lines in the top yielding 10 % of RILs grown in the individual environments of Belleville, IL in 2011 and Knoxville, TN in 2010 were selected by MAS when using QTLs identified by SAS or R/qtl **(Table 3.33)**. However, all five lines selected by MAS with the favorable allele for the four QTLs identified in Belleville, IL in 2011 using R/qtl were in the top yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.28).** So, unlike Group A the environment with the more desirable growing conditions only had slightly better results using MAS. This may be because Knoxville, TN and Belleville, IL are less than a maturity group apart for soybean production, whereas Wooster, OH and Knoxville, TN are a full maturity group apart.

Using SAS 14 QTLs were detected on chromosomes 1, 2, 3, 5, 6, 7, 8, 9, 11, 15, 17, 18 and 19 (**Table 3.32**). Five QTLS were detected on chromosomes 2, 5, 6, 7 and 12 using R/qtl (**Table 3.27**). Marker Gm06_20996124_T_C (60.21 cM) was associated with a yield QTL in Belleville, IL in 2011 using R/qtl and in Knoxville, TN in 2010 (58.54 cM) and from data averaged across Knoxville, TN in 2010, 2011 and Belleville, IL in 2011 (58.54 cM) using SAS (**Table 3.27; Table 3.32**). Yield QTLs were also associated with Gm01_29787876_G_A (59.29 cM) and Gm_09_12463468_C_T (31.76 cM) in Belleville, IL in 2011 and from data averaged across all environments using SAS (**Table 3.32**). Like Group A more QTLs were discovered in all environments using SAS, but using R/qtl more top yielding lines were identified. This suggests R/qtl is better for identifying QTLs and MAS, which agrees with the results reported in Group A.

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010

R/qtl

In 2010 in Knoxville, TN seven QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.37)**. This information was used to develop an YPM to select by MAS high yielding lines in subsequent years. Seven lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.38)**. However, only five MAS lines from that YPM were in the top yielding 10 % of RILs grown in Belleville, IL in 2011 and of those only three lines were in the top yielding 5 % of RILs grown in Belleville, IL in 2011**,** but the MAS YPM did not select the highest yielding line in this environment **(Table 3.38)**. Seven lines that were in the top yielding 10 % of RILs grown over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) were selected by MAS using an YPM and of those four lines were in the top yielding 5 % of RILs grown over the three environments, including the top yielding line 550 **(Table 3.38)**.

Previously when using only additive effects identified using R/qtl in Knoxville, TN in 2010 for MAS (**Table 3.30**) without using additive by additive effects in an YPM; only two lines was selected in the top yielding 10 % of RILs grown over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 and only one line was selected in the top yielding 5 % of RILs grown over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 (**Table 3.30**).

SAS

In 2010 in Knoxville, TN five QTLs were shown to have a significant interaction with two of the QTLs identified for yield using SAS **(Table 3.40)**. This information was used to develop an

YPM to select by MAS the top yielding lines in subsequent years. Fourteen lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS and of those ten lines were in the top yielding 5 % of RILS grown in Knoxville, TN in 2011, including the top six yielding lines **(Table 3.39)**. Only three lines that yielded in the top yielding 5 % of RILs grown in Belleville, IL in 2011 were selected by MAS using an YPM **(Table 3.39)**. Ten lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) were selected by MAS using a YPM and of those seven lines were in the top yielding 5 % of RILs combined over three environments, including the top two yielding lines 550 and 676 **(Table 3.39)**.

Earlier when MAS was conducted using only additive effects detected using SAS in Knoxville, TN in 2010 (**Table 3.35**) with no additive by additive effects in an YPM; only three lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011) and of those only one line was in the top yielding 5 %, combined over three environments, but it was the top yielding line (550) (**Table 3.35**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Belleville, IL 2011

R/qtl

In 2011 in Belleville, IL 21 QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.37)**. This information was used to develop an YPM to select by MAS high yielding lines at other testing environments. Only four lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those two lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.41)**. This contrasted with the eighteen lines from that YPM that were in the top yielding 10 % of RILs grown in Belleville, IL in 2011 and of those nine lines were in the top 5 yielding % of RILs grown in Belleville, IL in 2011, including the two top yielding lines 65 and 172 **(Table 3.41)**. Twelve lines that were in the top yielding 10 % of RILs grown over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) were selected by MAS using an YPM and of those four lines were in the top yielding 5 % of RILs grown over three environments, including the top yielding line 550 **(Table 3.41)**.

Previously when using only additive effects identified using R/qtl in Belleville, IL in 2011 with no additive by additive effects in a YPM; five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) and of those only two lines were in the top yielding 5 % of RILs combined over three environments, including the top yielding line 550 (**Table 3.30**).

SAS

In 2011 in Belleville, IL thirteen QTLs were shown to have a significant interaction with three of the QTLs identified for yield using SAS **(Table 3.40)**. That information was used to develop an YPM to select by MAS the top yielding lines at other testing environments. Five lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected using MAS and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.42)**. Thirteen lines that were in the top yielding 10 % of RILs grown in Belleville, IL in 2011 were selected by MAS using an YPM and of those seven lines were in the top yielding 5 % of RILs grown in Belleville, IL in 2011, including the top three lines **(Table 3.42)**. Ten lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) were selected by MAS using an

YPM and of those six lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.42)**.

Earlier when MAS was conducted using only additive effects detected using SAS in Belleville, IL in 2011 (**Table 3.35**) with no additive by additive effects in an YPM; only two lines were selected in the top yielding 5 % of RILs grown over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 (**Table 3.35**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010, 2011 and Bellville, IL 2011

R/qtl

From data averaged across Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 sixteen QTLs were shown to have a significant interaction with three of the QTLs identified for yield using R/qtl **(Table 3.37)**. This information was used to develop an YPM to select by MAS high yielding lines in different environments. Eight lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using a YPM and of those five lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, including three of the top five yielding lines **(Table 3.43)**. Eleven lines were selected by MAS using a YPM in the top yielding 10 % of RILs grown in Belleville, IL in 2011 and of those seven lines were in the top yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.43)**. Eleven lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) and of those five lines were in the top yielding 5 % of RILs grown over three environments **(Table 3.43)**.

Previously when using only additive effects identified using R/qtl combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011 for MAS (**Table 3.30**) without using epistatic effects in an YPM; five lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 and of those three lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011, including the top yielding line 550 (**Table 3.30**).

SAS

From data averaged across Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 27 QTLs were shown to have a significant interaction with seven of the QTLs identified for yield using SAS **(Table 3.40)**. This information was used to develop an YPM to select by MAS the top yielding lines in different environments. Five lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.44)**. Eleven lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown in Belleville, IL in 2011 and of those six lines were in the top yielding 5 % of RILs grown in Belleville, IL in 2011 **(Table 3.44)**. Seven lines that yielded in the top 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011) were selected by MAS using an YPM and of those four lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.44)**.

Previously when MAS was accomplished using only additive effects detected using SAS combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 (**Table 3.35**) without using epistatic effects in an YPM; only four lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 and of those three were in the top yielding 5 % combined over Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011 (**Table 3.35**).

Using the YPM more lines were selected than using only additive QTL MAS in Group B as in Group A. When using data combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011 in the YPM similar results were seen using QTLs identified by R/qtl as when using QTLs identified by SAS. So, in some instances similar selections were seen when using QTLs identified by SAS and R/qtl. However, when using data collected in the individual environments of Knoxville, TN in 2010 and Belleville, IL in 2011 in the YPM more top yielding lines were selected in their respective individual environment using QTLs identified by R/qtl. So, overall R/qtl was the best program to use for identifying yield QTLs to be used in the YPM.

Group C: Agronomic Traits

The effect and contribution of each source of variation to yield was evaluated through a combined analysis of variance over all environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) (**Table 3.45**), in Knoxville, TN in 2011 (**Table 3.46**) and in Portageville, MO in 2011 (**Table 3.47**). The environmental effect explained a significant ($P<0.001$) amount of variation in the model when all environments were evaluated (**Table 3.45**). Genotypes were also highly significant ($P<0.0001$) (**Table 3.45**). At the individual environments, genotypes were significant at Knoxville, TN in 2011 ($P<0.05$) and highly significant at Portageville, MO in 2011 ($P<0.0001$) (**Table 3.46; Table 3.47**). The genotype effect was similar in Knoxville, TN in 2010 and Portageville, MO in 2011. The maturity of Group C ranged from an early MG IV to a late MG IV, which are well adapted to Portageville, MO and Knoxville, TN (Sleper, 2006). However, Portageville, MO has growing conditions similar to Milan, TN and in the 2011 Tennessee State Variety Test (TSVT) Milan, TN had higher yields than those in Knoxville, TN in 2011 (Allen, 2011) which supports our observation of higher yield in Portageville, MO then Knoxville, TN.

In Group C, Portageville, MO had an average yield (3810 kg ha^{-1}) that was significantly ($p<0.01$) higher than the average yield in Knoxville, TN in 2010 (2188 kg ha^{-1}) and 2011 (1915 kg ha^{-1}) **(Table 3.48)**. Average maturity was significantly different between Portageville, MO in 2011 (281) and Knoxville, TN in 2011 (271), but no significant difference was seen between Knoxville, TN in 2010 (274) and Knoxville, TN in 2011 (271) or between Knoxville, TN in 2010 (274) and Portageville, MO in 2011 (281) **(Table 3.48).**

Group C: QTL Results

R/qtl

In 2010 in Knoxville, TN three QTLs were identified for yield using R/qtl **(Table 3.49)**. Using MAS to select lines with the favorable allele for these QTLs, six lines were selected that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those six lines three were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.50)**. To further validate allele effectiveness MAS was conducted to target reduced yield; five lines selected by MAS using the unfavorable allele for the three QTLs were in the bottom yielding 10% of RILs grown in Knoxville, TN in 2010 and three of those lines were in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.51)**.

In 2011 in Portageville, MO three QTLs were identified for yield using R/qtl **(Table 3.49)**. Using MAS to select lines with the favorable allele for these QTLs fives lines were selected that were in the top yielding 10 % of RILs grown in Portageville, MO in 2011 **(Table 3.50).** One of those five lines was line 263 and ranked 3^{rd} in yield. Using MAS to select lines with the unfavorable allele for the same three QTLs, five lines were selected in the bottom yielding 10 % of RILs grown in Portageville, MO in 2011 and of those one was in the bottom yielding 5 % of RILs grown in Portageville, MO in 2011, which was the 2nd lowest yielding line (982) **(Table 3.51)**.

From data combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 three QTLs were identified for yield using R/qtl **(Table 3.49)**. Using MAS to select lines with the favorable allele for these QTLs, five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those five lines two were in the top yielding 5 % of RILs combined over three environments **(Table 3.50)**. Line 378 was among the lines selected in the top yielding 5 % of RILs combined over three environments and ranked 4th in yield. Using MAS to select lines with the unfavorable allele for the same three QTLs, three lines were selected in the bottom yielding 10 % of RILs combined over three environments and two of those lines were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.51)**. Lines 953 and 540 were the two lines selected in the bottom yielding 5 % of RILs combined over three environments and were the 2nd and 3rd lowest yielding lines, respectively.

From the lines selected with the favorable allele for the three QTLs identified in Knoxville, TN in 2010 using MAS, three lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those one was in the top yielding 5 % of RILs combined over three environments **(Table 3.52)**. Further credibility of the yield QTL was demonstrated when four lines selected with the unfavorable alleles for the three QTLs identified in Knoxville, TN in 2010 using MAS were in the bottom yielding 10 % of RILs combined over three environments and of those one line was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.53)**.

From the lines selected with the favorable alleles for the three QTLs identified in Portageville, MO in 2011 using MAS, three lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those two were in the top yielding 5 % of RILs combined over three environments **(Table 3.52)**. Lines 263 and 378 were among the top yielding 5 % of RILs combined over three environments selected and ranked 3rd and 4th in yield, respectively. Three lines selected by MAS with the unfavorable allele for the same three QTLs identified in Portageville, MO in 2011 were in the bottom yielding 10 % of RILs combined over three environments and of those one was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.53)**.

SAS

In 2010 in Knoxville, TN six QTLs were identified for yield using SAS **(Table 3.54)**. Using MAS to select lines with the favorable allele for these QTLs, two lines were selected that were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010. One of those lines selected in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 was 760 and ranked 2nd in yield **(Table 3.55)**. Using MAS to select lines with the unfavorable allele for the same six QTLs, five lines were selected in the bottom yielding 10 % of RILs grown in Knoxville, TN in 2010 and only one of those lines were in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.56)**.

In 2011 in Portageville, MO five QTLs were identified for yield using SAS **(Table 3.54)**. Using MAS to select lines with the favorable allele for these QTLs six lines were selected that were in the top yielding 10 % of RILs grown in Portageville, MO in 2011 and of those three were in the top yielding 5 % of RILs grown in Portageville, MO in 2011 **(Table 3.55)**. Lines 352 and 263 were among the lines selected in the top yielding 5 % of RILs grown in that environment and ranked 2nd and 3rd in yield, respectively **(Table 3.55)**. Using MAS to select lines with the unfavorable allele for the same five QTLs, six lines were selected in the bottom yielding 10 % of RILs grown in Portageville, MO in 2011 and three of those lines were in the bottom yielding 5 % of RILs grown in Portageville, MO in 2011 **(Table 3.56)**. Lines 982 and 649 were selected in the bottom yielding 5 % of RILs grown in Portageville, MO in 2011 and were the 2nd and 3rd lowest yielding lines, respectively **(Table 3.56)**.

From data combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 ten QTLs were identified for yield using SAS **(Table 3.54)**. Using MAS to select lines with the favorable allele for these QTLs, four lines were selected that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those one line was in the top yielding 5 % of RILs combined over three environments **(Table 3.55)**. Line 450 was selected in the top yielding 5 % of RILs combined over three environments and ranked 2nd highest in yield. Using MAS to select lines with the unfavorable allele for the same ten QTLs, three lines were selected in the bottom yielding 5 % of RILs combined over three environments **(Table 3.56)**.

From the top lines selected with the favorable allele for the six QTLs identified in Knoxville, TN in 2010 using MAS, five lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and two were in the top yielding 5 % of RILs combined over three environments **(Table 3.57)**. Lines 450 and 263 were selected in the top yielding 5 % of RILs combined over three environments, which ranked 2nd and 3rd in yield, respectively **(Table 3.57).** Using MAS to select lines with the unfavorable allele for the same six QTLs, four lines were selected in the bottom yielding 10 % of

RILs combined over three environments and of those three were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.58)**.

From the lines selected with the favorable alleles for the five QTLs identified in Portageville, MO in 2011 using MAS, two lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those one line was in the top yielding 5 % of RILs combined over three environments **(Table 3.57)**. The one line in the top yielding 5 % was line 263 and it was the 3rd highest yielding line combined over environments **(Table 3.57).** Two lines selected by MAS with the unfavorable allele for the same five QTLs identified in Portageville, MO in 2011 were in the bottom yielding 10 % of RILs combined over three environments and of those one was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.58)**.

Seventeen QTLs were detected on chromosomes 1, 2, 3, 5, 6, 7, 9, 11, 12, 13, 16, 18 and 20 using SAS (**Table 3.54**). Using R/qtl seven QTLs were detected on chromosomes 1, 2, 6, 9, 13, 16 and 19 (**Table 3.49**). Although, the yields were higher in Portageville, MO in 2011 than in Knoxville, TN in 2010 similar selections were made by MAS in both environments **(Tables 3.50, 3.51)**. This may be because both Knoxville, TN and Portageville, MO are in the same maturity zone for growing soybeans and are equally adapted for the maturity of Group C. Again, a similar number of top yielding lines were selected by MAS for the favorable allele of the QTLs identified using SAS as MAS for the favorable allele of the QTLs identified using R/qtl in certain instances. However, like in Groups A and B more top yielding lines averaged overall were selected by MAS for the favorable allele of the QTLs identified using R/qtl. In addition, these results agree with the results from Groups A and B that suggest MAS produces better results when using an environment that is adaptable for the maturity group of the soybean.

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010

R/qtl

In 2010 in Knoxville, TN eight QTLs were shown to have a significant interaction with one of the QTLs identified for yield using R/qtl **(Table 3.59)**. This information was used to develop an YPM to select by MAS high yielding lines in subsequent years. Fourteen lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those eight lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, including the top 5 lines **(Table 3.60)**. However, only six MAS lines from that YPM were in the top yielding 10 % of RILs when grown in Portageville, MO in 2011 and yet two of those lines were in the top yielding 5 % of RILs, including the highest yielding line (213) in that environment **(Table 3.60)**. Twelve lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs combined over three environments, including the top two yielding lines 213 and 450 **(Table 3.60)**.

Previously when using only additive effects identified using R/qtl in Knoxville, TN in 2010 for MAS (**Table 3.52**) without using additive by additive effects in an YPM; only three lines were selected in the top yielding 10 % of RILs grown over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 (**Table 3.52**).

SAS

In 2010 in Knoxville, TN fifteen QTLs were shown to have a significant interaction with three of the QTLs identified for yield using SAS **(Table 3.62)**. This information was used to develop an YPM to select by MAS the top yielding lines in subsequent years. Eight lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011were selected by MAS using an YPM and of those five lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 (**Table 3.61)**. Only one line was selected by MAS using an YPM in the top 10 % of RILs grown in Portageville, MO in 2011 **(Table 3.61)**. Six lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by MAS using an YPM and of those only two lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.61)**.

Earlier when MAS was conducted using only additive effects detected using SAS in Knoxville, TN in 2010 (**Table 3.57**) without the benefit of using an YPM containing epistasis; only five lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) and of those only two lines were in the top yielding 5 % combined over three environments (**Table 3.57**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Portageville, MO 2011

R/qtl

In 2011 in Portageville, MO five QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.59)**. This information was used to develop an YPM to select by MAS high yielding lines at other testing environments. Only four lines that were in the top yielding 10 % of RILs grown in Knoxville, TN 2011 were selected by MAS using an YPM from Portageville, MO 2011 data and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.63)**. This contrasted with the eighteen lines from that YPM that were in the top yielding 10 % of RILs grown in Portageville, MO in

2011 and of those nine lines were in the top yielding 5 % of RILs grown in Portageville, MO in 2011, including the four top yielding lines **(Table 3.63)**. Moreover, the single environment MAS results were not as effective as multi-environment MAS where eleven lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by MAS using an YPM and of which six lines were in the top yielding 5 % of RILs combined over three environments, including the top yielding line 213 **(Table 3.63)**.

Previously when using only additive effects identified using R/qtl in Portageville, MO without using additive effects in an YPM; three lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 and of those two lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011(**Table 3.52**).

SAS

In 2011 in Portageville, MO twelve QTLs were shown to have a significant interaction with three of the QTLs identified for yield using SAS **(Table 3.62)**. This information was used to develop an YPM to select by MAS the top yielding lines at other testing environments. Five lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those three lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.64)**. Nine lines were in the top yielding 10 % of RILs grown in Portageville, MO in 2011 were selected by MAS using an YPM and of those seven lines were in the top yielding 5 % of RILs grown in Portageville, MO in 2011, including the top four lines **(Table 3.64)**. Eleven lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by

MAS using an YPM and of those seven lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.64)**.

Earlier when MAS conducted using only additive effects detected using SAS in Portageville, MO in 2011 (**Table 3.57**) without the benefit of using an YPM containing epistasis; only two lines was selected in the top yielding 10 % combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 in the top 10 % and one line in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 (**Table 3.57**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010 and 2011 and Portageville, MO 2011

R/qtl

From data averaged across Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 two QTLs were shown to have a significant interaction with one of the QTLs identified for yield using R/qtl **(Table 3.59)**. This information was used to develop an YPM to select by MAS high yielding lines in the individual environments. Nine lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and six of which were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, including the top three yielding lines **(Table 3.65)**. Eleven lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown in Portageville, MO in 2011 and of those seven lines were in the top yielding 5 % of RILs grown in Portageville, MO in 2011 **(Table 3.65)**. Seventeen lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by MAS using an YPM and of those nine lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.65)**.

Previously when using only additive effects identified using R/qtl combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 without using epistatic effects in an YPM; five lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011and of those two lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 (**Table 3.52**).

SAS

From data averaged across Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 eighteen QTLs were shown to have a significant interaction with six of the QTLs identified for yield using SAS **(Table 3.62)**. This information was used to develop an YPM to select by MAS the top yielding in individual environments. Nine lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.66)**. Ten lines that were in the top yielding 10 % of RILs grown in Portageville, MO in 2011 were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILS grown in Portageville, MO in 2011 **(Table 3.66)**. Sixteen lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011) were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.66)**.

Previously when MAS was accomplished using only additive effects identified using SAS combined over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011 (**Table 3.57**) without using epistatic effects in an YPM; only four lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011 and of those only one line was in the top yielding 5 % of RILs combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011 (**Table 3.57**).

Like in Groups A and B, in Group C more top yielding lines were selected using the YPM than using only additive effects for MAS. In Group C, when using the Knoxville, TN 2010 data to develop an YPM a considerable number of top yielding lines in Knoxville, TN in 2011 were selected by MAS. Using the YPM 63% of the top yielding 10 % of RILs grown in Knoxville, TN in 2011 and 72 % of the top yielding 5 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using QTLs identified by R/qtl from data collected in Knoxville, TN in 2010. This is important to note because when using an YPM it is important for selections made in one year to carry forth into subsequent years. While, this YPM does not predict 100% of the top yielding lines from one year to the next it does prove yield predictions using genotypic data warrants further study.

Group D: Agronomic Traits

The effect and contribution of each source of variation to yield was evaluated through a combined analysis of variance over all environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) (**Table 3.67**), in Knoxville, TN in 2011 (**Table 3.68**) and in Plymouth, NC in 2011 (**Table 3.69**). Genotypes were significant when all environments were evaluated ($P<0.001$) and at the individual environments of Knoxville, TN in 2011 ($P<0.01$) and Plymouth, NC in 2011 ($P<0.001$) (**Table 3.67; Table 3.68; Table 3.69**). The genotype effect was similar in Knoxville, TN in 2011 and Plymouth, NC in 2011. This may be due to the adapted maturity of Group D to both environments and the statistically similar yields between both environments.

In Group D, Plymouth, NC (2191 kg ha^{-1}) did not have significantly ($p<0.05$) different yields than Knoxville, TN in 2010 (2354 kg ha^{-1}) and in 2011 (1720 kg ha^{-1}) **(Table 3.70)**. So, unlike Groups A, B and C all growing environments had significantly similar yields in Group D. These results would be expected because the maturity of Group D ranged from an early MG V to a late MG V, which are similarly adapted to Knoxville, TN and Plymouth, NC (Sleper, 2006). Average lodging, height and maturity were also not significantly different across locations. **(Table 3.70).**

Group D: QTL Results

R/qtl

In 2010 in Knoxville, TN three QTLs were identified for yield using R/qtl **(Table 3.71)**. Using MAS to select lines with the favorable allele for these QTLs, seven lines were selected in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those seven lines four were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.72)**. Lines 94 and 766 were among the lines selected in the top yielding 5 % of RILs grown in that environment and ranked 2nd and 5th in yield, respectively. Conversely when MAS was conducted to target reduced yield to demonstrate allele effectiveness; three lines selected by MAS using the unfavorable allele for the same three QTLs were in the bottom yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those two lines were in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.73)**. Lines 850 and 719 were among the two lines selected in the bottom 5 % in that environment and ranked as the lowest and forth lowest yielding lines out of 222 lines.

In 2011 in Plymouth, NC three QTLs were identified for yield using R/qtl **(Table 3.71)**. Using MAS to select lines with the favorable allele for these QTLs seven lines were selected in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 and of those lines four were in the top yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.72).** One of those four lines (216) was in the top 5 and ranked 2nd in yield. Using MAS to select lines with the unfavorable allele for the same three QTLs, six lines were selected in the bottom yielding 10 % of RILs grown in Plymouth, NC in 2011 and of those five were in the bottom yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.73)**. MAS lines 770, 647 and 989, for the unfavorable allele were the three lowest yielding lines in that environment.

From data combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 three QTLs were identified for yield using R/qtl **(Table 3.71)**. Using MAS to select lines with the favorable allele for these QTLs, three lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those three lines only one line was in the top yielding 5 % of RILs combined over three environments **(Table 3.72)**. Using MAS to select lines with the unfavorable allele for the same three QTLs, six lines were selected in the bottom yielding 10 % of RILs combined over three environments and only one those lines were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.73)**.

From the lines selected with the favorable allele for the three QTLs identified in Knoxville, TN in 2010 using MAS, three lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those one was in the top yielding 5 % of RILs combined over three environments **(Table 3.74)**. Using MAS to select lines with the unfavorable allele for the same three QTLs, only one line was selected in the bottom yielding 5 % **(Table 3.75)**.

From the lines selected with the unfavorable alleles for the three QTLs identified in Plymouth, NC in 2011 using MAS, six lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those two were in the top yielding 5 % of RILs combined over three environments **(Table**

3.74). Only one line selected by MAS with the unfavorable alleles for the three QTLs identified in Plymouth, NC in 2011 was in the bottom yielding 5 % of RILs averaged over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011 **(Table 3.75)**.

SAS

In 2010 in Knoxville, TN five QTLs were identified for yield using SAS **(Table 3.76)**. Using MAS to select lines with the favorable allele for these QTLs, eight lines were selected in the top yielding 10 % of RILs grown in Knoxville, TN in 2010 and of those eight lines five were in the top yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.77)**. Lines 94 and 491 were selected in the top yielding 5 % of RILs in that environment and ranked 2nd and 4th in yield, respectively. Using MAS to select lines with the unfavorable allele for the same five QTLs, three lines were selected in the bottom yielding 10 % of RILs grown in Knoxville, TN in 2010 and two of those lines were selected in the bottom yielding 5 % of RILs grown in Knoxville, TN in 2010 **(Table 3.78)**. 719 was one of the two lines selected in the bottom yielding 5 % of RILs in that environment and was the lowest yielding line in Knoxville, TN in 2010.

In 2011 in Plymouth, NC six QTLs were identified for yield using SAS **(Table 3.76)**. Using MAS to select lines with the favorable allele for these QTLs five lines were selected in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 and three of those lines were in the top yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.77)**. The 2nd (216) and 4th (122) ranking lines were selected in the top yielding 5 % of RILs grown in that environment. Using MAS to select lines with the unfavorable allele for the same six QTLs, five lines were selected in the bottom yielding 10 % of RILs grown in Plymouth, NC in 2011 and three of those lines were in the bottom yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.78)**.

The lowest yielding line (770) and the 3rd lowest yielding line (989) were selected in the bottom yielding 5 % of RILs grown in that environment.

From data combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 nine QTLs were identified for yield using SAS **(Table 3.76)**. Using MAS to select lines with the favorable allele for these QTLs, four lines were selected in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those three were in the top yielding 5 % of RILs combined over three environments **(Table 3.77)**. Using MAS to select lines with the unfavorable allele for the same nine QTLs, two lines were selected in the bottom yielding 5 % of RILs combined over three environments **(Table 3.78)**. Line 648 was one of the two lines selected in the bottom yielding 5 % of RILs in that environment and was the lowest yielding line.

From the top lines selected with the favorable allele for the five QTLs identified in Knoxville, TN in 2010 using MAS, three lines were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those one was in the top yielding 5 % of RILs combined over three environments **(Table 3.79)**. Using MAS to select lines with the unfavorable allele for the same five QTLs identified in Knoxville, TN in 2010, two lines selected were in the bottom yielding 10 % of RILs combined over three environments and of those one was in the bottom yielding 5 % of RILs combined over three environments **(Table 3.80)**.

From the lines selected with the favorable alleles for the six QTLs identified in Plymouth, NC in 2011 using MAS, two lines were in the top yielding 5 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) **(Table 3.79)**. Line 81 was one of the lines selected in the top yielding 5 % of RILs in that environment and yielded

2nd averaged over all environments. Three bottom lines selected with the unfavorable allele for the same six QTLs identified in Plymouth, NC in 2011 were in the bottom yielding 10 % of RILs combined over three environments and of those two were in the bottom yielding 5 % of RILs combined over three environments **(Table 3.80)**.

In Group D more top yielding lines were selected by MAS in the individual environments (Knoxville, TN in 2010 and Plymouth, NC in 2011) than by MAS averaged across environments (Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011) using QTLs identified using SAS and R/qtl. Also, more bottom yielding lines were selected by MAS in the individual environments than by MAS averaged across environments using R/qtl.

In all four groups R/qtl was the best program to use because a genetic map can be produced, the program is more user friendly and fewer, more significant QTLs were identified, which improved selections. However, high yielding selections were made using both programs in all groups in all environments, including top yielding lines. In both programs more high yielding selections were made from the individual environment best adaptable for the maturity group.

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010

R/qtl

In 2010 in Knoxville, TN seven QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.81)**. This information was used to develop an YPM to select by MAS high yielding lines in subsequent years. Twelve lines were selected by MAS using an YPM in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 and of those six lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, including the top 4 yielding lines **(Table 3.82)**. However, only one MAS line from that YPM was in the top yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.82)**. Six lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) were selected by MAS using an YPM and of those four lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.82)**.

Earlier when MAS was conducted using only additive effects detected using R/qtl in Knoxville, TN in 2010 (**Table 3.74**) without the benefit of using an YPM containing epistasis; only three lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 and of those two lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.74**).

SAS

In 2010 in Knoxville, TN only two QTLs were shown to have a significant interaction with two of the QTLs identified for yield using SAS **(Table 3.84)**. This information was used to develop an YPM to select by MAS the top yielding lines in subsequent years. Eleven lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 (**Table 3.83)**. However, only one MAS line from that YPM was in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 **(Table 3.83)**. Eight lines that were in the top yielding 10 % were selected by MAS using an YPM combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those five lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.83)**.

Previously when using only additive effects identified using R/qtl in Knoxville, TN in 2010 for MAS (**Table 3.79**) without using additive by additive effects in an YPM; only three lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011and of those only one line was in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.79**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Plymouth, NC 2011

R/qtl

In 2011 in Plymouth, NC six QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.81)**. This information was used to develop an YPM to select by MAS high yielding lines at other environments. Five lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those four lines were in the top yielding 5 % of RILs grown in Knoxville, TN in 2011, which were the top four yielding lines **(Table 3.85)**. Thirteen lines that were in the top yielding 10 % grown in Plymouth, NC in 2011 were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.85)**. Nine lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those five lines were in the top yielding 5 % of RILs combined over three environments **(Table 3.85)**.

Previously when using only additive effects detected using R/qtl in Plymouth, NC in 2011 (**Table 3.74**) without using additive by additive effects in an YPM; six lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 and of those two lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.74**).

SAS

In 2011 in Plymouth, NC six QTLs were shown to have a significant interaction with four of the QTLs identified for yield using SAS **(Table 3.84)**. That information was used to develop an YPM to select by MAS the top yielding lines at other testing environments. No lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM **(Table 3.86)**. This contrasted with the sixteen lines from that YPM that were in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 and of those eight lines were in the top yielding 5 % of RILs grown in Plymouth, NC in 2011, including the top four lines **(Table 3.86)**. Moreover, only four lines from that YPM were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) and of those two lines were in the top yielding 5 % combined over three environments **(Table 3.86)**.

Previously when using only additive effects detected using SAS in Plymouth, NC in 2011 (**Table 3.79**) without the benefit of using an YPM containing epistasis; only two lines were selected in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.79**).

YPM: Including Mean Yield, Additive and Additive by Additive Effects from Knoxville, TN 2010 and 2011 and Plymouth, NC 2011

R/qtl

From data averaged across Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 five QTLs were shown to have a significant interaction with two of the QTLs identified for yield using R/qtl **(Table 3.81)**. This information was used to develop an YPM to select by MAS high yielding lines in different environments. Eleven lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and of those seven lines were in the top 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.87)**. Only three lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 and of those two lines were in the top 5 % of RILs grown in Plymouth, NC in 2011 **(Table 3.87)**. Fourteen lines that yielded in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) were selected by MAS using an YPM and of those nine lines were in the top yielding 5 % of RILs combined over three environments, including the top five yielding lines **(Table 3.87)**.

Previously when using only additive effects identified using R/qtl combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.74**) without using epistatic effects in an YPM; three lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 and of those only one line was in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.74**).

SAS

From data averaged across Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 seventeen QTLs were shown to have a significant interaction with six of the QTLs identified for yield using SAS **(Table 3.84)**. This information was sued to develop an YPM to select by MAS the top yielding lines in different environments. Only two lines that were in the top yielding 10 % of RILs grown in Knoxville, TN in 2011 were selected by MAS using an YPM and one line was in the top yielding 5 % of RILs grown in Knoxville, TN in 2011 **(Table 3.88)**. Eleven lines were selected by MAS using an YPM that were in the top yielding 10 % of RILs grown in Plymouth, NC in 2011 and of those eight lines were in the top yielding 5 % of RILs grown in

Plymouth, NC in 2011 **(Table 3.88)**. Ten lines that were in the top yielding 10 % of RILs combined over three environments (Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011) were selected by MAS using an YPM and of those six lines were in the top yielding 5 % of RIlLs combined over three environments **(Table 3.88)**.

Previously when MAS was accomplished using only additive effects identified using SAS combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.79**) without using epistatic effects in an YPM; only four lines were selected in the top yielding 10 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 and of those three lines were in the top yielding 5 % of RILs combined over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011 (**Table 3.79**).

Like in Groups A, B and C, in Group D more top yielding lines were selected using the YPM than using only additive QTL MAS. Also, in Group D when using data collected in one individual environment in the YPM very few top yielding lines were selected in another individual environment even though the environments were similar in latitude.

Discussion

In this study generally predictions made from an individual environment for targeted use in that environment were better than data averaged from across environments if one environment was more adaptable to the soybean maturity group. If the environments were similar for adapted maturity, a multi-environment YPM was best for predicting top yielding lines in multiple individual environments. Bernardo et al. (2008) proposed that if the early generation test environments are not representative of the targeted population of environments, then this might not be predictive of genotypes that are favorable across the broader sample of environments encountered in subsequent replicated trials. Sebastian et al. (2008) suggested environments with high error variance or environments suspected to be unrepresentative of the targeted environment should be excluded from the QTL analysis so that more valid QTL estimates can be obtained to construct the favorable genotype. This agrees with the results found in this study where the environment most adaptable to the maturity group made the best predictions.

A yield QTL was identified on chromosome 1 associated with marker Gm01_1494600_C_T (5.52 cM) using SAS and marker Gm01_1045893_G_A (5.88 cM) using R/qtl (**Table 3.89)**. Also, markers Gm01_1241762_A_C (4.6 cM) and Gm01_2747136_A_C (11.28 cM) were identified using SAS and associated with the same yield QTL. Two other yield QTLs were identified using SAS further down the chromosome near markers Gm01_29787876_G_A (59.29 cM) and Gm01_47115450_G_T (70.15 cM) and Gm01_54171147_G_T (118.27 cM) (**Table 3.89)**. Kabelka et al. (2004) conducted a QTL study with three maturity groups (MG II, MG III and MG IV) and in MG IV they detected a QTL for seed yield on chromosome 1 (position not reported). Smalley et al. (2004) reported three yield QTLs on chromosome 1 in regions similar to the ones reported in this study. The objective of their study was to identify QTL for yield in elite and PI germplasm using three populations that differed in their percent of PI parentage. They reported three yield QTLs significantly associated with markers Satt184 (8.3 cM), Satt368 (41.1 cM) and Satt436 (89.3 cM), respectively.

In Group A a yield QTL on chromosome 2 was identified in each individual environment and across all environments using SAS. SAS linked this yield QTL to markers Gm02_47790307_C_T (121.66 cM) and Gm02_49126947_T_C (127.25 cM) in Group A. The same QTL was also associated with markers Gm02_44803277_C_T (107.06 cM) using SAS in Group C. R/qtl linked it to marker Gm02_44803277_C_T (114.09 cM) and Gm02_42469280_A_C (105.17 cM) (**Table 3.89)**. A yield QTL was also identified on chromosome 2 near marker Gm02_49746270_A_G (146.54 cM) using SAS and Gm02_47790307_C_T (150.38 cM) using R/qtl. Another yield QTL on chromosome 2 was linked to marker Gm02_12770553_A_G (46.15 cM) using SAS and markers Gm02_6821311_A_C (38.24 cM) and Gm02_6820177_A_C (38.07 cM) using R/qtl. Smalley et al. (2004) reported a yield QTL on chromosome 2 linked to marker Satt 141 (52.8 cM) and Du et al (2009) reported a yield QTL near marker Satt546 (110 cM) on chromosome 2 in a RIL population from a cross between Kefeng1 and Nannong 1138-2.

On chromosome 3 only two QTLs were identified with both SAS and R/qtl. SAS identified these QTLs near markers Gm03_5264953_A_G (19.43 cM) and Gm03_39552601_T_C (87.68 cM) (**Table 3.89)**. R/qtl identified these QTLs near markers Gm03_2151432_A_G (14 cM) and Gm03_39559139_G_A (93.64 cM). Smalley et al (2004) detected two yield QTLs linked to markers Satt152 (16.3 cM) and Satt_091 (95.5 cM). In our study SAS also identified three yield QTLs associated with markers Gm03_47386481_A_C (120.71 cM), Gm03_838582_T_C (4.68 cM) and Gm03_21003884_A_G (44.15 cM). Smalley et al. (2004) also reported a yield QTL linked to marker Satt584 (35.4 cM), but no studies have reported any yield QTL in the region around the other two markers we identified using SAS.

A yield QTL on chromosome 4 was identified in both Knoxville, TN in 2010 and Wooster, OH in 2011 in Group A using R/qtl near markers Gm04_48782140_G_T (152.98 cM) and Gm04_48993297_T_G (154.16 cM), respectively. Another yield QTL on chromosome 4 was identified in both in Knoxville, TN in 2010 and across Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011 in Group D using SAS near markers Gm04_8247949_C_T (65.87 cM) and Gm04_8845668_G_T (63.93 cM), respectively (**Table 3.89)**. Guzman et al. (2007) identified a yield QTL on chromosome 4 associated with marker Satt399 (76.2 cM), which is the same region where Yuan et al. (2002) mapped a QTL in an Essex x Forrest cross. Yuan et al. (2002) reported that the yield QTL was only detected in one of four environments, while Guzman et al. reported the yield QTL was detected across four environments in 2004 and averaged across 2003 and 2004. Three yield QTLs on chromosome 4 were also identified by Smalley et al. (2004) near markers Satt578 (74 cM), Satt294 (105 cM) and Satt338 (173 cM). The location of these markers and the one reported in this study indicates that there may be a large region on chromosome 4 responsible for yield QTL.

Markers Gm05_31399360_G_A (41.55 cM), Gm05_30953466_G_T (39.76 cM) using SAS and Gm05_33176582_G_A (33.77 cM) using R/qtl were linked to a yield QTL on chromosome 5 (**Table 3.89)**. The yield QTL on chromosome 5 by Guzman et al. (2007) was near marker Satt300 (30.9 cM) in 2003, 2004 and across years. SAS also identified a yield QTL on chromosome 5 linked to marker Gm05_1128604_A_G (3.24 cM) and a yield QTL linked to marker Gm05_34850619_C_T (72.38 cM). R/qtl identified one additional QTL associated with marker Gm05_3485480_T_C (19.73 cM). A yield QTL linked to Satt276 (5.1 cM) and another yield QTL linked to markers Satt385 (69.9 cM) and Satt545 (75.3 cM) were reported by Smalley et al. (2004).

Satt557 (112.5 cM) was detected in 2003, 2004 and across years by Guzman et al. (2007) to be linked to a yield QTL on chromosome 6. However, they only reported marker Satt640 (30.5 cM) was linked to yield QTL on chromosome 6 in 2003. Specht et al. (2001) reported a yield QTL linked to marker Satt281 (43.6 cM) on chromosome 6, which was 10 cM from Satt640 (30.5 cM) reported by Guzman et al. in 2007. Smalley et al (2004) reported a yield QTL linked to Sat_062 (29.2 cM). These finding agree with the yield QTLs linked to marker Gm06_10864751_A_G (24.86 cM) found in Portageville, MO in 2011 using SAS and marker

Gm06_16723946_G_A (32.46 cM) found across environments using R/qtl in Group C in our study. Another yield QTL was found in Group B in both individual environments and across environments using both SAS and R/qtl associated with markers Gm06_17617727_G_T (55.04 cM), Gm06_20996124_T_C (60.21 cM) and Gm06_20996124_T_C (62.03 cM) identified using R/qtl and Gm06_20996124_T_C (58.54 cM) and Gm06_27540819_T_G (66.24 cM) identified using SAS. Kabelka et al. (2004) only reported one yield QTL on chromosome 6 and it was detected across three maturity groups (MG II, MG III and MG IV) and averaged over twelve environments.

Two yield QTLs on chromosome 7 have been reported by Specht et al. (2001) near markers Satt150 (17.6 cM) and Satt567 (36.2 cM) and Smalley et al. (2004) reported two yield QTLs near markers Satt 590 (12.4 cM) and Satt567 (45.5 cM). Orf et al. (1999) also reported a yield QTL near Satt150 (16.1 cM). In this study one yield QTL was identified using SAS linked to marker Gm07_4837493_A_G (11.06 cM) and marker Gm07_149664_T_C (1.34 cM) and marker Gm07_4008483_C_T (5.19 cM) using R/qtl (**Table 3.89)**. Another yield QTL was linked to makers Gm07_17460956_C_A (39.95 cM), Gm07_16814628_C_T (38.47 cM) and Gm07_18539902_T_G (42.42 cM) using SAS and Gm07_16144523_C_A (51.90 cM), Gm07_17362808_A_G (55.95 cM) and Gm07_18539902_T_G (61.37 cM) using R/qtl.

Only one yield QTL was identified on chromosome 8 using SAS and it was linked to Gm08_15866777_G_A (22.31 cM) (**Table 3.89)**. No QTLs were found using R/qtl. Smalley et al. (2004) linked Satt493 (23.3 cM) to a yield QTL on chromosome 8, but no other studies were found that reported a yield QTL on chromosome 8.

Yuan et al. (2002), Kabelka et al. (2004) and Smalley et al. (2004) reported yield QTL near marker Satt119 (20.3 cM) on chromosome 9. In this study a yield QTL was mapped near markers Gm09_18969901_T_C (28.52 cM) detected using R/qtl and Gm09_12463468_C_T (31.76 cM) detected using SAS. Guzamn et al. (2007) reported a yield QTL across 2003 and 2004 linked to Satt046 (45.6 cM) on chromosome 9. Smalley et al. (2004) and Yuan et al. (2002) also reported a yield QTL near markers Satt087 (7.3 cM) and Satt539 (4.03 cM), respectively on chromosome 9. Yield QTLs were also reported linked to markers Satt544 (72.8 cM) and Satt 273 (120 cM) by Smalley et al. (2004). In this study a yield QTL was associated with Gm09_6967374_C_T (15.94 cM), Gm09_3394608_G_A (7.76 cM) and Gm09_457853_A_G (5.23 cM) detected using SAS and Gm09_2634593_G_A (5.62 cM) using R/qtl. Also, a yield QTL was identified near marker Gm09_34191288_T_C (78.24 cM) using SAS.

No QTLs were reported on chromosome 10 or 11 using R/qtl. SAS detected two yield QTLs on chromosome 10 associated with Gm10_47585270_T_G (108.89 cM)/ Gm10_48428720_T_C (110.82 cM) and Gm10_571698_A_G (1.3 cM) (**Table 3.89)**. Kalbelka et al. (2004) and Smalley et al. (2004) reported a QTL for yield associated with Satt358 (2.4 cM) on chromosome 10. Satt358 was detected across three maturity groups (MG II, MG III and MG IV) averaged across twelve environments by Kalbelka et al. (2004). Csanadi et al. (2001) also detected an association between seed weight and Satt358. An additional yield QTL was reported by Smalley et al. (2004) associated with Satt477 (103.8 cM), Satt592 (120.5 cM) and Satt331 (127.9 cM). SAS also detected two yield QTLs on chromosome 11 associated with Gm11_5773052_G_A (20.42 cM)/ Gm11_7323949_A_G (26.24 cM)/ Gm11_7445495_G_A (26.72 cM)/ Gm11_4453218_T_C (16.23 cM) and Gm11_36807939_C_A (84.22 cM). Only one study has reported yield QTL within 10 cM of marker Gm11_36807939_C_A (84.22 cM). Smalley et al. (2004) reported a yield QTL linked to markers Satt444 (76.4 cM) and Satt359

(92.1 cM), respectively. In addition, they reported Satt509 (26.7 cM) was associated with a yield QTL on chromosome 11. Du et al (2009) reported a yield QTL near markers at 36.4 cM and 9.61 cM on chromosome 11.

Three yield QTLs were detected on chromosome 12 using SAS and R/qtl. Using SAS markers Gm12_1594873_A_G (3.64 cM) and Gm12_39962521_A_G (91.44 cM) were linked to two different yield QTLs. Du et al. (2009) and Kalbelka et al. (2004) reported a yield QTL near markers at 86 cM on chromosome 12. No studies were found that reported a yield QTL near a marker at 3 cM on chromosome 12, but Du et al. (2009) did report a yield QTL associated with marker Satt317 (11.71 cM). For our study using R/qtl only one QTL was detected and it was associated with marker Gm12_7135310_A_G (36.25 cM). Only one study was found that reported a yield QTL in the same region linked to marker Satt192 (41.1 cM) (Smalley et al., 2004).

One yield QTL was identified on chromosome 13 linked to markers Gm13_27348409_A_G (150.28 cM), Gm13_32183364_A_C (162.13 cM), and Gm13_29895148_C_T (154.76 cM) using SAS and Gm13_34751493_C_A (165.33 cM) and Gm13_27092408_C_T (150.77 cM) using R/qtl. Another yield QTL was identified using SAS linked to Gm13_34946643_T_C (180.68 cM). In 2001, Specht et al. reported Satt074 (143.40 cM) was linked to a yield QTL in a Minsoy x Noir 1 population of 236 RIL genotyped at 665 loci. In 2004, Smalley et al. reported Sat_074 (181.8 cM) to be linked to a yield QTL in two different populations with 184 SSR markers spaced 15 cM apart. The proximity of these markers and the span in which they stretch may indicate that the same yield QTL may have been detected in all studies.

Only one QTL was associated with yield on chromosome 14 (linked to Gm14_49107190_G_A) using SAS and no QTLs were detected using R/qtl. Concibido et al. (2003), Smalley et al. (2004) and Kabelka et al. (2004) reported a yield QTL detected by Satt168 (94 cM) on chromosome 14, which is 8 cM below Gm14_49107190_G_A (102.52 cM). Orf et al. (1999) and Smalley et al. (2004) reported yield QTL linked to Satt066 (97.3 cM), which is 5 cM from Gm14_49107190_G_A (102.52 cM). In this study only one yield QTL was mapped on chromosome 15 using SAS and R/qtl associated with markers Gm15_48028533_G_A, Gm15_43797502_G_T and Gm15_49231503_C_T at 72.40 cM, 72.68 cM, and 89.13 cM, respectively. A yield QTL was reported by Wang et al (2004) on chromosome 15 linked to marker Satt575 (2.3 cM).

The yield QTL on chromosome 16 linked to Gm16_6262227_C_T (10.66 cM), Gm16_5735654_A_G (8.95 cM), Gm16_6233586_A_G (14.23 cM), Gm16_6496577_A_C (14.86 cM) and Gm16_1339719_T_C (6.55 cM) is in the same region as the yield QTL mapped by Orf et al. (1999) and Guzman et al. (2007). Both studies mapped the QTL to markers near 11.7 cM on chromosome 16. In the population in the Guzman et al. (2007) study another yield QTL was mapped to chromosome 16 associated with Satt215 (44.8 cM) only in 2004. In the same population a yield QTL associated with Satt547 (67.7 cM) was detected in 2003, 2004 and across years. In a different population Satt414 (37.8 cM) and Satt622 (42.4 cM) were linked to a yield QTL in 2004 and across years, respectively.

A yield QTL identified by SAS associated with Gm17_13240263_C_T (30.29 cM) was in the same region as the yield QTL identified by R/qtl associated with Gm17_32687336_C_T (49.59 cM) and Gm17_12822621_A_G (35.12 cM). Reinprecht et al. (2006) and Orf et al (1999) identified a yield QTL associated with Satt002 (46.73 cM) and Smalley et al. (2004)

identified a yield QTL associated with Satt135 (34.7 cM) and Satt458 (34.7 cM). The proximity of these markers also indicates that the same yield QTL may have been detected in all studies, providing evidence for the credibility of MAS for yield utilizing this locus.

On chromosome 18 three yield QTLs were detected using SAS. One yield QTL was associated with markers Gm18_8772679_T_C (33.67 cM), Gm18_23913313_A_G (54.72 cM) and Gm18_15660496_T_G (44.64 cM). The second QTL was associated with Gm18_265662_T_C (1.19 cM) and the third QTL was associated with Gm18_58055444_T_C (112.85 cM). Smalley et al. (2004) also identified three yield QTLs on chromosome 18 associated with Satt309 (1.9 cM), Satt324 (25.9 cM) and Satt517 (103.2 cM), respectively. Satt324 has also been associated with a yield QTL on chromosome 18 at 37.47 cM (Reinprecht et al., 2006) and on chromosome 18 at 42.38 cM (Kabelka et al., 2004). R/qtl detected a yield QTL on chromosome 18 linked to Gm18_57988264_A_G (78.75 cM). In 2009, Du et al. reported a yield QTL associated with Satt223 (76.81 cM) and Satt288 (88.01 cM). These makers and the two reported in this study using R/qtl are 25 cM from Satt517, which indicates that they are independent QTL. However, Satt517 and Gm18_58055444_T_C are less than 10 cM apart and may be identifying the same QTL.

In Group A one yield QTL on chromosome 19 was identified in each individual environment and across environments using both SAS and R/qtl associated with Gm19_44937486_T_C (70.75 cM), Gm19_45198812_C_A (72.00), Gm19_44955912_T_G (76.84 cM), and Gm19_44964042_C_T (76.91 cM). Also, in one individual environment in Group B and Group D markers Gm19_45062248_T_C (77.05 cM) and Gm19_39246602_T_C (73.68 cM) were associated with the same QTL using SAS. The same QTL was identified in Group C associated with marker Gm19_46733772_T_C (84.11 cM) using R/qtl. The large effect of this interval on chromosome 19 could be due to the gene for growth habit (Dt1) which is located in the same interval at 89.1 cM. The locus for growth habit segregates in the Essex (determinate) by Williams (indeterminate) cross. Heatherly et al. (2004) found growth habit and increased yield are not independent and indeterminate growth habit can produce higher yields in early maturing soybean lines. This would agree with our discovery of a minor QTL from the Williams cultivar for increasing yield. Another yield QTL was identified using SAS associated with Gm19_2404683_A_G (25.12 cM). The marker Satt313 (32.3 cM) was found to be associated with seed weight on chromosome 19 in a cross between the cultivars Ma Belle x Proto (Csanadi et al., 2001). Guzman et al. (2007) reported a yield QTL with the same marker on chromosome 19 at 34.5 cM. Smalley et al. (2004) reported a yield QTL in the same region associated with Satt143 (31.8 cM), which are all less than 10 cM from the QTL reported in this study.

Gm20_43890641_G_T (54.79 cM), Gm20_46574547_T_C (65.04 cM) and Gm20_41827386_T_C (43.53 cM) were associated with a yield QTL on chromosome 20 using SAS. Satt354 (45.22 cM) reported by Reinprecht et al. (2006) and Satt270 (57.9 cM) reported by Smalley et al. (2004) were also associated with a yield QTL on chromosome 20. Another yield QTL was linked to Gm20_800671_A_G (1.83 cM) using SAS. Smalley et al. (2004) reported a yield QTL linked to Satt127 (15.5 cM) in three populations, however no other studies were found that reported QTL in that region of chromosome 20. No yield QTLs were detected using R/qtl on chromosome 20.

Yield is probably one of the most complex traits to characterize either from a phenotypic or genotypic prospective. Yield is affected by not only genetic factors, but also by environmental factors. This makes it difficult to use QTLs selected from one population in a few select environments and use them in another population in different environments. There are few reports of validated seed yield QTL in different environments and even fewer validating the reported QTL across diverse genetic backgrounds (Palomeque et al. 2009; Fasoula et al. 2004; Reyna and Sneller 2001). Palomeque et al. (2009) conducted a study to identify yield QTL in two different environments with two high yielding soybean cultivars. A cross between Canadian cultivar 'OAC Millennium' and Chinese cultivar 'Heinong 38' was evaluated in China and Canada in multiple environments from 2004 to 2006. Seven yield QTLs were identified of which five were found in at least two environments. Three of the QTLs were detected using multiple QTL mapping (MQM) and four were detected using single-factor ANOVA. To validate these seven markers Palomeque et al. (2010) evaluated a cross between Canadian cultivar 'Pioneer 9071' and Chinese cultivar '8902' in two environments in China and five environments in Canada in 2005 and 2006. No association between seed yield and QTL was observed. However, one of the seven QTL evaluated by Palomeque et al. (2010) (linked to Satt277) was previously reported as being associated with seed yield in diverse genetic backgrounds and environments by other researchers (Guzman et al. 2007; Orf et al. 1999; Smalley et al. 2004; Specht et al. 2001).

Hao et al. (2012) evaluated a population of 191 soybean landraces in five environments to detect molecular markers associated with soybean yield and its components using 1,536 SNPs. Using genome-wide association they identified 19 SNPs associated with yield. Most SNPs were detected only in a specific environment and only a small number of SNPs were identified in three or more environments.

Also, maturity has been shown to affect the verification or validation of yield QTL in soybean. Kabelka et al. (2004) only reported two out of fifteen reported yield QTLs were detected across three maturity groups (MG II, MG III and MG IV). In this study most QTL were detected in at least two groups, but some were only found in one group. In addition, some QTLs detected by Kabelka et al. (2004) in only one maturity group was found in multiple maturity groups in this study. This indicates that while some yield QTL may not be specific to particular maturity groups other yield QTL may be specific to maturity groups within certain genetic backgrounds. Although some of the genomic regions explained a small portion of genotypic variation, or were identified only in a specific environment, they could be important to understanding the genetic control of yield in soybean seeds. Evaluation of these QTL in distinct environments and in different genetic backgrounds along with demonstrated effectiveness of MAS will be the true test of the concept of molecular breeding for seed yield.

Both the environment and genetic background play an important role in the success of the use MAS. QTL for a specific trait are not always stable across environments and/or genetic backgrounds, therefore, their breeding value depends on the strength and stability of trait associations. When yield QTL are evaluated in different genetic backgrounds a variety of results can be obtained. Epistatic effects could be considered as one of the factors leading to the lack of validation of the QTL effect across different populations and environments. Another possibility could be the variability between the parental lines used to derive these populations is limited, i.e. the parents of the validation population or the current mapping population have less genetic variation then parents used to form the population for QTL detection. Potentially, with the genetic diversity of the parents in this study and the ancestry of each line in different cultivars the yield QTL found in this study can be found in different populations. In this study yield prediction models including epistatic effects were used to predict top yielding lines.

When using the YPM to make predictions the data collected from the environment that was more adaptable to a particular maturity group made the best selections in that environment and across environments. This was prominent in Groups A and B where the maturity groups were more adapted to the locations at OH and IL which are more northern in latitude than Knoxville, TN. In Groups C and D the multi-environment YPM predicted more top yielding lines in each individual environment and across environment compared to each individual environment being able to predict top yielding lines in other environments and across environments. Further research is needed to determine the best overall YPM to use to predict top yielding lines.

When making selections using only the marker information, R/qtl was the best statistical program to use. When making selections using the maker information, additive effects and the additive by additive effects multiple programs were used. Overall R/qtl did better when using yield prediction models. However, SAS sometimes made similar predictions and in a few instances better predicted the top yielding lines. While using the program Epistacy (Holland, 1998) to determine the additive by additive effects of significant markers that were pre-determined using SAS and R/qtl, it was determined that Epistacy could be used to scan all pairwise interactions to detect significant interactions. This would greatly decrease the time needed to test pairwise combinations of >1000 SNPs (results not reported in this study). In addition, more additive by additive effects (epistatic effects) could be used in the YPM. These interactions where neither marker identifies a significant effect, but where the two markers together create a significant epistatic effect could be very valuable in predicting quantitative traits. Thus Epistacy could help eliminate the need to test multiple statistical programs for MAS and simplify the process of using epistatic interactions in genomic selection.

Previous research has suggested that including MAS into a breeding program can increase the genetic gain for yield. Sebastian et al. (2010) conducted a study in which $F_{7:8}$ lines derived from elite cultivars were grown as plant-row yield trials in three environments. The objective of that study was to select for an improved genotype. Analysis was done using a mixed linear model and at statistically significant loci, the allele associated with the highest yield mean was considered the favorable allele for the purpose of selecting higher-yielding lines. The yield potential of the selected lines was then compared to their respective parents across multiple environments and years. The seed yields of the reselected lines were greater than the original five elite cultivars by an average of 3.1% and yield gains of up to 5.8% were confirmed in some of the selected lines. Two of the improved lines were released as improved cultivars.

There are only a few reported studies on using MAS in plant breeding for improving quantitative traits controlled by many loci. Most studies refer mainly to computer simulations using various data sets. Campos et al. (2009) adapted the Bayesian LASSO to arrive at a regression model where markers, pedigrees and covariates other than markers are considered jointly. The model was fitted to two data sets from wheat and mouse populations. Results showed that models using molecular markers had better prediction accuracy of grain yield in wheat than those based on pedigree. Crossa et al. (2010) conducted a MAS study using a wheat data set containing various traits, including yield and a maize data set with two disease traits. Separate models were fitted to each trait and environment. Results indicated models including marker information lead to improved predictive ability, but estimates of marker effects were different across environments. It was speculated that multiple environment prediction would allow information to be borrowed between correlated environments and could yield similar or even better predictions for individual environments. Using only 80 markers and 126 soybean

RILs Hu et al. (2011) used MAS to predict the genomic value of somatic embryo number for each line. The correlation coefficient between the observed and predicted embryo numbers was 0.33 when only the additive effects were used in prediction. When the epistatic effects were also included in the model, the correlation coefficient increased to 0.78. Data analysis was conducted using PROC QTL in SAS. However, when marker density is high, the Bayesian method in that QTL procedure (as used in their study) may be limited for handling all pair-wise interactions.

Most quantitative traits are controlled by multiple QTL. The contribution of each locus may be small or large, but the collective contribution of all loci is often significant. Including epistatic effects to predict the genomic values of plants can achieve enhanced gains for soybean improvement. The results from this study suggest using an YPM with additive and additive by additive effects detected from environments that are similar in latitude may lead to the best YPM for predicting seed yield in multiple individual environments. However, more top yielding lines in an individual environment can be predicted using an YPM with additive and additive by additive effects detected from the environment in which the selections will be made.

Conclusion

This study suggests that environment specific data continues to be valuable and that while MAS can successfully predict high yielding lines the very top yielding lines might be missed by MAS unless the prediction equation includes data from the environment in which the yield trial is conducted. This begs the question of resource management and effectiveness in identifying the most superior individuals in a population for a targeted trait of low heritability, like yield. Nevertheless, this study proves MAS from one year can successfully identify some of the top yielding lines in subsequent years and distant environments. This leads to the credibility of continuing further research to enhance the YPM approach for improved efficiency. With the knowledge of the QTL segregating in our Essex x Williams 82 population along with QTL discovered from other mapping populations, researchers and breeders should have a more complete picture of which QTL are available to utilize as tools for soybean yield improvement by MAS.

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Appendix B:

Chapter 3 Tables

Table 3.1 Combined analysis of variance and estimates of variance components for yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in three environments: Knoxville, TN in 2010 and 2011 and Wooster, OH in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	h^2	P-VALUE	F-VALUE
Environment	2	196901.11	428.07	68		<0.0001	2422.73
Reps (Env.)	2	5050.95	20.90	3		<0.0001	6.25
Genotypes	217	434.72	39.66	6	0.44	<0.0001	5.34
Genotypes x Env.	217	206.05	57.96	9		<0.0001	2.54
Error	434	81.27	84.09	14			

Table 3.2 Combined analysis of variance and estimates of variance components for yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Knoxville, TN in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	169.03	36.82	26	0.014	2.10
Genotypes	217	125.06	22.31	16	0.031	1.55
Error	218	80.44	80.44	58		

Table 3.3 Combined analysis of variance and estimates of variance components for yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Wooster, OH in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	993.87	21.94	10	<0.0001	12.93
Genotypes	217	309.66	124.04	54	<0.0001	3.77
Error	218	82.13	82.13	36		

Table 3.4 Mean seed yield, maturity, lodging, and height of 218 recombinant inbred lines in Group A, two parents and three commercial checks grown in Knoxville, TN in 2010 and 2011, Wooster, OH in 2011 and averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011.

ExW50K Group A		COMBINED OVER ENVIRONMENTS				TENNESSEE 2011				OHIO 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
481	01	3315.8	2	261	83	1434.5	3	249	75	4901.5	1	273	89	2472.6	2	260	86
833	02	3107.5	2	259	77	1226.2	3	248	61	4710.0	1	270	86	3037.0	2	260	84
978	03	3005.5	2	261	74	2368.4	2	246	39	4992.2	1	275	94	2412.1	3	263	89
689	04	2973.2	2	260	76	1861.2	3	249	53	5156.8	1	272	94	2465.9	2	260	81
144	05	2972.0	2	260	77	1918.3	3	248	62	4760.4	1	274	86	2237.4	2	259	81
463	06	2957.5	2	261	87	1975.7	3	249	85	4854.5	1	272	89	2042.6	2	263	86
675	07	2876.9	2	261	80	1296.8	2	250	53	4518.5	1	271	94	2916.0	3	262	91
IA3023	**08**	**2875.7**	**1**	**258**	**65**	**1068.3**	**2**	**251**	**56**	**4683.1**	**1**	**266**	**74**	**.**	**.**	**.**	**.**
578	09	2871.3	3	261	84	2243.8	4	249	79	4122.1	2	272	89	2358.4	3	262	84
814	10	2827.6	2	263	79	1488.3	2	251	64	5227.4	1	277	97	1740.2	2	260	76
756	11	2813.1	3	260	75	1921.9	5	249	74	4078.4	1	269	79	1847.7	2	262	71
502	12	2808.5	2	263	86	1125.4	4	252	72	4350.6	1	274	102	1975.4	2	263	84
292	13	2802.9	2	260	77	2019.1	3	248	65	5163.6	2	272	89	1975.4	2	259	79
896	14	2800.7	2	262	79	1447.9	3	253	65	4918.3	1	273	91	1948.5	2	260	81
632	15	2795.1	3	263	92	1696.5	4	251	79	3843.3	2	274	104	3063.9	4	263	94
774	16	2794.0	3	263	85	655.1	5	252	86	4508.4	2	277	97	2351.7	2	260	71
637	17	2757.0	2	262	81	1407.6	3	249	64	4357.3	2	275	97	2217.3	2	263	84
951	18	2748.1	2	262	79	1633.0	3	251	75	4562.2	1	275	86	2116.5	2	260	76
668	19	2746.9	3	260	76	1975.4	4	251	74	3540.9	1	266	69	2855.6	3	263	86
130	20	2724.6	2	262	80	2156.8	3	251	71	3779.4	1	273	86	2237.4	2	262	81
454	21	2717.8	2	260	77	1975.4	3	249	67	4394.2	2	270	99	2082.9	2	260	66
146	22	2713.5	1	260	67	920.8	1	249	25	4666.3	1	270	91	2553.2	2	261	84
751	23	2691.0	2	260	85	913.8	4	251	74	4639.5	1	272	94	1713.3	2	258	86
767	24	2685.5	2	261	78	1521.9	2	248	48	4521.9	3	274	102	1894.8	3	260	84
757	25	2683.2	2	261	85	1639.7	3	252	95	4421.1	2	272	84	1706.6	2	260	76
156	26	2637.2	2	260	74	1663.0	3	250	77	4088.5	1	270	81	1982.1	2	260	64
928	27	2632.7	2	260	83	1468.1	3	250	66	4474.9	1	274	97	1961.9	2	258	86
90	28	2631.6	2	262	83	1736.9	3	253	76	3833.2	1	274	86	2324.8	3	259	86
66	29	2628.3	2	263	76	1199.3	2	250	44	4474.9	2	278	99	2210.6	2	262	84
487	30	2621.5	2	261	79	1263.2	3	252	66	4085.2	1	269	86	2344.9	3	262	84
669	31	2614.8	2	263	80	1196.0	3	250	86	3779.4	1	277	84	2089.6	2	263	69
559	32	2609.2	2	260	76	2133.3	2	246	41	4998.9	2	272	107	2143.4	2	261	81
134	33	2607.0	2	262	75	1249.7	2	249	58	4434.5	1	276	84	2136.6	2	261	84
892	34	2605.8	2	260	77	1904.8	4	250	70	4081.8	1	271	84	2129.9	2	258	76
143	35	2603.6	3	258	79	2519.6	4	250	76	3416.6	1	267	79	1874.6	3	257	81
583	36	2602.5	3	261	82	1679.8	3	250	74	3873.5	1	273	84	2029.1	4	260	89
148	37	2591.4	2	259	78	1041.4	2	249	44	4562.2	1	272	97	2291.2	2	256	94
344	38	2591.3	2	260	82	1861.2	2	251	53	4370.7	2	271	107	2009.0	3	258	86
117	39	2586.8	2	261	81	1945.2	2	248	65	3725.7	1	274	86	2089.6	3	261	91
854	40	2586.8	2	261	72	1148.9	3	251	46	3917.2	1	273	81	2492.7	1	260	89
604	41	2576.7	2	261	69	719.2	2	252	50	4498.4	2	273	89	1787.3	3	259	69
18	42	2568.9	2	261	80	1928.4	3	251	66	3997.8	1	270	91	1780.5	2	262	81
807	43	2568.9	2	258	75	1783.9	2	247	67	4374.1	1	268	81	1968.7	2	258	76
754	44	2554.3	2	262	76	2513.2	3	253	48	4572.3	1	275	91	2177.0	2	260	89
866	45	2548.7	2	261	78	1152.3	3	251	75	3614.8	1	274	76	2257.6	2	260	84
590	46	2535.3	1	261	70	1626.0	2	252	66	3540.9	1	271	89	1780.5	1	259	56
278	47	2528.6	2	261	71	907.1	3	253	65	4105.3	1	272	84	1773.8	2	258	64
1004	48	2528.6	2	259	72	876.8	2	249	72	3944.1	1	269	76	2170.2	2	258	69
155	49	2520.6	2	259	76	1841.0	4	252	67	3268.8	1	267	76	2842.1	2	260	84
600	50	2514.0	2	261	74	1360.6	2	252	65	3934.0	1	270	81	1955.2	2	261	76
291	51	2512.9	2	262	84	1269.9	2	249	66	4024.7	1	277	94	1841.0	3	260	91
878	52	2512.9	2	260	77	1888.0	3	250	71	3960.9	1	270	84	1854.4	2	259	76
592	53	2505.1	2	263	75	732.4	3	251	70	3487.2	1	277	84	1982.1	2	261	71
125	54	2503.9	2	259	72	1730.1	3	249	70	3987.7	1	270	84	1794.0	2	257	64
799	55	2501.8	3	262	81	1780.5	5	252	69	3944.1	1	271	89	2257.6	3	263	86
Essex	**56**	**2499.5**	**2**	**269**	**62**	**1098.6**	**3**	**250**	**46**	**3900.4**	**1**	**289**	**79**	**.**	**.**	**.**	**.**
489	57	2499.5	2	260	76	1696.5	4	250	66	4562.2	1	270	94	1673.0	2	260	69
919	58	2498.3	2	262	84	1783.9	4	250	76	3806.3	1	274	89	2398.7	2	262	86
203	59	2495.0	2	262	73	1918.3	2	251	60	4169.1	1	274	79	2365.1	2	260	81
865	60	2495.0	2	262	88	1773.8	3	250	79	3147.9	1	274	97	2479.3	3	262	89
709	61	2486.0	3	260	85	698.8	4	249	77	3823.1	2	268	89	1814.1	3	262	89
290	62	2481.5	2	259	72	1673.0	4	252	75	3782.8	1	268	76	1820.8	2	258	66
981	63	2469.2	2	258	77	2042.6	3	251	85	3285.6	1	264	76	1753.7	2	260	69
211	64	2464.8	2	262	75	1189.3	3	250	58	4636.1	2	275	94	1632.7	2	262	74
988	65	2463.6	3	264	83	1562.2	4	253	75	3648.4	1	276	97	1699.9	3	263	79
749	66	2459.2	2	262	77	1720.1	3	249	72	4044.8	1	276	91	1290.0	3	262	69
610	67	2456.9	2	260	72	823.1	3	248	58	3873.5	1	271	89	2069.5	2	261	69
104	68	2451.3	2	258	75	1182.5	3	248	64	3362.9	1	268	81	2808.5	2	259	81
58	69	2449.1	2	262	85	1629.4	3	250	69	3682.0	1	275	94	2035.9	2	263	91
428	70	2447.9	2	261	79	1313.6	2	250	48	3729.0	1	276	97	1740.2	3	259	91

Table 3.4 Continued.

ExW50K Group A		COMBINED OVER ENVIRONMENTS				TENNESSEE 2011				OHIO 2011				TENNESSEE 2010			
LINE	RANK	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT
		kg ha^{-1}			cm	kg ha^{-1}			cm	kg ha^{-1}			cm	kg ha^{-1}			cm
353	72	2441.2	2	262	62	1061.6	2	244	72	3440.1	1	279	69	2022.4	2	263	46
Williams82	**73**	**2439.0**	**2**	**260**	**67**	**1340.4**	**3**	**249**	**52**	**3537.6**	**1**	**272**	**81**	.	.	.	.
84	74	2439.0	2	260	76	1202.7	3	249	71	3991.1	1	269	81	2123.2	2	261	76
451	75	2439.0	2	260	77	1676.4	2	250	39	4374.1	2	274	99	1894.8	3	257	94
IA3024	**76**	**2435.6**	**1**	**257**	**59**	**1249.7**	**2**	**250**	**47**	**3621.5**	**1**	**265**	**71**	.	.	.	.
949	77	2433.4	2	261	83	1565.5	3	247	72	3907.1	1	275	97	1854.4	2	262	79
396	78	2421.1	2	261	75	2109.5	2	249	66	3796.2	1	274	84	1847.7	2	262	74
524	79	2420.0	2	262	72	1394.2	3	251	48	3799.6	1	276	86	2257.6	2	260	81
133	80	2415.5	2	263	87	1790.6	4	251	81	3547.6	1	277	91	1908.2	2	260	89
626	81	2399.8	2	261	60	1122.1	4	250	86	2721.2	1	273	43	2533.1	1	261	51
403	82	2394.1	2	260	70	853.0	2	250	55	3534.2	1	270	84	1538.7	2	260	71
494	83	2389.7	3	262	89	500.6	5	248	80	4169.1	1	276	97	1673.0	2	262	91
995	84	2380.8	2	258	81	856.7	2	245	72	3393.1	1	270	84	2385.2	2	258	86
883	85	2378.5	2	259	82	1605.8	3	252	72	3661.9	2	267	91	1585.7	2	258	81
93	86	2376.3	2	261	76	1777.2	4	252	79	3396.5	1	271	69	1955.2	1	260	81
829	87	2375.2	2	261	80	1575.6	3	247	79	3430.0	1	273	79	2056.0	2	263	84
920	88	2372.9	2	262	75	1461.4	3	251	69	3628.3	1	275	79	1706.6	2	262	76
812	89	2369.6	2	260	85	1515.1	4	249	76	3645.1	1	272	91	1679.8	2	260	86
423	90	2360.6	2	262	58	1874.3	3	249	71	3406.5	1	277	56	1955.2	1	261	48
788	91	2359.6	2	256	64	1384.1	3	250	52	3698.8	1	263	74	1632.7	1	256	66
242	92	2353.9	1	261	65	1065.0	2	251	50	3866.8	1	272	79	1894.8	1	260	66
500	93	2351.7	3	263	91	2099.7	4	253	84	3850.0	1	275	102	1343.8	3	261	89
743	94	2351.7	2	259	75	2042.6	2	247	48	3752.6	1	271	86	2143.4	2	258	91
734	95	2350.5	2	262	71	1998.9	2	247	51	3833.2	1	275	91	2150.1	2	263	71
740	96	2337.2	2	262	68	1159.0	2	250	52	3967.6	1	274	76	1740.2	2	262	76
537	97	2337.1	2	261	78	1199.3	3	250	70	3584.6	1	272	84	1639.4	2	260	81
13	98	2333.7	2	260	74	1098.6	2	248	56	3772.7	1	272	86	2129.9	3	259	79
581	99	2333.6	2	262	59	1904.8	2	252	51	3265.4	1	272	64	1491.6	2	263	64
62	100	2332.6	2	259	80	1609.2	3	250	76	3278.9	1	268	76	2109.8	2	259	86
591	101	2329.3	2	259	69	2045.9	2	248	70	3594.7	1	269	74	1767.1	2	260	64
447	102	2327.0	2	260	77	1048.2	3	249	76	3601.4	1	272	79	1773.8	2	260	76
120	103	2320.4	1	262	65	1156.0	1	250	30	4280.0	1	273	89	1525.2	2	262	76
28	104	2319.2	2	261	84	1730.1	3	252	79	3258.7	1	270	89	1968.7	2	260	84
790	105	2313.6	2	261	55	1303.8	3	250	62	3776.1	1	274	53	1780.5	1	260	48
86	106	2305.7	2	260	67	1481.5	4	251	67	3944.1	1	273	74	1491.6	1	258	61
444	107	2303.5	2	258	72	1605.8	2	248	50	3393.1	1	266	81	2277.7	2	260	86
301	108	2292.3	2	256	69	1001.1	2	251	75	3225.1	1	266	69	1632.7	2	251	64
341	109	2287.8	2	259	69	1394.2	3	247	66	3225.1	1	272	69	1626.0	2	260	74
916	110	2285.6	2	261	69	1290.0	2	246	48	3930.6	1	276	89	1982.1	2	261	71
598	111	2272.2	2	257	65	1652.9	3	250	61	2872.4	1	267	69	1673.0	1	256	66
856	112	2266.5	2	262	67	1857.8	2	250	50	3453.6	1	275	79	2197.1	2	260	74
960	113	2264.3	1	259	67	1054.9	2	249	56	3581.2	1	269	74	1679.8	1	258	71
543	114	2263.2	2	261	51	1394.2	2	250	58	4138.9	1	274	89	1451.3	2	260	5
957	115	2263.2	2	258	76	1246.4	4	249	86	4051.6	1	266	81	1397.6	1	260	61
71	116	2260.9	2	261	80	1783.9	3	251	69	3366.2	2	272	91	1632.7	2	259	79
LD00-3309	**117**	**2260.9**	**2**	**258**	**65**	**2261.2**	**3**	**248**	**52**	**4521.9**	**1**	**267**	**79**	.	.	.	.
253	118	2259.8	1	261	64	1787.3	2	248	44	4505.1	1	274	84	1652.9	1	262	64
61	119	2258.7	2	261	53	1528.6	3	248	65	3359.5	1	274	48	1888.0	1	262	46
266	120	2258.7	2	262	82	1861.2	3	248	76	3571.1	1	276	84	2217.3	2	262	86
948	121	2249.7	2	260	64	1538.7	3	248	67	3759.3	1	273	91	1364.0	1	260	33
472	122	2240.8	2	262	69	2143.4	3	251	58	3305.7	1	274	74	1706.6	2	261	74
336	123	2238.5	2	260	72	944.0	4	249	70	2916.0	1	269	79	1968.7	2	261	69
609	124	2237.5	1	256	60	1427.8	1	250	27	4038.1	1	263	81	1955.2	2	256	71
710	125	2235.2	2	263	77	930.6	2	246	42	3702.2	1	279	99	2304.6	2	263	89
940	126	2232.9	2	258	64	1044.8	2	247	47	3806.3	1	265	74	1914.9	2	261	71
954	127	2231.9	2	259	71	1434.5	2	251	55	3309.1	1	268	81	1753.7	2	257	76
515	128	2231.8	1	259	50	1202.7	2	250	42	3090.7	1	266	53	2479.3	1	260	53
204	129	2228.5	2	258	72	1125.4	3	250	81	2852.2	1	266	69	1914.9	1	258	66
260	130	2228.5	2	261	79	2103.0	3	252	79	3218.4	1	268	81	1679.8	2	262	76
930	131	2212.8	2	258	69	1797.3	4	249	66	3369.6	1	269	74	1437.9	1	257	69
737	132	2210.6	2	262	63	1458.0	2	251	69	3910.5	1	273	79	1471.5	2	262	41
358	133	2203.8	2	260	69	1142.2	2	248	47	3493.9	1	272	81	2056.0	2	261	79
945	134	2192.6	2	259	71	1626.0	2	248	51	3981.0	1	272	86	1552.1	2	257	76
286	135	2191.5	2	261	69	1041.4	3	249	75	3248.6	1	271	69	1565.5	1	262	64
73	136	2183.7	2	260	48	2197.1	3	249	74	2694.3	1	270	36	1659.6	1	263	36
720	137	2181.4	2	262	71	853.3	2	250	51	3698.8	1	275	89	1914.9	2	261	74
603	138	2174.7	2	259	60	1444.6	2	250	51	3819.8	1	265	69	1498.3	2	261	61
170	139	2164.6	2	259	80	1632.7	3	250	75	2842.1	1	267	84	1666.3	2	260	81
639	140	2163.5	2	260	48	1290.0	3	250	61	2637.2	1	268	36	2445.7	1	262	48
224	141	2162.4	2	262	75	1437.9	4	252	71	3460.3	1	275	76	1572.2	2	261	79
433	142	2147.8	2	258	80	1239.7	2	249	51	4014.6	2	268	104	1115.4	2	258	86
106	143	2141.1	2	262	74	1038.1	2	250	53	3524.1	1	274	89	1861.2	2	263	79
59	144	2138.9	1	260	65	960.8	1	251	30	3648.4	1	269	84	1807.4	2	261	81
851	145	2136.6	1	260	49	1350.5	2	250	46	2879.1	1	270	58	2304.6	1	261	43
929	146	2132.2	2	262	73	1830.9	3	250	74	3604.7	1	273	89	1323.6	2	262	56
126	147	2125.3	2	257	72	1834.0	2	247	52	2969.8	1	270	84	1572.2	2	256	81
630	148	2121.0	1	259	74	1478.2	2	247	64	3463.6	1	271	86	1780.5	1	259	71
912	149	2118.7	2	258	75	1108.6	3	249	81	2778.3	1	266	64	1511.8	1	258	79
337	150	2096.3	2	261	68	2012.3	4	250	66	4484.9	1	274	89	860.0	2	260	48

Table 3.4 Continued.

ExW50K Group A		COMBINED OVER ENVIRONMENTS				TENNESSEE 2011				OHIO 2011				TENNESSEE 2010			
LINE	RANK	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT
		kg ha^{-1}			cm	kg ha^{-1}			cm	kg ha^{-1}			cm	kg ha^{-1}			cm
480	151	2089.6	2	259	69	2573.4	3	252	79	2432.3	1	266	74	1693.2	2	258	53
735	152	2088.5	2	261	71	1249.7	4	250	77	3063.9	1	272	76	1202.7	2	260	58
994	153	2058.3	2	262	46	1364.0	3	251	66	2912.7	1	274	66	1699.9	2	262	5
775	154	2057.1	2	260	63	1747.2	2	251	50	3708.9	1	269	76	1807.4	2	259	64
48	155	2037.0	2	257	71	1535.3	2	251	55	2727.9	1	264	76	1847.7	3	258	81
549	156	2031.4	2	258	64	685.3	3	251	58	2906.0	1	267	66	1794.0	1	258	66
388	157	2028.0	2	262	54	1350.5	4	250	69	2855.6	1	276	43	1505.1	1	259	51
145	158	2021.3	2	257	80	1521.9	3	248	69	2848.9	1	265	79	1693.2	3	257	91
261	159	2021.3	2	260	79	987.7	4	249	89	2872.4	1	272	79	1088.5	2	260	69
914	160	2017.9	1	256	62	1706.6	2	250	52	3359.5	1	266	74	1585.7	1	253	61
376	161	2014.6	2	259	74	547.6	3	252	75	3151.2	1	264	76	1619.3	2	262	71
361	162	2001.1	2	261	67	393.1	2	249	56	3369.6	1	274	71	1491.6	2	260	74
595	163	1953.0	1	260	60	2271.3	1	252	34	3561.1	1	271	76	1565.5	2	258	69
305	164	1949.6	2	262	66	1414.3	2	249	39	2791.7	1	277	79	2056.0	2	261	79
601	165	1945.2	2	261	49	1206.1	4	250	60	2795.1	1	272	41	1679.8	1	260	46
241	166	1942.9	2	257	74	1300.1	2	246	66	3188.2	1	265	79	1202.7	4	261	76
64	167	1936.2	1	260	46	1683.1	2	248	70	2378.5	1	271	36	1746.9	1	260	33
391	168	1933.9	1	257	64	1619.3	2	247	61	2986.6	1	266	74	1464.7	1	257	58
955	169	1921.6	2	258	55	1340.4	4	250	86	3033.6	1	268	38	1296.8	1	257	41
10	170	1907.1	2	261	73	930.6	2	249	61	3117.6	1	273	79	1673.0	2	260	79
587	171	1902.6	2	260	55	2284.5	3	246	80	2422.2	1	271	38	1605.8	1	262	48
1014	172	1894.8	1	259	60	1058.2	1	250	37	3201.6	1	270	76	1605.8	1	258	66
21	173	1889.2	2	259	53	2012.3	3	247	93	2116.5	1	271	30	1538.7	1	260	36
407	174	1881.2	2	260	74	1404.3	2	250	48	3037.0	1	270	84	1753.7	3	260	89
693	175	1867.9	1	258	46	1122.4	2	245	72	2418.8	1	268	30	1323.6	1	260	36
108	176	1865.6	1	259	50	1998.9	2	246	71	2388.6	1	270	41	1209.4	1	260	38
627	177	1855.6	1	259	47	1118.7	2	251	46	2805.2	1	270	46	1639.4	1	258	51
316	178	1839.9	1	259	43	1830.9	2	251	53	2566.7	1	268	36	1538.7	1	259	41
975	179	1822.0	1	259	63	1612.3	2	253	47	2516.3	1	267	74	1733.5	1	259	69
721	180	1817.5	2	263	64	1854.4	2	251	46	3201.6	2	275	81	1397.6	2	262	66
901	181	1817.5	2	260	44	900.3	3	252	56	2533.1	1	270	43	1471.5	1	259	33
112	182	1805.2	1	260	44	1531.9	2	248	66	2633.8	1	271	33	1249.7	1	261	33
624	183	1770.5	1	257	41	1945.2	2	249	51	2707.8	1	264	43	994.4	1	258	30
119	184	1743.6	2	256	71	1340.4	4	246	76	2398.7	1	265	71	1491.6	2	258	66
167	185	1739.1	1	257	61	1985.5	2	250	65	2415.5	1	265	64	1511.8	1	256	53
699	186	1705.6	1	258	37	1820.8	1	251	33	2617.1	1	267	41	1377.4	1	257	38
534	187	1699.9	1	255	49	1787.3	2	248	69	1894.8	1	262	36	1263.2	1	257	43
166	188	1693.2	2	260	47	1290.0	3	250	58	1978.7	1	269	38	1437.9	1	260	43
997	189	1667.4	1	260	56	1471.5	1	252	37	2741.4	1	266	66	1404.3	2	262	66
907	190	1663.0	2	256	58	2066.1	2	245	41	3121.0	1	267	74	967.5	2	257	61
464	191	1660.8	2	258	39	1710.0	3	252	55	1736.9	1	264	36	1269.9	1	258	25
279	192	1637.2	1	261	42	1760.4	1	251	41	3037.0	1	272	51	967.5	1	260	36
421	193	1562.2	2	258	49	1720.1	4	253	74	1689.8	1	266	23	1303.5	1	257	51
825	194	1554.3	1	259	40	1639.4	2	250	52	1743.6	1	268	30	1431.1	1	259	38
965	195	1516.3	1	260	40	1101.9	2	249	53	2129.9	1	271	30	1364.0	1	260	36
496	196	1500.6	1	263	37	1861.2	1	249	34	2543.1	1	277	33	1458.0	1	262	43
289	197	1499.5	2	259	50	1841.0	4	250	72	2368.4	1	266	43	1088.5	1	262	36
45	198	1496.0	1	259	68	537.2	1	248	37	2210.6	1	268	86	1740.2	2	260	81
654	199	1486.0	1	258	52	1844.4	2	251	60	2274.4	1	266	53	893.6	1	259	43
89	200	1481.5	2	256	43	1790.6	3	250	69	1652.9	1	262	25	1001.1	1	256	36
527	201	1481.5	1	259	39	1941.8	2	251	61	1579.0	1	266	18	1471.5	1	261	38
248	202	1460.3	2	258	46	621.5	4	249	67	1857.8	1	266	33	1458.0	1	258	38
893	203	1443.5	2	258	45	1535.3	3	251	77	1518.5	1	265	25	907.1	1	259	33
200	204	1426.7	1	259	39	1122.4	2	249	57	1713.3	1	267	30	933.9	1	260	28
493	205	1425.6	2	257	52	1327.0	4	249	83	1760.4	1	263	36	819.7	1	258	38
739	206	1394.2	2	258	48	1303.8	3	249	80	1757.0	1	266	23	967.5	1	258	41
150	207	1390.8	2	256	41	1451.0	3	251	61	1565.5	1	263	30	1565.5	1	256	30
60	208	1340.4	1	260	39	1017.9	2	250	51	1948.5	1	270	28	1054.9	1	260	38
959	209	1336.0	1	259	41	1531.9	2	250	61	1746.9	1	267	25	1014.6	1	261	36
277	210	1321.4	2	255	45	1706.6	3	245	64	1269.9	1	262	30	833.2	1	257	41
724	211	1303.5	2	259	42	1068.3	3	249	72	981.1	1	266	15	1075.0	1	261	38
410	212	1245.3	1	258	40	1693.2	2	251	62	1411.0	1	262	28	920.5	1	261	30
931	213	1243.0	2	259	44	977.6	3	248	69	749.2	1	267	23	1182.5	1	261	41
915	214	1216.1	2	256	44	944.0	4	247	71	1175.8	1	265	23	766.0	1	258	38
800	215	1206.1	2	257	46	1364.0	3	251	76	1091.8	1	263	25	745.8	1	258	36
974	216	1206.1	2	260	51	1216.1	3	250	64	1770.5	1	272	56	745.8	1	258	33
379	217	1189.3	1	260	34	1723.4	1	247	34	2166.9	1	272	33	853.3	1	260	36
105	218	1180.3	1	258	38	1266.5	2	250	60	1152.3	1	265	18	1122.1	1	260	36
1015	219	1150.1	2	258	41	1646.2	3	250	62	1552.1	1	269	25	839.9	1	256	36
876	220	1145.5	2	261	68	1723.4	4	250	72	689.0	1	273	50	2264.3	2	261	81
202	221	1060.6	2	257	43	950.7	3	250	65	1058.2	1	262	33	1001.1	1	260	30
615	222	991.1	1	259	32	1609.2	2	251	39	1390.8	1	263	25	759.2	1	262	30
372	223	774.9	1	257	30	1273.3	1	249	32	1246.4	1	263	23	685.3	1	260	36
	Mean	2188.9	1.8	259.9	66.6	1486.7	2.4	249.4	62.6	3339.1	1.1	270.3	71.4	1740.8	1.8	259.9	65.9
	LSD	772.7	1.1	3.3	7.0	992.3	1.8	5.8	12.9	992.3	1.8	5.8	12.9	992.3	1.8	5.8	12.9

†MAT is maturity date according to the Julian calendar

‡LODG is the lodge score reported on a 1-5 scale

$LSD_{0.05}$ is Least Significance Difference at the 0.05 probability level.

Table 3.5 Quantitative trait loci identified using R/qtl located on various chromosomes associated with yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	70.65	3.25	8.25	5.04	W
Knoxville, TN 2010	Gm02_707483_A_G	2	D1b	5.25	3.07	6.7	2.48	E
Knoxville, TN 2010	Gm04_48782140_G_T	4	C1	152.98	2.48	6.4	2.13	E
Wooster, OH 2011	Gm19_45198812_C_A	19	L	72.00	3.28	9.5	2.40	W
Wooster, OH 2011	Gm03_2151432_A_G	3	N	14.00	3.21	8.3	4.33	E
Wooster, OH 2011	Gm04_48993297_T_G	4	C1	154.16	2.78	5.2	3.18	E
Knoxville, TN 2010-11 Wooster, OH 2011	Gm19_44937486_T_C	19	L	70.75	3.75	7.2	3.17	W
Knoxville, TN 2010-11 Wooster, OH 2011	Gm05_33176582_G_A	5	A1	33.77	3.44	7.8	2.56	W
Knoxville, TN 2010-11 Wooster, OH 2011	Gm02_47790307_C_T	2	D1b	150.38	2.56	5.7	3.26	E

†Additive effect refers to the quantitative change in yield that is associated with the favorable allele from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.6 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using R/qtl in each environment in Group A. Those MAS lines were compared to the top yielding 10 % of lines in the environment from which they were selected. The MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					WOOSTER, OH 2011					KNOXVILLE, TN 2010-11 WOOSTER, OH 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
28	01	632	3063.9	01	59	01	[bb]**814**	5227.4	01	71	01	[cc]**481**	3319	01
45	02	833	3037.0	02	62	02	292	5166.9	02	90	02	[cc]**833**	3111	02
58	03	675	2916.0	03	71	03	[bb]**689**	5160.2	03	125	03	978	3003	03
[a]**90**	04	668	2855.6	04	86	04	559	4998.9	04	[cc]**144**	04	689	2977	04
[aa]**104**	05	155	2842.1	05	[bb]**144**	05	978	4992.2	05	156	05	[cc]**144**	2970	05
106	06	[aa]**104**	2808.5	06	224	06	896	4918.3	06	211	06	[cc]**463**	2956	06
117	07	[aa]**146**	2553.2	07	261	07	[bb]**481**	4904.9	07	224	07	675	2876	07
120	08	626	2533.1	08	337	08	[bb]**463**	4857.8	08	260	08	578	2869	08
130	09	854	2492.7	09	341	09	[bb]**144**	4763.8	09	[c]**292**	09	[cc]**814**	2829	09
134	10	865	2479.3	10	344	10	833	4710.0	10	344	10	756	2815	10
144	11	515	2479.3	11	358	11	146	4669.7	11	[cc]**463**	11	502	2809	11
[aa]**146**	12	[a]**481**	2472.6	12	428	12	[b]**751**	4642.8	12	[cc]**481**	12	[c]**292**	2802	12
156	13	689	2465.9	13	[bb]**463**	13	211	4636.1	13	543	13	[c]**896**	2802	13
[a]**203**	14	639	2445.7	14	[bb]**481**	14	754	4575.6	14	583	14	632	2795	14
204	15	978	2412.1	15	524	15	148	4562.2	15	710	15	774	2795	15
211	16	919	2398.7	16	592	16	489	4562.2	16	[c]**751**	16	637	2755	16
266	17	995	2385.2	17	[bb]**689**	17	951	4562.2	17	767	17	[c]**951**	2748	17
291	18	[a]**203**	2365.1	18	737	18	767	4521.9	18	[cc]**814**	18	668	2748	18
292	19	578	2358.4	19	[b]**751**	19	675	4521.9	19	[cc]**833**	19	130	2728	19
358	20	774	2351.7	20	756	20	[b]**774**	4508.4	20	[c]**896**	20	454	2721	20
[a]**481**	21	[a]**487**	2344.9	21	[b]**774**	21	253	4508.4	21	912	21	146	2714	21
[a]**487**	22	[a]**90**	2324.8	22	[bb]**814**	22	604	4501.7	22	[c]**951**	22	[c]**751**	2694	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Wooster, OH in 2011
[bb] Top 5% yield in Wooster, OH in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011

Table 3.7 MAS identifying the bottom 10 % of lines containing unfavorable allele for the yield QTLs detected using R/qtl in each environment in Group A. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					**WOOSTER, OH 2011**					**KNOXVILLE, TN 2010-11 WOOSTER, OH 2011**				
MAS		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
[aa]**1015**	197	[a]**60**	1054.9	197	60	197	739	1760.4	197	997	197	248	1458.0	197
21	198	959	1014.6	198	[bb]**105**	198	[b]**959**	1746.9	198	[cc]**1015**	198	893	1444.6	198
[a]**60**	199	[a]**89**	1001.1	199	108	199	825	1746.9	199	10	199	200	1424.4	199
[a]**89**	200	[a]**202**	1001.1	200	[b]**150**	200	464	1740.2	200	[c]**60**	200	[c]**493**	1424.4	200
[a]**200**	201	624	994.4	201	166	201	200	1713.3	201	84	201	[c]**739**	1397.6	201
[a]**202**	202	[a]**907**	967.5	202	204	202	421	1693.2	202	[cc]**105**	202	[c]**150**	1390.8	202
286	203	279	967.5	203	[bb]**277**	203	89	1652.9	203	[c]**150**	203	[c]**60**	1343.8	203
361	204	739	967.5	204	289	204	527	1579.0	204	[cc]**202**	204	959	1337.1	204
376	205	[a]**200**	933.9	205	407	205	[b]**150**	1565.5	205	289	205	277	1323.6	205
391	206	410	920.5	206	433	206	1015	1552.1	206	[cc]**379**	206	[c]**724**	1303.5	206
421	207	893	907.1	207	480	207	893	1518.5	207	407	207	410	1243.0	207
433	208	[aa]**654**	893.6	208	581	208	410	1411.0	208	421	208	[cc]**931**	1243.0	208
480	209	337	860.0	209	[bb]**615**	209	[bb]**615**	1390.8	209	433	209	[cc]**915**	1216.1	209
581	210	379	853.3	210	624	210	[bb]**277**	1269.9	210	[c]**493**	210	800	1209.4	210
590	211	[aa]**1015**	839.9	211	[bb]**724**	211	372	1249.7	211	527	211	[cc]**974**	1209.4	211
639	212	277	833.2	212	[bb]**800**	212	[bb]**915**	1175.8	212	[c]**724**	212	[cc]**379**	1189.3	212
[aa]**654**	213	493	819.7	213	851	213	[bb]**105**	1155.7	213	[c]**739**	213	[cc]**105**	1182.5	213
[aa]**800**	214	915	766.0	214	901	214	[bb]**800**	1095.2	214	901	214	[cc]**1015**	1148.9	214
851	215	615	759.2	215	[bb]**915**	215	202	1061.6	215	907	215	876	1142.2	215
[a]**907**	216	[aa]**800**	745.8	216	[bb]**931**	216	[bb]**724**	981.0	216	[cc]**915**	216	[cc]**202**	1061.6	216
948	217	974	745.8	217	[b]**959**	217	[bb]**931**	752.5	217	[cc]**931**	217	615	994.4	217
965	218	372	685.3	218	974	218	876	689.0	218	[cc]**974**	218	372	772.7	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Wooster, OH in 2011
[bb] Bottom 5% yield in Wooster, OH in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011

Table 3.8 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using R/qtl in each environment in Group A compared to the top yielding 10 % of lines averaged over all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
28	01	59	01	71	01	**[aabbcc]481**	3319.2	01
45	02	62	02	90	02	**[cc]833**	3110.9	02
58	03	71	03	125	03	978	3003.4	03
90	04	86	04	**[cc]144**	04	**[bb]689**	2976.5	04
104	05	**[bb]144**	05	156	05	**[aabbcc]144**	2969.8	05
106	06	224	06	211	06	**[bbcc]463**	2956.4	06
117	07	261	07	224	07	675	2875.7	07
120	08	337	08	260	08	578	2869.1	08
[a]130	09	341	09	**[c]292**	09	**[bbcc]814**	2828.7	09
134	10	344	10	344	10	**[bb]756**	2815.3	10
[aa]144	11	358	11	**[cc]463**	11	502	2808.5	11
[a]146	12	428	12	**[cc]481**	12	**[ac]292**	2801.8	12
156	13	**[bb]463**	13	543	13	**[c]896**	2801.8	13
203	14	**[bb]481**	14	583	14	632	2795.1	14
204	15	524	15	710	15	**[b]774**	2795.1	15
211	16	592	16	751	16	637	2754.8	16
266	17	**[bb]689**	17	767	17	951	2748.1	17
291	18	737	18	**[cc]814**	18	668	2748.1	18
[a]292	19	**[b]751**	19	**[cc]833**	19	**[a]130**	2727.9	19
358	20	**[bb]756**	20	**[c]896**	20	454	2721.2	20
[aa]481	21	**[b]774**	21	912	21	**[a]146**	2714.5	21
487	22	**[bb]814**	22	951	22	**[b]751**	2694.3	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011

Table 3.9 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using R/qtl in each environment in Group A compared to the bottom yielding 10 % of lines averaged over all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
[aa]1015	197	**[b]60**	197	997	197	248	1458.0	197
21	198	**[bb]105**	198	**[c]1015**	198	893	1444.6	198
[a]60	199	108	199	10	199	**[a]200**	1424.4	199
89	200	**[b]150**	200	**[c]60**	200	**[c]493**	1424.4	200
[a]200	201	166	201	84	201	**[c]739**	1397.6	201
[aa]202	202	204	202	**[cc]105**	202	**[bc]150**	1390.8	202
286	203	**[b]277**	203	**[c]150**	203	**[abc]60**	1343.8	203
361	204	289	204	**[cc]202**	204	**[b]959**	1337.1	204
376	205	407	205	289	205	**[b]277**	1323.6	205
391	206	433	206	**[cc]379**	206	**[bc]724**	1303.5	206
421	207	480	207	407	207	410	1243.0	207
433	208	581	208	421	208	**[bbcc]931**	1243.0	208
480	209	**[bb]615**	209	433	209	**[bbcc]915**	1216.1	209
581	210	624	210	**[c]493**	210	**[aabb]800**	1209.4	210
590	211	**[b]724**	211	527	211	**[bbcc]974**	1209.4	211
639	212	**[bb]800**	212	**[c]724**	212	**[cc]379**	1189.3	212
654	213	851	213	**[c]739**	213	**[bbcc]105**	1182.5	213
[aa]800	214	901	214	901	214	**[aac]1015**	1148.9	214
851	215	**[bb]915**	215	907	215	876	1142.2	215
907	216	**[bb]931**	216	**[cc]915**	216	**[aacc]202**	1061.6	216
948	217	**[b]959**	217	**[cc]931**	217	**[bb]615**	994.4	217
965	218	**[bb]974**	218	**[cc]974**	218	372	772.7	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011

Table 3.10 Quantitative trait loci identified using SAS located on various chromosomes associated with yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE EFFECT[†]	FAVORABLE ALLELE	P-VALUE
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	76.71	8.17	5.75	W	<0.0001
Knoxville, TN 2010	Gm15_43797502_G_T	15	E	72.68	6.38	1.88	W	0.002
Knoxville, TN 2010	Gm02_47790307_C_T	2	D1b	121.66	6.04	3.39	E	0.0028
Knoxville, TN 2010	Gm09_6967374_C_T	9	K	15.94	4.64	0.88	E	0.0106
Wooster, OH 2011	Gm19_44955912_T_G	19	L	76.84	7.98	-4.22	W	<0.0001
Wooster, OH 2011	Gm10_47585270_T_G	10	O	108.89	5.35	2.27	E	0.0049
Wooster, OH 2011	Gm02_49126947_T_C	2	D1b	127.25	5.31	3.44	E	0.0051
Wooster, OH 2011	Gm01_1494600_C_T	1	D1a	5.52	4.73	2.44	E	0.009
Knoxville, TN 2010-11 Wooster, OH 2011	Gm19_44964042_C_T	19	L	76.91	8.12	3.21	W	<0.0001
Knoxville, TN 2010-11 Wooster, OH 2011	Gm18_8772679_T_C	18	D2	33.67	6.88	2.83	W	0.0002
Knoxville, TN 2010-11 Wooster, OH 2011	Gm11_5773052_G_A	11	B1	20.42	6.53	3.80	E	0.0018
Knoxville, TN 2010-11 Wooster, OH 2011	Gm13_27348409_A_G	13	F	150.28	6.07	4.13	E	0.0006
Knoxville, TN 2010-11 Wooster, OH 2011	Gm14_49107190_G_A	14	B2	102.52	5.97	6.14	W	0.003
Knoxville, TN 2010-11 Wooster, OH 2011	Gm03_47386481_A_C	3	N	120.71	5.67	5.81	E	0.004
Knoxville, TN 2010-11 Wooster, OH 2011	Gm02_49126947_T_C	2	D1b	127.25	5.07	5.82	E	0.0071

[†]Additive effect refers to the quantitative change in yield that is associated with the favorable allele from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.11 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using SAS in each environment in Group A. Those MAS lines were compared to the top yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					WOOSTER, OH 2011					KNOXVILLE, TN 2010-11 WOOSTER, OH 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
18	01	632	3063.9	01	278	01	814	5227.4	01	28	01	481	3319.2	01
[a]**90**	02	833	3037.0	02	[bb]**292**	02	[bb]**292**	5166.9	02	204	02	833	3110.9	02
120	03	675	2916.0	03	[b]**754**	03	689	5160.2	03	211	03	978	3003.4	03
143	04	[aa]**668**	2855.6	04	756	04	559	4998.9	04	290	04	[cc]**689**	2976.5	04
144	05	155	2842.1	05	62	05	978	4992.2	05	305	05	144	2969.8	05
[a]**203**	06	104	2808.5	06	125	06	[bb]**896**	4918.3	06	[cc]**502**	06	463	2956.4	06
204	07	146	2553.2	07	145	07	481	4904.9	07	537	07	675	2875.7	07
266	08	626	2533.1	08	[bb]**146**	08	463	4857.8	08	595	08	578	2869.0	08
291	09	854	2492.7	09	261	09	144	4763.8	09	600	09	814	2828.7	09
305	10	865	2479.3	10	291	10	833	4710.0	10	604	10	[cc]**756**	2815.3	10
489	11	515	2479.3	11	337	11	[bb]**146**	4669.7	11	[cc]**689**	11	[cc]**502**	2808.5	11
524	12	481	2472.6	12	341	12	751	4642.8	12	749	12	292	2801.8	12
549	13	[a]**689**	2465.9	13	396	13	211	4636.1	13	[cc]**756**	13	896	2801.8	13
[aa]**668**	14	639	2445.7	14	428	14	[b]**754**	4575.6	14	807	14	632	2795.1	14
[a]**689**	15	978	2412.1	15	[b]**489**	15	148	4562.2	15	854	15	774	2795.1	15
754	16	919	2398.7	16	537	16	[b]**489**	4562.2	16	876	16	637	2754.8	16
756	17	995	2385.2	17	637	17	951	4562.2	17	892	17	951	2748.1	17
[a]**774**	18	[a]**203**	2365.1	18	[b]**767**	18	[b]**767**	4521.9	18	920	18	668	2748.1	18
775	19	578	2358.4	19	892	19	675	4521.9	19	930	19	130	2727.9	19
829	20	[a]**774**	2351.7	20	[bb]**896**	20	774	4508.4	20	960	20	454	2721.2	20
928	21	487	2344.9	21	928	21	253	4508.4	21	18	21	146	2714.5	21
940	22	[a]**90**	2324.8	22	960	22	604	4501.7	22	45	22	751	2694.3	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Wooster, OH in 2011
[bb] Top 5% yield in Wooster, OH in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011

Table 3.12 MAS identifying the bottom 10 % of lines containing the unfavorable allele for the yield QTLs detected using SAS in each environment in Group A. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					**WOOSTER, OH 2011**					**KNOXVILLE, TN 2010-11 WOOSTER, OH 2011**				
MAS		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
916	197	60	1054.9	197	955	197	739	1760.4	197	767	197	248	1458.0	197
930	198	[a]**959**	1014.6	198	965	198	959	1746.9	198	[cc]**800**	198	893	1444.6	198
931	199	89	1001.1	199	981	199	825	1746.9	199	856	199	200	1424.4	199
951	200	[a]**202**	1001.1	200	21	200	464	1740.2	200	883	200	493	1424.4	200
954	201	624	994.4	201	[bb]**105**	201	200	1713.3	201	912	201	739	1397.6	201
957	202	[a]**907**	967.5	202	166	202	421	1693.2	202	[cc]**931**	202	150	1390.8	202
[a]**959**	203	279	967.5	203	248	203	89	1652.9	203	948	203	60	1343.8	203
965	204	[a]**739**	967.5	204	[bb]**277**	204	527	1579.0	204	[c]**959**	204	[c]**959**	1337.1	204
[aa]**974**	205	200	933.9	205	361	205	150	1565.5	205	965	205	277	1323.6	205
108	206	410	920.5	206	[bb]**372**	206	[b]**1015**	1552.1	206	[cc]**974**	206	724	1303.5	206
119	207	893	907.1	207	388	207	893	1518.5	207	[cc]**1015**	207	410	1243.0	207
[a]**202**	208	654	893.6	208	493	208	410	1411.0	208	108	208	[cc]**931**	1243.0	208
[aa]**372**	209	337	860.0	209	598	209	[bb]**615**	1390.8	209	361	209	915	1216.1	209
391	210	379	853.3	210	[bb]**615**	210	[bb]**277**	1269.9	210	376	210	[cc]**800**	1209.4	210
421	211	1015	839.9	211	654	211	[bb]**372**	1249.7	211	391	211	[cc]**974**	1209.4	211
433	212	277	833.2	212	693	212	915	1175.8	212	433	212	379	1189.3	212
590	213	493	819.7	213	721	213	[bb]**105**	1155.7	213	496	213	105	1182.5	213
721	214	915	766.0	214	[bb]**800**	214	[bb]**800**	1095.2	214	587	214	[cc]**1015**	1148.9	214
[a]**739**	215	615	759.2	215	912	215	202	1061.6	215	590	215	876	1142.2	215
[aa]**800**	216	[aa]**800**	745.8	216	954	216	724	981.0	216	693	216	202	1061.6	216
851	217	[aa]**974**	745.8	217	974	217	931	752.5	217	851	217	615	994.4	217
[a]**907**	218	[aa]**372**	685.3	218	[b]**1015**	218	876	689.0	218	901	218	372	772.7	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Wooster, OH in 2011
[bb] Bottom 5% yield in Wooster, OH in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Wooster, OH in 2011

Table 3.13 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using SAS in each environment in Group A compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
18	01	278	01	28	01	481	3319.2	01
90	02	**[b]292**	02	204	02	833	3110.9	02
120	03	754	03	211	03	978	3003.4	03
143	04	**[bb]756**	04	290	04	**[aabbcc]689**	2976.5	04
[aa]144	05	62	05	305	05	**[aa]144**	2969.8	05
203	06	125	06	**[cc]502**	06	463	2956.4	06
204	07	145	07	537	07	675	2875.7	07
266	08	**[b]146**	08	595	08	578	2869.0	08
291	09	261	09	600	09	814	2828.7	09
305	10	291	10	604	10	**[aabbcc]756**	2815.3	10
489	11	337	11	**[cc]689**	11	**[cc]502**	2808.5	11
524	12	341	12	749	12	**[b]292**	2801.8	12
549	13	396	13	**[cc]756**	13	**[b]896**	2801.8	13
[a]668	14	428	14	807	14	632	2795.1	14
[aa]689	15	489	15	854	15	**[a]774**	2795.1	15
754	16	537	16	876	16	**[b]637**	2754.8	16
[aa]756	17	**[b]637**	17	892	17	951	2748.1	17
[a]774	18	767	18	920	18	**[a]668**	2748.1	18
775	19	892	19	930	19	130	2727.9	19
829	20	**[b]896**	20	960	20	454	2721.2	20
928	21	928	21	18	21	**[b]146**	2714.5	21
940	22	960	22	45	22	751	2694.3	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011

Table 3.14 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using SAS in each environment in Group A compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
916	197	955	197	767	197	**[b]248**	1458.0	197
930	198	965	198	**[cc]800**	198	893	1444.6	198
[aa]931	199	981	199	856	199	200	1424.4	199
951	200	21	200	883	200	**[b]493**	1424.4	200
954	201	**[bb]105**	201	912	201	**[a]739**	1397.6	201
957	202	166	202	**[cc]931**	202	150	1390.8	202
[a]959	203	**[b]248**	203	948	203	60	1343.8	203
965	204	**[b]277**	204	**[c]959**	204	**[ac]959**	1337.1	204
[aa]974	205	361	205	965	205	**[b]277**	1323.6	205
108	206	**[bb]372**	206	**[cc]974**	206	724	1303.5	206
119	207	388	207	**[cc]1015**	207	410	1243.0	207
[aa]202	208	**[b]493**	208	108	208	**[aacc]931**	1243.0	208
[aa]372	209	598	209	361	209	915	1216.1	209
391	210	**[bb]615**	210	376	210	**[aabbcc]800**	1209.4	210
421	211	654	211	391	211	**[aabbcc]974**	1209.4	211
433	212	693	212	433	212	379	1189.3	212
590	213	721	213	496	213	**[bb]105**	1182.5	213
721	214	**[bb]800**	214	587	214	**[bbcc]1015**	1148.9	214
[a]739	215	912	215	590	215	876	1142.2	215
[aa]800	216	954	216	693	216	**[aa]202**	1061.6	216
851	217	**[bb]974**	217	851	217	**[bb]615**	994.4	217
907	218	**[bb]1015**	218	901	218	**[aabb]372**	772.7	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011

Table 3.15 Significant (P<0.01) epistatic interactions between loci for yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using R/qtl and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	70.65	W	GM15_10059948_T_C	15	E	15.82	3.12	5.80	3.01
						GM15_50338705_T_C	15	E	79.15	2.77	5.83	3.31
						GM20_41180602_G_A	20	I	64.75	3.01	5.72	3.10
Knoxville, TN 2010	Gm04_48782140_G_T	4	C1	152.98	E	GM06_45433980_G_A	6	C2	71.44	4.22	-0.46	3.09
						GM11_37065128_T_C	11	B1	58.28	4.20	-1.43	1.59
Wooster, OH 2011	Gm19_45198812_C_A	19	L	72.00	W	GM04_11182315_A_G	4	C1	17.58	3.54	0.19	5.91
						GM05_32908802_T_C	5	A1	51.74	5.14	-1.30	5.46
						GM13_28429921_T_C	13	F	44.70	3.68	-0.14	5.81
						GM20_12318232_A_G	20	I	19.37	3.52	5.18	-0.49
Wooster, OH 2011	Gm04_48993297_T_G	4	C1	154.16	E	GM06_49103970_C_T	6	C2	77.21	4.65	-0.65	5.77
						GM10_37618173_A_G	10	O	59.15	5.92	-2.44	4.68
						GM19_44478931_A_G	19	L	69.94	2.67	0.90	6.10
Knoxville, TN 2010-11 Wooster, OH 2011	Gm19_44937486_T_C	19	L	70.75	W	GM05_39611177_C_T	5	A1	62.28	1.94	4.83	7.09
						GM11_38762112_G_T	11	B1	60.95	1.78	4.65	6.70
						GM15_49657706_C_T	15	E	78.08	3.70	7.32	4.30
						GM19_42189531_T_C	19	L	66.34	1.66	9.48	5.19
Knoxville, TN 2010-11 Wooster, OH 2011	Gm05_33176582_G_A	5	A1	33.77	W	GM02_32518097_T_C	2	D1b	51.13	3.69	0.95	-1.62
						GM16_28901653_G_A	16	J	45.44	3.66	1.27	-1.24
						GM20_34223656_G_A	20	I	53.81	3.89	1.40	-1.32
Knoxville, TN 2010-11 Wooster, OH 2011	Gm02_47790307_C_T	2	D1b	150.38	E	GM02_46778366_G_A	2	D1b	73.55	4.42	-1.89	2.85
						GM04_29535808_A_G	4	C1	46.44	3.64	0.04	2.73
						GM18_48533018_G_A	18	D2	76.31	4.13	-0.03	2.88
						GM19_50486916_C_T	19	L	79.38	4.14	0.29	3.13

†Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.16 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by R/qtl to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[abbcc]**833**	01	[aa]**668**	2415.5	814	5227.4	[cc]**481**	3319.2
[bbcc]**481**	02	978	2390.3	292	5166.9	[cc]**833**	3110.9
[aa]**155**	03	632	2380.2	689	5160.2	978	3003.4
[abcc]**675**	04	754	2345.1	559	4998.9	689	2976.5
[bc]**774**	05	[aa]**155**	2341.6	978	4992.2	[cc]**144**	2969.8
[aac]**668**	06	578	2301.1	896	4918.3	463	2956.4
104	07	[aa]**130**	2197.1	[bb]**481**	4904.9	[cc]**675**	2875.7
62	08	143	2197.1	463	4857.8	578	2869.0
[a]**90**	09	689	2163.5	[bb]**144**	4763.8	814	2828.7
[bc]**951**	10	203	2141.7	[bb]**833**	4710.0	756	2815.3
854	11	559	2138.3	146	4669.7	502	2808.5
995	12	480	2133.3	751	4642.8	292	2801.8
[a]**734**	13	[a]**833**	2131.6	211	4636.1	896	2801.8
[a]**919**	14	[a]**865**	2126.6	754	4575.6	632	2795.1
799	15	[a]**675**	2106.4	148	4562.2	[c]**774**	2795.1
1004	16	743	2093.0	489	4562.2	637	2754.8
524	17	[a]**919**	2091.3	[b]**951**	4562.2	[c]**951**	2748.1
[aac]**130**	18	[a]**144**	2077.9	767	4521.9	[c]**668**	2748.1
[a]**865**	19	[a]**734**	2074.5	[b]**675**	4521.9	[c]**130**	2727.9
[abbcc]**144**	20	266	2039.2	[b]**774**	4508.4	[c]**454**	2721.2
156	21	[a]**90**	2030.8	253	4508.4	146	2714.5
[ac]**454**	22	[a]**454**	2029.1	604	4501.7	751	2694.3

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.17 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by SAS to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[a]**266**	01	668	2415.5	814	5227.4	[cc]**481**	3319.2
[bbcc]**481**	02	978	2390.3	292	5166.9	[cc]**833**	3110.9
[abcc]**675**	03	632	2380.2	689	5160.2	978	3003.4
358	04	754	2345.1	559	4998.9	689	2976.5
487	05	155	2341.6	978	4992.2	144	2969.8
[a]**919**	06	[aa]**578**	2301.1	896	4918.3	463	2956.4
[aac]**130**	07	[aa]**130**	2197.1	[bb]**481**	4904.9	[cc]**675**	2875.7
104	08	143	2197.1	463	4857.8	[cc]**578**	2869.0
[b]**148**	09	689	2163.5	144	4763.8	814	2828.7
[a]**865**	10	203	2141.7	[bb]**833**	4710.0	756	2815.3
28	11	559	2138.3	146	4669.7	[cc]**502**	2808.5
892	12	480	2133.3	751	4642.8	292	2801.8
[abbcc]**833**	13	[a]**833**	2131.6	211	4636.1	896	2801.8
854	14	[a]**865**	2126.6	754	4575.6	632	2795.1
[cc]**502**	15	[a]**675**	2106.4	[b]**148**	4562.2	[c]**774**	2795.1
117	16	743	2093.0	489	4562.2	637	2754.8
[bc]**774**	17	[a]**919**	2091.3	951	4562.2	951	2748.1
[a]**90**	18	144	2077.9	767	4521.9	668	2748.1
600	19	[a]**734**	2074.5	[b]**675**	4521.9	[c]**130**	2727.9
[aacc]**578**	20	[a]**266**	2039.2	[b]**774**	4508.4	454	2721.2
524	21	[a]**90**	2030.8	253	4508.4	146	2714.5
[a]**734**	22	454	2029.1	604	4501.7	751	2694.3

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.18 Significant (P<0.01) epistatic interactions between loci for yield in 218 RILs in Group A derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using SAS and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	76.71	W	GM15_10059948_T_C	15	E	17.20	3.12	5.80	3.01
						GM15_50338705_T_C	15	E	86.05	2.77	5.83	3.31
						GM20_41180602_G_A	20	I	70.39	3.01	5.72	3.10
Knoxville, TN 2010	Gm15_43797502_G_T	15	E	72.68	W	GM03_40881828_T_G	3	N	69.88	4.67	-2.65	0.44
						GM10_43894668_A_G	10	O	75.03	3.72	0.17	-2.50
						GM12_38433319_G_A	12	H	65.70	5.78	0.33	-3.11
						GM19_47909005_A_G	19	L	81.90	3.44	-2.78	-4.66
						GM20_26172915_T_C	20	I	44.74	3.75	-2.40	0.24
Knoxville, TN 2010	Gm02_47790307_C_T	2	D1b	121.66	E	GM02_47271538_C_T	2	D1b	80.81	4.07	-1.45	5.76
						GM09_18598782_G_A	9	K	31.79	3.88	2.72	-0.03
						GM15_10416352_C_T	15	E	17.81	4.13	2.98	0.07
Wooster, OH 2011	Gm19_44955912_T_G	19	L	76.84	W	GM15_49657706_C_T	15	E	84.88	3.83	15.80	9.18
						GM17_12291268_A_C	17	D2	21.01	2.20	14.68	9.70
						GM20_45983354_A_C	20	I	78.60	2.85	15.19	9.57
Wooster, OH 2011	Gm10_47585270_T_G	10	O	108.89	E	GM09_20919517_G_T	9	K	35.76	4.05	4.27	-1.73
						GM15_12899200_C_T	15	E	22.05	4.52	3.46	-2.82
						GM16_29930067_A_G	16	J	51.16	3.70	-2.11	3.31
						GM19_49766146_G_A	19	L	85.07	5.38	-2.16	4.94
Wooster, OH 2011	Gm02_49126947_T_C	2	D1b	127.25	E	GM02_42899434_T_C	2	D1b	73.33	5.75	6.47	-0.68
						GM19_48071332_C_A	19	L	82.17	4.79	-0.42	6.11

Table 3.18 Continued.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010-11 Wooster, OH 2011	Gm19_44964042_C_T	19	L	76.91	W	GM05_39611177_C_T	5	A1	67.71	2.25	4.95	7.45
						GM11_30346591_A_G	11	B1	51.87	1.74	4.65	6.73
						GM15_49657706_C_T	15	E	84.88	3.74	7.49	4.40
						GM17_37769057_A_G	17	D2	64.56	1.87	6.80	4.64
						GM19_44658979_A_G	19	L	76.34	1.93	12.14	4.05
Knoxville, TN 2010-11 Wooster, OH 2011	Gm13_27348409_A_G	13	F	150.28	E	GM09_15428656_T_C	9	K	26.37	4.34	2.13	-0.66
						GM12_33656706_G_A	12	H	57.53	6.10	-0.90	2.44
Knoxville, TN 2010-11 Wooster, OH 2011	Gm14_49107190_G_A	14	B2	102.52	W	GM06_48262402_A_G	6	C2	82.50	4.69	-2.58	0.74
						GM17_13589025_G_A	17	D2	23.23	4.11	-2.92	-0.08
Knoxville, TN 2010-11 Wooster, OH 2011	Gm03_47386481_A_C	3	N	120.71	E	GM03_40881828_T_G	3	N	69.88	4.24	2.52	-0.45
						GM19_40201430_T_C	19	L	68.72	3.35	-0.21	2.33
Knoxville, TN 2010-11 Wooster, OH 2011	Gm02_49126947_T_C	2	D1b	127.25	E	GM02_42852580_G_A	2	D1b	73.25	3.99	2.81	-0.04
						GM05_35096373_A_G	5	A1	59.99	3.88	0.20	2.89
						GM19_47254555_T_C	19	L	80.78	4.04	0.01	2.85

† Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.19 Yield prediction model (YPM) developed using QTLs detected in Wooster, OH in 2011 by R/qtl to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments**.** These lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
WOOSTER, OH 2011		KNOXVILLE, TN 2011		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aabbcc]**689**	01	668	2415.5	[bb]**814**	5227.4	[cc]**481**	3319.2
[bbcc]**481**	02	[aa]**978**	2390.3	[bb]**292**	5166.9	[cc]**833**	3110.9
[bc]**951**	03	632	2380.2	[bb]**689**	5160.2	[cc]**978**	3003.4
[bbcc]**463**	04	754	2345.1	559	4998.9	[cc]**689**	2976.5
[abbcc]**144**	05	155	2341.6	[bb]**978**	4992.2	[cc]**144**	2969.8
[bc]**774**	06	578	2301.1	[bb]**896**	4918.3	[cc]**463**	2956.4
[bbcc]**814**	07	130	2197.1	[bb]**481**	4904.9	[cc]**675**	2875.7
[aabbcc]**978**	08	143	2197.1	[bb]**463**	4857.8	578	2869.0
[bbc]**292**	09	[aa]**689**	2163.5	[bb]**144**	4763.8	[cc]**814**	2828.7
[c]**637**	10	203	2141.7	[bb]**833**	4710.0	756	2815.3
[b]**211**	11	559	2138.3	146	4669.7	502	2808.5
[bc]**751**	12	480	2133.3	[b]**751**	4642.8	[c]**292**	2801.8
[bbc]**896**	13	[a]**833**	2131.6	[b]**211**	4636.1	[c]**896**	2801.8
487	14	865	2126.6	754	4575.6	632	2795.1
[c]**146**	15	[a]**675**	2106.4	148	4562.2	[c]**774**	2795.1
854	16	743	2093.0	[b]**489**	4562.2	[c]**637**	2754.8
[b]**489**	17	919	2091.3	[b]**951**	4562.2	[c]**951**	2748.1
[abcc]**675**	18	[a]**144**	2077.9	767	4521.9	668	2748.1
86	19	734	2074.5	[b]**675**	4521.9	130	2727.9
[abbcc]**833**	20	266	2039.2	[b]**774**	4508.4	[c]**454**	2721.2
72	21	90	2030.8	253	4508.4	[c]**146**	2714.5
[ac]**454**	22	[a]**454**	2029.1	604	4501.7	[c]**751**	2694.3

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.20 Yield prediction model (YPM) developed using QTLs detected in Wooster, OH in 2011 by SAS to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
WOOSTER, OH 2011		KNOXVILLE, TN 2011		WOOSTER, OH 2011		KNOXVILLE, TN 2010-11 WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bbc]**896**	01	668	2415.5	[bb]**814**	5227.4	481	3319.2
[bbc]**292**	02	978	2390.3	[bb]**292**	5166.9	833	3110.9
[bc]**774**	03	632	2380.2	[bb]**689**	5160.2	978	3003.4
337	04	754	2345.1	[bb]**559**	4998.9	[cc]**689**	2976.5
[aabbcc]**689**	05	155	2341.6	978	4992.2	[cc]**144**	2969.8
[b]**211**	06	578	2301.1	[bb]**896**	4918.3	463	2956.4
290	07	130	2197.1	481	4904.9	675	2875.7
[bbcc]**814**	08	143	2197.1	463	4857.8	578	2869.0
[aa]**203**	09	[aa]**689**	2163.5	[bb]**144**	4763.8	[cc]**814**	2828.7
278	10	[aa]**203**	2141.7	833	4710.0	756	2815.3
134	11	[aa]**559**	2138.3	146	4669.7	[cc]**502**	2808.5
[cc]**502**	12	480	2133.3	[b]**751**	4642.8	[c]**292**	2801.8
928	13	833	2131.6	[b]**211**	4636.1	[c]**896**	2801.8
[c]**637**	14	865	2126.6	754	4575.6	632	2795.1
[bc]**751**	15	675	2106.4	[b]**148**	4562.2	[c]**774**	2795.1
[b]**148**	16	743	2093.0	489	4562.2	[c]**637**	2754.8
757	17	919	2091.3	[b]**951**	4562.2	[c]**951**	2748.1
609	18	[a]**144**	2077.9	767	4521.9	668	2748.1
[abbcc]**144**	19	734	2074.5	675	4521.9	130	2727.9
[aabb]**559**	20	266	2039.2	[b]**774**	4508.4	454	2721.2
[bc]**951**	21	90	2030.8	253	4508.4	146	2714.5
481	22	454	2029.1	604	4501.7	[c]**751**	2694.3

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.21 Yield prediction model (YPM) developed using QTLs detected over three environments by R/qtl to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 WOOSTER, OH 2011				KNOXVILLE, TN 2011		WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
134	01	**[aa]481**	3319.2	668	2415.5	814	5227.4
[aabcc]144	02	**[aa]833**	3110.9	**[bb]978**	2390.3	**[cc]292**	5166.9
[aacc]481	03	**[aa]978**	3003.4	632	2380.2	**[cc]689**	5160.2
[acc]146	04	689	2976.5	**[bb]754**	2345.1	559	4998.9
[bb]203	05	**[aa]144**	2969.8	155	2341.6	**[cc]978**	4992.2
[aabbcc]978	06	**[aa]463**	2956.4	**[bb]578**	2301.1	**[cc]896**	4918.3
[aabcc]833	07	**[aa]675**	2875.7	130	2197.1	**[cc]481**	4904.9
[bbc]754	08	**[aa]578**	2869.0	143	2197.1	**[cc]463**	4857.8
[b]919	09	814	2828.7	**[bb]689**	2163.5	**[cc]144**	4763.8
[ac]774	10	756	2815.3	**[bb]203**	2141.7	**[cc]833**	4710.0
[acc]896	11	502	2808.5	559	2138.3	**[cc]146**	4669.7
451	12	**[a]292**	2801.8	480	2133.3	**[c]751**	4642.8
[bbcc]689	13	**[a]896**	2801.8	**[b]833**	2131.6	211	4636.1
[c]148	14	632	2795.1	865	2126.6	**[c]754**	4575.6
[aabc]675	15	**[a]774**	2795.1	**[b]675**	2106.4	**[c]148**	4562.2
[aacc]463	16	637	2754.8	743	2093.0	489	4562.2
156	17	951	2748.1	**[b]919**	2091.3	951	4562.2
[acc]292	18	668	2748.1	**[b]144**	2077.9	767	4521.9
756	19	130	2727.9	734	2074.5	**[c]675**	4521.9
[aabb]578	20	454	2721.2	266	2039.2	**[c]774**	4508.4
807	21	**[a]146**	2714.5	90	2030.8	253	4508.4
[ac]751	22	**[a]751**	2694.3	454	2029.1	604	4501.7

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.22 Yield prediction model (YPM) developed using QTLs detected over three environments by SAS to select by MAS the top yielding 10 % of RILs in Group A grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 WOOSTER, OH 2011				KNOXVILLE, TN 2011		WOOSTER, OH 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bbc]754	01	**[aa]481**	3319.2	**[bb]668**	2415.5	**[cc]814**	5227.4
[acc]896	02	**[aa]833**	3110.9	**[bb]978**	2390.3	**[cc]292**	5166.9
[aabbcc]978	03	**[aa]978**	3003.4	632	2380.2	**[cc]689**	5160.2
[aabcc]144	04	**[aa]689**	2976.5	**[bb]754**	2345.1	559	4998.9
[aabbcc]689	05	**[aa]144**	2969.8	155	2341.6	**[cc]978**	4992.2
[aacc]481	06	463	2956.4	578	2301.1	**[cc]896**	4918.3
[aa]756	07	675	2875.7	130	2197.1	**[cc]481**	4904.9
278	08	578	2869.0	143	2197.1	463	4857.8
[bb]203	09	**[aa]814**	2828.7	**[bb]689**	2163.5	**[cc]144**	4763.8
[aacc]814	10	**[aa]756**	2815.3	**[bb]203**	2141.7	**[cc]833**	4710.0
[ac]751	11	**[aa]502**	2808.5	559	2138.3	**[cc]146**	4669.7
[acc]146	12	**[a]292**	2801.8	480	2133.3	**[c]751**	4642.8
[aa]502	13	**[a]896**	2801.8	**[b]833**	2131.6	**[c]211**	4636.1
[b]90	14	632	2795.1	865	2126.6	**[c]754**	4575.6
[acc]292	15	774	2795.1	675	2106.4	148	4562.2
125	16	637	2754.8	743	2093.0	**[c]489**	4562.2
[c]211	17	951	2748.1	919	2091.3	951	4562.2
[c]489	18	**[a]668**	2748.1	**[b]144**	2077.9	767	4521.9
[abb]668	19	130	2727.9	734	2074.5	675	4521.9
[aabcc]833	20	454	2721.2	266	2039.2	774	4508.4
995	21	**[a]146**	2714.5	**[b]90**	2030.8	253	4508.4
156	22	**[a]751**	2694.3	454	2029.1	604	4501.7

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Wooster, OH in 2011 and combined over Knoxville, TN in 2010, 2011 and Wooster, OH in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.23 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in three environments: Knoxville, TN in 2010 and 2011 and Belleville, IL in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	h^2	P-VALUE	F-VALUE
Environment	2	46030.86	102.69	56		<0.0001	1385.84
Reps (Env.)	2	847.84	3.02	2		<0.0001	25.74
Genotypes	220	182.17	15.51	8	0.40	0.0002	5.48
Genotypes x Env.	220	89.12	27.94	15		0.004	2.64
Error	440	33.23	33.83	19			

Table 3.24 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Knoxville, TN in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	63.26	30.28	34	0.024	1.50
Genotypes	220	78.58	18.24	21	0.012	1.86
Error	221	42.09	40.4	45		

Table 3.25 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Belleville, IL in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	684.03	46.37	53	<0.0001	27.54
Genotypes	220	54.96	15.1	18	<0.0001	2.21
Error	221	24.83	24.63	29		

Table 3.26 Mean seed yield, maturity, lodging and height of 221 recombinant inbred lines in Group B and two commercial checks grown in Knoxville, TN in 2010 and 2011, Belleville, IL in 2011 and averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011.

ExW50K Group B		ACROSS LOCATIONS				TENNESSEE 2011				ILLINOIS 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha⁻¹	LODG†	MAT‡	HGT cm	YIELD kg ha⁻¹	LODG†	MAT‡	HGT cm	YIELD kg ha⁻¹	LODG†	MAT‡	HGT cm	YIELD kg ha⁻¹	LODG†	MAT‡	HGT cm
550	01	3135.5	1.8	278	45	2072.8	2.0	271	58	4081.8	1.5	291	71	3252.0	2	273	56
676	02	3123.2	1.5	278	69	1935.1	1.5	270	52	4128.8	1.0	291	76	3305.7	2	273	79
IA4005	**03**	**3069.0**	**1.6**	**277**	**45**	**2065.1**	**1.9**	**263**	**7**	**4072.8**	**1.3**	**290**	**83**	**.**	**.**	**.**	**.**
172	04	3044.8	2.8	277	97	2062.7	3.0	269	89	4202.7	2.5	288	112	2869.0	3	273	91
722	05	3015.7	3.2	275	90	2375.2	4.0	274	128	3863.4	2.5	285	71	2808.5	3	267	71
681	06	3006.8	2.5	274	69	1760.4	3.0	267	84	3678.7	2.5	289	64	3581.2	2	267	58
LD00-3309	**07**	**2932.8**	**1.8**	**275**	**75**	**2062.7**	**2.0**	**268**	**56**	**3803.0**	**1.5**	**283**	**94**	**.**	**.**	**.**	**.**
702	08	2917.2	2.5	275	97	2344.9	4.5	273	100	3645.1	1.0	284	98	2761.5	2	269	91
332	09	2908.2	1.8	274	59	2079.5	2.5	267	48	3695.5	1.0	287	70	2949.6	2	270	58
888	10	2903.7	2.2	274	72	2066.1	2.5	273	66	3897.0	2.0	284	77	2748.1	2	266	71
1013	11	2903.4	2.8	278	95	2139.0	2.5	269	76	3500.6	3.0	292	113	3070.6	3	273	97
665	12	2901.5	2.2	276	72	2096.3	3.5	265	72	3584.6	1.0	290	74	3023.6	2	273	69
330	13	2889.2	2.5	274	77	2123.2	2.0	267	56	3661.9	2.5	286	102	2882.5	3	269	74
197	14	2878.0	2.3	277	77	1673.0	3.0	268	69	3473.7	2.0	289	88	3487.2	2	273	76
694	15	2873.5	2.7	279	88	2301.3	3.5	272	80	3221.8	2.5	291	94	3097.5	2	273	89
970	16	2865.7	2.5	278	73	1928.4	2.5	270	58	3860.1	3.0	290	80	2808.5	2	273	81
346	17	2863.4	2.3	277	86	2257.6	3.5	271	122	3732.4	1.5	289	77	2600.3	2	270	58
383	18	2861.2	2.2	276	79	1451.3	3.0	270	81	4007.9	1.5	288	85	3124.3	2	269	71
1008	19	2860.1	2.0	276	72	1958.6	2.0	269	55	3732.4	2.0	289	77	2889.2	2	270	84
362	20	2853.3	2.8	279	81	2049.3	2.5	270	67	3903.7	3.0	293	95	2607.0	3	273	81
826	21	2852.2	3.5	276	81	1750.3	3.0	266	74	4078.4	3.5	290	93	2727.9	4	273	76
881	22	2847.7	1.7	273	63	1982.1	2.0	266	51	4021.3	1.0	287	72	2539.8	2	266	66
65	23	2843.3	2.2	275	73	2351.7	3.0	269	84	4263.2	1.5	287	80	1914.9	2	268	56
922	24	2843.3	3.3	279	108	2136.6	3.5	272	113	3839.9	2.5	291	116	2553.2	4	273	94
518	25	2833.2	3.3	279	88	2415.5	2.0	274	64	3315.8	4.0	291	113	2768.2	4	273	89
272	26	2830.9	2.0	276	57	1773.8	2.0	268	41	3782.8	2.0	286	80	2936.2	2	273	51
619	27	2825.3	2.0	278	72	1810.8	2.0	271	61	3917.2	2.0	289	80	2748.1	2	273	76
439	28	2822.0	2.0	273	75	1918.3	3.0	271	84	4075.1	1.0	284	77	2472.6	2	265	64
738	29	2822.0	2.8	276	71	1743.6	3.5	273	84	3772.7	3.0	289	65	2949.6	2	267	64
413	30	2817.5	3.5	278	111	2190.4	4.5	270	123	3285.6	3.0	292	117	2976.5	3	273	94
872	31	2817.5	2.0	277	79	2180.3	2.0	270	47	3846.6	2.0	291	102	2425.6	2	270	89
162	32	2814.1	2.2	277	74	2056.0	2.0	268	60	3799.6	2.5	291	89	2586.8	2	273	74
184	33	2814.1	2.0	274	84	2173.6	2.5	269	76	3507.3	1.5	286	83	2761.5	2	268	94
411	34	2789.5	1.8	271	72	1659.6	2.0	264	70	3806.3	1.5	284	75	2902.6	2	266	71
321	35	2788.7	2.5	275	65	2100.7	2.0	265	55	3604.7	2.5	290	79	2660.7	3	269	61
672	36	2782.8	2.3	278	88	2523.0	2.0	270	56	3272.2	2.0	292	99	2553.2	3	273	109
415	37	2780.5	2.5	276	90	2311.3	3.5	271	90	3577.9	2.0	290	97	2452.4	2	267	84
625	38	2778.3	2.7	277	83	2042.6	3.0	271	97	3873.5	3.0	290	84	2418.8	2	270	69
998	39	2773.8	2.3	275	83	1770.5	2.5	265	62	3903.7	2.5	289	97	2647.3	2	273	89
205	40	2772.7	2.3	275	79	2422.2	4.0	269	112	3524.1	1.0	286	67	2371.8	2	270	58
887	41	2772.7	2.7	278	82	1632.7	4.0	271	85	3749.2	2.0	292	85	2936.2	2	270	76
478	42	2771.6	3.5	276	75	2052.7	3.0	267	67	3157.9	4.5	289	77	3104.2	3	273	81
1002	43	2771.6	2.2	275	70	2015.7	2.0	266	46	3537.6	2.5	289	80	2761.5	2	269	84
793	44	2770.1	3.5	278	91	1688.8	2.5	271	74	3907.1	4.0	289	107	2714.5	4	273	94
753	45	2767.1	3.2	276	96	2079.5	3.5	270	83	3661.9	3.0	287	104	2559.9	3	270	102
298	46	2764.9	2.8	277	70	2109.8	3.5	268	74	3551.0	3.0	289	65	2633.8	2	273	71
375	47	2760.4	2.7	272	81	1817.5	4.0	265	99	3883.6	2.0	285	81	2580.1	2	267	64
397	48	2758.1	2.0	274	78	2143.4	2.5	270	81	3416.6	1.5	288	74	2714.5	2	264	79
900	49	2758.1	2.0	276	83	2039.2	2.0	273	58	3587.9	2.0	286	99	2647.3	2	270	91
879	50	2757.0	2.2	275	72	1834.3	2.5	271	74	3856.7	2.0	288	61	2580.1	2	267	81
570	51	2753.7	2.3	274	71	1965.3	3.0	269	81	4004.5	2.0	285	71	2291.2	2	267	61
561	52	2752.6	2.3	274	79	1931.7	2.5	268	79	3504.0	2.5	286	84	2822.0	2	267	74
307	53	2744.7	2.7	277	62	2079.5	2.0	271	52	3601.4	3.0	289	80	2553.2	3	270	53
431	54	2741.4	3.5	277	102	1995.5	3.0	270	100	3372.9	3.5	290	113	2855.6	4	273	94
367	55	2732.4	3.3	279	65	1878.0	4.0	273	95	3725.7	3.0	292	93	2593.5	3	273	8
88	56	2729.0	3.0	275	90	2066.1	3.5	270	93	3695.5	2.5	286	94	2425.6	3	270	84
792	57	2729.0	2.3	273	66	1995.5	2.0	267	62	3671.9	3.0	285	75	2519.6	2	268	61
25	58	2715.6	2.7	275	73	1820.8	3.0	266	64	3604.7	2.0	289	86	2721.2	3	270	69
804	59	2714.5	1.8	277	66	2093.0	2.0	268	42	3416.6	1.5	289	74	2633.8	2	273	81
123	60	2710.0	3.0	274	95	1921.6	2.5	260	65	3648.4	3.5	290	123	2559.9	3	273	97
392	61	2707.8	2.8	274	74	2129.9	2.0	269	55	3520.8	3.5	285	80	2472.6	3	267	86
728	62	2707.8	2.3	275	73	2187.0	3.5	266	74	3470.4	1.5	290	77	2465.9	2	269	69
42	63	2705.5	2.2	277	79	1663.0	3.0	268	76	3436.8	1.5	291	80	3016.8	2	273	81
259	64	2699.9	1.8	271	69	1938.4	2.0	267	46	3198.2	1.5	284	75	2963.1	2	264	86
322	65	2699.9	2.7	276	76	1918.3	3.5	268	76	3635.0	2.5	290	84	2546.5	2	270	69
171	66	2696.6	2.0	273	81	2277.7	3.0	269	93	3621.5	1.0	283	81	2190.4	2	267	69
708	67	2696.6	1.8	276	66	1750.3	2.0	267	51	3537.6	1.5	287	91	2801.8	2	273	56
294	68	2695.4	3.5	278	107	2143.4	5.0	270	107	3275.5	2.5	292	113	2667.4	3	273	102
939	69	2689.5	2.2	276	77	2165.9	2.5	272	70	3537.6	2.0	287	86	2365.1	2	270	76
7	70	2685.4	2.2	274	73	1646.2	3.5	266	75	3372.9	1.0	288	79	3037.0	2	268	66
886	71	2684.2	2.2	274	79	1931.7	2.5	268	76	3554.4	2.0	285	83	2566.7	2	270	79
884	72	2676.4	2.0	276	83	1888.0	2.0	269	56	3339.3	2.0	287	103	2801.8	2	273	91
32	73	2670.8	2.5	276	99	1965.3	2.0	266	64	3406.5	2.5	290	113	2640.6	3	273	122
783	74	2657.4	1.8	278	75	1918.3	2.0	271	56	3339.3	1.5	290	95	2714.5	2	273	74

Table 3.26 Continued.

ExW50K Group B		ACROSS LOCATIONS				TENNESSEE 2011				ILLINOIS 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
470	75	2656.2	3.2	276	101	2052.7	3.5	268	103	3383.0	3.0	291	116	2533.1	3	270	84
329	76	2645.0	3.3	277	98	1414.3	3.0	271	80	3954.1	4.0	288	118	2566.7	3	273	97
Essex	**77**	**2643.9**	**2.0**	**278**	**65**	**1676.4**	**2.5**	**271**	**44**	**3611.5**	**1.5**	**286**	**86**	**.**	**.**	**.**	**.**
354	78	2643.9	3.3	276	89	1797.3	5.0	272	103	3534.2	2.0	289	76	2600.3	3	268	89
189	79	2640.6	3.3	277	102	1421.1	5.0	267	94	3510.7	3.0	290	116	2990.0	2	273	97
47	80	2638.3	3.8	278	83	1972.0	2.5	270	53	3168.0	5.0	290	113	2774.9	4	273	84
597	81	2636.1	2.5	273	69	1542.0	2.5	266	47	3571.1	3.0	286	77	2795.1	2	267	81
227	82	2633.8	3.0	279	92	1810.8	2.5	272	66	3443.5	2.5	292	119	2647.3	4	273	91
422	83	2632.7	2.8	275	84	1847.7	3.5	263	62	3537.6	2.0	292	105	2512.9	3	270	84
302	84	2629.4	3.2	274	102	2244.1	4.0	271	105	3359.5	2.5	285	107	2284.5	3	267	94
853	85	2629.4	1.8	275	68	2022.4	2.0	271	47	3735.8	1.5	287	76	2129.9	2	268	81
77	86	2627.1	4.0	275	100	2113.1	3.5	266	83	3322.5	4.5	291	112	2445.7	4	269	107
707	87	2627.1	3.0	275	78	1676.4	3.5	268	81	3833.2	3.5	289	84	2371.8	2	269	69
384	88	2624.9	3.0	277	103	1965.3	4.0	273	117	3786.2	3.0	289	119	2123.2	2	270	74
731	89	2619.3	2.7	276	91	2032.5	3.0	268	89	3803.0	3.0	289	102	2022.4	2	270	81
24	90	2614.8	3.3	276	97	2368.4	3.0	269	76	3661.9	4.0	290	123	1814.1	3	269	91
38	91	2614.8	2.8	275	100	1676.4	3.5	262	91	3372.9	2.0	290	112	2795.1	3	273	97
778	92	2614.8	1.8	275	64	2029.1	2.0	268	43	3470.4	1.5	287	77	2344.9	2	269	71
342	93	2610.3	2.7	274	65	1518.5	3.5	272	71	3900.4	2.5	285	64	2412.1	2	266	61
567	94	2609.2	2.3	276	82	2163.5	2.0	270	50	3413.3	3.0	289	112	2250.9	2	270	84
795	95	2609.2	2.5	272	65	1841.0	2.5	265	62	3426.7	3.0	285	72	2559.9	2	267	61
986	96	2608.1	2.8	276	81	1841.0	2.5	271	90	3530.8	3.0	290	75	2452.4	3	268	79
357	97	2596.9	2.3	277	65	1626.0	3.5	274	50	3624.9	1.5	288	79	2539.8	2	270	66
533	98	2596.9	2.2	275	64	1555.4	3.0	268	66	3984.4	1.5	287	72	2250.9	2	269	53
687	99	2596.9	4.0	275	93	1807.4	4.5	268	131	3141.1	4.5	288	85	2842.1	3	268	64
128	100	2595.8	2.5	276	66	1673.0	2.0	266	48	3661.9	2.5	291	83	2452.4	3	270	69
653	101	2590.2	1.8	276	72	1380.8	2.5	269	71	3406.5	1.0	286	74	2983.2	2	273	71
437	102	2585.7	2.7	277	96	1928.4	2.5	271	75	3940.7	2.5	291	122	1888.0	3	270	91
946	103	2585.7	2.3	274	75	1495.0	3.0	268	79	3561.1	2.0	287	79	2701.0	2	266	69
218	104	2582.3	2.7	277	92	1491.6	2.0	266	52	3352.8	2.0	292	108	2902.6	4	273	117
5	105	2580.1	3.0	279	91	1713.3	3.0	270	69	3446.8	3.0	289	113	.	.	.	.
452	106	2580.1	2.0	273	78	1723.4	2.5	268	91	3456.9	1.5	287	74	2559.9	2	266	69
831	107	2575.6	2.0	277	71	2183.7	2.5	273	60	3352.8	1.5	288	76	2190.4	2	269	76
8	108	2570.0	2.5	276	74	2069.5	3.0	272	90	3537.6	1.5	289	74	2103.0	3	267	58
366	109	2567.8	3.5	279	88	1780.5	3.5	272	90	3322.5	4.0	291	97	2600.3	3	273	79
163	110	2565.5	2.2	273	80	1854.4	2.0	269	48	3430.0	2.5	285	107	2412.1	2	266	84
275	111	2565.5	2.3	269	80	1481.5	3.0	263	74	3386.4	2.0	277	94	2828.7	2	267	71
99	112	2564.4	2.7	275	94	2129.9	3.0	266	75	3379.7	2.0	288	116	2183.7	3	271	91
486	113	2563.3	3.2	275	73	1602.5	3.0	271	80	3561.1	3.5	287	76	2526.3	3	267	64
127	114	2562.2	2.0	274	61	1998.9	2.5	267	69	3745.8	1.5	287	108	1941.8	2	268	5
267	115	2561.1	3.3	278	86	1417.7	2.0	271	69	3362.9	4.0	289	109	2902.6	4	273	81
968	116	2558.8	2.0	272	85	1867.9	2.0	259	58	3362.9	2.0	289	112	2445.7	2	269	84
569	117	2557.7	3.3	276	80	1961.9	2.5	268	97	3829.8	4.5	291	76	1881.3	3	268	69
11	118	2545.4	2.3	273	90	1394.2	3.0	265	76	3970.9	2.0	286	113	2271.0	2	270	81
952	119	2545.4	1.7	276	59	2234.1	2.0	267	55	3608.1	1.0	290	58	1794.0	2	270	64
46	120	2542.0	3.5	277	89	2076.2	3.0	270	89	3043.7	4.5	290	89	2506.2	3	270	89
82	121	2529.7	2.2	273	71	1757.0	3.0	265	61	3540.9	1.5	285	71	2291.2	2	268	81
92	122	2527.5	3.0	272	98	1686.5	3.5	263	108	3456.9	2.5	285	95	2439.0	3	267	91
380	123	2527.5	3.0	276	78	1579.0	2.0	263	52	3228.5	4.0	291	89	2774.9	3	273	94
638	124	2527.5	2.3	273	95	2126.6	3.0	267	79	3547.6	2.0	286	113	1908.2	2	267	94
355	125	2524.1	2.3	274	81	1545.4	2.0	261	66	3399.8	3.0	287	108	2627.1	2	273	69
326	126	2519.6	1.7	272	62	2062.7	2.0	270	53	3198.2	1.0	284	64	2297.9	2	264	69
726	127	2517.4	2.3	273	69	2039.2	2.0	263	53	3248.6	3.0	289	81	2264.3	2	268	71
683	128	2516.3	2.7	276	97	2002.3	3.0	272	80	3591.3	2.0	287	105	1955.2	3	269	107
114	129	2515.1	2.7	275	85	1572.2	3.5	260	90	3500.6	2.5	292	91	2472.6	2	272	74
351	130	2514.0	3.7	274	74	1619.3	2.5	262	46	3624.9	4.5	290	84	2297.9	4	270	91
519	131	2514.0	2.2	273	65	1773.8	3.5	270	86	3342.7	1.0	284	55	2425.6	2	265	53
498	132	2511.5	3.3	277	89	1520.9	4.0	274	83	3574.5	2.0	288	102	2439.0	4	270	84
217	133	2510.7	2.2	274	91	1871.2	2.5	264	83	3551.0	2.0	288	110	2109.8	2	271	81
312	134	2509.5	2.2	276	58	1800.7	2.0	272	53	3174.7	1.5	286	62	2553.2	3	269	58
747	135	2508.4	2.7	276	87	1626.0	3.0	268	71	3561.1	2.0	291	99	2338.2	3	269	91
691	136	2506.2	2.3	272	91	1911.6	3.0	270	81	2966.4	1.0	279	97	2640.6	3	267	94
54	137	2501.7	2.2	276	70	1878.0	3.0	271	74	3443.5	1.5	288	77	2183.7	2	269	58
586	138	2490.5	2.5	273	78	1101.9	4.0	268	88	3534.2	1.5	285	69	2835.4	2	266	79
542	139	2489.4	1.8	273	70	1471.5	2.0	267	44	3443.5	1.5	284	90	2553.2	2	269	76
230	140	2488.3	3.0	274	67	1636.1	2.0	264	44	3295.7	4.0	289	80	2533.1	3	270	76
234	141	2486.0	3.2	275	96	1327.0	3.5	269	71	3470.4	2.0	287	110	2660.7	4	270	107
547	142	2481.5	3.0	275	80	2257.6	2.0	269	55	3305.7	3.0	287	102	1881.3	4	269	84
250	143	2477.1	2.2	277	75	1390.8	2.0	271	56	3379.7	2.5	290	89	2660.7	2	269	79
111	144	2470.4	1.8	275	70	2116.5	2.0	270	58	2996.7	1.5	287	85	2297.9	2	267	66
247	145	2469.2	2.5	277	78	1693.2	3.0	270	85	3678.7	2.5	291	83	2035.9	2	270	66
780	146	2468.1	2.7	276	88	1884.7	3.0	270	89	3201.6	2.0	287	93	2318.1	3	270	84
17	147	2456.9	2.7	276	78	2009.0	3.5	271	80	3453.6	2.5	288	88	1908.2	2	269	66
196	148	2456.9	2.0	274	72	1411.0	3.0	259	58	3339.3	1.0	289	81	2620.4	2	273	76
852	149	2456.9	2.2	274	85	1750.3	3.0	268	79	3403.2	1.5	285	94	2217.3	2	270	81
293	150	2454.7	2.8	277	81	2140.0	1.5	270	47	3409.9	4.0	291	122	1814.1	3	270	74
153	151	2453.6	3.3	275	99	2402.0	3.0	270	81	2754.8	4.0	286	126	2203.8	3	270	89
880	152	2453.6	1.8	273	66	1753.7	2.0	266	56	3248.6	1.5	287	77	2358.4	2	267	64
110	153	2443.5	2.5	275	78	2086.2	3.5	269	85	3121.0	2.0	287	84	2123.2	2	270	66

Table 3.26 Continued.

ExW50K Group B		ACROSS LOCATIONS				TENNESSEE 2011				ILLINOIS 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
116	154	2433.4	1.7	274	65	1390.8	2.0	264	55	3463.6	1.0	289	80	2445.7	2	270	61
646	155	2423.3	2.7	272	102	1955.2	4.0	271	113	3547.6	2.0	281	107	1767.1	2	265	86
385	156	2422.2	3.0	277	91	2271.0	3.0	273	81	3262.1	3.0	288	117	1733.5	3	270	74
1001	157	2421.1	2.5	275	69	2079.5	3.0	270	74	3194.9	2.5	287	66	1988.8	2	267	66
663	158	2414.4	2.3	274	84	2015.7	3.5	270	88	3057.1	1.5	283	90	2170.2	2	269	74
264	159	2412.1	2.5	273	69	2015.7	3.5	265	72	3205.0	2.0	286	70	2015.7	2	268	66
551	160	2409.9	3.3	275	64	1458.0	3.0	267	71	3587.9	4.0	289	114	2183.7	3	269	8
655	161	2402.0	3.3	275	91	2035.9	2.5	264	77	3376.3	4.5	290	118	1794.0	3	270	76
860	162	2399.8	2.7	272	64	1531.9	3.0	264	62	3477.1	3.0	286	75	2190.4	2	268	53
256	163	2396.4	2.5	276	63	1417.7	1.5	267	47	3621.5	3.0	290	72	2150.1	3	270	69
947	164	2385.2	2.5	276	94	1998.9	3.0	272	83	3235.2	2.5	286	110	1921.6	2	270	89
520	165	2381.9	2.3	274	91	2129.9	2.0	266	60	3309.1	3.0	288	118	1706.6	2	269	94
695	166	2381.9	2.2	272	64	1458.0	3.0	266	79	3712.2	1.5	283	67	1975.4	2	267	46
568	167	2379.6	1.7	276	57	2173.6	2.0	269	44	3594.7	2.0	290	71	1370.7	1	269	56
257	168	2377.1	1.7	277	59	1473.8	2.0	272	38	3628.3	1.0	290	76	2029.1	2	269	64
269	169	2373.7	2.2	275	68	1588.0	2.5	271	67	3329.3	2.0	286	71	2203.8	2	268	66
554	170	2371.8	2.5	275	91	1908.2	3.0	265	89	3433.4	2.5	290	113	1773.8	2	270	71
606	171	2371.8	2.8	275	73	1787.3	2.5	269	75	3312.5	4.0	290	75	2015.7	2	267	69
765	172	2364.0	2.0	275	87	2005.6	3.0	273	79	3252.0	1.0	283	112	1834.3	2	268	71
313	173	2361.7	3.0	272	78	2015.7	3.5	261	62	3470.4	3.5	287	103	1599.1	2	267	69
251	174	2360.6	2.2	273	69	1841.0	3.0	260	64	3413.3	1.5	287	80	1827.6	2	271	64
473	175	2359.5	1.5	275	63	1552.1	2.0	270	66	3329.3	1.5	287	64	2197.1	1	268	58
417	176	2357.2	3.3	274	105	1736.9	4.0	268	105	3252.0	3.0	289	116	2082.9	3	266	94
98	177	2356.1	3.3	273	73	1975.4	3.5	268	65	3238.6	3.5	285	77	1854.4	3	267	76
446	178	2356.1	1.8	276	59	1595.8	2.0	267	42	3618.2	1.5	290	90	1854.4	2	270	46
132	179	2355.0	2.8	277	80	2170.2	2.5	271	64	2596.9	3.0	290	97	2297.9	3	271	81
718	180	2355.0	3.5	276	105	1925.0	2.5	268	75	3440.1	4.0	289	132	1699.9	4	271	107
925	181	2350.5	2.8	274	91	1397.6	4.5	263	91	3134.4	2.0	290	90	2519.6	2	269	91
560	182	2343.8	2.5	276	87	2146.7	3.5	273	95	3010.1	2.0	289	102	1874.6	2	267	64
395	183	2341.6	1.7	273	66	1894.8	2.0	270	56	2966.4	1.0	284	75	2163.5	2	266	66
580	184	2338.2	2.0	275	76	1780.5	2.0	270	43	3285.6	2.0	288	108	1948.5	2	268	76
467	185	2329.3	2.7	278	90	1807.4	3.0	271	76	3238.6	2.0	292	110	1941.8	3	271	84
983	186	2324.8	2.2	276	85	2213.9	3.5	271	113	3470.4	1.0	288	75	1290.0	2	270	66
667	187	2320.3	2.0	276	64	1824.2	2.0	271	55	3215.0	2.0	290	75	1921.6	2	268	61
742	188	2320.3	2.2	275	64	1632.7	3.0	270	76	3097.5	1.5	286	64	2230.7	2	269	53
304	189	2319.2	2.2	276	64	1733.5	3.0	270	60	3423.3	1.5	289	76	1800.7	2	268	56
370	190	2313.6	2.2	276	86	2019.1	3.5	272	84	3463.6	1.0	286	103	1458.0	2	270	71
26	191	2311.3	2.8	275	97	2035.9	3.5	268	76	3272.2	3.0	287	132	1626.0	2	270	84
215	192	2297.9	2.2	275	85	1777.2	2.5	265	71	3403.2	2.0	289	107	1713.3	2	272	76
131	193	2291.2	2.3	274	77	1797.3	3.0	269	88	2993.3	2.0	285	80	2082.9	2	268	64
961	194	2277.7	1.8	271	60	1451.3	2.0	267	47	3507.3	1.5	283	81	1874.6	2	264	51
16	195	2275.5	3.0	274	94	1172.5	3.5	261	84	3671.9	2.5	291	110	1982.1	3	269	89
479	196	2275.5	2.5	272	101	2207.2	4.0	271	114	3255.4	1.5	280	104	1364.0	2	266	84
499	197	2272.1	2.3	275	85	2059.4	3.5	271	75	2627.1	1.5	284	100	2129.9	2	270	79
652	198	2267.7	3.2	275	103	1790.6	4.0	274	117	3124.3	2.5	286	110	1888.0	3	267	81
660	199	2264.3	2.2	275	72	1891.4	2.5	267	66	3349.4	2.0	288	90	1552.1	2	270	61
644	200	2262.1	2.3	275	91	1763.7	2.5	269	81	3114.3	2.5	288	109	1908.2	2	268	84
577	201	2253.4	2.2	273	78	1838.6	2.5	270	76	3396.5	2.0	283	93	1525.2	2	265	66
511	202	2247.5	2.2	275	71	1703.3	2.0	270	52	3198.2	2.5	287	89	1841.0	2	267	71
107	203	2224.0	2.0	271	60	1935.1	3.0	268	61	3124.3	1.0	282	74	1612.6	2	264	46
594	204	2213.9	2.7	276	98	1904.8	4.0	270	107	2680.9	2.0	289	95	2056.0	2	270	91
483	205	2209.4	2.7	274	58	1384.1	3.5	269	67	3013.5	2.5	285	62	2230.7	2	268	43
245	206	2203.8	2.7	273	58	1128.8	2.5	257	29	3581.2	3.5	291	80	1901.5	2	270	66
661	207	2203.8	2.7	274	85	1807.4	3.0	267	65	2942.9	2.0	288	99	1861.2	3	267	91
643	208	2197.1	2.2	276	66	1646.2	3.0	268	81	3272.2	1.5	291	61	1673.0	2	270	56
698	209	2177.7	2.8	274	71	1265.5	3.5	268	71	3366.2	3.0	287	85	1901.5	2	268	56
608	210	2171.4	2.2	269	61	1145.6	1.5	259	39	2922.8	3.0	284	79	2445.7	2	265	64
177	211	2163.5	2.8	272	81	1075.0	2.0	261	41	3433.4	3.5	286	118	1982.1	3	269	84
360	212	2163.5	2.8	277	75	1028.0	2.0	267	43	2909.3	4.5	291	97	2553.2	2	273	86
933	213	2157.9	2.3	275	85	1531.9	2.0	271	46	3194.9	3.0	286	117	1746.9	2	267	91
744	214	2155.7	2.3	272	88	1965.3	2.5	273	75	2956.4	2.5	279	105	1545.4	2	264	84
429	215	2146.7	2.5	274	66	1632.7	3.5	269	76	3181.4	2.0	286	77	1626.0	2	268	46
324	216	2134.4	3.2	274	64	1572.2	4.0	269	77	2633.8	3.5	286	70	2197.1	2	267	46
871	217	2125.4	2.7	275	77	1746.9	3.5	272	79	2694.3	2.5	285	67	1935.1	2	267	84
657	218	2123.2	2.2	274	75	1528.6	3.0	262	91	3302.4	1.5	289	77	1538.7	2	270	56
416	219	2118.7	2.0	273	68	1891.4	3.5	271	90	3181.4	1.5	282	76	1283.3	1	265	38
432	220	2078.4	1.5	273	55	1693.2	2.5	260	81	3393.1	2.0	292	84	1148.9	.	267	.
768	221	2051.2	1.7	272	66	170.3	1.5	262	42	3423.3	1.5	287	83	2559.9	2	268	74
9	222	2032.5	1.8	270	68	1300.1	2.0	262	69	3151.2	1.5	283	69	1646.2	2	264	66
398	223	1937.3	2.0	274	72	1458.0	2.5	267	58	2486.0	1.5	288	93	1867.9	2	268	66
30	224	1885.5	2.7	277	67	472.7	3.5	273	62	3423.3	2.5	289	84	1760.4	2	270	56
68	225	1851.9	2.3	276	91	1534.3	3.0	270	108	2308.0	2.0	289	84	1713.3	2	269	81
659	226	1668.5	1.3	268	40	1612.6	2.0	264	46	1800.7	1.0	277	28	1592.4	1	264	46
	Mean	2538.6	2.5	274.9	78.8	1834.6	2.8	268	72.2	3445.3	2.3	287.5	89.9	2327.3	2.4	269.2	74.6
	LSD	510.6	1.1	4.5	27.4	892.2	2.0	7.9	48.5	892.2	2.0	7.9	48.5	892.2	2.0	7.9	48.5

†MAT is maturity date according to the Julian calendar

‡LODG is the lodge score reported on a 1-5 scale

$LSD_{0.05}$ is Least Significance Difference at the 0.05 probability level.

Table 3.27 Quantitative trait loci identified using R/qtl located on various chromosomes associated with yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT[†]	FAVORABLE ALLELE
Knoxville, TN 2010	Gm07_16144523_C_A	7	M	51.90	3.65	6.67	1.87	W
Knoxville, TN 2010	Gm06_17617727_G_T	6	C2	55.04	2.82	3.42	3.70	W
Belleville, IL 2011	Gm06_20996124_T_C	6	C2	60.21	5.56	10.48	5.26	W
Belleville, IL 2011	Gm12_7135310_A_G	12	H	36.25	3.71	6.22	2.28	W
Belleville, IL 2011	Gm05_3485480_T_C	5	A1	19.73	2.66	5.86	1.61	W
Belleville, IL 2011	Gm02_44803277_C_T	2	D1b	114.09	2.83	4.66	2.10	W
Knoxville, TN 2010-11 Belleville, IL 2011	Gm07_17362808_A_G	7	M	55.95	5.31	8.20	2.04	W
Knoxville, TN 2010-11 Belleville, IL 2011	Gm06_20996124_T_C	6	C2	62.03	3.92	6.23	3.22	W
Knoxville, TN 2010-11 Belleville, IL 2011	Gm02_42469280_A_C	2	D1b	105.17	2.65	4.07	1.16	W

[†]Additive effect refers to the quantitative change in yield that is associated with the favorable allele from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.28 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using R/qtl in each environment in Group B. Those MAS lines were compared to the top yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					**BELLEVILLE, IL 2011**					**KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011**				
MAS		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
[aa]7	01	681	3581.2	01	**[bb]65**	01	**[bb]65**	4266.6	01	25	01	**[cc]550**	3137.8	01
25	02	197	3487.2	02	114	02	172	4206.1	02	46	02	676	3124.3	02
32	03	676	3305.7	03	128	03	676	4132.2	03	**[c]65**	03	172	3043.7	03
[aa]42	04	550	3252.0	04	218	04	**[bb]550**	4085.2	04	116	04	722	3016.8	04
46	05	383	3124.3	05	275	05	**[bb]826**	4078.4	05	123	05	**[cc]681**	3010.1	05
65	06	478	3104.2	06	298	06	439	4078.4	06	128	06	702	2916.0	06
88	07	694	3097.5	07	467	07	**[bb]881**	4024.7	07	184	07	**[cc]332**	2909.3	07
123	08	1013	3070.6	08	**[bb]550**	08	383	4011.2	08	227	08	888	2902.6	08
128	09	**[aa]7**	3037.0	09	569	09	570	4004.5	09	298	09	1013	2902.6	09
162	10	665	3023.6	10	681	10	533	3984.4	10	**[cc]332**	10	665	2902.6	10
171	11	**[aa]42**	3016.8	11	738	11	**[bb]11**	3970.9	11	342	11	330	2889.2	11
184	12	**[a]189**	2990.0	12	**[bb]826**	12	329	3957.5	12	**[c]362**	12	197	2875.7	12
[a]189	13	653	2983.2	13	**[bb]881**	13	437	3944.1	13	415	13	694	2875.7	13
205	14	413	2976.5	14	922	14	619	3917.2	14	431	14	970	2869.0	14
227	15	**[a]259**	2963.1	15	**[bb]11**	15	793	3910.5	15	**[cc]550**	15	346	2862.3	15
230	16	**[a]332**	2949.6	16	24	16	362	3903.7	16	551	16	383	2862.3	16
[a]259	17	738	2949.6	17	46	17	998	3903.7	17	561	17	1008	2862.3	17
298	18	272	2936.2	18	92	18	342	3903.7	18	569	18	**[c]362**	2855.6	18
312	19	887	2936.2	19	98	19	888	3897.0	19	619	19	826	2855.6	19
324	20	411	2902.6	20	116	20	375	3883.6	20	**[cc]681**	20	881	2848.9	20
[a]332	21	218	2902.6	21	127	21	625	3876.9	21	707	21	**[c]65**	2842.1	21
342	22	267	2902.6	22	131	22	722	3863.4	22	753	22	922	2842.1	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Belleville, IL in 2011
[bb] Top 5% yield in Belleville, IL in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011

Table 3.29 MAS identifying the bottom 10 % of lines containing the unfavorable allele for the yield QTLs detected using R/qtl in each environment in Group B. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					BELLEVILLE, IL 2011					KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
98	197	385	1733.5	197	[b]**744**	197	742	3097.5	197	780	197	483	2210.6	197
114	198	215	1713.3	198	747	198	663	3057.1	198	783	198	245	2203.8	198
163	199	68	1713.3	199	765	199	46	3043.7	199	792	199	661	2203.8	199
177	200	520	1706.6	200	783	200	[b]**483**	3016.8	200	804	200	643	2197.1	200
247	201	718	1699.9	201	792	201	[b]**560**	3010.1	201	852	201	698	2177.0	201
264	202	643	1673.0	202	804	202	[b]**111**	2996.7	202	[cc]**871**	202	608	2170.2	202
267	203	9	1646.2	203	831	203	131	2996.7	203	880	203	177	2163.5	203
307	204	26	1626.0	204	860	204	395	2969.8	204	925	204	360	2163.5	204
322	205	429	1626.0	205	[bb]**871**	205	691	2969.8	205	[c]**933**	205	[c]**933**	2156.8	205
357	206	107	1612.6	206	884	206	[b]**744**	2956.4	206	947	206	[c]**744**	2156.8	206
360	207	313	1599.1	207	887	207	661	2942.9	207	983	207	429	2150.1	207
[aa]**370**	208	659	1592.4	208	925	208	608	2922.8	208	1008	208	324	2136.6	208
446	209	660	1552.1	209	947	209	[bb]**360**	2909.3	209	16	209	[cc]**871**	2123.2	209
452	210	[aa]**744**	1545.4	210	107	210	[bb]**153**	2754.8	210	267	210	657	2123.2	210
533	211	657	1538.7	211	[b]**111**	211	[bb]**871**	2694.3	211	370	211	416	2116.5	211
554	212	[aa]**577**	1525.2	212	[bb]**153**	212	594	2680.9	212	417	212	432	2076.2	212
[aa]**577**	213	[aa]**370**	1458.0	213	[bb]**360**	213	324	2633.8	213	446	213	768	2049.3	213
646	214	568	1370.7	214	[b]**483**	214	499	2627.1	214	577	214	9	2035.9	214
691	215	479	1364.0	215	[b]**560**	215	132	2600.3	215	691	215	398	1935.1	215
698	216	983	1290.0	216	577	216	398	2486.0	216	[c]**744**	216	30	1888.0	216
[aa]**744**	217	416	1283.3	217	[bb]**659**	217	68	2311.3	217	853	217	68	1854.4	217
860	218	432	1148.9	218	853	218	[bb]**659**	1800.7	218	860	218	659	1666.3	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Belleville, IL in 2011
[bb] Bottom 5% yield in Belleville, IL in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011

Table 3.30 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using R/qtl in each environment in Group B compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
7	01	[b]**65**	01	25	01	[bbcc]**550**	3137.8	01
25	02	114	02	46	02	676	3124.3	02
32	03	128	03	[c]**65**	03	172	3043.7	03
42	04	218	04	116	04	722	3016.8	04
46	05	275	05	123	05	[bbcc]**681**	3010.1	05
[a]**65**	06	298	06	128	06	702	2916.0	06
88	07	467	07	184	07	[aacc]**332**	2909.3	07
123	08	[bb]**550**	08	227	08	888	2902.6	08
128	09	569	09	298	09	1013	2902.6	09
162	10	[bb]**681**	10	[cc]**332**	10	665	2902.6	10
171	11	738	11	342	11	330	2889.2	11
184	12	[b]**826**	12	[c]**362**	12	197	2875.7	12
189	13	[b]**881**	13	415	13	694	2875.7	13
205	14	[b]**922**	14	431	14	970	2869.0	14
227	15	11	15	[cc]**550**	15	346	2862.3	15
230	16	24	16	551	16	383	2862.3	16
259	17	46	17	561	17	1008	2862.3	17
298	18	92	18	569	18	[c]**362**	2855.6	18
312	19	98	19	619	19	[b]**826**	2855.6	19
324	20	116	20	[cc]**681**	20	[b]**881**	2848.9	20
[aa]**332**	21	127	21	707	21	[ac]**65**	2842.1	21
342	22	131	22	753	22	[b]**922**	2842.1	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011

Table 3.31 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using R/qtl in each environment in Group B compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
98	197	[b]**744**	197	780	197	483	2210.6	197
114	198	747	198	783	198	245	2203.8	198
163	199	765	199	792	199	661	2203.8	199
[a]**177**	200	783	200	804	200	643	2197.1	200
247	201	792	201	852	201	[a]**698**	2177.0	201
264	202	804	202	[cc]**871**	202	608	2170.2	202
267	203	831	203	880	203	[a]**177**	2163.5	203
307	204	860	204	925	204	[ab]**360**	2163.5	204
322	205	[bb]**871**	205	[c]**933**	205	[c]**933**	2156.8	205
357	206	884	206	947	206	[abc]**744**	2156.8	206
[a]**360**	207	887	207	983	207	429	2150.1	207
370	208	925	208	1008	208	324	2136.6	208
446	209	947	209	16	209	[bbcc]**871**	2123.2	209
452	210	107	210	267	210	657	2123.2	210
533	211	111	211	370	211	416	2116.5	211
554	212	153	212	417	212	432	2076.2	212
577	213	[b]**360**	213	446	213	768	2049.3	213
646	214	483	214	577	214	9	2035.9	214
691	215	560	215	691	215	398	1935.1	215
[a]**698**	216	577	216	[c]**744**	216	30	1888.0	216
[a]**744**	217	[bb]**659**	217	853	217	68	1854.4	217
860	218	853	218	860	218	[bb]**659**	1666.3	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011

Table 3.32 Quantitative trait loci identified using SAS located on various chromosomes associated with yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE	P-VALUE
Knoxville, TN 2010	Gm01_1241762_A_C	1	D1a	4.60	8.50	2.24	W	0.0003
Knoxville, TN 2010	Gm02_12770553_A_G	2	D1b	46.15	6.29	1.69	W	0.0022
Knoxville, TN 2010	Gm06_20996124_T_C	6	C2	58.54	9.03	7.90	W	0.0002
Knoxville, TN 2010	Gm19_45062248_T_C	19	L	77.05	6.10	2.56	W	0.0005
Belleville, IL 2011	Gm01_29787876_G_A	1	D1a	59.29	10.02	0.92	E	<.0001
Belleville, IL 2011	Gm03_5264953_A_G	3	N	19.43	5.58	0.36	E	0.001
Belleville, IL 2011	Gm06_27540819_T_G	6	C2	66.24	10.29	4.48	W	<.0001
Belleville, IL 2011	Gm09_12463468_C_T	9	K	31.76	9.79	0.02	W	<.0001
Belleville, IL 2011	Gm17_13240263_C_T	17	D2	30.29	6.86	1.22	E	0.0002
Belleville, IL 2011	Gm20_800671_A_G	20	I	1.83	7.78	1.18	W	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm01_29787876_G_A	1	D1a	59.29	8.08	1.00	E	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm05_30953466_G_T	5	A1	39.76	7.68	1.60	W	0.0005
Knoxville, TN 2010-11 Belleville, IL 2011	Gm07_17460956_C_A	7	M	39.95	14.85	1.90	W	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm06_20996124_T_C	6	C2	58.54	10.63	4.03	W	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm08_15866777_G_A	8	A2	22.31	7.09	0.35	E	0.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm09_12463468_C_T	9	K	31.76	7.11	0.45	W	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm10_571698_A_G	10	O	1.30	6.48	0.14	E	0.0016
Knoxville, TN 2010-11 Belleville, IL 2011	Gm11_7323949_A_G	11	B1	26.24	6.83	0.28	E	0.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm15_49231503_C_T	15	E	89.13	7.60	0.98	W	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm18_23913313_A_G	18	G	54.72	7.42	0.38	E	<.0001
Knoxville, TN 2010-11 Belleville, IL 2011	Gm19_2404683_A_G	19	L	25.12	6.39	0.87	W	0.0017

†Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.33 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using SAS in each environment in Group B. Those MAS lines were compared to the top yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					BELLEVILLE, IL 2011					KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
17	01	681	3581.2	01	123	01	65	4266.6	01	380	01	550	3137.8	01
88	02	197	3487.2	02	25	02	172	4206.1	02	384	02	[cc]**676**	3124.3	02
245	03	676	3305.7	03	162	03	[bb]**676**	4132.2	03	413	03	172	3043.7	03
250	04	[aa]**550**	3252.0	04	247	04	550	4085.2	04	7	04	722	3016.8	04
256	05	383	3124.3	05	264	05	826	4078.4	05	25	05	681	3010.1	05
[a]**259**	06	478	3104.2	06	302	06	439	4078.4	06	46	06	[cc]**702**	2916.0	06
269	07	694	3097.5	07	312	07	881	4024.7	07	256	07	332	2909.3	07
307	08	1013	3070.6	08	321	08	383	4011.2	08	302	08	[cc]**888**	2902.6	08
346	09	7	3037.0	09	367	09	[bb]**570**	4004.5	09	397	09	1013	2902.6	09
362	10	665	3023.6	10	380	10	533	3984.4	10	431	10	665	2902.6	10
367	11	42	3016.8	11	397	11	11	3970.9	11	619	11	330	2889.2	11
392	12	189	2990.0	12	511	12	329	3957.5	12	663	12	197	2875.7	12
[a]**411**	13	653	2983.2	13	519	13	437	3944.1	13	[cc]**676**	13	[c]**694**	2875.7	13
473	14	413	2976.5	14	[bb]**570**	14	619	3917.2	14	[c]**694**	14	970	2869.0	14
533	15	[a]**259**	2963.1	15	652	15	793	3910.5	15	[cc]**702**	15	346	2862.3	15
[aa]**550**	16	332	2949.6	16	[bb]**676**	16	362	3903.7	16	731	16	383	2862.3	16
570	17	738	2949.6	17	681	17	998	3903.7	17	804	17	1008	2862.3	17
619	18	272	2936.2	18	718	18	342	3903.7	18	[cc]**888**	18	362	2855.6	18
657	19	887	2936.2	19	872	19	888	3897.0	19	939	19	826	2855.6	19
667	20	[a]**411**	2902.6	20	887	20	375	3883.6	20	946	20	881	2848.9	20
742	21	218	2902.6	21	933	21	625	3876.9	21	8	21	65	2842.1	21
795	22	267	2902.6	22	946	22	722	3863.4	22	24	22	922	2842.1	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Belleville, IL in 2011
[bb] Top 5% yield in Belleville, IL in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011

Table 3.34 MAS identifying the bottom 10 % of lines containing the unfavorable allele for the yield QTLs detected using SAS in each environment in Group B. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					BELLEVILLE, IL 2011					KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
594	197	385	1733.5	197	947	197	742	3097.5	197	1008	197	483	2210.6	197
625	198	215	1713.3	198	1008	198	663	3057.1	198	65	198	245	2203.8	198
646	199	68	1713.3	199	9	199	46	3043.7	199	**[cc]68**	199	661	2203.8	199
652	200	520	1706.6	200	47	200	483	3016.8	200	251	200	643	2197.1	200
[aa]659	201	718	1699.9	201	**[bb]68**	201	560	3010.1	201	307	201	**[c]698**	2177.0	201
661	202	643	1673.0	202	**[bb]132**	202	111	2996.7	202	383	202	608	2170.2	202
780	203	9	1646.2	203	257	203	131	2996.7	203	422	203	177	2163.5	203
852	204	26	1626.0	204	267	204	395	2969.8	204	499	204	360	2163.5	204
900	205	429	1626.0	205	272	205	**[b]691**	2969.8	205	554	205	933	2156.8	205
933	206	107	1612.6	206	370	206	744	2956.4	206	653	206	744	2156.8	206
947	207	313	1599.1	207	**[bb]398**	207	661	2942.9	207	747	207	429	2150.1	207
986	208	**[aa]659**	1592.4	208	446	208	608	2922.8	208	860	208	324	2136.6	208
16	209	660	1552.1	209	498	209	360	2909.3	209	886	209	871	2123.2	209
132	210	**[aa]744**	1545.4	210	568	210	153	2754.8	210	107	210	657	2123.2	210
470	211	657	1538.7	211	586	211	871	2694.3	211	234	211	416	2116.5	211
[aa]479	212	577	1525.2	212	**[bb]594**	212	**[bb]594**	2680.9	212	366	212	432	2076.2	212
483	213	370	1458.0	213	660	213	324	2633.8	213	577	213	768	2049.3	213
498	214	568	1370.7	214	**[b]691**	214	499	2627.1	214	646	214	9	2035.9	214
560	215	**[aa]479**	1364.0	215	747	215	**[bb]132**	2600.3	215	**[cc]659**	215	398	1935.1	215
655	216	983	1290.0	216	107	216	**[bb]398**	2486.0	216	695	216	30	1888.0	216
691	217	416	1283.3	217	646	217	**[bb]68**	2311.3	217	**[c]698**	217	**[cc]68**	1854.4	217
[aa]744	218	432	1148.9	218	**[bb]659**	218	**[bb]659**	1800.7	218	722	218	**[cc]659**	1666.3	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Belleville, IL in 2011
[bb] Bottom 5% yield in Belleville, IL in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Belleville, IL in 2011

Table 3.35 MAS identifying the top 10 % of lines containing the favorable alleles for QTLs detected using SAS in each environment in Group B compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
17	01	123	01	380	01	**[aa]550**	3137.8	01
88	02	25	02	384	02	**[bbcc]676**	3124.3	02
245	03	162	03	413	03	172	3043.7	03
250	04	247	04	7	04	722	3016.8	04
256	05	264	05	25	05	**[bb]681**	3010.1	05
259	06	302	06	46	06	**[cc]702**	2916.0	06
269	07	312	07	256	07	332	2909.3	07
307	08	321	08	302	08	**[cc]888**	2902.6	08
[a]346	09	367	09	397	09	1013	2902.6	09
[a]362	10	380	10	431	10	665	2902.6	10
367	11	397	11	619	11	330	2889.2	11
392	12	511	12	663	12	197	2875.7	12
411	13	519	13	**[cc]676**	13	**[c]694**	2875.7	13
473	14	570	14	**[c]694**	14	970	2869.0	14
533	15	652	15	**[cc]702**	15	**[a]346**	2862.3	15
[aa]550	16	**[bb]676**	16	731	16	383	2862.3	16
570	17	**[bb]681**	17	804	17	1008	2862.3	17
619	18	718	18	**[cc]888**	18	**[a]362**	2855.6	18
657	19	872	19	939	19	826	2855.6	19
667	20	887	20	946	20	881	2848.9	20
742	21	933	21	8	21	65	2842.1	21
795	22	946	22	24	22	922	2842.1	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011

Table 3.36 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using SAS in each environment in Group B compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
594	197	947	197	1008	197	483	2210.6	197
625	198	1008	198	65	198	245	2203.8	198
646	199	**[bb]9**	199	**[cc]68**	199	**[a]661**	2203.8	199
652	200	47	200	251	200	643	2197.1	200
[aa]659	201	**[bb]68**	201	307	201	**[c]698**	2177.0	201
[a]661	202	132	202	383	202	608	2170.2	202
780	203	257	203	422	203	177	2163.5	203
852	204	267	204	499	204	360	2163.5	204
900	205	272	205	554	205	**[a]933**	2156.8	205
[a]933	206	370	206	653	206	**[a]744**	2156.8	206
947	207	**[bb]398**	207	747	207	429	2150.1	207
986	208	446	208	860	208	324	2136.6	208
16	209	498	209	886	209	871	2123.2	209
132	210	568	210	107	210	657	2123.2	210
470	211	586	211	234	211	416	2116.5	211
479	212	594	212	366	212	432	2076.2	212
483	213	660	213	577	213	768	2049.3	213
498	214	691	214	646	214	**[bb]9**	2035.9	214
560	215	747	215	**[cc]659**	215	**[bb]398**	1935.1	215
655	216	107	216	695	216	30	1888.0	216
691	217	646	217	**[c]698**	217	**[bbcc]68**	1854.4	217
[a]744	218	**[bb]659**	218	722	218	**[aabbcc]659**	1666.3	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011

Table 3.37 Significant (P<0.01) epistatic interactions between loci for yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using R/qtl and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm07_16144523_C_A	7	M	51.90	W	GM01_46579445_G_A	1	D1a	109.34	3.84	-3.14	-0.50
						GM05_39673657_T_G	5	A1	93.13	5.84	0.07	-3.09
						GM06_19653985_A_G	6	C2	46.14	3.28	4.47	-2.21
						GM11_17113172_G_A	11	B1	40.17	6.25	-3.25	-0.06
Knoxville, TN 2010	Gm06_17617727_G_T	6	C2	55.04	W	GM07_42111727_C_T	7	M	98.85	4.61	0.16	-4.33
						GM14_12556387_T_C	14	B2	29.48	3.95	-4.82	-0.71
						GM20_44554028_G_A	20	I	104.59	4.05	-4.47	-0.56
Belleville, IL 2011	Gm06_20996124_T_C	6	C2	60.21	W	GM01_29990637_T_C	1	D1a	70.40	11.69	-12.86	-1.60
						GM02_13771227_A_G	2	D1b	32.33	5.09	-5.87	-0.45
						GM03_37376203_C_T	3	N	87.74	6.20	0.16	-5.94
						GM04_48819142_A_C	4	C1	114.60	8.85	-9.47	-1.41
						GM07_35091912_G_T	7	M	82.38	7.20	-1.02	-7.42
						GM08_12693852_G_A	8	A2	29.80	9.62	-12.82	-2.23
						GM10_47833380_A_G	10	O	112.28	9.09	-2.18	-12.64
						GM11_36811720_C_A	11	B1	86.41	3.41	-5.78	-1.44
						GM12_33656706_G_A	12	H	79.01	11.36	-1.32	-13.05
						GM13_26705499_C_T	13	F	62.69	11.37	-1.30	-12.39
						GM14_19103544_T_C	14	B2	44.84	12.69	-1.20	-12.80
						GM15_49375283_T_C	15	E	115.90	11.04	-1.40	-12.77
						GM16_29081010_A_G	16	J	68.27	5.32	-0.20	-6.09
						GM17_36966551_A_C	17	D2	86.78	10.09	-12.87	-2.11
						GM18_52455765_C_A	18	G	123.14	4.69	-5.38	-0.42
						GM19_33586981_A_G	19	L	78.84	3.95	-1.80	-7.12
Belleville, IL 2011	Gm02_44803277_C_T	2	D1b	114.09	W	GM01_51416475_G_A	1	D1a	120.70	3.57	-2.14	-0.19
						GM02_11182262_C_T	2	D1b	26.25	4.65	-2.50	-0.23
						GM06_41416032_T_C	6	C2	97.22	3.55	-3.85	-0.92
						GM07_15590266_C_T	7	M	36.60	5.25	0.09	-2.28
						GM17_15834164_T_C	17	D2	37.17	3.56	-2.04	-0.10

Table 3.37 Continued.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010-11												
Belleville, IL 2011	Gm07_17362808_A_G	7	M	55.95	W	GM_01-5021663_A_G	1	D1a	11.79	3.98	-0.27	-1.68
						GM06_20835584_T_C	6	C2	48.91	4.90	3.04	-1.35
						GM06_20996124_T_C	6	C2	62.03	4.82	2.43	-1.40
						GM13_26707540_C_T	13	F	62.69	4.42	-1.58	-0.08
						GM15_11274131_A_G	15	E	26.47	3.60	-1.56	-0.18
						GM18_58266066_T_C	18	G	136.77	5.41	-1.63	-0.03
Knoxville, TN 2010-11												
Belleville, IL 2011	Gm06_20996124_T_C	6	C2	62.03	W	GM01_29990637_T_C	1	D1a	70.40	4.93	31.75	36.68
						GM07_17460956_C_A	7	M	40.99	4.79	36.21	35.23
						GM08_12693852_G_A	8	A2	29.80	4.71	31.89	36.46
						GM10_47858822_C_T	10	O	112.34	4.03	36.51	31.63
						GM12_33657269_G_T	12	H	79.01	4.83	36.55	31.77
						GM13_26707540_C_T	13	F	62.69	3.72	36.55	31.42
						GM15_49375283_T_C	15	E	115.90	5.43	36.55	31.18
						GM19_45082401_G_A	19	L	105.83	4.78	36.56	31.72
Knoxville, TN 2010-11												
Belleville, IL 2011	Gm02_42469280_A_C	2	D1b	105.17	W	GM12_34378311_T_C	12	H	80.70	5.31	0.17	-1.58
						GM16_29150479_A_G	16	J	68.43	3.65	0.15	-1.28

†Additive by additive effect refers to the quantitative change in yield that is associated with the combination of the additive effect of locus 1 with the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1
MLG = molecular linkage group; CHR = chromosome

Table 3.38 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by R/qtl to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aac]**197**	01	694	2699.4	65	4266.6	[cc]**550**	3137.8
[aa]**413**	02	[aa]**681**	2670.8	172	4206.1	676	3124.3
[bbc]**383**	03	[aa]**550**	2662.4	676	4132.2	172	3043.7
[a]**431**	04	676	2620.4	[bb]**550**	4085.2	[cc]**722**	3016.8
267	05	[aa]**1013**	2604.8	826	4078.4	[cc]**681**	3010.1
783	06	518	2591.9	439	4078.4	702	2916.0
[aacc]**1013**	07	[aa]**722**	2591.9	[bb]**881**	4024.7	332	2909.3
[aacc]**681**	08	[aa]**413**	2583.5	[bb]**383**	4011.2	888	2902.6
597	09	[aa]**197**	2580.1	570	4004.5	[cc]**1013**	2902.6
653	10	478	2578.4	533	3984.4	665	2902.6
7	11	665	2559.9	11	3970.9	330	2889.2
[bbc]**881**	12	702	2553.2	[b]**329**	3957.5	[c]**197**	2875.7
886	13	672	2538.1	437	3944.1	694	2875.7
691	14	332	2514.6	619	3917.2	970	2869.0
422	15	330	2502.8	793	3910.5	346	2862.3
[aabbcc]**550**	16	184	2467.6	362	3903.7	[c]**383**	2862.3
42	17	172	2465.9	998	3903.7	1008	2862.3
230	18	259	2450.8	342	3903.7	362	2855.6
[b]**329**	19	346	2428.9	888	3897.0	826	2855.6
411	20	397	2428.9	375	3883.6	[c]**881**	2848.9
275	21	[a]**431**	2425.6	625	3876.9	65	2842.1
[aabcc]**722**	22	1008	2423.9	[b]**722**	3863.4	922	2842.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.39 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by SAS to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aac]**197**	01	[aa]**694**	2699.4	65	4266.6	[cc]**550**	3137.8
[aacc]**681**	02	[aa]**681**	2670.8	172	4206.1	[cc]**676**	3124.3
[aabbcc]**550**	03	[aa]**550**	2662.4	[bb]**676**	4132.2	172	3043.7
[aabbcc]**676**	04	[aa]**676**	2620.4	[bb]**550**	4085.2	722	3016.8
586	05	[aa]**1013**	2604.8	826	4078.4	[cc]**681**	3010.1
561	06	[aa]**518**	2591.9	439	4078.4	702	2916.0
[bbc]**383**	07	722	2591.9	881	4024.7	[cc]**332**	2909.3
[aacc]**665**	08	[aa]**413**	2583.5	[bb]**383**	4011.2	888	2902.6
272	09	[aa]**197**	2580.1	570	4004.5	[cc]**1013**	2902.6
887	10	[aa]**478**	2578.4	533	3984.4	[cc]**665**	2902.6
[acc]**330**	11	[aa]**665**	2559.9	11	3970.9	[cc]**330**	2889.2
[aa]**478**	12	702	2553.2	329	3957.5	[c]**197**	2875.7
[a]**259**	13	672	2538.1	437	3944.1	[c]**694**	2875.7
[aac]**694**	14	[a]**332**	2514.6	619	3917.2	970	2869.0
42	15	[a]**330**	2502.8	793	3910.5	346	2862.3
[aa]**518**	16	[a]**184**	2467.6	362	3903.7	[c]**383**	2862.3
[a]**184**	17	172	2465.9	998	3903.7	1008	2862.3
[aacc]**1013**	18	[a]**259**	2450.8	342	3903.7	362	2855.6
[aa]**413**	19	346	2428.9	888	3897.0	826	2855.6
[acc]**332**	20	397	2428.9	375	3883.6	881	2848.9
738	21	431	2425.6	625	3876.9	65	2842.1
687	22	1008	2423.9	722	3863.4	922	2842.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.40 Significant (P<0.01) epistatic interactions between loci for yield in 221 RILs in Group B derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using SAS and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

											ADDITIVE X ADDITIVE EFFECT†	
ENVIRONMENT	**LOCUS 1**	**CHR**	**MLG**	**LOC (cM)**	**FAVORABLE ALLELE**	**LOCUS 2**	**CHR**	**MLG**	**LOC (cM)**	**R^2 (%)**	**E**	**W**
Knoxville, TN 2010	Gm02_12770553_A_G	2	D1b	46.15	W	GM04_45110392_G_A	4	C1	94.77	4.33	-1.61	1.16
						GM05_40675941_A_G	5	A1	85.45	4.02	0.98	-1.62
						GM09_16674947_T_C	9	K	35.03	4.83	-1.77	1.14
						GM17_16523531_A_C	17	D2	34.71	3.63	-1.38	1.18
Knoxville, TN 2010	Gm06_20996124_T_C	6	C2	58.54	W	GM02_49616128_C_A	2	D1b	104.24	5.10	-7.14	1.51
Belleville, IL 2011	Gm01_29787876_G_A	1	D1a	59.29	E	GM01_47327886_T_C	1	D1a	99.43	4.12	0.04	1.90
						GM17_12891830_C_T	17	D2	27.08	4.44	1.31	-0.63
						GM19_33747911_T_C	19	L	70.90	3.94	1.34	-0.51
Belleville, IL 2011	Gm09_12463468_C_T	9	K	31.76	W	GM04_33044652_A_C	4	C1	69.42	8.00	1.48	-1.32
						GM08_11971276_T_C	8	A2	25.15	4.90	-1.03	1.10
						GM09_40619828_C_A	9	K	85.34	4.82	-0.96	1.14
						GM10_47833380_A_G	10	O	100.49	4.02	-0.77	1.19
						GM11_10999596_T_C	11	B1	23.11	7.28	-1.47	1.17
						GM15_10416352_C_T	15	E	21.88	4.01	-0.75	1.23
						GM18_26198552_T_C	18	G	55.04	5.50	1.31	-1.05
Belleville, IL 2011	Gm17_13240263_C_T	17	D2	30.29	E	GM01_35522185_A_C	1	D1a	74.63	4.27	1.44	-0.45
						GM02_10568008_G_A	2	D1b	22.20	4.20	-0.23	1.65
						GM11_38762898_A_G	11	B1	81.43	7.20	-0.79	1.73
Knoxville, TN 2010-11 Belleville, IL 2011	Gm01_29787876_G_A	1	D1a	59.59	E	GM01_47165807_C_T	1	D1a	99.09	3.84	1.54	-0.32
						GM04_43830188_C_T	4	C1	92.08	5.16	1.31	-0.20
						GM11_38454564_A_G	11	B1	80.79	5.14	-0.47	1.14
						GM17_16310183_G_A	17	D2	34.27	3.75	1.09	-0.30
						GM19_33262731_G_A	19	L	69.88	3.62	1.19	-0.15
Knoxville, TN 2010-11 Belleville, IL 2011	Gm05_30953466_G_T	5	A1	7.68	W	GM08_15866777_G_A	8	A2	33.33	3.52	-1.44	-0.12
						GM03_45054251_A_C	3	N	94.65	3.62	-0.05	-1.39
						GM08_16267207_T_C	8	A2	34.17	4.35	-1.59	-0.06
						GM13_31424193_T_G	13	F	66.02	3.97	-0.03	-1.48

Table.40 Continued.

ENVIRONMENT	LOCUS 1	CHR	MLG			LOCUS 2	CHR	MLG		R^2 (%)	ADDITIVE X ADDITIVE EFFECT[†] E	W
Knoxville, TN 2010-11 Belleville, IL 2011	Gm07_17460956_C_A	7	M	14.85	W	GM01_50216637_T_C	1	D1a	105.50	3.59	-0.34	-1.69
						GM06_20396381_A_G	6	C2	42.85	4.85	3.04	-1.38
						GM13_26707540_C_T	13	F	56.11	5.11	-1.68	-0.04
						GM15_11274131_A_G	15	E	23.69	-1.56	-0.18	3.57
						GM18_58266066_T_C	18	G	122.41	6.15	-1.70	-0.01
Knoxville, TN 2010-11 Belleville, IL 2011	Gm08_15866777_G_A	8	A2	22.31	E	GM05_31446565_T_C	5	A1	66.06	4.91	-0.52	1.00
Knoxville, TN 2010-11 Belleville, IL 2011	Gm09_12463468_C_T	9	K	31.76	W	GM02_10074856_T_C	2	D1b	21.17	3.61	-0.98	0.37
						GM04_26622759_G_A	4	C1	55.93	5.05	0.77	-0.87
						GM11_10999596_T_C	11	B1	23.11	9.58	-1.43	0.79
						GM15_10376148_G_A	15	E	21.80	4.39	-0.82	0.73
						GM17_11662531_T_C	17	D2	24.50	4.16	-0.76	0.67
						GM18_26198552_T_C	18	G	55.04	4.01	0.60	-0.87
Knoxville, TN 2010-11 Belleville, IL 2011	Gm15_49231503_C_T	15	E	89.13	W	GM10_44142724_T_G	10	O	92.74	5.55	0.27	-1.35
						GM12_36456298_A_G	12	H	76.59	3.54	-1.23	0.07
						GM13_30189048_C_T	13	F	63.42	6.37	-1.35	0.39
						GM14_49107190_G_A	14	B2	103.17	3.59	-1.08	0.22
						GM19_46278942_A_G	19	L	97.22	4.32	0.34	-1.12
Knoxville, TN 2010-11 Belleville, IL 2011	Gm18_23913313_A_G	18	G	54.72	E	GM03_38058453_C_T	3	N	79.95	4.58	0.95	-0.53

[†]Additive by additive effect refers to the quantitative change in yield that is associated with the combination of the additive effect of locus 1 with the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1; MLG = molecular linkage group; CHR = chromosome

Table 3.41 Yield prediction model (YPM) developed using QTLs detected in Belleville, IL in 2011 by R/qtl to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
BELLEVILLE, IL 2011		KNOXVILLE, TN 2011		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bb]533	01	694	2699.4	**[bb]65**	4266.6	**[cc]550**	3137.8
[bbc]383	02	681	2670.8	**[bb]172**	4206.1	676	3124.3
[bb]439	03	**[aa]550**	2662.4	676	4132.2	**[cc]172**	3043.7
[bbc]65	04	676	2620.4	**[bb]550**	4085.2	**[cc]722**	3016.8
[b]437	05	1013	2604.8	**[bb]826**	4078.4	681	3010.1
[bcc]888	06	518	2591.9	**[bb]439**	4078.4	702	2916.0
[aabbcc]550	07	**[aa]722**	2591.9	**[bb]881**	4024.7	332	2909.3
[bb]570	08	413	2583.5	**[bb]383**	4011.2	**[cc]888**	2902.6
[bbc]881	09	197	2580.1	**[bb]570**	4004.5	1013	2902.6
[b]375	10	478	2578.4	**[bb]533**	3984.4	665	2902.6
[b]793	11	665	2559.9	11	3970.9	330	2889.2
[ac]1008	12	702	2553.2	**[b]329**	3957.5	197	2875.7
[c]922	13	672	2538.1	**[b]437**	3944.1	694	2875.7
[b]998	14	332	2514.6	**[b]619**	3917.2	**[c]970**	2869.0
[b]329	15	330	2502.8	**[b]793**	3910.5	346	2862.3
384	16	184	2467.6	**[b]362**	3903.7	**[c]383**	2862.3
[b]619	17	**[a]172**	2465.9	**[b]998**	3903.7	**[c]1008**	2862.3
[aabcc]722	18	259	2450.8	342	3903.7	**[c]362**	2855.6
[bbc]826	19	346	2428.9	**[b]888**	3897.0	**[c]826**	2855.6
[abbcc]172	20	397	2428.9	**[b]375**	3883.6	**[c]881**	2848.9
[bc]362	21	431	2425.6	625	3876.9	**[c]65**	2842.1
[c]970	22	**[a]1008**	2423.9	**[b]722**	3863.4	**[c]922**	2842.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.42 Yield prediction model (YPM) developed using QTLs detected in Belleville, IL in 2011 by SAS to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
BELLEVILLE, IL 2011		KNOXVILLE, TN 2011		BELLEVILLE, IL 2011		KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[abbcc]172	01	694	2699.4	**[bb]65**	4266.6	550	3137.8
367	02	**[aa]681**	2670.8	**[bb]172**	4206.1	**[cc]676**	3124.3
[bb]570	03	550	2662.4	**[bb]676**	4132.2	**[cc]172**	3043.7
[b]329	04	**[aa]676**	2620.4	550	4085.2	**[cc]722**	3016.8
88	05	1013	2604.8	**[bb]826**	4078.4	**[cc]681**	3010.1
[bb]439	06	518	2591.9	**[bb]439**	4078.4	702	2916.0
[aabbcc]676	07	**[aa]722**	2591.9	881	4024.7	**[cc]332**	2909.3
[c]970	08	413	2583.5	**[bb]383**	4011.2	**[cc]888**	2902.6
342	09	197	2580.1	**[bb]570**	4004.5	1013	2902.6
[b]998	10	478	2578.4	533	3984.4	665	2902.6
[bbc]826	11	665	2559.9	11	3970.9	330	2889.2
872	12	702	2553.2	**[b]329**	3957.5	197	2875.7
[aacc]681	13	672	2538.1	437	3944.1	694	2875.7
[aabcc]722	14	**[a]332**	2514.6	**[b]619**	3917.2	**[c]970**	2869.0
[b]375	15	330	2502.8	793	3910.5	346	2862.3
707	16	184	2467.6	362	3903.7	**[c]383**	2862.3
[b]619	17	**[a]172**	2465.9	**[b]998**	3903.7	1008	2862.3
[bbc]65	18	259	2450.8	342	3903.7	362	2855.6
[bbc]383	19	346	2428.9	**[b]888**	3897.0	**[c]826**	2855.6
[acc]332	20	397	2428.9	**[b]375**	3883.6	881	2848.9
695	21	431	2425.6	625	3876.9	**[c]65**	2842.1
[bcc]888	22	1008	2423.9	**[b]722**	3863.4	922	2842.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.43 Yield prediction model (YPM) developed using QTLs detected over three environments by R/qtl to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		**YIELD ($kg\ ha^{-1}$)**					
KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011				**KNOXVILLE, TN 2011**		**BELLEVILLE, IL 2011**	
LINE	**RANK**	**LINE**	**YIELD**	**LINE**	**YIELD**	**LINE**	**YIELD**
[abb]**197**	01	[aa]**550**	3137.8	694	2699.4	65	4266.6
[aabb]**681**	02	[aa]**676**	3124.3	[bb]**681**	2670.8	[cc]**172**	4206.1
[aabcc]**172**	03	[aa]**172**	3043.7	[bb]**550**	2662.4	[cc]**676**	4132.2
[bbc]**722**	04	722	3016.8	[bb]**676**	2620.4	[cc]**550**	4085.2
[acc]**383**	05	[aa]**681**	3010.1	1013	2604.8	826	4078.4
272	06	702	2916.0	518	2591.9	439	4078.4
[aabbcc]**676**	07	332	2909.3	[bb]**722**	2591.9	[cc]**881**	4024.7
586	08	[aa]**888**	2902.6	413	2583.5	[cc]**383**	4011.2
[a]**970**	09	1013	2902.6	[bb]**197**	2580.1	[cc]**570**	4004.5
[ab]**1008**	10	665	2902.6	478	2578.4	[cc]**533**	3984.4
[cc]**570**	11	[a]**330**	2889.2	665	2559.9	11	3970.9
[ab]**330**	12	[a]**197**	2875.7	702	2553.2	[c]**329**	3957.5
[c]**329**	13	694	2875.7	672	2538.1	437	3944.1
411	14	[a]**970**	2869.0	332	2514.6	619	3917.2
[aac]**888**	15	346	2862.3	[b]**330**	2502.8	793	3910.5
900	16	[a]**383**	2862.3	184	2467.6	362	3903.7
[c]**375**	17	[a]**1008**	2862.3	[b]**172**	2465.9	998	3903.7
[acc]**881**	18	362	2855.6	259	2450.8	342	3903.7
321	19	826	2855.6	346	2428.9	[c]**888**	3897.0
653	20	[a]**881**	2848.9	397	2428.9	[c]**375**	3883.6
[aabbcc]**550**	21	65	2842.1	431	2425.6	625	3876.9
[cc]**533**	22	922	2842.1	[b]**1008**	2423.9	[c]**722**	3863.4

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.44 Yield prediction model (YPM) developed using QTLs detected over three environments by SAS to select by MAS the top yielding 10 % of RILs in Group B grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		**YIELD ($kg\ ha^{-1}$)**					
KNOXVILLE, TN 2010-11 BELLEVILLE, IL 2011				**KNOXVILLE, TN 2011**		**BELLEVILLE, IL 2011**	
LINE	**RANK**	**LINE**	**YIELD**	**LINE**	**YIELD**	**LINE**	**YIELD**
[aabb]**681**	01	550	3137.8	694	2699.4	65	4266.6
367	02	[aa]**676**	3124.3	[bb]**681**	2670.8	[cc]**172**	4206.1
[aabcc]**172**	03	[aa]**172**	3043.7	550	2662.4	[cc]**676**	4132.2
[aabbcc]**676**	04	722	3016.8	[bb]**676**	2620.4	550	4085.2
[a]**970**	05	[aa]**681**	3010.1	1013	2604.8	[cc]**826**	4078.4
88	06	702	2916.0	518	2591.9	[cc]**439**	4078.4
[c]**329**	07	[aa]**332**	2909.3	722	2591.9	881	4024.7
[c]**998**	08	888	2902.6	413	2583.5	[cc]**383**	4011.2
[cc]**570**	09	1013	2902.6	[bb]**197**	2580.1	[cc]**570**	4004.5
[aab]**332**	10	665	2902.6	478	2578.4	533	3984.4
[acc]**383**	11	330	2889.2	665	2559.9	11	3970.9
[acc]**826**	12	[a]**197**	2875.7	702	2553.2	[c]**329**	3957.5
357	13	694	2875.7	672	2538.1	437	3944.1
[c]**342**	14	[a]**970**	2869.0	[b]**332**	2514.6	[c]**619**	3917.2
[cc]**439**	15	346	2862.3	330	2502.8	793	3910.5
46	16	[a]**383**	2862.3	184	2467.6	362	3903.7
[abb]**197**	17	1008	2862.3	[b]**172**	2465.9	[c]**998**	3903.7
804	18	362	2855.6	259	2450.8	[c]**342**	3903.7
380	19	[a]**826**	2855.6	346	2428.9	888	3897.0
[c]**619**	20	881	2848.9	397	2428.9	[c]**375**	3883.6
[c]**375**	21	65	2842.1	431	2425.6	625	3876.9
872	22	922	2842.1	1008	2423.9	722	3863.4

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Belleville, IL in 2011 and combined over Knoxville, TN in 2010, 2011 and Belleville, IL in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.45 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in three environments: Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	h^2	P-VALUE	F-VALUE
Environment	2	86957.2	191.24	60		<0.0001	1980.47
Reps (Env.)	2	2826.39	12.26	4		<0.0001	64.38
Genotypes	215	275.33	24.20	8	0.42	<0.0001	6.27
Genotypes x Env.	215	135.08	45.59	14		<0.0001	3.07
Error	430	43.9	43.89	14			

Table 3.46 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Knoxville, TN in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	561.43	41.42	36	0.001	10.93
Genotypes	215	77.7	23.17	20	0.03	1.51
Error	216	51.35	50.89	44		

Table 3.47 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Portageville, MO in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	691.3	43.06	41	<0.0001	26.26
Genotypes	215	90.05	26.9	25	<0.0001	2.46
Error	216	36.55	36.24	34		

Table 3.48 Mean seed yield, maturity, lodging and height of 216 recombinant inbred lines in Group C, two parents and two commercial checks grown in Knoxville, TN in 2010 and 2011, Portageville, MO in 2011 and averaged over Knoxville, TN in 2010 and 2011 and Portageville, MO in 2011.

ExW50K Group C		ACROSS LOCATIONS				TENNESSEE 2011				MISSOURI 2011				TENNESSEE 2010			
LINE	RANK	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT	YIELD	LODG†	MAT‡	HGT
		kg ha-1			cm	kg ha-1			cm	kg ha-1			cm	kg ha-1			cm
213	01	3331.5	2.3	275	80	1857.8	2.5	269	69	5301.3	2.5	282	86	2835.4	2	274	84
5002T	**02**	**3327.6**	**1.5**	**276**	**57**	**1874.6**	**2.0**	**270**	**47**	**4780.6**	**1.0**	**281**	**66**	**.**	**.**	**.**	**.**
450	03	3258.7	2.5	275	73	2418.8	4.0	268	55	4696.6	1.5	282	89	2660.7	2	275	76
263	04	3247.5	2.1	277	74	2462.5	2.3	277	72	4760.4	2.0	282	74	2519.6	2	273	76
378	05	3180.3	2.7	276	87	2126.6	3.0	272	83	4417.7	2.0	282	89	2996.7	3	275	89
938	06	3155.7	1.9	277	62	2331.5	2.3	275	58	4300.2	1.5	282	57	2835.4	2	274	71
TN09-008	**07**	**3141.1**	**2.5**	**276**	**81**	**1437.9**	**3.5**	**268**	**80**	**4844.4**	**1.5**	**284**	**81**	**.**	**.**	**.**	**.**
867	08	3121.0	2.7	276	92	1978.7	3.0	270	95	4468.1	2.0	282	97	2916.0	3	275	84
183	09	3098.6	2.2	274	70	2523.0	2.0	269	64	4353.9	2.5	279	80	2418.8	2	274	66
Essex	**10**	**3097.5**	**2.5**	**276**	**81**	**1891.4**	**4.0**	**272**	**86**	**4303.5**	**1.0**	**279**	**76**	**.**	**.**	**.**	**.**
908	11	3090.7	2.4	277	77	2334.9	2.2	274	37	4592.4	3.0	283	109	2344.9	2	273	84
505	12	3087.4	3.0	274	90	2213.9	4.0	269	112	4589.1	2.0	281	83	2459.2	3	273	76
426	13	3080.7	3.0	275	99	1874.6	3.0	269	74	4182.6	3.0	283	131	3184.8	3	274	94
607	14	3060.5	2.7	275	87	2015.7	4.0	271	91	4706.7	2.0	280	86	2459.2	2	273	84
760	15	3057.1	3.8	275	113	1427.8	4.5	268	97	4552.1	3.0	283	126	3191.5	4	275	117
612	16	3057.1	2.2	273	74	2731.3	2.5	270	69	4323.7	1.0	277	72	2116.5	3	273	81
78	17	3053.8	3.0	276	104	2066.1	3.0	272	90	4239.7	3.0	283	126	2855.6	3	275	97
165	18	3040.3	3.0	275	100	2230.7	3.0	269	74	4505.1	3.0	282	127	2385.2	3	274	99
199	19	3040.3	2.7	276	85	2563.3	3.0	274	80	3903.7	2.0	282	86	2654.0	3	274	89
932	20	2996.7	2.7	276	91	1696.5	2.5	271	67	4128.8	2.5	281	118	3164.6	3	275	89
553	21	2988.8	2.7	275	98	1898.1	2.0	271	51	4347.2	2.0	282	135	2721.2	4	274	109
1006	22	2984.4	3.2	276	96	1820.8	2.5	271	62	4471.5	3.0	282	126	2660.7	4	275	99
368	23	2966.4	2.7	275	88	2432.3	2.5	270	69	4249.8	2.5	282	100	2217.3	3	273	94
803	24	2964.2	2.7	275	93	2133.3	4.0	271	116	4380.8	2.0	281	71	2378.5	2	273	91
485	25	2962.0	2.7	275	91	2267.7	3.0	267	85	4293.4	2.0	282	104	2324.8	3	275	84
460	26	2960.8	3.3	276	98	2321.4	3.5	272	77	3960.9	3.5	282	109	2600.3	3	275	107
680	27	2960.8	2.0	274	68	1787.3	2.5	268	60	4649.5	1.5	281	70	2445.7	2	273	74
596	28	2944.0	3.0	275	106	2143.4	3.5	270	77	4437.9	2.5	282	133	2250.9	3	273	107
897	29	2930.6	2.8	276	93	2156.8	3.5	271	95	4209.5	3.0	282	99	2425.6	2	274	84
198	30	2902.6	2.5	275	89	1841.0	4.5	270	109	3856.7	1.0	282	76	3010.1	2	274	81
956	31	2899.2	2.3	276	83	2321.4	3.0	273	79	4300.2	2.0	282	83	2076.2	2	273	89
235	32	2895.9	2.5	274	101	2076.2	4.0	274	88	4105.3	1.5	276	122	2506.2	2	273	94
352	33	2886.9	2.4	276	76	1679.8	2.6	272	53	4911.6	2.5	283	103	2069.5	2	275	71
898	34	2881.3	1.7	277	75	1827.6	1.2	274	55	4149.0	2.0	282	79	2667.4	2	275	91
359	35	2874.6	3.3	276	69	2398.7	3.0	272	69	3786.2	3.0	283	127	2439.0	4	273	10
732	36	2874.6	3.3	274	93	2059.4	3.5	267	77	4266.6	3.5	282	112	2297.9	3	274	89
849	37	2860.1	3.0	275	84	2600.3	4.5	272	107	3507.3	1.5	280	71	2472.6	3	274	74
764	38	2855.6	1.7	275	67	2415.5	1.5	271	53	3665.2	1.5	281	70	2486.0	2	274	79
270	39	2853.3	2.8	275	90	1948.5	3.5	269	74	4387.5	3.0	282	119	2224.0	2	273	76
448	40	2853.3	2.3	276	87	2193.8	3.0	273	77	3463.6	2.0	282	103	2902.6	2	274	81
141	41	2853.3	2.0	274	64	1488.3	3.0	272	80	4579.0	1.0	278	58	2492.7	2	273	53
299	42	2852.2	1.8	274	67	1847.7	2.5	268	58	4162.4	1.0	281	71	2546.5	2	274	71
430	43	2845.5	1.6	274	61	2724.6	1.7	271	48	3722.3	1.0	279	62	2089.6	2	273	71
435	44	2845.5	2.5	275	79	2405.4	3.5	271	84	3772.7	2.0	280	81	2358.4	2	273	71
845	45	2842.1	3.3	275	102	2045.9	3.5	269	80	4001.2	3.5	283	126	2479.3	3	274	99
63	46	2838.8	1.8	275	69	2294.5	2.0	271	62	3473.7	1.5	281	86	2748.1	2	274	58
870	47	2836.5	2.7	274	86	2217.3	4.5	271	105	3880.2	1.5	278	70	2412.1	2	273	81
784	48	2836.5	2.0	275	93	2321.4	2.5	271	77	4078.4	1.5	280	110	2109.8	2	273	91
373	49	2835.4	2.2	276	90	2059.4	1.6	274	46	4108.7	3.0	282	135	2338.2	2	273	89
979	50	2835.4	3.8	276	112	2093.0	3.5	273	85	4350.6	4.0	283	144	2062.7	4	273	107
469	51	2828.7	2.2	274	75	1474.8	3.5	266	83	3994.4	1.0	282	74	3016.8	2	275	69
121	52	2820.9	3.3	277	61	1689.8	5.0	273	27	4246.4	2.0	283	71	2526.3	3	275	84
535	53	2813.0	3.8	277	99	2489.4	3.5	272	88	4054.9	4.0	283	127	1894.8	4	275	84
633	54	2802.9	3.5	276	104	1713.3	4.0	271	114	4296.8	3.5	284	117	2398.7	3	273	81
620	55	2798.5	3.5	276	96	1857.8	2.5	272	72	3574.5	4.0	283	130	2963.1	4	274	86
820	56	2798.5	3.2	276	102	2183.7	3.5	271	85	3927.3	3.0	282	131	2284.5	3	275	91
748	57	2797.3	3.7	275	91	2069.5	3.5	271	76	4226.3	3.5	283	121	2096.3	4	273	76
674	58	2797.3	3.2	273	100	1965.3	4.0	268	95	4370.7	2.5	279	119	2056.0	3	273	86
696	59	2797.3	2.8	274	93	2274.4	4.5	271	112	4001.2	2.0	280	81	2116.5	2	273	86
588	60	2789.5	3.3	275	103	2049.3	3.0	269	70	4249.8	4.0	283	133	2069.5	3	274	107
371	61	2787.3	2.3	274	82	2509.5	2.5	270	56	3964.2	2.5	281	114	1888.0	2	273	76
306	62	2785.0	3.0	274	83	2009.0	2.5	269	62	4007.9	3.5	280	99	2338.2	3	273	89
101	63	2783.9	2.3	274	79	2089.6	3.0	267	85	3823.1	2.0	281	70	2439.0	2	274	81
786	64	2780.5	1.9	276	62	2321.4	2.3	274	61	3803.0	1.5	280	67	2217.3	2	275	58
36	65	2772.7	2.7	276	78	1182.5	3.5	272	80	4602.5	1.5	281	69	2533.1	3	275	86
20	66	2771.6	3.8	277	110	1518.5	4.5	272	97	4024.7	3.0	283	123	.	.	.	.
572	67	2767.1	2.5	276	96	2072.8	3.5	271	109	4461.4	2.0	284	89	1767.1	2	273	89
436	68	2766.0	2.3	275	87	1837.6	3.5	271	112	4162.4	1.5	281	76	2297.9	2	275	74
622	69	2760.4	3.8	277	116	2328.1	3.5	272	123	3977.6	4.0	283	136	1975.4	4	275	89
400	70	2760.4	2.0	275	69	2395.3	2.0	274	46	3897.0	2.0	278	91	1988.8	2	273	69
276	71	2759.3	3.2	274	102	2113.1	4.5	269	91	3759.3	2.0	280	127	2405.4	3	273	89
393	72	2758.1	1.7	276	64	2119.8	2.0	272	55	4226.3	1.0	283	72	1928.4	2	274	66

Table 3.48 Continued.

ExW50K Group C		ACROSS LOCATIONS				Tennessee 2011				Missouri 2011				Tennessee 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
221	73	2757.0	3.3	275	111	2143.4	3.5	270	113	3668.6	3.5	282	131	2459.2	3	273	89
159	74	2746.9	3.2	275	87	1716.7	4.5	268	102	3850.0	2.0	282	76	2674.2	3	274	84
636	75	2744.7	3.7	276	113	2324.8	3.5	274	110	3813.0	3.5	282	131	2096.3	4	273	97
154	76	2743.6	4.2	276	116	1878.0	4.5	270	108	4209.5	4.0	284	132	2143.4	4	275	107
536	77	2743.6	2.5	277	92	1874.6	3.5	273	85	3997.8	2.0	282	117	2358.4	2	275	74
389	78	2741.4	2.2	275	79	2173.6	3.0	272	104	4269.9	1.5	280	61	1780.5	2	274	71
818	79	2735.7	2.0	272	72	1881.1	3.0	261	71	3907.1	1.0	281	57	2418.8	2	273	89
55	80	2732.4	2.2	273	78	1901.5	3.0	266	88	3923.9	1.5	280	64	2371.8	2	273	84
377	81	2732.4	1.8	274	68	1568.9	2.5	268	69	3886.9	1.0	280	74	2741.4	2	274	61
419	82	2725.7	2.8	276	105	2240.8	4.0	274	97	3839.9	2.5	282	112	2096.3	2	273	107
582	83	2722.3	3.8	277	105	1763.7	4.0	273	107	4212.8	3.5	282	127	2190.4	4	275	81
877	84	2721.2	3.7	276	104	1908.2	3.5	272	98	3984.4	3.5	282	117	2271.0	4	275	97
545	85	2721.2	3.0	275	105	2150.1	4.0	271	107	3997.8	3.0	283	135	2015.7	2	273	74
255	86	2714.5	3.8	276	100	2586.8	2.5	270	75	3460.3	4.0	284	137	2096.3	5	275	89
282	87	2713.4	2.8	275	87	1723.4	4.5	271	109	4374.1	2.0	280	81	2042.6	2	274	71
808	88	2706.6	3.3	275	103	2207.2	3.0	271	79	3561.1	4.0	281	133	2351.7	3	273	97
507	89	2699.9	1.4	275	55	2271.0	2.2	273	38	3598.0	1.0	279	57	2230.7	1	274	69
616	90	2697.7	4.2	275	106	1622.6	5.0	270	104	4085.2	3.5	282	127	2385.2	4	275	86
791	91	2697.7	3.8	276	97	2025.8	3.5	270	77	3997.8	4.0	283	127	2069.5	4	275	86
325	92	2696.6	2.8	274	103	2133.3	3.5	270	105	3994.4	3.0	281	122	1961.9	2	273	81
964	93	2696.6	2.5	274	94	2489.4	3.0	271	76	3584.6	2.5	278	113	2015.7	2	273	91
752	94	2696.6	2.2	275	76	1955.2	3.5	271	95	4071.7	1.0	281	60	2062.7	2	274	74
320	95	2689.8	3.5	276	104	1743.6	4.0	270	98	4478.2	3.5	283	123	1847.7	3	275	91
862	96	2687.6	3.5	276	110	1427.8	3.5	271	110	4054.9	3.0	283	118	2580.1	4	274	102
401	97	2687.6	2.8	276	97	2025.8	3.5	271	83	3322.5	2.0	283	117	2714.5	3	275	91
335	98	2685.4	1.7	273	69	1931.7	2.0	266	64	3577.9	1.0	280	70	2546.5	2	273	74
240	99	2676.4	3.5	276	103	2227.3	3.5	272	79	4202.7	3.0	281	124	1599.1	4	274	107
798	100	2675.3	2.0	275	61	2129.9	2.4	274	53	3645.1	1.5	280	65	2250.9	2	273	64
149	101	2671.9	3.0	276	121	1867.9	4.5	272	119	3688.7	2.5	282	126	2459.2	2	273	117
238	102	2670.8	1.7	269	69	1209.4	2.0	252	75	4101.9	1.0	279	52	2701.0	2	275	79
558	103	2664.1	2.5	275	84	2183.7	4.0	269	98	3732.4	1.5	282	102	2076.2	2	274	53
1020	104	2656.2	2.1	277	57	1948.5	2.8	276	32	3876.9	1.5	281	75	2143.4	2	275	64
80	105	2656.2	2.2	275	77	2109.8	2.5	271	67	4125.5	2.0	283	81	1733.5	2	273	81
869	106	2652.9	3.3	277	97	2166.9	2.5	274	58	3359.5	3.5	283	141	2432.3	4	275	91
671	107	2650.6	2.5	274	62	1316.9	3.5	270	76	3436.8	1.0	279	53	3198.2	3	274	56
679	108	2646.2	2.3	273	84	2207.2	4.0	268	98	3621.5	1.0	278	86	2109.8	2	274	69
441	109	2645.0	2.7	277	84	2385.2	2.0	274	50	3668.6	3.0	282	119	1881.3	3	274	84
730	110	2642.8	1.4	276	65	1864.5	1.2	273	53	3430.0	1.0	281	62	2633.8	2	274	79
249	111	2642.8	2.0	275	79	1867.9	3.0	270	74	3554.4	1.0	282	95	2506.2	2	274	69
318	112	2637.2	3.3	275	99	1958.6	3.5	270	88	4044.8	3.5	282	124	1908.2	3	274	84
308	113	2636.1	3.8	277	113	2267.7	3.5	274	95	3241.9	4.0	283	133	2398.7	4	273	109
895	114	2636.1	3.3	276	97	1679.8	4.5	275	94	3883.6	3.5	279	113	2344.9	2	273	84
656	115	2636.1	2.7	275	90	2227.3	2.0	270	53	3645.1	3.0	282	121	2035.9	3	274	97
641	116	2623.8	2.3	276	99	1474.8	2.4	274	64	3715.6	2.5	281	118	2680.9	2	274	114
921	117	2617.1	4.2	276	100	1851.1	4.0	273	116	3742.5	3.5	280	110	2257.6	5	274	74
813	118	2612.6	3.5	277	98	1716.7	3.5	274	86	3910.5	4.0	283	124	2210.6	3	275	84
941	119	2605.8	3.3	275	113	1531.9	4.0	270	114	4108.7	3.0	282	130	2177.0	3	273	97
265	120	2605.8	2.8	275	81	1548.7	4.0	274	97	3110.9	1.5	277	74	3157.9	3	274	74
1005	121	2604.7	2.3	275	70	2019.1	3.5	271	70	3772.7	1.5	281	61	2022.4	2	273	79
662	122	2602.5	2.9	276	104	2244.1	1.7	274	62	3372.9	3.0	283	127	2190.4	4	273	122
382	123	2600.3	2.0	275	71	1941.8	3.0	269	77	3010.1	1.0	283	65	2848.9	2	274	71
523	124	2600.3	1.7	276	59	1871.2	2.0	270	50	2939.6	1.0	282	56	2990.0	2	275	71
506	125	2596.9	3.5	275	103	1505.1	3.5	271	79	4249.8	4.0	282	128	2035.9	3	273	102
755	126	2594.7	2.3	275	75	2213.9	3.0	273	83	3567.8	2.0	281	75	2002.3	2	273	66
906	127	2593.5	2.8	274	86	1713.3	4.0	270	118	3836.5	1.5	280	71	2230.7	3	273	69
497	128	2592.4	2.2	274	69	1736.9	3.5	270	74	4024.7	1.0	279	61	2015.7	2	273	71
418	129	2589.1	3.2	278	86	2637.2	1.5	275	30	3571.1	4.0	283	137	1558.8	4	275	91
85	130	2587.9	2.7	275	89	1914.9	5.0	272	124	3584.6	1.0	279	71	2264.3	2	275	71
963	131	2586.9	2.5	277	80	1599.3	2.4	277	11	4407.7	3.0	281	133	1753.7	2	274	97
492	132	2583.5	2.8	276	110	1347.2	4.0	274	103	4347.2	2.5	281	124	2056.0	2	273	102
966	133	2583.5	2.7	275	92	1689.8	4.0	272	99	4602.5	2.0	282	105	1458.0	2	273	71
797	134	2575.6	3.8	275	103	1555.4	3.5	266	81	4007.9	4.0	283	133	2163.5	4	275	94
758	135	2574.5	2.1	277	82	2267.7	2.2	275	58	3366.2	2.0	283	112	2089.6	2	274	76
387	136	2573.4	3.0	275	85	2559.9	2.5	270	75	3648.4	3.5	282	112	1511.8	3	273	69
273	137	2572.3	2.6	277	88	2035.9	1.4	274	56	3886.9	3.5	283	128	1794.0	3	274	81
151	138	2571.1	1.7	274	66	1770.5	2.0	268	61	3671.9	1.0	281	77	2271.0	2	275	61
1003	139	2570.0	2.7	275	92	2240.8	2.5	270	81	3299.0	2.5	282	109	2170.2	3	274	86
135	140	2564.4	4.2	265	115	1767.1	4.5	271	118	3601.4	4.0	251	136	2324.8	4	273	91
364	141	2559.9	2.2	275	75	1572.2	3.5	271	88	3635.0	1.0	281	65	2472.6	2	274	71
715	142	2559.9	2.2	276	84	2254.2	3.5	272	110	3504.0	1.0	280	77	1921.6	2	275	64
Williams82	**143**	**2559.9**	**1.8**	**271**	**76**	**2533.1**	**2.0**	**274**	**56**	**2586.8**	**1.5**	**268**	**97**	**.**	**.**	**.**	**.**
904	144	2559.9	1.3	274	56	2482.7	2.0	273	66	3181.4	1.0	274	41	2015.7	1	274	61
977	145	2556.6	3.5	275	112	1982.1	4.5	270	108	3947.4	4.0	282	137	1740.2	2	274	91
91	146	2552.1	3.5	276	103	1935.1	3.0	271	79	3396.5	3.5	283	133	2324.8	4	275	97
468	147	2549.9	3.2	277	85	1495.0	2.5	276	50	3601.4	3.0	281	109	2553.2	4	274	97
311	148	2545.4	3.2	277	93	1501.7	2.5	275	65	4461.4	4.0	282	132	1673.0	3	273	81
891	149	2545.4	3.0	276	94	1904.8	3.5	271	83	3870.1	3.5	282	116	1861.2	2	275	84

Table 3.48 Continued.

ExW50K Group C		ACROSS LOCATIONS				Tennessee 2011				Missouri 2011				Tennessee 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
634	150	2531.9	3.0	275	83	1706.6	3.5	270	66	3786.2	2.5	281	109	2103.0	3	275	74
466	151	2527.5	2.0	275	72	1814.1	3.0	270	77	2959.7	1.0	280	69	2808.5	2	275	69
49	152	2521.9	3.0	277	94	1770.5	2.4	274	55	3860.1	3.5	283	136	1935.1	3	274	91
613	153	2516.3	2.8	277	82	2022.4	4.5	274	103	3383.0	2.0	281	74	2143.4	2	275	69
70	154	2508.4	2.2	276	74	2045.9	3.5	272	80	3396.5	1.0	281	71	2082.9	2	274	71
243	155	2503.9	2.3	275	86	1955.2	3.5	269	94	3863.4	1.5	281	91	1693.2	2	275	71
369	156	2502.8	4.2	275	98	1683.1	3.5	271	75	3574.5	4.0	282	128	2250.9	5	273	91
136	157	2500.6	2.3	275	78	1948.5	3.5	272	76	3268.8	1.5	281	77	2284.5	2	273	81
811	158	2491.6	3.0	276	98	1951.9	3.0	270	77	3231.8	3.0	282	128	2291.2	3	275	89
827	159	2491.6	2.8	274	92	1592.4	2.5	269	60	3463.6	3.0	280	123	2418.8	3	273	94
635	160	2489.4	2.7	275	92	2274.4	2.5	271	64	2963.1	2.5	279	121	2230.7	3	275	91
449	161	2484.9	3.7	275	116	1770.5	4.0	271	121	4105.3	4.0	282	142	1579.0	3	274	84
504	162	2476.0	2.0	274	73	2009.0	3.0	269	90	3584.6	1.0	278	66	1834.3	2	275	64
556	163	2473.7	3.2	276	98	2045.9	3.0	271	72	3211.7	2.5	282	122	2163.5	4	274	99
593	164	2471.5	3.5	275	99	1830.9	3.5	270	88	4004.5	4.0	282	118	1579.0	3	273	91
232	165	2469.2	2.5	275	75	1713.3	2.0	271	52	3611.5	2.5	281	102	2082.9	3	274	71
640	167	2460.3	3.3	273	84	1478.2	4.0	269	74	4048.2	3.0	279	104	1854.4	3	273	74
746	168	2458.0	2.8	275	108	1122.1	4.0	270	108	3974.3	2.5	282	122	2277.7	2	273	94
129	169	2455.8	3.2	276	88	1931.7	2.5	271	61	3178.1	3.0	282	121	2257.6	4	274	84
405	170	2443.5	3.2	275	107	2049.3	4.5	273	110	3386.4	2.0	281	118	1894.8	3	273	91
513	171	2434.5	3.0	277	95	2338.2	1.4	275	69	3366.2	3.5	283	121	1599.1	4	275	97
875	172	2433.4	3.2	276	94	2093.0	2.5	270	79	3299.0	3.0	282	107	1908.2	4	275	97
927	173	2431.2	3.0	276	94	1827.6	3.0	273	80	3174.7	3.0	281	112	2291.2	3	275	91
713	174	2431.2	2.7	274	87	2277.7	2.0	271	57	3456.9	3.0	280	121	1558.8	3	273	84
552	175	2431.2	1.5	275	54	1646.2	2.0	271	53	3611.5	0.5	280	57	2035.9	2	274	51
565	176	2430.0	4.0	276	103	1421.1	5.0	272	99	4007.9	4.0	283	135	1861.2	3	273	76
327	177	2426.7	2.2	273	77	1501.7	3.0	266	89	3823.1	1.5	280	71	1955.2	2	273	71
109	178	2423.4	1.5	275	74	1155.8	1.1	271	57	3944.1	1.5	281	84	2170.2	2	273	81
219	179	2420.0	2.3	274	79	1202.7	3.5	269	81	4034.8	1.5	279	75	2022.4	2	273	81
585	180	2415.5	2.7	275	94	1444.6	3.5	269	94	3665.2	2.5	283	104	2136.6	2	275	84
868	181	2412.1	2.1	276	85	2213.9	2.4	274	61	2912.7	2.0	280	109	2109.8	2	274	84
574	182	2403.2	3.2	275	118	997.8	4.5	270	130	3732.4	3.0	281	124	2479.3	2	273	99
936	183	2400.9	4.3	275	108	1615.9	4.0	272	123	3436.8	4.0	281	112	2150.1	5	273	89
39	184	2400.9	3.7	275	109	1750.3	4.5	269	93	3604.7	3.5	282	144	1847.7	3	274	91
100	185	2395.3	3.3	275	100	1599.1	2.0	266	77	3692.1	4.0	284	124	1894.8	4	275	99
525	186	2394.2	2.9	277	97	1135.5	2.3	275	71	3581.2	3.5	282	127	2465.9	3	273	94
911	187	2394.2	3.5	275	103	1179.2	4.5	269	99	3383.0	3.0	282	116	2620.4	3	275	94
666	188	2384.1	3.2	273	101	1686.5	2.5	263	80	4048.2	4.0	283	140	1417.7	3	273	84
300	189	2377.4	2.2	275	61	1867.9	3.5	269	69	3329.3	1.0	282	65	1935.1	2	275	51
310	190	2371.8	3.0	275	103	1814.1	4.5	269	132	3608.1	2.5	282	103	1693.2	2	273	74
982	191	2365.1	2.5	274	90	1837.6	2.5	267	51	2832.1	2.0	281	113	2425.6	3	273	107
394	192	2358.4	2.3	275	80	1656.2	4.0	271	116	3604.7	1.0	280	62	1814.1	2	275	61
649	193	2357.2	2.5	275	97	1904.8	3.5	272	100	2855.6	2.0	280	107	2311.3	2	273	84
685	194	2356.1	2.3	275	91	1763.7	2.0	268	60	3121.0	2.0	282	118	2183.7	3	274	94
40	195	2352.8	2.8	274	95	1820.8	2.5	268	72	3873.5	4.0	282	137	1364.0	2	273	76
563	196	2348.3	2.1	277	73	2227.3	1.2	274	52	3252.0	3.0	284	95	1565.5	2	273	71
785	197	2341.6	2.3	276	97	1478.2	1.4	275	69	3470.4	1.5	280	124	2076.2	4	273	97
717	198	2340.4	2.2	275	75	2039.2	3.5	272	71	3376.3	1.0	279	76	1605.8	2	273	76
532	199	2337.1	3.2	275	97	1951.9	3.0	269	79	3346.1	3.5	283	117	1713.3	3	273	97
832	200	2331.5	3.8	276	101	1696.5	3.5	270	93	3719.0	4.0	283	113	1579.0	4	274	97
495	201	2331.5	2.2	274	67	1424.4	3.5	270	67	3594.7	1.0	278	66	1975.4	2	273	69
571	202	2323.7	3.5	275	99	1935.1	3.5	269	65	3349.4	4.0	283	132	1686.5	3	273	99
950	203	2316.9	2.5	275	89	1720.1	3.0	272	86	3208.3	2.5	280	100	2022.4	2	273	81
771	204	2305.7	2.2	275	79	1760.4	2.5	272	57	3134.4	2.0	280	109	2022.4	2	273	71
727	205	2302.4	3.7	275	105	1545.4	4.5	271	110	3144.5	3.5	282	116	2217.3	3	273	89
712	206	2291.2	3.3	275	99	1985.5	4.0	270	98	3329.3	3.0	283	114	1558.8	3	273	86
684	207	2271.0	2.1	275	77	1300.1	2.3	274	66	3396.5	2.0	280	77	2116.5	2	273	89
51	208	2237.4	1.5	275	55	1941.8	2.5	269	62	3238.6	1.0	281	55	1531.9	1	274	48
769	209	2201.6	3.7	276	111	1105.3	5.0	272	113	3537.6	3.0	282	124	1961.9	3	275	97
438	210	2198.2	1.7	277	58	2133.3	2.0	274	62	2929.5	1.0	282	52	1531.9	2	275	61
934	211	2193.8	2.8	277	89	1538.7	2.5	273	70	3403.2	4.0	283	122	1639.4	2	274	76
303	212	2189.3	2.7	275	94	1713.3	3.5	270	86	3483.8	2.5	281	113	1370.7	2	274	84
390	213	2177.0	3.0	274	106	1713.3	4.0	269	102	3372.9	3.0	282	126	1444.6	2	273	91
239	214	2174.7	2.3	274	77	1481.5	3.5	269	100	3470.4	1.5	281	66	1572.2	2	273	64
944	215	2165.8	1.8	273	76	1253.1	1.5	266	36	3362.9	2.0	279	108	1881.3	2	275	84
44	216	2149.0	1.8	276	62	1518.5	2.0	271	51	3430.0	1.5	281	76	1498.3	2	275	58
579	217	2122.1	2.7	272	79	1384.1	5.0	267	103	3188.2	1.0	277	66	1794.0	2	273	69
759	218	2109.8	3.8	275	95	1347.2	3.5	267	84	3161.3	4.0	284	121	1820.8	4	275	81
540	219	2059.4	2.0	275	76	1424.4	4.0	270	93	3302.4	1.0	282	66	1451.3	1	275	69
953	220	2017.9	2.5	275	89	1901.5	3.0	272	83	2640.6	2.5	281	112	1511.8	2	273	74
323	221	1993.3	2.3	276	73	1478.2	3.5	271	71	2996.7	1.5	281	79	1505.1	2	275	69
	Mean	2643.9	2.7	275.1	88.0	1915.1	3.2	270.6	80.0	3810.7	2.4	280.9	101.3	2188.0	2.7	273.9	82.6
	LSD	577.8	1.8	4.3	12.7	1083.1	1.5	7.5	22.4	1083.1	1.5	7.5	22.4	1083.1	1.5	7.5	22.4

†MAT is maturity date according to the Julian calendar

‡LODG is the lodge score reported on a 1-5 scale;

$LSD_{0.05}$ is Least Significance Difference at the 0.05 probability level.

Table 3.49 Quantitative trait loci identified using R/qtl located on various chromosomes associated with yield in 216 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE
Knoxville, TN 2010	Gm19_46733772_T_C	19	L	84.11	2.87	6.10	1.85	W
Knoxville, TN 2010	Gm01_1045893_G_A	1	D1a	5.88	2.63	5.45	1.18	E
Knoxville, TN 2010	Gm02_6821311_A_C	2	D1b	38.24	2.35	4.35	1.18	E
Portageville, MO	Gm16_6262227_C_T	16	J	10.66	3.18	5.25	3.09	E
Portageville, MO	Gm13_34751493_C_A	13	F	165.33	3.17	5.02	1.16	W
Portageville, MO	Gm09_18969901_T_C	9	K	28.52	2.32	3.81	2.77	W
Knoxville, TN 2010-11 Portageville, MO 2011	Gm06_16723946_G_A	6	C2	32.46	3.72	5.57	2.64	W
Knoxville, TN 2010-11 Portageville, MO 2011	Gm16_5735654_A_G	16	J	8.95	3.71	4.61	1.80	W
Knoxville, TN 2010-11 Portageville, MO 2011	Gm02_6820177_A_C	2	D1b	38.07	3.25	4.31	1.80	W

†Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.50 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using R/qtl in each environment in Group C. Those MAS lines were compared to the top yielding 10 % of lines in the environment(s) from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					**PORTAGEVILLE, MO 2011**					**KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011**				
MAS		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
36	01	671	3198.2	01	78	01	213	5301.3	01	109	01	213	3332.6	01
159	02	760	3191.5	02	101	02	352	4911.6	02	[c]**165**	02	450	3258.7	02
[aa]**198**	03	426	3184.8	03	232	03	[bb]**263**	4763.8	03	303	03	263	3245.3	03
[a]**238**	04	932	3164.6	04	235	04	607	4710.0	04	306	04	[cc]**378**	3178.1	04
239	05	[aa]**265**	3157.9	05	[b]**311**	05	450	4696.6	05	308	05	938	3157.9	05
[aa]**265**	06	469	3016.8	06	[b]**320**	06	680	4649.5	06	311	06	867	3124.3	06
335	07	[aa]**198**	3010.1	07	327	07	36	4602.5	07	327	07	183	3097.5	07
373	08	378	2996.7	08	[b]**378**	08	966	4602.5	08	[c]**368**	08	908	3090.7	08
394	09	[aa]**523**	2990.0	09	666	09	908	4595.8	09	[cc]**378**	09	[cc]**505**	3090.7	09
[aa]**523**	10	620	2963.1	10	717	10	505	4589.1	10	400	10	426	3084.0	10
607	11	867	2916.0	11	944	11	141	4582.4	11	441	11	607	3063.9	11
759	12	448	2902.6	12	953	12	760	4555.5	12	448	12	[c]**612**	3057.1	12
803	13	[a]**78**	2855.6	13	1020	13	165	4508.4	13	460	13	760	3057.1	13
956	14	382	2848.9	14	44	14	[b]**320**	4481.6	14	492	14	78	3057.1	14
49	15	213	2835.4	15	109	15	1006	4474.9	15	[cc]**505**	15	[c]**165**	3043.7	15
55	16	938	2835.4	16	159	16	867	4468.1	16	532	16	199	3043.7	16
[a]**63**	17	466	2808.5	17	221	17	[b]**311**	4461.4	17	571	17	932	2996.7	17
70	18	[a]**63**	2748.1	18	[bb]**263**	18	572	4461.4	18	579	18	553	2990.0	18
[a]**78**	19	377	2741.4	19	265	19	596	4441.3	19	[c]**612**	19	1006	2983.2	19
85	20	553	2721.2	20	[b]**270**	20	[b]**378**	4421.1	20	633	20	[c]**368**	2969.8	20
91	21	401	2714.5	21	276	21	963	4407.7	21	679	21	803	2963.1	21
109	22	[a]**238**	2701.0	22	282	22	[b]**270**	4387.5	22	730	22	485	2963.1	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Portageville, MO in 2011
[bb] Top 5% yield in Portageville, MO in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011

Table 3.51 MAS identifying the bottom 10 % of lines containing unfavorable allele for the yield QTLs detected using R/qtl in each environment in Group C. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PORTAGEVILLE, MO 2011					KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
[aa]**387**	197	240	1599.1	197	525	197	811	3231.8	197	895	197	495	2331.5	197
419	198	513	1599.1	198	[b]**556**	198	[b]**556**	3211.7	198	897	198	832	2331.5	198
[aa]**438**	199	[a]**449**	1579.0	199	613	199	[b]**950**	3211.7	199	906	199	571	2324.8	199
[a]**449**	200	[a]**593**	1579.0	200	641	200	579	3191.5	200	921	200	[c]**950**	2318.1	200
460	201	832	1579.0	201	679	201	904	3184.8	201	938	201	771	2304.6	201
556	202	239	1572.2	202	[b]**685**	202	129	3178.1	202	[c]**950**	202	727	2304.6	202
585	203	563	1565.5	203	712	203	927	3178.1	203	[cc]**953**	203	712	2291.2	203
[a]**593**	204	418	1558.8	204	715	204	[b]**759**	3164.6	204	964	204	684	2271.0	204
612	205	713	1558.8	205	732	205	727	3144.5	205	979	205	51	2237.4	205
634	206	712	1558.8	206	[b]**759**	206	771	3137.8	206	982	206	769	2203.8	206
684	207	51	1531.9	207	760	207	[b]**685**	3124.3	207	1005	207	438	2197.1	207
758	208	[aa]**438**	1531.9	208	797	208	265	3110.9	208	49	208	934	2197.1	208
811	209	[aa]**387**	1511.8	209	818	209	382	3010.1	209	373	209	303	2190.4	209
849	210	953	1511.8	210	845	210	323	2996.7	210	418	210	390	2177.0	210
869	211	323	1505.1	211	849	211	635	2963.1	211	426	211	239	2177.0	211
908	212	44	1498.3	212	862	212	466	2963.1	212	[cc]**540**	212	944	2163.5	212
934	213	[aa]**966**	1458.0	213	875	213	523	2942.9	213	563	213	44	2150.1	213
941	214	540	1451.3	214	877	214	438	2929.5	214	565	214	579	2123.2	214
950	215	390	1444.6	215	906	215	868	2916.0	215	574	215	759	2109.8	215
[aa]**966**	216	666	1417.7	216	938	216	649	2855.6	216	845	216	[cc]**540**	2062.7	216
977	217	303	1370.7	217	[b]**950**	217	[bb]**982**	2835.4	217	849	217	[cc]**953**	2015.7	217
1020	218	40	1364.0	218	[bb]**982**	218	953	2640.6	218	870	218	323	1995.5	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Portageville, MO in 2011
[bb] Bottom 5% yield in Belleville, IL in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011

Table 3.52 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using R/qtl in each environment in Group C compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
36	01	**[b]78**	01	109	01	213	3332.6	01
159	02	101	02	**[c]165**	02	450	3258.7	02
198	03	232	03	303	03	**[bb]263**	3245.3	03
238	04	235	04	306	04	**[bbcc]378**	3178.1	04
239	05	311	05	308	05	938	3157.9	05
265	06	320	06	311	06	867	3124.3	06
335	07	327	07	327	07	183	3097.5	07
373	08	**[bb]378**	08	**[c]368**	08	908	3090.7	08
394	09	666	09	**[cc]378**	09	**[cc]505**	3090.7	09
523	10	717	10	400	10	426	3084.0	10
[aa]607	11	944	11	441	11	**[aa]607**	3063.9	11
759	12	953	12	448	12	**[c]612**	3057.1	12
[a]803	13	1020	13	460	13	760	3057.1	13
956	14	44	14	492	14	**[ab]78**	3057.1	14
49	15	109	15	**[cc]505**	15	**[c]165**	3043.7	15
55	16	159	16	532	16	199	3043.7	16
63	17	221	17	571	17	932	2996.7	17
70	18	**[bb]263**	18	579	18	553	2990.0	18
[a]78	19	265	19	**[c]612**	19	1006	2983.2	19
85	20	270	20	633	20	**[c]368**	2969.8	20
91	21	276	21	679	21	**[a]803**	2963.1	21
109	22	282	22	730	22	485	2963.1	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011

Table 3.53 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using R/qtl in each environment in Group C compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
387	197	525	197	895	197	495	2331.5	197
419	198	556	198	897	198	832	2331.5	198
[a]438	199	613	199	906	199	571	2324.8	199
449	200	641	200	921	200	**[abc]950**	2318.1	200
460	201	679	201	938	201	771	2304.6	201
556	202	685	202	**[c]950**	202	727	2304.6	202
585	203	**[b]712**	203	**[cc]953**	203	**[b]712**	2291.2	203
593	204	715	204	964	204	**[a]684**	2271.0	204
612	205	732	205	979	205	51	2237.4	205
634	206	**[bb]759**	206	982	206	769	2203.8	206
[a]684	207	760	207	1005	207	**[a]438**	2197.1	207
758	208	797	208	49	208	**[aa]934**	2197.1	208
811	209	818	209	373	209	303	2190.4	209
849	210	845	210	418	210	390	2177.0	210
869	211	849	211	426	211	239	2177.0	211
908	212	862	212	**[cc]540**	212	944	2163.5	212
[aa]934	213	875	213	563	213	44	2150.1	213
941	214	877	214	565	214	579	2123.2	214
[a]950	215	906	215	574	215	**[bb]759**	2109.8	215
966	216	938	216	845	216	**[cc]540**	2062.7	216
977	217	**[b]950**	217	849	217	**[cc]953**	2015.7	217
1020	218	982	218	870	218	323	1995.5	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011

Table 3.54 Quantitative trait loci identified using SAS located on various chromosomes associated with yield in 216 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE	P-VALUE
Knoxville, TN 2010	Gm01_2747136_A_C	1	D1a	11.28	7.32	-1.30 (w)	W	0.0008
Knoxville, TN 2010	Gm20_43890641_G_T	20	I	54.79	6.70	-2.67 (w)	W	0.0015
Knoxville, TN 2010	Gm02_44803277_C_T	2	D1b	107.06	6.11	-0.51 (w)	W	0.0026
Knoxville, TN 2010	Gm07_16814628_C_T	7	M	38.47	5.41	-0.83 (w)	W	0.0051
Knoxville, TN 2010	Gm12_1594873_A_G	12	H	3.64	5.34	-0.62 (w)	W	0.0055
Knoxville, TN 2010	Gm05_1128604_A_G	5	A1	3.24	4.95	-0.52 (w)	W	0.0024
Portageville, MO 2011	Gm16_6233586_A_G	16	J	14.23	8.39	3.13 (e)	E	0.0003
Portageville, MO 2011	Gm13_34946643_T_C	13	F	180.68	7.28	2.90 (e)	E	0.0009
Portageville, MO 2011	Gm09_34191288_T_C	9	K	78.24	6.88	-3.47 (w)	W	0.0013
Portageville, MO 2011	Gm06_10864751_A_G	6	C2	24.86	5.61	-2.83 (w)	W	0.0042
Portageville, MO 2011	Gm03_838582_T_C	3	N	4.68	4.82	-2.34 (w)	W	0.0089
Knoxville, TN 2010-11 Portageville, MO 2011	Gm20_46574547_T_C	20	I	65.04	8.90	-1.72 (w)	W	0.0001
Knoxville, TN 2010-11 Portageville, MO 2011	Gm16_6496577_A_C	16	J	14.86	7.62	0.42 (e)	E	0.0005
Knoxville, TN 2010-11 Portageville, MO 2011	Gm03_21003884_A_G	3	N	44.15	6.76	0.37 (e)	E	0.0012
Knoxville, TN 2010-11 Portageville, MO 2011	Gm13_32183364_A_C	13	F	162.13	6.32	0.02 (e)	E	0.0019
Knoxville, TN 2010-11 Portageville, MO 2011	Gm12_39962521_A_G	12	H	91.44	6.07	1.54 (e)	E	0.0004
Knoxville, TN 2010-11 Portageville, MO 2011	Gm11_7445495_G_A	11	B1	26.72	5.97	0.67 (e)	E	0.0026
Knoxville, TN 2010-11 Portageville, MO 2011	Gm18_265662_T_C	18	G	1.19	5.71	0.96 (e)	E	0.0007
Knoxville, TN 2010-11 Portageville, MO 2011	Gm05_34850619_C_T	5	A1	72.38	5.71	-0.27 (w)	W	0.0007
Knoxville, TN 2010-11 Portageville, MO 2011	Gm07_4837493_A_G	7	M	11.06	5.71	2.04 (e)	E	0.0007
Knoxville, TN 2010-11 Portageville, MO 2011	Gm02_49746270_A_G	2	D1b	146.54	5.40	-1.19 (w)	W	0.0046

†Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.55 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using SAS in each environment in Group C. Those MAS lines were compared to the top yielding 10 % of lines in the environment(s) from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PORTAGEVILLE, MO 2011					KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
450	01	671	3198.2	01	[bb]**263**	01	213	5301.3	01	85	01	213	3332.6	01
221	02	[aa]**760**	3191.5	02	748	02	[bb]**352**	4911.6	02	235	02	[cc]**450**	3258.7	02
306	03	426	3184.8	03	[bb]**36**	03	[bb]**263**	4763.8	03	282	03	263	3245.3	03
325	04	932	3164.6	04	80	04	607	4710.0	04	364	04	378	3178.1	04
400	05	265	3157.9	05	109	05	450	4696.6	05	400	05	938	3157.9	05
[aa]**469**	06	[aa]**469**	3016.8	06	219	06	680	4649.5	06	401	06	867	3124.3	06
525	07	198	3010.1	07	273	07	[bb]**36**	4602.5	07	[cc]**450**	07	183	3097.5	07
[aa]**760**	08	378	2996.7	08	282	08	966	4602.5	08	492	08	908	3090.7	08
797	09	523	2990.0	09	[b]**320**	09	908	4595.8	09	616	09	505	3090.7	09
798	10	620	2963.1	10	[bb]**352**	10	505	4589.1	10	633	10	426	3084.0	10
875	11	867	2916.0	11	359	11	141	4582.4	11	748	11	607	3063.9	11
982	12	448	2902.6	12	441	12	760	4555.5	12	941	12	612	3057.1	12
121	13	78	2855.6	13	466	13	165	4508.4	13	[c]**78**	13	760	3057.1	13
149	14	382	2848.9	14	492	14	[b]**320**	4481.6	14	[c]**199**	14	[c]**78**	3057.1	14
159	15	213	2835.4	15	535	15	1006	4474.9	15	303	15	165	3043.7	15
165	16	938	2835.4	16	545	16	867	4468.1	16	369	16	[c]**199**	3043.7	16
199	17	466	2808.5	17	552	17	311	4461.4	17	393	17	932	2996.7	17
232	18	63	2748.1	18	553	18	[b]**572**	4461.4	18	419	18	553	2990.0	18
263	19	377	2741.4	19	571	19	[b]**596**	4441.3	19	438	19	1006	2983.2	19
273	20	553	2721.2	20	[b]**572**	20	378	4421.1	20	441	20	368	2969.8	20
276	21	401	2714.5	21	579	21	963	4407.7	21	506	21	803	2963.1	21
299	22	238	2701.0	22	[b]**596**	22	270	4387.5	22	[c]**553**	22	485	2963.1	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Portageville, MO in 2011
[bb] Top 5% yield in Portageville, MO in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011

Table 3.56 MAS identifying the bottom 10 % of lines containing the unfavorable allele for the yield QTLs detected using SAS in each environment in Group C. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PORTAGEVILLE, MO 2011					KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
382	197	[a]**240**	1599.1	197	921	197	[b]**811**	3231.8	197	213	197	495	2331.5	197
[a]**418**	198	513	1599.1	198	[b]**927**	198	556	3211.7	198	219	198	832	2331.5	198
504	199	449	1579.0	199	964	199	[b]**950**	3211.7	199	[cc]**239**	199	571	2324.8	199
532	200	[a]**593**	1579.0	200	[bb]**982**	200	579	3191.5	200	387	200	950	2318.1	200
579	201	832	1579.0	201	1003	201	904	3184.8	201	405	201	771	2304.6	201
612	202	[a]**239**	1572.2	202	1006	202	129	3178.1	202	435	202	727	2304.6	202
674	203	563	1565.5	203	70	203	[b]**927**	3178.1	203	466	203	712	2291.2	203
696	204	[a]**418**	1558.8	204	159	204	759	3164.6	204	468	204	684	2271.0	204
769	205	713	1558.8	205	300	205	727	3144.5	205	507	205	51	2237.4	205
897	206	712	1558.8	206	393	206	771	3137.8	206	525	206	769	2203.8	206
921	207	51	1531.9	207	507	207	685	3124.3	207	558	207	438	2197.1	207
938	208	438	1531.9	208	[bb]**523**	208	265	3110.9	208	[cc]**579**	208	934	2197.1	208
944	209	387	1511.8	209	540	209	382	3010.1	209	585	209	303	2190.4	209
964	210	953	1511.8	210	558	210	323	2996.7	210	813	210	390	2177.0	210
[aa]**966**	211	323	1505.1	211	582	211	635	2963.1	211	818	211	[cc]**239**	2177.0	211
1005	212	44	1498.3	212	585	212	466	2963.1	212	849	212	944	2163.5	212
[a]**239**	213	[aa]**966**	1458.0	213	620	213	[bb]**523**	2942.9	213	869	213	44	2150.1	213
[a]**240**	214	540	1451.3	214	[bb]**649**	214	438	2929.5	214	877	214	[cc]**579**	2123.2	214
536	215	390	1444.6	215	671	215	868	2916.0	215	964	215	759	2109.8	215
[a]**593**	216	666	1417.7	216	758	216	[bb]**649**	2855.6	216	378	216	[cc]**540**	2062.7	216
820	217	303	1370.7	217	[b]**811**	217	[bb]**982**	2835.4	217	[cc]**540**	217	953	2015.7	217
1020	218	40	1364.0	218	[b]**950**	218	953	2640.6	218	845	218	323	1995.5	218

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Portageville, MO in 2011
[bb] Bottom 5% yield in Portageville, MO in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Portageville, MO in 2011

Table 3.57 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using SAS in each environment in Group C compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
[aa]450	01	**[bb]263**	01	85	01	213	3332.6	01
221	02	748	02	235	02	**[aacc]450**	3258.7	02
306	03	36	03	282	03	**[aabb]263**	3245.3	03
325	04	80	04	364	04	378	3178.1	04
400	05	109	05	400	05	938	3157.9	05
469	06	219	06	401	06	867	3124.3	06
525	07	273	07	**[cc]450**	07	183	3097.5	07
[a]760	08	282	08	492	08	908	3090.7	08
797	09	320	09	616	09	505	3090.7	09
798	10	352	10	633	10	426	3084.0	10
875	11	359	11	748	11	607	3063.9	11
982	12	441	12	941	12	612	3057.1	12
121	13	466	13	**[c]78**	13	**[a]760**	3057.1	13
149	14	492	14	**[c]199**	14	**[c]78**	3057.1	14
159	15	535	15	303	15	**[a]165**	3043.7	15
[a]165	16	545	16	369	16	**[ac]199**	3043.7	16
[a]199	17	552	17	393	17	932	2996.7	17
232	18	**[b]553**	18	419	18	**[bc]553**	2990.0	18
[aa]263	19	571	19	438	19	1006	2983.2	19
273	20	572	20	441	20	368	2969.8	20
276	21	579	21	506	21	803	2963.1	21
299	22	596	22	**[c]553**	22	485	2963.1	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011

Table 3.58 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using SAS in each environment in Group C compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
382	197	921	197	213	197	495	2331.5	197
418	198	927	198	219	198	832	2331.5	198
504	199	964	199	**[cc]239**	199	571	2324.8	199
532	200	982	200	387	200	**[b]950**	2318.1	200
[aa]579	201	1003	201	405	201	771	2304.6	201
612	202	1006	202	435	202	727	2304.6	202
674	203	70	203	466	203	712	2291.2	203
696	204	159	204	468	204	684	2271.0	204
[a]769	205	300	205	507	205	51	2237.4	205
897	206	393	206	525	206	**[a]769**	2203.8	206
921	207	507	207	558	207	438	2197.1	207
938	208	523	208	**[cc]579**	208	934	2197.1	208
[aa]944	209	**[bb]540**	209	585	209	303	2190.4	209
964	210	558	210	813	210	390	2177.0	210
966	211	582	211	818	211	**[aacc]239**	2177.0	211
1005	212	585	212	849	212	**[aa]944**	2163.5	212
[aa]239	213	620	213	869	213	44	2150.1	213
240	214	649	214	877	214	**[aacc]579**	2123.2	214
536	215	671	215	964	215	759	2109.8	215
593	216	758	216	378	216	**[bbcc]540**	2062.7	216
820	217	811	217	**[cc]540**	217	953	2015.7	217
1020	218	**[b]950**	218	845	218	323	1995.5	218

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011

Table 3.59 Significant (P<0.01) epistatic interactions between loci for yield in 216 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using R/qtl and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm19_46733772_T_C	19	L	84.11	W	GM02_44803277_C_T	2	D1b	99.56	1.53	-1.88	-0.43
						GM05_39686377_T_C	5	A1	88.19	2.21	-1.89	-0.11
						GM06_16450669_T_C	6	C2	36.56	2.74	1.82	-1.58
						GM08_39969061_C_T	8	A2	88.82	2.73	-2.39	-0.40
						GM09_45833394_G_A	9	K	101.85	2.98	-2.34	-0.29
						GM10_36871822_T_G	10	O	81.94	3.26	-0.07	-2.18
						GM13_20628643_G_T	13	F	45.84	3.30	-0.02	-2.15
						GM18_60221294_C_T	18	G	133.83	3.14	-0.15	-2.25
Portageville, MO	Gm13_34751493_C_A	13	F	165.33	W	GM02_46971562_G_A	2	D1b	104.38	5.84	3.21	-0.14
						GM12_34600990_C_T	12	H	76.89	5.43	3.37	0.17
Portageville, MO	Gm09_18969901_T_C	9	K	28.52	W	GM05_32329300_T_G	5	A	71.84	5.42	0.38	-2.91
						GM13_25895304_C_T	13	F	57.55	5.39	0.31	-2.84
						GM17_13589025_G_A	17	D2	30.20	3.89	-2.78	-0.12
Knoxville, TN 2010-11 Portageville, MO 2011	Gm06_16723946_G_A	6	C2	32.46	W	GM04_46940182_G_T	4	C1	104.31	3.96	-2.75	0.47
						GM06_47833095_T_G	6	C2	106.30	4.72	-3.73	0.19

†Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.60 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by R/qtl to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
671	01	**[aa]199**	2608.7	**[bb]213**	5301.3	**[cc]213**	3332.6
[ac]932	02	**[aa]938**	2583.5	352	4911.6	**[cc]450**	3258.7
265	03	**[aa]378**	2561.6	263	4763.8	263	3245.3
[aabcc]378	04	**[aa]448**	2548.2	607	4710.0	**[cc]378**	3178.1
[aac]78	05	**[aa]450**	2539.8	**[bb]450**	4696.6	**[cc]938**	3157.9
[bc]760	06	849	2536.4	680	4649.5	**[cc]867**	3124.3
[aacc]426	07	**[aa]426**	2529.7	36	4602.5	183	3097.5
[a]198	08	**[aa]63**	2521.3	966	4602.5	908	3090.7
[a]523	09	263	2491.1	908	4595.8	505	3090.7
[aa]448	10	183	2470.9	505	4589.1	**[cc]426**	3084.0
[a]382	11	**[aa]78**	2460.8	141	4582.4	607	3063.9
[a]620	12	460	2460.8	**[b]760**	4555.5	612	3057.1
[aacc]938	13	764	2450.8	165	4508.4	**[c]760**	3057.1
[bbcc]213	14	**[a]867**	2447.4	320	4481.6	**[c]78**	3057.1
[bcc]378	15	**[a]932**	2430.6	**[b]1006**	4474.9	165	3043.7
[c]553	16	**[a]523**	2430.6	**[b]867**	4468.1	**[c]199**	3043.7
[abcc]867	17	**[a]198**	2425.6	311	4461.4	**[c]932**	2996.7
[aa]63	18	612	2423.9	572	4461.4	**[c]553**	2990.0
898	19	359	2418.8	596	4441.3	**[c]1006**	2983.2
[aabbcc]450	20	**[a]620**	2410.4	**[b]378**	4421.1	368	2969.8
[bc]1006	21	430	2407.1	963	4407.7	803	2963.1
[aac]199	22	**[a]382**	2395.3	270	4387.5	485	2963.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively
†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.61 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by SAS to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aacc]426	01	199	2608.7	213	5301.3	213	3332.6
[a]382	02	**[aa]938**	2583.5	352	4911.6	450	3258.7
845	03	378	2561.6	263	4763.8	263	3245.3
[a]198	04	448	2548.2	607	4710.0	378	3178.1
982	05	450	2539.8	450	4696.6	**[cc]938**	3157.9
641	06	**[aa]849**	2536.4	680	4649.5	867	3124.3
[aac]78	07	**[aa]426**	2529.7	36	4602.5	183	3097.5
[aa]63	08	**[aa]63**	2521.3	966	4602.5	908	3090.7
[bc]760	09	263	2491.1	908	4595.8	505	3090.7
401	10	183	2470.9	505	4589.1	**[cc]426**	3084.0
121	11	**[aa]78**	2460.8	141	4582.4	607	3063.9
377	12	460	2460.8	**[b]760**	4555.5	612	3057.1
238	13	764	2450.8	165	4508.4	**[c]760**	3057.1
911	14	867	2447.4	320	4481.6	**[c]78**	3057.1
[a]523	15	932	2430.6	1006	4474.9	165	3043.7
[c]553	16	**[a]523**	2430.6	867	4468.1	199	3043.7
818	17	**[a]198**	2425.6	311	4461.4	932	2996.7
[aa]849	18	612	2423.9	572	4461.4	**[c]553**	2990.0
435	19	359	2418.8	596	4441.3	1006	2983.2
[c]368	20	620	2410.4	378	4421.1	**[c]368**	2969.8
91	21	430	2407.1	963	4407.7	803	2963.1
[aacc]938	22	**[a]382**	2395.3	270	4387.5	485	2963.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively
†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.62 Significant (P<0.01) epistatic interactions between loci for yield in 216 RILs in Group C derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using SAS and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm20_43890641_G_T	20	I	54.79	W	GM04_44269200_C_A	4	C1	98.38	3.67	-0.17	-2.44
						GM05_30931540_G_A	5	A1	68.74	5.23	-2.67	0.10
						GM12_14694597_G_T	12	H	32.65	3.50	-2.51	-0.23
						GM15_48313076_A_C	15	E	107.36	3.86	-2.50	-0.19
Knoxville, TN 2010	Gm02_44803277_C_T	2	D1b	107.06	W	GM05_36762481_G_A	5	A1	81.69	4.94	0.99	-1.61
						GM07_42867486_A_G	7	M	95.26	3.73	0.89	-1.34
						GM09_38902035_A_G	9	K	86.45	7.99	1.42	-1.95
						GM14_41157194_A_C	14	B2	91.46	6.05	-1.34	1.59
Knoxville, TN 2010	Gm07_16814628_C_T	7	M	38.47	W	GM04_31211384_C_T	4	C1	69.36	3.59	0.67	-1.52
						GM08_14311616_T_C	8	A2	31.80	3.63	-1.59	0.59
						GM12_14579106_A_G	12	H	32.40	3.45	-1.56	0.56
						GM13_33821100_A_G	13	F	75.16	4.76	0.77	-1.79
						GM14_10176632_C_T	14	B2	22.61	3.77	0.80	-1.43
						GM18_25859813_G_A	18	G	57.47	3.56	0.68	-1.52
						GM19_38075013_G_A	19	L	84.61	3.99	-1.35	0.99
Portageville, MO 2011	Gm13_34946643_T_C	13	F	180.68	E	GM02_48594877_C_T	2	D1b	107.99	5.53	3.11	-0.12
						GM10_39818480_G_A	10	O	88.49	4.01	-0.15	2.58
						GM12_34600990_C_T	12	H	76.89	5.39	3.26	0.07
Portageville, MO 2011	Gm09_34191288_T_C	9	K	78.24	W	GM10_43808257_T_C	10	O	97.35	3.82	-3.09	-0.35
						GM12_15394023_C_T	12	H	34.21	6.75	-3.31	0.27
						GM13_26311075_C_A	13	F	58.47	3.74	-0.38	-3.05
						GM15_14046246_T_G	15	E	31.21	4.59	0.07	-2.94
						GM17_13487812_A_G	17	D2	29.97	4.44	-3.18	-0.26
						GM19_49206071_G_A	19	L	109.35	3.41	-0.54	-3.13
						GM20_43196719_T_C	20	I	95.99	4.60	-0.34	-3.36
Portageville, MO 2011	Gm06_10864751_A_G	6	C2	24.86	W	GM13_28191307_T_C	13	F	62.65	6.12	0.30	-3.03
						GM14_42787602_A_G	6	C2	95.08	3.87	-0.28	-3.07

Table 3.62 Continued.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT[†] E	W
Knoxville, TN 2010-11 Portageville, MO 2011	Gm20_46574547_T_C	20	I	65.04	W	GM03_37432542_C_A	3	N	83.18	7.80	-1.89	0.83
						GM04_44765666_T_C	4	C1	99.48	3.98	0.71	-1.10
						GM06_44116624_T_C	6	C2	74.85	3.91	-1.94	0.32
						GM12_33680937_T_G	12	H	74.85	4.22	-1.15	0.70
						GM16_29973174_T_C	16	J	66.61	5.48	0.67	-1.55
Knoxville, TN 2010-11 Portageville, MO 2011	Gm03_21003884_A_G	3	N	44.15	E	GM04_44267306_T_C	4	C1	98.37	5.31	0.91	-1.30
Knoxville, TN 2010-11 Portageville, MO 2011	Gm13_32183364_A_C	13	F	162.13	E	GM13_23774236_T_G	13	F	52.83	4.71	1.87	-0.23
						GM17_39483942_A_C	17	D2	87.74	3.56	-0.47	1.37
						GM19_37728693_G_A	19	L	83.84	5.93	-0.28	2.13
Knoxville, TN 2010-11 Portageville, MO 2011	Gm12_39962521_A_G	12	H	91.44	E	GM01_47115450_G_T	1	D1a	104.70	6.00	-0.08	2.37
						GM02_14479985_A_C	2	D1b	32.18	4.24	0.10	2.18
						GM13_37624457_T_C	13	F	83.61	3.94	1.78	-0.19
Knoxville, TN 2010-11 Portageville, MO 2011	Gm05_34850619_C_T	5	A1	72.38	W	GM14_12850710_T_C	14	B2	28.56	5.89	0.97	-1.34
						GM20_37924589_A_G	20	I	84.28	4.91	-1.21	0.92
Knoxville, TN 2010-11 Portageville, MO 2011	Gm02_49746270_A_G	2	D1b	146.54	W	GM02_47268207_C_T	2	D1b	105.04	4.12	1.68	-0.71
						GM11_30346591_A_G	11	B1	67.44	3.69	1.16	-0.74
						GM18_53801740_T_C	18	G	119.56	5.60	-1.31	1.07
						GM19_40567680_A_G	19	L	90.15	4.33	1.24	-0.84

[†]Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.63 Yield prediction model (YPM) developed using QTLs detected in Portageville, MO in 2011 by R/qtl to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bb]352	01	199	2608.7	**[bb]213**	5301.3	**[cc]213**	3332.6
[bb]680	02	938	2583.5	**[bb]352**	4911.6	450	3258.7
[aac]78	03	**[aa]378**	2561.6	**[bb]263**	4763.8	**[cc]263**	3245.3
[aabbcc]263	04	448	2548.2	**[bb]607**	4710.0	**[cc]378**	3178.1
[abcc]867	05	450	2539.8	450	4696.6	938	3157.9
[bbcc]213	06	849	2536.4	**[bb]680**	4649.5	**[cc]867**	3124.3
[b]572	07	426	2529.7	**[bb]36**	4602.5	183	3097.5
[bbcc]505	08	63	2521.3	**[bb]966**	4602.5	908	3090.7
[b]596	09	**[aa]263**	2491.1	908	4595.8	**[cc]505**	3090.7
[b]270	10	183	2470.9	**[bb]505**	4589.1	426	3084.0
[bb]966	11	**[aa]78**	2460.8	**[bb]141**	4582.4	**[cc]607**	3063.9
[bc]1006	12	460	2460.8	**[b]760**	4555.5	612	3057.1
[bb]141	13	764	2450.8	165	4508.4	**[c]760**	3057.1
[aabcc]378	14	**[a]867**	2447.4	**[b]320**	4481.6	**[c]78**	3057.1
[bbcc]607	15	932	2430.6	**[b]1006**	4474.9	165	3043.7
[b]320	16	523	2430.6	**[b]867**	4468.1	199	3043.7
[b]311	17	198	2425.6	**[b]311**	4461.4	932	2996.7
[bb]36	18	612	2423.9	**[b]572**	4461.4	**[c]553**	2990.0
[c]368	19	359	2418.8	**[b]596**	4441.3	**[c]1006**	2983.2
[bc]760	20	620	2410.4	**[b]378**	4421.1	**[c]368**	2969.8
897	21	430	2407.1	963	4407.7	803	2963.1
[c]553	22	382	2395.3	**[b]270**	4387.5	485	2963.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.64 Yield prediction model (YPM) developed using QTLs detected in Portageville, MO in 2011 by SAS to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011		KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bbcc]213	01	199	2608.7	**[bb]213**	5301.3	**[cc]213**	3332.6
[bbcc]505	02	**[aa]938**	2583.5	**[bb]352**	4911.6	450	3258.7
[bb]141	03	378	2561.6	**[bb]263**	4763.8	**[cc]263**	3245.3
[aacc]426	04	448	2548.2	**[bb]607**	4710.0	378	3178.1
[bb]966	05	450	2539.8	450	4696.6	**[cc]938**	3157.9
956	06	849	2536.4	680	4649.5	**[cc]867**	3124.3
506	07	**[aa]426**	2529.7	36	4602.5	183	3097.5
535	08	63	2521.3	**[bb]966**	4602.5	908	3090.7
[bb]352	09	**[aa]263**	2491.1	908	4595.8	**[cc]505**	3090.7
[abcc]867	10	183	2470.9	**[bb]505**	4589.1	**[cc]426**	3084.0
820	11	78	2460.8	**[bb]141**	4582.4	**[cc]607**	3063.9
[aacc]938	12	460	2460.8	760	4555.5	612	3057.1
449	13	764	2450.8	165	4508.4	760	3057.1
[aabbcc]263	14	**[a]867**	2447.4	320	4481.6	78	3057.1
[bbcc]607	15	**[a]932**	2430.6	**[b]1006**	4474.9	165	3043.7
400	16	523	2430.6	**[b]867**	4468.1	199	3043.7
784	17	198	2425.6	311	4461.4	**[c]932**	2996.7
219	18	612	2423.9	572	4461.4	**[c]553**	2990.0
[ac]932	19	359	2418.8	596	4441.3	**[c]1006**	2983.2
[c]553	20	620	2410.4	378	4421.1	**[c]368**	2969.8
[c]368	21	430	2407.1	963	4407.7	803	2963.1
[bc]1006	22	382	2395.3	270	4387.5	485	2963.1

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.65 Yield prediction model (YPM) developed using QTLs detected over three environments by R/qtl to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011				KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aabbcc]263	01	**[aa]213**	3332.6	**[bb]199**	2608.7	**[cc]213**	5301.3
[aabc]867	02	**[aa]450**	3258.7	**[bb]938**	2583.5	352	4911.6
[aacc]213	03	**[aa]263**	3245.3	**[bb]378**	2561.6	**[cc]263**	4763.8
932	04	**[aa]378**	3178.1	448	2548.2	**[cc]607**	4710.0
[ab]612	05	**[aa]938**	3157.9	**[bb]450**	2539.8	**[cc]450**	4696.6
[ac]760	06	**[aa]867**	3124.3	849	2536.4	**[cc]680**	4649.5
[aabbcc]450	07	183	3097.5	426	2529.7	36	4602.5
[aacc]505	08	**[aa]908**	3090.7	63	2521.3	966	4602.5
[aabb]938	09	**[aa]505**	3090.7	**[bb]263**	2491.1	**[cc]908**	4595.8
[ac]165	10	426	3084.0	183	2470.9	**[cc]505**	4589.1
633	11	**[aa]607**	3063.9	**[bb]78**	2460.8	141	4582.4
[aabbc]378	12	**[a]612**	3057.1	460	2460.8	**[c]760**	4555.5
[ab]932	13	**[a]760**	3057.1	764	2450.8	**[c]165**	4508.4
[abb]78	14	**[a]78**	3057.1	**[b]867**	2447.4	320	4481.6
786	15	**[a]165**	3043.7	**[b]932**	2430.6	1006	4474.9
[a]553	16	**[a]199**	3043.7	523	2430.6	**[c]867**	4468.1
956	17	**[a]932**	2996.7	198	2425.6	311	4461.4
[aacc]607	18	**[a]553**	2990.0	**[b]612**	2423.9	572	4461.4
[a]803	19	1006	2983.2	359	2418.8	596	4441.3
[aacc]908	20	368	2969.8	620	2410.4	**[c]378**	4421.1
[abb]199	21	**[a]803**	2963.1	430	2407.1	963	4407.7
[cc]680	22	485	2963.1	382	2395.3	270	4387.5

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.66 Yield prediction model (YPM) developed using QTLs detected over three environments by SAS to select by MAS the top yielding 10 % of RILs in Group C grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 PORTAGEVILLE, MO 2011				KNOXVILLE, TN 2011		PORTAGEVILLE, MO 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aabbcc]450	01	**[aa]213**	3332.6	**[bb]199**	2608.7	**[cc]213**	5301.3
[a]553	02	**[aa]450**	3258.7	938	2583.5	352	4911.6
[abb]78	03	**[aa]263**	3245.3	378	2561.6	**[cc]263**	4763.8
748	04	378	3178.1	448	2548.2	**[cc]607**	4710.0
[aacc]607	05	938	3157.9	**[bb]450**	2539.8	**[cc]450**	4696.6
[ab]932	06	**[aa]867**	3124.3	**[bb]849**	2536.4	**[cc]680**	4649.5
[aacc]213	07	183	3097.5	426	2529.7	36	4602.5
[aacc]505	08	908	3090.7	**[bb]63**	2521.3	966	4602.5
[aabc]867	09	**[aa]505**	3090.7	**[bb]263**	2491.1	908	4595.8
[cc]680	10	426	3084.0	183	2470.9	**[cc]505**	4589.1
[ac]1006	11	**[aa]607**	3063.9	**[bb]78**	2460.8	141	4582.4
435	12	612	3057.1	460	2460.8	**[c]760**	4555.5
[ac]165	13	**[a]760**	3057.1	**[b]764**	2450.8	**[c]165**	4508.4
[ac]760	14	**[a]78**	3057.1	**[b]867**	2447.4	320	4481.6
[aabbcc]263	15	**[a]165**	3043.7	**[b]932**	2430.6	**[c]1006**	4474.9
[a]803	16	**[a]199**	3043.7	523	2430.6	**[c]867**	4468.1
[a]368	17	**[a]932**	2996.7	198	2425.6	311	4461.4
[bb]849	18	**[a]553**	2990.0	612	2423.9	572	4461.4
[bb]63	19	**[a]1006**	2983.2	359	2418.8	596	4441.3
[b]764	20	**[a]368**	2969.8	620	2410.4	378	4421.1
[abb]199	21	**[a]803**	2963.1	430	2407.1	963	4407.7
[a]485	22	**[a]485**	2963.1	382	2395.3	270	4387.5

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Portageville, MO in 2011 and combined over Knoxville, TN in 2010, 2011 and Portageville, MO in 2011, respectively

[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.67 Combined analysis of variance and estimates of variance components for yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in three environments: Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011.

SOURCE	DF	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	h^2	P-VALUE	F-VALUE
Environment	2	9916.48	40.47	36		<0.0001	138.83
Reps (Env.)	2	421.62	1.13	1		0.0051	5.94
Genotypes	219	185.34	14.92	13	0.38	0.0002	2.59
Genotypes x E	219	100.09	13.14	12		0.001	1.40
Error	438	71.42	42.44	38			

Table 3.68 Combined analysis of variance and estimates of variance components for yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Knoxville, TN in 2011.

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	69.32	69.32	17.89	25	0.01	1.29
Genotypes	219	14685.59	94.53	20.51	28	0.002	1.76
Error	220	12473.27	53.53	33.82	47		

Table 3.69 Combined analysis of variance and estimates of variance components for yield in 221 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1 evaluated in Plymouth, NC in 2011.

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	VARIANCE COMPONENT	PERCENT OF TOTAL	P-VALUE	F-VALUE
Reps	1	731.28	731.28	79.41	34	0.004	8.11
Genotypes	219	3308.70	142.62	66.18	28	0.0003	1.58
Error	220	20026.70	90.21	90.79	38		

Table 3.70 Mean seed yield, maturity, lodging and height of 220 recombinant inbred lines in Group D and three commercial checks grown in Knoxville, TN in 2010 and 2011, Plymouth, NC in 2011 and averaged over Knoxville, TN in 2010 and 2011 and Plymouth, NC in 2011.

ExW50K Group D		ACROSS LOCATIONS				TENNESSEE 2011				NORTH CAROLINA 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
5601T	**01**	**2707.8**	**3.9**	**275**	**97**	**2706.5**	**3.0**	**275**	**117**	**.**	**4.8**	**.**	**76**	**.**	**.**	**.**	**.**
864	02	2648.2	3.8	279	120	1985.5	4.5	279	98	1746.9	3.0	277	140	2985.9	4	278	122
81	03	2641.2	3.2	276	84	2160.2	3.0	275	99	2748.1	2.5	276	72	3015.5	4	276	81
686	04	2603.4	3.6	277	102	2291.2	3.0	273	84	3205.0	3.8	283	114	2340.9	4	278	109
530	05	2601.6	3.7	277	109	2381.9	4.5	274	109	2677.5	3.5	279	127	2745.4	3	277	91
918	06	2581.9	3.4	281	77	1878.0	3.5	275	65	1666.3	2.8	280	81	3059.2	4	285	86
122	07	2547.4	3.9	278	105	1972.0	4.0	275	116	3265.4	3.8	281	109	2404.7	4	277	89
605	08	2540.3	3.5	279	121	1739.0	4.5	277	119	2566.7	3.0	280	113	3059.8	3	277	132
984	09	2532.6	3.2	279	101	2170.2	4.0	277	102	3151.2	3.5	279	121	2310.0	2	277	81
491	10	2529.0	3.0	279	78	1582.3	4.5	271	99	2680.9	2.5	282	64	3323.9	2	284	71
706	11	2516.7	4.2	275	112	2281.1	4.5	272	110	2435.6	4.0	279	107	3337.3	4	279	119
847	12	2493.6	3.3	278	87	1656.2	4.5	273	126	2140.0	2.5	278	70	2787.7	3	283	66
531	13	2488.3	2.6	274	82	2311.3	3.5	273	110	2533.1	2.3	274	70	2620.4	2	276	66
220	14	2479.8	3.2	279	99	1898.1	2.0	278	70	2825.3	3.5	281	130	2715.8	4	279	97
846	15	2461.2	3.8	276	123	1965.3	4.0	273	107	3037.0	3.5	281	135	2697.0	4	276	127
688	16	2460.9	3.7	279	109	1921.6	3.5	279	90	1280.0	3.5	277	130	2256.2	4	276	107
917	17	2452.7	3.9	282	108	1562.2	4.0	274	99	2808.5	3.8	279	119	2805.9	4	283	107
647	18	2445.7	3.5	276	112	1921.6	3.5	274	88	1012.2	3.0	262	123	2975.8	4	276	124
1010	19	2438.1	2.3	277	69	1871.2	3.0	275	85	2633.8	2.0	281	57	2711.8	2	279	66
94	20	2436.1	3.5	278	93	1978.7	4.0	275	108	1820.8	2.5	281	79	3508.7	4	279	91
23	21	2435.9	3.1	276	96	1639.4	4.5	275	131	2825.3	2.8	277	70	2842.8	2	277	86
682	22	2429.4	3.8	277	105	1615.9	5.0	275	114	3178.1	3.5	280	118	2685.6	3	276	84
Osage	**23**	**2418.8**	**2.8**	**274**	**87**	**1024.6**	**3.5**	**270**	**102**	**3813.0**	**2.0**	**277**	**72**	**.**	**.**	**.**	**.**
118	24	2418.4	2.5	274	69	2217.3	3.5	275	86	2620.4	2.0	272	61	2417.5	2	276	58
314	25	2410.3	2.9	277	83	1938.4	4.5	274	126	2697.7	2.3	278	64	2594.9	2	278	61
75	26	2403.6	3.5	282	108	2133.3	2.5	275	89	2318.1	4.0	288	119	2759.5	4	284	117
773	27	2403.3	3.5	277	111	1847.7	3.5	274	95	1118.7	4.0	278	122	1892.1	3	279	117
618	28	2401.4	3.0	279	73	1864.5	3.5	273	86	2250.9	2.5	275	70	2772.9	3	283	64
228	29	2400.9	4.3	280	114	2230.7	5.0	271	104	2348.3	3.8	286	133	2623.8	4	283	104
810	30	2399.4	4.2	278	110	1676.4	4.0	273	118	2146.7	3.5	285	122	2703.1	5	279	91
315	31	2398.2	3.1	275	101	1689.8	3.0	271	86	2825.3	3.3	277	121	2679.5	3	277	97
475	32	2389.2	3.3	279	106	2640.6	3.5	278	95	2362.1	3.3	281	117	2164.9	3	279	107
434	33	2388.2	3.9	278	113	1515.1	5.0	275	123	3087.4	3.8	283	119	2562.0	3	277	97
517	34	2387.3	2.8	276	84	1777.2	4.5	274	118	2701.0	2.0	275	70	2683.6	2	279	64
510	35	2383.9	3.9	280	104	1948.5	4.0	275	105	2378.5	3.8	281	116	2824.7	4	283	91
461	36	2382.6	3.8	276	105	2116.5	3.5	274	104	1444.6	4.0	276	118	3586.6	4	277	94
909	37	2373.2	3.6	280	111	2559.9	4.0	277	104	2428.9	3.8	290	123	1912.2	3	276	107
57	38	2368.9	4.1	279	114	1978.7	4.0	270	117	3020.2	4.3	290	118	2107.8	4	277	107
779	39	2362.2	3.1	278	92	1555.4	4.5	277	110	1780.5	2.8	282	80	2652.0	2	278	86
741	40	2358.6	3.9	280	113	2173.6	4.0	273	99	1269.9	3.8	275	118	2822.7	4	284	122
12	41	2355.5	3.2	276	81	1703.3	3.0	271	86	2254.2	3.5	277	75	3108.9	3	279	81
602	42	2351.9	4.4	283	133	1978.7	4.0	273	109	2822.0	4.3	283	157	2305.3	5	286	132
287	43	2346.9	3.6	278	98	1626.0	4.0	274	105	2526.3	3.8	279	100	2888.5	3	282	89
522	44	2335.3	2.5	281	90	2140.0	3.0	278	93	2093.0	2.5	281	95	2772.9	2	285	81
476	45	2334.0	3.5	278	91	2106.4	4.5	275	76	2774.9	3.0	281	112	2120.5	3	278	84
890	46	2303.9	3.0	276	104	1955.2	2.5	269	76	2654.0	3.5	280	122	2299.2	3	276	114
987	47	2302.8	2.9	277	81	1820.8	4.5	278	113	2321.4	2.3	281	70	1936.4	2	276	61
138	48	2301.3	3.4	280	121	2022.4	3.0	278	113	2650.6	3.3	284	135	2230.7	4	279	114
140	49	2292.5	4.1	278	111	1327.0	4.5	274	104	2822.0	3.8	282	113	2728.6	4	278	117
161	50	2287.6	2.8	276	85	1461.4	4.0	273	104	2526.3	2.3	276	70	2875.1	2	279	81
855	51	2287.6	3.9	278	106	1743.6	3.5	277	97	2973.2	3.3	278	114	2844.8	5	276	107
809	52	2286.5	4.0	276	101	1730.1	4.0	271	114	2818.6	4.0	280	102	2287.1	4	276	86
705	53	2246.2	4.2	277	98	1716.7	5.0	275	108	1931.7	3.5	274	99	2008.3	4	276	86
83	54	2243.7	3.8	281	113	1773.8	5.0	277	119	2583.5	3.5	282	128	2373.8	3	284	91
910	55	2242.1	3.1	278	108	1669.7	3.0	274	85	2990.0	3.3	285	116	2627.8	3	279	122
334	56	2237.0	3.0	278	96	1955.2	3.5	273	85	2056.0	3.5	278	113	2699.7	2	282	89
766	57	2234.5	3.3	277	91	1696.5	3.5	274	104	2042.6	3.5	272	72	3159.3	3	284	97
285	58	2229.1	2.4	276	81	1746.9	2.5	272	85	2355.0	2.8	277	80	2585.5	2	278	79
271	59	2225.2	2.8	276	91	1794.0	3.0	274	71	2515.9	3.5	278	119	2365.8	2	277	81
456	60	2222.6	3.4	281	115	1730.1	4.0	276	88	2926.1	3.3	290	142	2011.7	3	277	114
992	61	2219.1	3.0	277	75	1898.1	3.5	274	85	1837.2	2.5	277	72	2531.7	3	276	69
262	62	2215.5	2.9	277	75	2197.1	3.5	279	95	1535.3	2.3	276	65	2914.0	3	276	66
268	63	2215.3	3.1	278	105	1938.4	4.0	274	122	2486.0	3.3	282	107	2221.3	2	279	86
333	64	2215.0	2.8	277	101	1824.2	3.5	273	114	2523.0	2.8	279	107	2297.9	2	279	81
343	65	2213.9	3.0	278	89	1481.5	4.5	271	107	2002.3	2.5	281	79	3157.9	2	282	81
157	66	2212.1	3.0	277	83	1777.2	4.5	274	103	2227.3	2.5	279	65	2631.8	2	277	81
996	67	2210.0	3.8	277	115	2059.4	4.0	274	121	1407.6	3.3	277	117	2733.3	4	277	107
124	68	2204.3	3.3	274	91	1779.3	4.0	267	62	2224.0	3.0	277	118	2609.7	3	279	91
538	69	2197.1	4.0	279	122	1894.8	4.0	279	112	2472.6	4.0	280	137	2224.0	4	279	117
573	71	2195.1	2.8	279	91	2093.0	2.0	274	58	1746.9	3.5	277	132	1771.1	3	277	81
236	70	2195.1	4.2	279	114	1723.4	5.0	274	130	3033.6	3.5	286	114	1828.2	4	278	99

Table 3.70 Continued.

ExW50K Group D		ACROSS LOCATIONS				TENNESSEE 2011				NORTH CAROLINA 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
412	72	2190.4	3.3	282	109	1750.3	3.0	274	88	1948.5	3.8	288	117	2872.4	3	283	122
226	73	2187.9	3.6	280	107	2072.8	3.0	272	88	1773.8	3.8	283	113	2717.2	4	285	119
52	74	2187.5	3.6	279	119	2116.5	4.5	273	113	2119.8	3.3	287	128	2326.1	3	278	117
670	75	2175.4	2.8	278	83	2015.7	2.0	277	62	1357.2	3.3	278	99	1923.6	3	276	86
770	76	2172.7	3.1	274	85	2035.9	4.0	273	105	1005.9	2.3	278	60	2439.7	3	276	89
328	77	2170.5	3.8	280	104	1283.3	4.5	276	121	2338.2	3.0	280	100	2889.8	4	283	91
539	78	2168.4	3.7	281	104	1478.2	3.5	275	102	2281.1	3.5	285	126	2746.1	4	283	84
168	79	2163.1	3.7	278	91	1884.7	4.5	277	93	2045.9	3.5	280	100	2558.6	3	277	81
628	80	2155.0	2.3	275	69	1619.3	3.0	270	102	2566.7	2.0	282	51	1872.6	2	276	56
374	81	2151.6	3.3	279	99	2045.9	3.5	279	94	2375.2	3.5	281	112	2033.8	3	276	91
338	82	2150.5	3.8	279	117	1548.7	4.5	275	124	2311.3	3.8	281	127	2591.5	3	282	99
319	83	2149.9	3.5	276	97	2580.1	3.5	272	86	1767.1	4.0	279	113	2102.4	3	276	91
874	84	2149.0	3.0	276	85	1397.6	2.0	273	43	2129.9	3.0	282	113	2835.4	4	277	99
508	85	2143.1	3.7	278	122	1696.5	3.5	273	102	2153.4	3.5	280	157	2579.4	4	282	107
216	86	2138.7	3.8	276	92	789.5	3.5	265	66	3423.3	3.8	283	126	2203.2	4	279	84
41	87	2135.3	3.1	275	76	1935.1	3.0	271	89	1921.6	3.3	277	72	2549.2	3	276	66
566	88	2134.4	3.5	278	112	1572.2	4.0	273	103	2721.2	3.5	285	126	2452.4	3	278	107
848	89	2134.2	3.3	278	101	1911.6	3.5	277	90	1985.5	3.3	280	116	2351.0	3	276	97
824	90	2130.1	3.6	278	97	1639.4	3.5	276	94	1814.1	3.3	276	104	2261.6	4	277	94
621	92	2129.7	3.6	275	78	1639.4	3.5	274	79	1612.6	3.3	284	86	2498.8	4	276	69
402	91	2129.7	2.8	277	70	1807.4	3.0	275	75	2015.7	3.5	274	74	2566.0	2	283	61
331	93	2127.5	3.3	278	120	1760.4	3.5	274	109	2217.3	3.5	285	128	2404.7	3	276	122
516	94	2119.8	4.6	278	116	551.0	5.0	273	105	2926.1	3.8	279	137	2882.5	5	283	107
206	95	2115.8	3.7	279	117	2294.5	4.5	275	119	1713.3	3.5	284	112	2339.6	3	279	119
631	96	2114.5	4.3	277	108	2140.0	5.0	275	119	2244.1	4.0	285	113	1976.1	4	276	91
440	97	2113.3	3.8	276	106	1484.9	3.5	273	119	2338.2	3.8	277	103	2516.9	4	277	97
733	98	2105.7	3.3	278	94	2146.7	4.5	277	122	1067.8	2.5	275	86	1781.9	3	278	74
905	99	2103.9	3.5	278	119	910.4	5.0	275	124	2647.3	3.5	281	126	2495.4	2	277	107
711	100	2100.6	3.5	277	104	1518.5	3.0	275	89	1478.2	3.5	279	117	2347.6	4	278	107
1016	101	2099.9	3.4	277	97	2019.1	3.5	274	110	2012.3	3.8	281	108	2006.3	3	276	74
347	102	2099.5	3.3	281	106	2368.4	3.0	277	76	1535.3	2.8	281	126	2394.7	4	284	117
584	103	2097.0	4.1	277	99	1726.8	3.0	274	89	2771.6	4.3	289	128	2202.5	5	278	81
459	104	2089.4	3.0	275	78	1750.3	3.0	272	105	1424.4	3.0	273	65	3093.4	3	279	64
160	105	2088.7	2.3	275	75	1888.0	4.0	274	114	2234.1	2.0	275	58	2144.0	1	277	53
420	106	2085.6	3.5	279	102	1878.0	2.5	274	84	2237.4	4.0	282	124	2141.3	4	282	97
894	107	2081.1	4.0	277	101	1612.6	5.0	273	114	1773.8	4.0	286	107	1976.7	3	277	81
201	108	2080.2	2.6	277	88	2486.0	3.5	275	118	1099.1	2.3	278	71	2656.0	2	279	76
989	109	2076.4	3.3	277	86	2140.0	4.0	277	114	1031.9	3.0	281	77	1767.8	3	276	66
37	110	2071.7	4.0	281	118	2035.9	3.0	277	102	1495.0	4.0	281	119	2684.2	5	285	132
555	112	2068.1	4.0	276	111	1481.5	3.0	273	77	1951.9	4.0	281	124	2092.3	5	276	132
386	111	2068.1	3.4	277	91	1179.2	5.0	274	99	2586.8	2.3	282	99	2438.3	3	276	76
195	113	2067.9	3.5	277	102	1471.5	4.5	273	112	2727.9	4.0	283	110	2004.3	2	276	84
Essex	**114**	**2064.4**	**3.6**	**276**	**90**	**1615.9**	**5.0**	**277**	**114**	**2512.9**	**2.3**	**275**	**66**	**.**	**.**	**.**	**.**
972	115	2064.3	3.2	276	76	1800.7	4.0	277	93	1036.6	3.5	279	72	2080.9	2	276	64
404	116	2061.8	3.8	275	93	1488.3	3.0	270	85	2197.1	4.3	279	110	2500.1	4	276	84
1012	117	2061.4	3.6	277	99	1491.6	4.0	276	107	2274.4	3.8	278	100	2058.7	3	276	89
762	118	2060.7	4.2	277	106	1794.0	3.5	274	108	2385.2	4.0	279	119	2244.8	5	277	91
835	119	2059.2	3.7	275	105	2143.4	5.0	274	107	2721.2	3.0	279	110	1853.8	3	276	97
521	120	2052.9	2.9	278	94	1807.4	2.0	278	66	2459.2	3.8	280	121	1892.1	3	276	97
363	121	2041.5	2.9	275	92	1232.9	3.0	269	77	2536.4	3.8	279	113	2355.0	2	278	86
33	122	2040.3	4.1	278	123	1642.8	4.5	276	114	1686.5	3.8	281	133	2791.7	4	278	122
971	123	2039.9	4.3	278	104	2344.9	4.5	272	110	2311.3	4.5	275	105	1880.0	4	279	97
629	124	2039.7	4.3	277	96	1750.3	3.5	274	104	2227.3	4.3	281	108	1802.0	5	276	76
222	125	2035.4	3.0	278	89	1837.6	3.0	273	72	1565.5	3.0	279	104	2703.1	3	282	91
281	126	2024.2	4.2	273	111	1407.6	4.5	273	103	1592.4	4.0	271	123	3072.6	4	276	107
763	127	2022.6	3.9	278	106	1579.0	5.0	276	104	1847.7	3.8	274	108	2103.7	3	279	107
414	128	2022.2	2.3	275	77	1861.2	2.5	277	69	2509.5	2.5	271	85	1695.9	2	276	79
113	129	2021.3	2.8	278	73	1693.2	4.0	271	100	2045.9	2.3	278	62	2324.8	2	285	56
1021	130	2018.6	2.9	277	81	1817.5	3.5	275	98	2922.8	3.3	258	71	2562.0	2	279	74
231	131	2017.3	3.3	276	81	1515.1	4.5	272	97	1888.0	2.5	277	69	2648.6	3	279	79
716	132	2017.0	3.7	279	88	1259.8	4.5	273	112	2019.1	2.5	284	70	2187.7	4	286	84
781	133	2015.2	3.1	277	102	1820.8	3.0	272	100	1726.8	3.3	282	118	2444.4	3	276	89
819	134	2015.0	3.3	276	101	1746.9	4.5	275	103	1891.4	3.5	280	112	2215.3	2	276	89
1000	135	2013.0	2.7	275	75	1528.6	4.0	273	110	2277.7	2.0	277	64	2528.4	2	276	51
926	136	2010.3	3.5	278	102	1767.1	2.5	275	84	1384.1	4.0	276	117	2184.3	4	278	107
152	137	2009.2	2.8	276	71	2140.0	4.0	273	83	2015.7	2.3	280	70	1871.9	2	276	61
103	138	2009.0	3.2	272	79	1436.6	3.5	267	83	1945.2	3.0	273	74	2645.3	3	276	81
834	139	2007.9	3.7	277	105	2250.9	4.0	275	102	2180.3	4.0	280	117	1958.6	3	276	97
53	140	2007.6	3.8	278	114	1720.1	4.5	274	122	1599.1	3.0	278	121	2703.7	4	283	99
805	141	2006.1	2.7	277	83	2213.9	3.5	274	93	2842.1	2.5	281	79	1644.1	2	277	79
381	142	1998.8	4.0	275	94	1733.5	4.0	278	95	1125.0	4.0	273	79	3137.8	4	276	107
902	143	1995.8	2.8	278	88	1273.3	3.5	273	76	2906.0	3.0	286	97	2627.8	2	276	91
969	144	1992.4	2.6	275	66	1592.4	3.5	272	83	1894.8	2.3	275	56	2097.0	2	277	58
923	145	1987.0	3.4	277	89	1390.8	3.0	275	76	2079.5	3.3	281	94	2904.0	4	276	97
87	146	1986.4	3.2	275	94	2056.0	3.0	270	94	1874.6	3.5	277	107	2028.5	3	279	81
345	147	1986.4	3.0	274	89	1757.0	4.5	271	113	1901.5	2.5	276	74	2300.6	2	276	81
501	148	1983.7	2.8	277	80	2324.8	2.0	277	60	1330.4	3.3	277	98	2295.9	3	276	81
348	149	1978.7	3.3	277	92	2143.4	3.5	277	86	1790.6	3.3	279	112	2002.3	3	276	79
697	150	1973.6	4.0	277	107	1525.2	5.0	274	100	1300.1	4.0	274	132	1933.1	3	276	89
457	151	1972.2	3.8	277	141	1585.7	5.0	270	105	1592.4	3.3	278	70	2738.7	3	284	249

Table 3.70 Continued.

ExW50K Group D		ACROSS LOCATIONS				TENNESSEE 2011				NORTH CAROLINA 2011				TENNESSEE 2010			
LINE	RANK	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm	YIELD kg ha^{-1}	LODG†	MAT‡	HGT cm
802	152	1965.5	3.8	278	104	1609.2	5.0	276	102	2160.2	3.3	281	113	2312.0	3	276	97
139	153	1962.4	4.4	279	116	1767.1	4.5	275	117	1750.3	3.8	278	123	2369.8	5	284	107
284	154	1957.0	2.9	276	90	2143.4	2.5	275	71	1404.3	3.3	277	114	2323.4	3	276	84
455	155	1952.5	4.3	276	113	1723.4	4.0	271	112	2042.6	4.0	282	117	2091.6	5	276	109
823	156	1950.7	3.7	275	104	1259.8	3.5	271	93	2489.4	3.5	279	113	2701.0	4	277	107
526	157	1945.8	3.5	279	92	826.4	4.0	276	90	2677.5	2.5	278	79	2333.5	4	283	107
999	158	1939.1	2.5	275	80	1985.5	2.5	271	66	1982.1	3.0	279	95	2424.2	2	276	79
1019	159	1938.9	4.3	276	112	1382.8	5.0	267	91	1676.4	4.0	279	126	2760.8	4	279	119
782	160	1938.9	4.4	280	109	1659.6	4.5	274	93	1861.2	3.8	282	133	2430.3	5	283	102
816	161	1936.0	4.3	282	99	1834.3	5.0	275	112	1958.6	4.0	278	95	1826.9	4	286	91
548	162	1934.6	2.6	276	69	1683.1	2.0	273	62	2630.5	2.8	279	70	2330.1	3	278	76
96	163	1930.6	3.0	277	103	1851.1	4.0	275	114	1777.2	3.0	280	104	2163.5	2	276	91
406	164	1930.1	3.3	277	115	1599.1	3.5	275	99	1663.0	3.5	276	130	2528.4	3	279	117
484	165	1924.1	3.7	278	75	1965.3	3.5	278	81	2580.1	3.5	280	135	1226.9	4	276	8
5002T	**166**	**1921.6**	**2.6**	**273**	**78**	**1919.8**	**3.0**	**273**	**91**	**.**	**2.3**	**.**	**65**	**.**	**.**	**.**	**.**
817	167	1919.4	2.5	279	76	1488.3	3.5	277	94	2082.9	2.0	277	55	2311.3	2	284	79
503	168	1918.1	4.1	275	95	1673.0	4.5	276	109	1847.7	3.8	274	99	2233.4	4	276	76
514	169	1897.9	4.3	281	117	1612.6	4.0	272	81	1693.2	3.8	287	141	2387.9	5	285	130
35	170	1891.4	3.7	279	103	1367.3	3.0	273	81	1447.9	4.0	282	112	2858.9	4	283	117
512	171	1885.8	3.7	278	106	1746.9	3.0	277	90	2146.7	4.0	279	131	1763.7	4	277	97
1018	172	1884.9	2.9	276	94	1152.3	4.0	273	119	1673.0	2.8	278	77	2490.1	2	277	86
692	173	1878.9	3.5	276	110	1468.1	4.5	273	121	2462.5	4.0	280	116	2606.3	2	276	94
850	174	1878.6	3.1	275	100	2264.3	3.0	272	100	2274.4	4.3	281	119	1386.1	2	276	81
714	175	1877.3	2.7	277	95	1757.0	3.5	277	81	2603.6	2.5	277	113	2396.7	2	276	91
673	176	1866.1	2.9	276	98	1901.5	2.5	273	83	1797.3	3.3	274	112	2339.6	3	277	99
562	177	1863.0	3.3	277	87	1521.9	2.5	275	85	2378.5	3.3	282	102	2115.1	4	276	74
529	178	1847.3	3.8	277	102	1269.9	3.5	266	69	1867.9	3.8	282	130	2404.1	4	284	107
651	179	1844.2	3.0	273	83	1732.2	3.5	268	64	2586.8	2.5	281	89	2157.5	3	276	97
700	180	1843.9	2.8	276	94	1878.0	4.0	274	113	3013.5	2.5	279	77	2353.7	2	279	91
214	181	1833.6	3.9	272	99	843.2	5.0	259	80	1874.6	3.8	279	110	2783.0	3	279	107
546	182	1829.8	2.7	275	82	1646.2	4.0	272	114	1790.6	2.0	276	64	2052.7	2	276	69
723	183	1829.1	3.2	276	71	1867.9	2.5	275	72	1444.6	3.0	278	65	1667.7	4	278	76
50	184	1828.5	3.2	274	88	1441.2	5.0	271	108	1118.6	2.5	274	79	2928.8	2	276	76
15	185	1820.2	2.8	277	86	1434.5	3.5	276	91	1488.3	3.0	279	90	2537.8	2	276	76
296	186	1820.2	2.3	278	99	1565.5	2.0	271	55	1746.9	3.0	284	136	2148.1	2	278	107
777	187	1817.0	2.5	276	80	2082.9	3.0	273	98	2879.1	2.5	285	70	2246.2	2	277	74
873	188	1814.8	3.0	277	91	2244.1	3.0	276	89	2213.9	4.0	279	102	1453.3	2	276	84
899	189	1804.5	3.5	277	105	1555.4	2.5	273	64	2086.2	4.0	281	118	2084.2	4	279	132
1007	190	1798.0	3.8	276	99	1105.3	4.0	273	81	2731.3	3.5	278	127	2011.0	4	276	89
258	191	1795.3	3.3	276	93	1343.8	3.0	270	88	2442.4	4.0	281	98	1599.8	3	276	94
937	192	1785.7	3.5	278	110	1844.4	3.0	275	98	1091.5	3.5	275	117	2128.6	4	277	117
623	193	1784.8	3.3	278	114	1824.2	3.5	273	95	2973.2	3.5	279	131	1917.6	3	276	117
137	194	1780.3	3.3	271	90	1461.4	5.0	273	126	1484.9	3.0	264	75	2394.7	2	276	69
677	195	1780.1	3.3	275	80	1189.3	4.0	272	104	1841.0	2.8	283	71	2353.7	3	278	66
488	196	1775.6	3.5	276	83	1427.8	4.5	276	95	2056.0	3.0	275	79	1843.0	3	276	76
815	197	1772.0	2.4	276	84	1081.8	2.5	273	65	2146.7	2.8	276	104	2087.6	2	276	84
645	198	1767.3	3.7	281	102	1249.7	4.0	277	116	3299.0	4.0	279	116	1808.1	3	282	76
678	199	1762.6	4.2	278	104	1048.2	3.5	274	76	2986.6	4.0	279	142	2398.7	5	276	94
458	200	1762.4	4.4	272	105	1306.8	5.0	275	118	1710.0	4.3	265	104	2270.4	4	276	94
745	201	1760.2	2.0	275	61	1545.4	2.0	274	58	2143.4	2.0	279	57	2465.2	2	276	66
885	202	1753.2	2.5	277	73	1152.3	3.5	274	84	2657.4	2.0	280	62	1977.4	2	279	74
576	203	1745.8	2.8	277	62	1589.0	2.5	273	56	2361.7	2.8	279	81	1615.9	3	279	48
339	204	1737.4	3.2	277	87	1138.9	4.0	270	110	1413.9	2.5	278	74	2659.4	3	284	76
729	205	1734.0	3.3	276	100	1827.6	4.0	275	104	2388.6	3.0	278	103	1929.7	3	276	94
474	206	1733.7	3.6	276	111	1182.5	3.0	269	91	1562.2	3.8	282	110	2456.5	4	276	132
789	207	1714.5	3.3	277	121	907.1	3.5	271	95	1975.4	3.5	281	136	2375.2	3	279	132
409	208	1706.8	4.0	284	121	1384.1	4.0	273	104	1874.6	4.0	290	137	1861.8	4	288	122
76	209	1653.1	3.7	279	112	1746.9	3.0	276	95	1864.5	4.0	283	121	1347.8	4	279	119
990	210	1651.1	3.3	278	108	1538.7	4.5	274	123	2227.3	2.5	281	104	2682.2	3	279	97
980	211	1622.0	3.8	276	95	1165.7	3.5	272	88	3117.6	3.8	277	103	2114.5	4	276	94
102	212	1617.3	3.1	274	81	1249.7	4.5	271	113	1636.1	2.8	272	75	1966.0	2	278	56
528	213	1587.5	4.1	276	69	1464.7	3.5	274	90	1498.3	3.8	279	103	1799.3	5	276	13
477	214	1581.2	3.6	272	91	1044.8	4.5	259	64	1988.8	3.3	280	117	1710.0	3	276	91
225	215	1562.6	2.8	269	77	2056.0	4.5	273	113	1065.8	1.8	259	57	1731.5	2	276	61
365	216	1554.8	4.0	276	109	1377.4	4.0	274	98	1216.1	4.0	275	97	2070.8	4	278	132
349	217	1554.6	3.6	275	96	1364.0	4.5	276	108	1427.4	3.3	273	90	1872.6	3	277	89
772	218	1547.0	4.4	277	108	1646.2	5.0	276	112	3470.0	3.3	277	89	2562.0	5	278	122
976	219	1541.9	2.4	276	83	1844.4	3.0	276	58	1585.7	2.3	283	98	2012.3	2	276	94
736	220	1516.7	3.8	276	106	1474.8	4.5	273	109	2079.5	3.8	282	102	2171.6	3	279	107
575	221	1513.8	3.9	276	99	1367.3	5.0	276	110	2032.5	3.8	278	118	1427.1	3	276	69
719	222	1459.1	2.4	279	66	1337.1	2.0	275	58	1951.9	2.3	275	62	1021.3	3	279	79
690	223	1435.9	3.6	275	87	1054.9	4.5	269	98	1562.2	3.3	278	80	1972.7	3	279	84
942	224	1238.3	4.4	276	97	1095.2	5.0	275	108	2287.8	4.3	284	95	1615.2	4	276	89
648	225	1232.3	3.3	270	102	1431.1	3.0	271	88	1642.8	3.8	276	102	1825.6	3	276	117
	Mean	2069.1	3.4	276.0	97.0	1720.4	3.7	273.6	97.0	2191.2	3.3	279.0	101.7	2354.9	3	278.4	92.0
	LSD	740.4	1.3	4.0	42.9	1278.6	2.1	7.0	74.0	1278.6	2.1	7.0	74.0	1278.6	2.1	7.0	74.0

†MAT is maturity date according to the Julian calendar

‡LODG is the lodge score reported on a 1-5 scale

$LSD_{0.05}$ is Least Significance Difference at the 0.05 probability level.

Table 3.71 Quantitative trait loci identified using R/qtl located on various chromosomes associated with yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE
Knoxville, TN 2010	Gm07_18539902_T_G	7	M	61.37	3.52	8.83	2.67	W
Knoxville, TN 2010	Gm18_57988264_A_G	18	G	78.75	2.79	6.57	2.44	E
Knoxville, TN 2010	Gm13_27092408_C_T	13	F	150.77	2.75	6.18	2.21	E
Plymouth, NC 2011	Gm09_2634593_G_A	9	K	5.62	3.02	7.87	3.09	E
Plymouth, NC 2011	Gm03_39559139_G_A	3	N	93.64	2.78	7.38	3.09	E
Plymouth, NC 2011	Gm17_32687336_C_T	17	D2	49.59	2.47	5.71	2.92	E
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm07_4008483_C_T	7	M	5.19	2.92	8.64	1.86	W
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm15_48028533_G_A	15	E	72.40	2.77	6.49	1.86	W
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm17_12822621_A_G	17	D2	35.12	2.56	4.86	1.09	E

†Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.72 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using R/qtl in each environment in Group D. Those MAS lines compared to the top yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					**PLYMOUTH, NC 2011**					**KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011**				
MAS		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**			**MAS**		**YIELD (kg ha^{-1})**		
Line	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**	**Line**	**Rank**	**Line**	**Yld**	**Rank**
[aa]**12**	01	461	3587.9	01	118	01	772	3467.0	01	[c]**23**	01	864	2734.6	01
[aa]**94**	02	[aa]**94**	3507.3	02	140	02	[bb]**216**	3426.7	02	140	02	81	2647.3	02
[a]**161**	03	706	3339.3	03	[bb]**216**	03	645	3299.0	03	157	03	686	2640.6	03
271	04	491	3325.9	04	[bb]**236**	04	122	3265.4	04	195	04	[cc]**530**	2600.3	04
296	05	[aa]**766**	3157.9	05	347	05	686	3205.0	05	216	05	918	2600.3	05
[a]**328**	06	343	3157.9	06	363	06	[bb]**682**	3178.1	06	231	06	122	2580.1	06
331	07	[aa]**381**	3137.8	07	[b]**456**	07	[bb]**984**	3151.2	07	236	07	605	2546.5	07
[aa]**381**	08	[aa]**12**	3110.9	08	530	08	980	3117.6	08	268	08	984	2539.8	08
434	09	459	3090.7	09	531	09	434	3090.7	09	333	09	491	2533.1	09
476	10	281	3070.6	10	631	10	846	3037.0	10	334	10	706	2526.3	10
514	11	605	3057.1	11	[bb]**682**	11	[bb]**236**	3037.0	11	338	11	847	2519.6	11
530	12	[a]**918**	3057.1	12	[b]**777**	12	57	3023.6	12	347	12	[c]**531**	2492.7	12
566	13	81	3016.8	13	781	13	700	3016.8	13	348	13	220	2486.0	13
621	14	864	2983.2	14	802	14	910	2990.0	14	402	14	846	2479.3	14
673	15	647	2976.5	15	810	15	678	2990.0	15	440	15	688	2459.2	15
700	16	50	2929.5	16	834	16	623	2976.5	16	514	16	917	2459.2	16
733	17	262	2916.0	17	[b]**855**	17	[b]**855**	2976.5	17	[cc]**530**	17	647	2452.4	17
[aa]**766**	18	923	2902.6	18	885	18	[b]**456**	2929.5	18	[c]**531**	18	1010	2439.0	18
823	19	[a]**328**	2889.2	19	909	19	516	2929.5	19	651	19	94	2439.0	19
855	20	287	2889.2	20	[bb]**984**	20	1021	2922.8	20	766	20	[c]**23**	2439.0	20
910	21	516	2882.5	21	990	21	902	2909.3	21	770	21	682	2432.3	21
[a]**918**	22	[a]**161**	2875.7	22	1010	22	[b]**777**	2882.5	22	823	22	118	2418.8	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Plymouth, NC in 2011
[bb] Top 5% yield in Plymouth, NC in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011

Table 3.73 MAS identifying the bottom 10 % of lines containing the unfavorable allele for yield QTLs detected using R/qtl in each environment in Group D. Those MAS lines were compared to the bottom yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PLYMOUTH, NC 2011					KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
333	201	648	1827.6	201	343	201	459	1424.4	201	[c]**990**	201	[c]**339**	1737.4	201
374	202	645	1807.4	202	[bb]**381**	202	339	1411.0	202	996	202	729	1734.0	202
386	203	[a]**629**	1800.7	203	420	203	996	1411.0	203	999	203	474	1733.7	203
457	204	528	1800.7	204	455	204	284	1404.3	204	1012	204	789	1714.5	204
501	205	733	1780.5	205	461	205	[b]**926**	1384.1	205	1018	205	409	1706.8	205
510	206	573	1773.8	206	484	206	670	1357.2	206	[c]**76**	206	[c]**76**	1653.1	206
562	207	989	1767.1	207	508	207	501	1330.4	207	281	207	[c]**990**	1651.1	207
584	208	512	1767.1	208	575	208	697	1303.5	208	[c]**339**	208	980	1622.0	208
628	209	225	1733.5	209	645	209	688	1283.3	209	345	209	102	1617.3	209
[a]**629**	210	477	1713.3	210	[bb]**647**	210	741	1269.9	210	[c]**349**	210	528	1587.5	210
631	211	414	1693.2	211	673	211	365	1216.1	211	404	211	477	1581.2	211
677	212	723	1666.3	212	711	212	[bb]**381**	1122.1	212	584	212	225	1562.6	212
678	213	805	1646.2	213	[bb]**770**	213	[bb]**773**	1118.6	213	692	213	365	1554.8	213
686	214	576	1619.3	214	[bb]**773**	214	50	1118.4	214	711	214	[c]**349**	1554.6	214
[aa]**719**	215	942	1612.6	215	874	215	201	1099.1	215	[c]**772**	215	[c]**772**	1547.0	215
824	216	258	1599.1	216	894	216	937	1091.5	216	782	216	976	1541.9	216
847	217	873	1451.3	217	899	217	733	1067.8	217	817	217	736	1516.7	217
[aa]**850**	218	575	1424.4	218	918	218	225	1065.8	218	834	218	575	1513.8	218
894	219	[aa]**850**	1384.1	219	[b]**926**	219	972	1036.6	219	873	219	719	1459.1	219
923	220	76	1350.5	220	969	220	[bb]**989**	1031.9	220	874	220	690	1435.9	220
926	221	484	1229.6	221	[bb]**989**	221	[bb]**647**	1012.2	221	[cc]**942**	221	[cc]**942**	1238.3	221
972	222	[aa]**719**	1021.3	222	1019	222	[bb]**770**	1005.9	222	992	222	648	1232.3	222

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Plymouth, NC in 2011
[bb] Bottom 5% yield in Plymouth, NC in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011

Table 3.74 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using R/qtl in each environment in Group D compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
12	01	[b]**118**	01	[c]**23**	01	864	2734.6	01
[a]**94**	02	140	02	140	02	81	2647.3	02
161	03	216	03	157	03	686	2640.6	03
271	04	236	04	195	04	[aabbcc]**530**	2600.3	04
296	05	347	05	216	05	[aa]**918**	2600.3	05
328	06	363	06	231	06	122	2580.1	06
331	07	456	07	236	07	605	2546.5	07
381	08	[bb]**530**	08	268	08	[bb]**984**	2539.8	08
434	09	[b]**531**	09	333	09	491	2533.1	09
476	10	631	10	334	10	706	2526.3	10
514	11	[b]**682**	11	338	11	847	2519.6	11
[aa]**530**	12	777	12	347	12	[bc]**531**	2492.7	12
566	13	781	13	348	13	220	2486.0	13
621	14	802	14	402	14	846	2479.3	14
673	15	810	15	440	15	688	2459.2	15
700	16	834	16	514	16	917	2459.2	16
733	17	855	17	[cc]**530**	17	647	2452.4	17
766	18	885	18	[c]**531**	18	[b]**1010**	2439.0	18
823	19	909	19	651	19	[a]**94**	2439.0	19
855	20	[bb]**984**	20	766	20	[c]**23**	2439.0	20
910	21	990	21	770	21	[b]**682**	2432.3	21
[aa]**918**	22	[b]**1010**	22	823	22	[b]**118**	2418.8	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011

Table 3.75 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using R/qtl in each environment in Group D compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
333	201	343	201	[c]**990**	201	[cc]**339**	1737.4	201
374	202	381	202	996	202	729	1734.0	202
386	203	420	203	999	203	474	1733.7	203
457	204	455	204	1012	204	789	1714.5	204
501	205	461	205	1018	205	409	1706.8	205
510	206	484	206	[c]**76**	206	[c]**76**	1653.1	206
562	207	508	207	281	207	[c]**990**	1651.1	207
584	208	[bb]**575**	208	[cc]**339**	208	980	1622.0	208
628	209	645	209	345	209	102	1617.3	209
629	210	647	210	[c]**349**	210	528	1587.5	210
631	211	673	211	404	211	477	1581.2	211
677	212	711	212	584	212	225	1562.6	212
678	213	770	213	692	213	365	1554.8	213
686	214	773	214	711	214	[c]**349**	1554.6	214
[aa]**719**	215	874	215	[cc]**772**	215	[cc]**772**	1547.0	215
824	216	894	216	782	216	976	1541.9	216
847	217	899	217	817	217	736	1516.7	217
850	218	918	218	834	218	[bb]**575**	1513.8	218
894	219	926	219	873	219	[aa]**719**	1459.1	219
923	220	969	220	874	220	690	1435.9	220
926	221	989	221	[cc]**942**	221	[cc]**942**	1238.3	221
972	222	1019	222	992	222	648	1232.3	222

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011

Table 3.76 Quantitative trait loci identified using SAS located on various chromosomes associated with yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE EFFECT†	FAVORABLE ALLELE	P-VALUE
Knoxville, TN 2010	Gm04_8247949_C_T	4	C1	65.87	6.79	0.97	W	0.0014
Knoxville, TN 2010	Gm07_18539902_T_G	7	M	42.42	5.69	3.04	W	0.0039
Knoxville, TN 2010	Gm11_4453218_T_C	11	B1	16.23	5.66	2.88	E	0.004
Knoxville, TN 2010	Gm01_54171147_G_T	1	D1a	118.27	4.91	1.81	E	0.0082
Knoxville, TN 2010	Gm18_58055444_T_C	18	G	112.85	4.72	2.72	E	0.0034
Plymouth, NC 2011	Gm07_149664_T_C	7	M	1.34	11.29	5.43	W	<.0001
Plymouth, NC 2011	Gm09_457853_A_G	9	K	5.23	6.06	4.10	E	0.0027
Plymouth, NC 2011	Gm19_39246602_T_C	19	L	73.68	5.66	3.38	E	0.0009
Plymouth, NC 2011	Gm03_39552601_T_C	3	N	87.68	5.54	3.81	E	0.0045
Plymouth, NC 2011	Gm18_15660496_T_G	18	G	44.64	4.92	0.85	E	0.0025
Plymouth, NC 2011	Gm13_29895148_C_T	13	F	154.76	4.73	2.54	W	0.0098
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm13_11355266_T_C	13	F	35.49	6.73	1.34	E	0.0002
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm11_36807939_C_A	11	B1	84.22	5.95	1.25	E	0.0027
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm05_31399360_G_A	5	A1	41.55	5.71	0.99	W	0.0007
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm01_47115450_G_T	1	D1a	70.15	5.61	0.24	E	0.0008
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm10_48428720_T_C	10	O	110.82	5.46	0.11	E	0.001
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm16_1339719_T_C	16	J	6.55	5.39	1.81	W	0.0011
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm20_41827386_T_C	20	I	43.53	5.15	0.82	E	0.0016
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm04_8845668_G_T	4	C1	63.93	4.84	0.28	E	0.0081
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm09_3394608_G_A	9	K	7.76	4.53	1.20	E	0.0037

†Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.77 MAS identifying the top 10 % of lines containing the favorable allele for the yield QTLs detected using SAS in each environment in Group D. Those MAS were compared to the top yielding 10 % of lines in the environment from which they were selected. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PLYMOUTH, NC 2011					KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
402	01	461	3587.9	01	[bb]**122**	01	772	3467.0	01	37	01	864	2734.6	01
1019	02	[aa]**94**	3507.3	02	[bb]**216**	02	[bb]**216**	3426.7	02	57	02	81	2647.3	02
[aa]**12**	03	706	3339.3	03	[bb]**236**	03	645	3299.0	03	103	03	[cc]**686**	2640.6	03
33	04	[aa]**491**	3325.9	04	823	04	[bb]**122**	3265.4	04	137	04	[cc]**530**	2600.3	04
[a]50	05	766	3157.9	05	923	05	686	3205.0	05	168	05	918	2600.3	05
75	06	343	3157.9	06	1016	06	682	3178.1	06	[c]**220**	06	122	2580.1	06
[aa]**94**	07	[aa]**381**	3137.8	07	76	07	984	3151.2	07	262	07	605	2546.5	07
[a]**161**	08	[aa]**12**	3110.9	08	81	08	980	3117.6	08	328	08	984	2539.8	08
220	09	459	3090.7	09	140	09	434	3090.7	09	374	09	[cc]**491**	2533.1	09
271	10	[aa]**281**	3070.6	10	152	10	846	3037.0	10	404	10	706	2526.3	10
[aa]**281**	11	605	3057.1	11	206	11	[bb]**236**	3037.0	11	461	11	847	2519.6	11
284	12	918	3057.1	12	226	12	57	3023.6	12	[cc]**491**	12	531	2492.7	12
319	13	81	3016.8	13	228	13	700	3016.8	13	517	13	[c]**220**	2486.0	13
[a]**328**	14	864	2983.2	14	258	14	910	2990.0	14	[cc]**530**	14	846	2479.3	14
[aa]**381**	15	647	2976.5	15	363	15	[b]**678**	2990.0	15	546	15	688	2459.2	15
404	16	50	2929.5	16	[b]**456**	16	623	2976.5	16	548	16	917	2459.2	16
412	17	262	2916.0	17	512	17	855	2976.5	17	566	17	647	2452.4	17
458	18	923	2902.6	18	618	18	[b]**456**	2929.5	18	573	18	1010	2439.0	18
474	19	[a]**328**	2889.2	19	631	19	516	2929.5	19	673	19	94	2439.0	19
[aa]**491**	20	287	2889.2	20	651	20	1021	2922.8	20	[cc]**686**	20	23	2439.0	20
[a]**516**	21	[a]**516**	2882.5	21	[b]**678**	21	902	2909.3	21	690	21	682	2432.3	21
566	22	[a]**161**	2875.7	22	781	22	777	2882.5	22	815	22	118	2418.8	22

[a] Top 10% yield in Knoxville, TN in 2010
[aa] Top 5% yield in Knoxville, TN in 2010
[b] Top 10% yield in Plymouth, NC in 2011
[bb] Top 5% yield in Plymouth, NC in 2011
[c] Top 10% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011
[cc] Top 5% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011

Table 3.78 MAS identifying the bottom 10 % of lines containing the unfavorable allele for the yield QTLs detected using SAS in each environment in Group D. Those Mas were compared to the bottom yielding 10 % of lines in the environment(s) from which they were selected. Those MAS lines whose yield values were among the bottom yielding 10 % are indicated in bold.

KNOXVILLE, TN 2010					PLYMOUTH, NC 2011					KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011				
MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})			MAS		YIELD (kg ha^{-1})		
Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank	Line	Rank	Line	Yld	Rank
682	201	648	1827.6	201	343	201	[b]**459**	1424.4	201	420	201	339	1737.4	201
697	202	645	1807.4	202	345	202	339	1411.0	202	434	202	729	1734.0	202
[aa]**723**	203	629	1800.7	203	[bb]**381**	203	996	1411.0	203	459	203	474	1733.7	203
781	204	528	1800.7	204	[b]**459**	204	284	1404.3	204	477	204	789	1714.5	204
782	205	733	1780.5	205	461	205	926	1384.1	205	539	205	409	1706.8	205
847	206	573	1773.8	206	514	206	[b]**670**	1357.2	206	555	206	76	1653.1	206
899	207	[a]**989**	1767.1	207	555	207	501	1330.4	207	[cc]**575**	207	990	1651.1	207
923	208	512	1767.1	208	573	208	697	1303.5	208	584	208	980	1622.0	208
926	209	225	1733.5	209	575	209	688	1283.3	209	602	209	102	1617.3	209
937	210	477	1713.3	210	621	210	741	1269.9	210	605	210	528	1587.5	210
[a]**989**	211	414	1693.2	211	[b]**670**	211	365	1216.1	211	[cc]**648**	211	477	1581.2	211
999	212	[aa]**723**	1666.3	212	706	212	[bb]**381**	1122.1	212	762	212	225	1562.6	212
1010	213	805	1646.2	213	[bb]**770**	213	773	1118.7	213	802	213	365	1554.8	213
87	214	576	1619.3	214	779	214	50	1121.9	214	823	214	349	1554.6	214
201	215	942	1612.6	215	789	215	201	1102.8	215	846	215	772	1547.0	215
314	216	258	1599.1	216	890	216	937	1114.5	216	855	216	976	1541.9	216
584	217	873	1451.3	217	976	217	733	1098.3	217	864	217	736	1516.7	217
628	218	575	1424.4	218	[bb]**989**	218	225	1120.1	218	873	218	[cc]**575**	1513.8	218
[aa]**719**	219	850	1384.1	219	1019	219	972	1093.0	219	874	219	719	1459.1	219
729	220	76	1350.5	220	96	220	[bb]**989**	1117.4	220	894	220	690	1435.9	220
762	221	484	1229.6	221	222	221	647	1102.3	221	1012	221	942	1238.3	221
885	222	[aa]**719**	1021.3	222	434	222	[bb]**770**	1115.8	222	1016	222	[cc]**648**	1232.3	222

[a] Bottom 10% yield in Knoxville, TN in 2010
[aa] Bottom 5% yield in Knoxville, TN in 2010
[b] Bottom 10% yield in Plymouth, NC in 2011
[bb] Bottom 5% yield in Plymouth, NC in 2011
[c] Bottom 10% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011
[cc] Bottom 5% yield averaged over Knoxville, TN in 2010-11 and Plymouth, NC in 2011

Table 3.79 MAS identifying the top 10 % of lines containing the favorable allele for QTLs detected using SAS in each environment in Group D compared to the top yielding 10 % of lines averaged across all environments. Those MAS lines whose yield values were among the top yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
402	01	**[bb]122**	01	37	01	864	2734.6	01
1019	02	216	02	57	02	**[bb]81**	2647.3	02
12	03	236	03	103	03	**[cc]686**	2640.6	03
33	04	823	04	137	04	**[cc]530**	2600.3	04
50	05	923	05	168	05	918	2600.3	05
75	06	1016	06	**[c]220**	06	**[bb]122**	2580.1	06
[a]94	07	76	07	262	07	605	2546.5	07
161	08	**[bb]81**	08	328	08	984	2539.8	08
[a]220	09	140	09	374	09	**[aacc]491**	2533.1	09
271	10	152	10	404	10	706	2526.3	10
281	11	206	11	461	11	847	2519.6	11
284	12	226	12	**[cc]491**	12	531	2492.7	12
319	13	228	13	517	13	**[c]220**	2486.0	13
328	14	258	14	**[cc]530**	14	846	2479.3	14
381	15	363	15	546	15	688	2459.2	15
404	16	456	16	548	16	917	2459.2	16
412	17	512	17	566	17	647	2452.4	17
458	18	618	18	573	18	1010	2439.0	18
474	19	631	19	673	19	**[a]94**	2439.0	19
[aa]491	20	651	20	**[cc]686**	20	23	2439.0	20
516	21	678	21	690	21	682	2432.3	21
566	22	781	22	815	22	118	2418.8	22

[a b c] Top 10% yield, [aa bb cc] Top 5% yield averaged over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011

Table 3.80 MAS identifying the bottom 10 % of lines containing the unfavorable allele for QTLs detected using SAS in each environment in Group D compared to the bottom yielding 10 % of lines averaged across all environments. Those MAS lines that yielded among the bottom yielding 10 % are indicated in bold.

MARKER ASSISTED SELECTIONS						YIELD (kg ha^{-1})		
KNOXVILLE, TN 2010		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011		
LINE	RANK	LINE	RANK	LINE	RANK	LINE	YEILD	RANK
682	201	343	201	990	201	339	1737.4	201
697	202	345	202	996	202	**[a]729**	1733.95	202
723	203	381	203	459	203	474	1733.72	203
781	204	459	204	**[c]477**	204	**[b]789**	1714.47	204
782	205	461	205	539	205	409	1706.85	205
847	206	514	206	555	206	76	1653.1	206
899	207	555	207	**[cc]575**	207	990	1651.08	207
923	208	573	208	584	208	980	1621.97	208
926	209	**[bb]575**	209	[cc]602	209	102	1617.26	209
937	210	621	210	605	210	528	1587.48	210
989	211	670	211	**[cc]648**	211	**[c]477**	1581.2	211
999	212	706	212	762	212	225	1562.62	212
1010	213	770	213	802	213	365	1554.78	213
87	214	779	214	823	214	349	1554.64	214
201	215	**[b]789**	215	846	215	772	1547.03	215
314	216	890	216	855	216	**[bb]976**	1541.88	216
584	217	**[bb]976**	217	864	217	736	1516.7	217
628	218	989	218	873	218	**[bb]575**	1513.79	218
[aa]719	219	1019	219	874	219	**[aa]719**	1459.15	219
[a]729	220	96	220	894	220	690	1435.85	220
762	221	222	221	1012	221	942	1238.31	221
885	222	434	222	1016	222	**[cc]648**	1232.26	222

[a b c] Bottom 10% yield, [aa bb cc] Bottom 5% yield averaged over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011

Table 3.81 Significant (P<0.01) epistatic interactions between loci for yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using R/qtl and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010	Gm07_18539902_T_G	7	M	61.37	W	GM08_19730595_T_C	8	A2	43.85	3.63	-0.14	-2.65
						GM09_38671215_T_C	9	K	85.94	4.25	-0.08	-2.86
						GM13_31873907_C_T	13	F	70.83	4.06	-2.61	0.09
						GM17_36810061_G_A	17	D2	81.80	3.79	-2.93	-0.35
Knoxville, TN 2010	Gm13_27092408_C_T	13	F	150.77	E	GM06_14356253_C_T	6	C2	31.90	6.58	-1.76	2.04
						GM09_38995035_C_T	9	K	86.66	3.59	0.31	2.94
						GM12_38128613_C_T	12	H	84.73	7.39	-0.67	2.89
Plymouth, NC 2011	Gm03_39559139_G_A	3	N	93.64	E	GM17_12926227_C_T	17	D2	28.72	8.50	3.39	-1.79
Plymouth, NC 2011	Gm17_32687336_C_T	17	D2	49.59	E	GM05_41748937_A_G	5	A1	92.78	7.42	-0.35	4.39
						GM06_47297459_G_A	6	C2	105.11	4.11	-1.06	2.84
						GM09_32922675_G_A	9	K	73.16	5.96	0.68	4.64
						GM12_39893147_C_T	12	H	88.65	3.85	3.60	0.20
						GM18_60158659_A_G	18	G	133.69	4.92	3.60	-0.19
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm15_48028533_G_A	15	E	72.4	W	GM01_49121708_G_T	1	D1a	109.16	4.71	-1.29	0.45
						GM04_11433919_T_C	4	C1	25.41	4.47	0.33	-1.35
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm17_12822621_A_G	17	D2	35.12	E	GM03_41402437_A_C	3	N	92.01	4.31	1.47	-0.20
						GM06_11630759_A_G	6	C2	25.85	4.74	1.80	-0.04
						GM19_35565632_C_T	19	L	79.03	4.16	-0.02	1.68

†Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.82 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by R/qtl to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aa]**461**	01	[aa]**461**	2851.5	772	3467.0	864	2734.6
[aac]**94**	02	[aa]**706**	2809.2	216	3426.7	[cc]**81**	2647.3
[aacc]**81**	03	[aa]**94**	2743.7	645	3299.0	686	2640.6
[a]**381**	04	[aa]**81**	2587.8	122	3265.4	530	2600.3
[a]**459**	05	201	2571.0	686	3205.0	[cc]**918**	2600.3
334	06	530	2563.6	682	3178.1	122	2580.1
161	07	262	2555.6	984	3151.2	605	2546.5
[bbc]**846**	08	[aa]**741**	2498.1	980	3117.6	984	2539.8
[aacc]**706**	09	864	2485.7	434	3090.7	[cc]**491**	2533.1
226	10	[aa]**918**	2468.6	[bb]**846**	3037.0	[cc]**706**	2526.3
[a]**766**	11	531	2465.9	236	3037.0	847	2519.6
140	12	522	2456.5	57	3023.6	531	2492.7
281	13	[a]**491**	2453.1	700	3016.8	220	2486.0
328	14	647	2448.7	910	2990.0	[c]**846**	2479.3
[aacc]**918**	15	75	2446.4	678	2990.0	688	2459.2
[a]**12**	16	[a]**381**	2435.6	623	2976.5	917	2459.2
548	17	[a]**766**	2427.9	855	2976.5	647	2452.4
[a]**228**	18	[a]**228**	2427.2	456	2929.5	1010	2439.0
[acc]**491**	19	[a]**459**	2421.9	516	2929.5	[c]**94**	2439.0
[aa]**741**	20	[a]**12**	2406.1	1021	2922.8	23	2439.0
35	21	475	2402.7	902	2909.3	682	2432.3
508	22	605	2399.4	777	2882.5	118	2418.8

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.83 Yield prediction model (YPM) developed using QTLs detected in Knoxville, TN in 2010 by SAS to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010		KNOXVILLE, TN 2011		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aac]**94**	01	[aa]**461**	2851.5	772	3467.0	864	2734.6
[acc]**491**	02	[aa]**706**	2809.2	216	3426.7	810	2647.3
[a]**12**	03	[aa]**94**	2743.7	645	3299.0	686	2640.6
281	04	[aa]**81**	2587.8	122	3265.4	[cc]**530**	2600.3
381	05	201	2571.0	686	3205.0	[cc]**918**	2600.3
[a]**766**	06	[aa]**530**	2563.6	682	3178.1	122	2580.1
[aacc]**918**	07	262	2555.6	984	3151.2	[cc]**605**	2546.5
874	08	741	2498.1	980	3117.6	984	2539.8
[aacc]**530**	09	864	2485.7	434	3090.7	[cc]**491**	2533.1
[acc]**605**	10	[aa]**918**	2468.6	846	3037.0	[cc]**706**	2526.3
[aa]**461**	11	531	2465.9	236	3037.0	847	2519.6
[b]**516**	12	522	2456.5	57	3023.6	531	2492.7
412	13	[a]**491**	2453.1	700	3016.8	220	2486.0
328	14	[a]**647**	2448.7	910	2990.0	846	2479.3
[ac]**647**	15	75	2446.4	678	2990.0	688	2459.2
1019	16	381	2435.6	623	2976.5	917	2459.2
161	17	[a]**766**	2427.9	855	2976.5	[c]**647**	2452.4
402	18	228	2427.2	456	2929.5	1010	2439.0
33	19	459	2421.9	[b]**516**	2929.5	[c]**94**	2439.0
[aacc]**706**	20	[a]**12**	2406.1	1021	2922.8	[c]**23**	2439.0
[c]**23**	21	475	2402.7	902	2909.3	682	2432.3
[aa]**81**	22	[a]**605**	2399.4	777	2882.5	118	2418.8

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.84 Significant (P<0.01) epistatic interactions between loci for yield in 220 RILs in Group D derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. Locus 1 indicates the markers where yield QTL were detected using SAS and locus 2 indicates the markers where QTL(s) were detected using Epistacy in SAS that were interacting with the yield QTL at locus 1.

											ADDITIVE X ADDITIVE EFFECT†	
ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	E	W
Knoxville, TN 2010	Gm01_54171147_G_T	1	D1a	118.27	E	GM03_43341179_T_C	3	N	96.31	3.75	0.16	2.64
Knoxville, TN 2010	Gm18_58055444_T_C	18	G	112.85	E	GM12_38118136_C_T	12	H	84.71	4.09	-0.27	2.28
Plymouth, NC 2011	Gm03_39552601_T_C	3	N	87.68	E	GM17_12926227_C_T	17	D2	28.72	8.50	3.39	-1.79
Plymouth, NC 2011	Gm13_29895148_C_T	13	F	154.76	W	GM06_16524166_A_G	6	C2	36.72	3.79	-6.85	-0.99
						GM07_15547905_A_G	7	M	34.55	4.20	-3.34	0.20
Plymouth, NC 2011	Gm18_15660496_T_G	18	G	44.64	E	GM13_27705537_G_A	13	F	61.57	4.31	2.08	-1.33
						GM17_33343495_A_G	17	D2	74.10	3.82	2.49	-0.79
Plymouth, NC 2011	Gm19_39246602_T_C	19	L	73.68	E	GM10_46788615_A_G	10	O	103.97	6.49	-0.23	4.07
						GM18_52455765_C_A	18	G	116.57	5.57	3.88	-0.24
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm01_47115450_G_T	1	D1a	70.15	E	GM06_49868054_G_A	6	C2	110.82	4.88	0.95	-0.75
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm05_31399360_G_A	5	A1	41.55	W	GM03_44983539_T_C	3	N	99.96	4.36	0.18	-1.41
						GM11_37237023_G_T	11	B1	82.75	5.30	0.47	-1.37
						GM10_48643490_T_C	10	O	108.10	5.88	-5.24	2.80

Table 3.84 Continued.

ENVIRONMENT	LOCUS 1	CHR	MLG	LOC (cM)	FAVORABLE ALLELE	LOCUS 2	CHR	MLG	LOC (cM)	R^2 (%)	ADDITIVE X ADDITIVE EFFECT† E	W
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm10_48428720_T_C	10	O	110.82	E	GM05_32329300_T_G	5	A1	71.84	4.53	0.22	-1.58
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm11_36807939_C_A	11	B1	84.22	E	GM05_31399360_G_A	5	A1	69.78	3.90	1.25	-0.30
						GM02_47462924_G_A	2	D1b	105.47	5.00	-0.55	1.28
						GM03_16491445_A_G	3	N	36.65	4.94	-0.55	1.27
						GM04_33044652_A_C	4	C1	73.43	4.89	1.47	-0.25
						GM05_39568162_C_T	5	A1	87.93	4.65	-0.07	1.67
						GM07_15862402_G_T	7	M	35.25	4.40	-0.53	1.14
						GM13_27705537_G_A	13	F	61.57	3.56	-0.02	1.49
						GM15_12224277_T_C	15	E	27.17	4.28	1.32	-0.32
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm13_11355266_T_C	13	F	25.49	E	GM17_38085822_A_G	17	D2	84.64	3.93	0.18	1.78
Knoxville, TN 2010-11 Plymouth, NC 2011	Gm20_41827386_T_C	20	I	45.53	E	GM03_39717853_A_G	3	N	88.26	8.21	1.43	-0.87
						GM07_18539902_T_G	7	M	41.20	3.96	1.15	-0.45
						GM09_31659985_T_C	9	K	70.36	3.93	-0.20	1.45

†Additive by additive effect refers to the quantitative change in yield that is associated with the epistatic combination of the additive genetic effect of locus 1 having the favorable allele with the additive genetic effect of the homozygous state of locus 2 from (E) Essex 15-86-1 or (W) Williams 82-11-43-1

Table 3.85 Yield prediction model (YPM) developed using QTLs detected in Plymouth, NC in 2011 by R/qtl to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
PLYMOUTH, NC 2011		KNOXVILLE, TN 2011		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bb]216	01	**[aa]461**	2851.5	772	3467.0	864	2734.6
[bb]236	02	**[aa]706**	2809.2	**[bb]216**	3426.7	**[bb]81**	2647.3
[b]1021	03	**[aa]94**	2743.7	645	3299.0	686	2640.6
[bbcc]984	04	**[aa]81**	2587.8	122	3265.4	**[cc]530**	2600.3
[b]57	05	201	2571.0	686	3205.0	918	2600.3
[b]700	06	530	2563.6	**[bb]682**	3178.1	122	2580.1
[b]623	07	262	2555.6	**[bb]984**	3151.2	605	2546.5
[c]1010	08	741	2498.1	980	3117.6	**[cc]984**	2539.8
885	09	864	2485.7	**[bb]434**	3090.7	491	2533.1
[b]456	10	918	2468.6	**[bb]846**	3037.0	**[bb]706**	2526.3
[b]855	11	531	2465.9	**[bb]236**	3037.0	847	2519.6
[bbc]846	12	522	2456.5	**[b]57**	3023.6	531	2492.7
[a]491	13	**[a]491**	2453.1	**[b]700**	3016.8	220	2486.0
[bbc]682	14	647	2448.7	910	2990.0	**[c]846**	2479.3
[cc]530	15	75	2446.4	678	2990.0	688	2459.2
[bb]434	16	381	2435.6	**[b]623**	2976.5	917	2459.2
[c]118	17	766	2427.9	**[b]855**	2976.5	647	2452.4
[aa]461	18	228	2427.2	**[b]456**	2929.5	**[c]1010**	2439.0
[b]777	19	459	2421.9	516	2929.5	**[bb]94**	2439.0
[aabb]706	20	12	2406.1	**[b]1021**	2922.8	23	2439.0
[aabb]94	21	475	2402.7	902	2909.3	**[c]682**	2432.3
[aabb]81	22	605	2399.4	**[b]777**	2882.5	**[c]118**	2418.8

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
†YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.86 Yield prediction model (YPM) developed using QTLs detected in Plymouth, NC in 2011 by SAS to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM†		YIELD (kg ha^{-1})					
PLYMOUTH, NC 2011		KNOXVILLE, TN 2011		PLYMOUTH, NC 2011		KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[bbcc]984	01	461	2851.5	**[bb]772**	3467.0	864	2734.6
[bbcc]122	02	706	2809.2	**[bb]216**	3426.7	81	2647.3
456	03	94	2743.7	**[bb]645**	3299.0	686	2640.6
[bb]216	04	81	2587.8	**[bb]122**	3265.4	530	2600.3
[bb]236	05	201	2571.0	686	3205.0	918	2600.3
823	06	530	2563.6	**[bb]682**	3178.1	**[cc]122**	2580.1
[b]902	07	262	2555.6	**[bb]984**	3151.2	605	2546.5
1007	08	741	2498.1	980	3117.6	**[cc]984**	2539.8
[bbc]682	09	864	2485.7	434	3090.7	491	2533.1
140	10	918	2468.6	**[bb]846**	3037.0	706	2526.3
[bbc]846	11	531	2465.9	**[bb]236**	3037.0	847	2519.6
[b]678	12	522	2456.5	**[b]57**	3023.6	531	2492.7
[bb]645	13	491	2453.1	**[b]700**	3016.8	220	2486.0
[bb]772	14	647	2448.7	**[b]910**	2990.0	**[c]846**	2479.3
[b]700	15	75	2446.4	**[b]678**	2990.0	688	2459.2
[b]1021	16	381	2435.6	**[b]623**	2976.5	917	2459.2
[b]57	17	766	2427.9	855	2976.5	647	2452.4
363	18	228	2427.2	456	2929.5	1010	2439.0
521	19	459	2421.9	**[b]516**	2929.5	94	2439.0
[b]623	20	12	2406.1	**[b]1021**	2922.8	23	2439.0
[b]910	21	475	2402.7	**[b]902**	2909.3	**[c]682**	2432.3
[b]516	22	605	2399.4	777	2882.5	118	2418.8

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
†YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.87 Yield prediction model (YPM) developed using QTLs detected over three environments in 2011 by R/qtl to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011				KNOXVILLE, TN 2011		PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[aabb]530	01	**[aa]864**	2734.6	461	2851.5	772	3467.0
[a]23	02	**[aa]81**	2647.3	706	2809.2	216	3426.7
[aabb]918	03	**[aa]686**	2640.6	**[bb]94**	2743.7	645	3299.0
[aab]605	04	**[aa]530**	2600.3	**[bb]81**	2587.8	122	3265.4
[aabb]864	05	**[aa]918**	2600.3	201	2571.0	**[cc]686**	3205.0
[a]1010	06	122	2580.1	**[bb]530**	2563.6	682	3178.1
[abb]531	07	**[aa]605**	2546.5	**[bb]262**	2555.6	**[cc]984**	3151.2
[b]475	08	**[aa]984**	2539.8	741	2498.1	980	3117.6
[abb]94	09	**[aa]491**	2533.1	**[bb]864**	2485.7	434	3090.7
268	10	706	2526.3	**[bb]918**	2468.6	846	3037.0
[aabb]686	11	**[aa]847**	2519.6	**[bb]531**	2465.9	236	3037.0
[aa]847	12	**[a]531**	2492.7	522	2456.5	**[c]57**	3023.6
[ab]647	13	220	2486.0	**[b]491**	2453.1	700	3016.8
314	14	846	2479.3	**[b]647**	2448.7	910	2990.0
[aabb]81	15	688	2459.2	75	2446.4	678	2990.0
[aab]491	16	917	2459.2	381	2435.6	623	2976.5
[aacc]984	17	**[a]647**	2452.4	766	2427.9	855	2976.5
909	18	**[a]1010**	2439.0	228	2427.2	456	2929.5
[bb]262	19	**[a]94**	2439.0	459	2421.9	516	2929.5
[c]57	20	**[a]23**	2439.0	12	2406.1	1021	2922.8
140	21	682	2432.3	**[b]475**	2402.7	902	2909.3
287	22	118	2418.8	**[b]605**	2399.4	777	2882.5

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (R/qtl) and additive by additive effects (Episatcy)

Table 3.88 Yield prediction model (YPM) developed using QTLs detected over three environments in 2011 by SAS to select by MAS the top yielding 10 % of RILs in Group D grown in individual environments and averaged across multiple environments. These MAS lines are indicated in bold.

YPM[†]		YIELD (kg ha^{-1})					
KNOXVILLE, TN 2010-11 PLYMOUTH, NC 2011				KNOXVILLE, TN 2011		PLYMOUTH, NC 2011	
LINE	RANK	LINE	YIELD	LINE	YIELD	LINE	YIELD
[acc]682	01	864	2734.6	461	2851.5	772	3467.0
[a]1010	02	**[aa]81**	2647.3	706	2809.2	**[cc]216**	3426.7
[aacc]122	03	**[aa]686**	2640.6	94	2743.7	645	3299.0
[aab]491	04	530	2600.3	**[bb]81**	2587.8	**[cc]122**	3265.4
809	05	918	2600.3	201	2571.0	**[cc]686**	3205.0
[aabb]81	06	**[aa]122**	2580.1	530	2563.6	**[cc]682**	3178.1
314	07	605	2546.5	262	2555.6	**[cc]984**	3151.2
1019	08	**[aa]984**	2539.8	741	2498.1	980	3117.6
[c]456	09	**[aa]491**	2533.1	864	2485.7	**[cc]434**	3090.7
987	10	706	2526.3	918	2468.6	**[cc]846**	3037.0
[cc]216	11	**[aa]847**	2519.6	531	2465.9	**[cc]236**	3037.0
692	12	531	2492.7	522	2456.5	57	3023.6
271	13	220	2486.0	**[b]491**	2453.1	**[c]700**	3016.8
[c]700	14	**[a]846**	2479.3	647	2448.7	910	2990.0
[acc]846	15	688	2459.2	75	2446.4	678	2990.0
[cc]236	16	917	2459.2	381	2435.6	623	2976.5
[aacc]984	17	647	2452.4	766	2427.9	**[c]855**	2976.5
[aa]847	18	**[a]1010**	2439.0	228	2427.2	**[c]456**	2929.5
[c]855	19	94	2439.0	459	2421.9	516	2929.5
[a]23	20	**[a]23**	2439.0	12	2406.1	1021	2922.8
140	21	**[a]682**	2432.3	475	2402.7	902	2909.3
526	22	118	2418.8	605	2399.4	777	2882.5

[a b c] the top 10% , [aa bb cc] Top 5% of RILs at Knoxville, TN in 2011, Plymouth, NC in 2011 and combined over Knoxville, TN in 2010, 2011 and Plymouth, NC in 2011, respectively
[†]YPM indicates what environment the data for the model was collected: mean yield, additive effects (SAS) and additive by additive effects (Episatcy)

Table 3.89 Quantitative trait loci identified using R/qtl or SAS located on various molecular linkage groups associated with yield in 875 RILs derived from a cross between Essex 86-15-1 x Williams 82-11-43-1. The lines were divided into four groups based on maturity and number of RILs and grown in two environments.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADD. EFFECT†	FAV. ALLELE	P-VALUE	PROGRAM	GROUP
Knoxville, TN 2010	Gm01_1241762_A_C	1	D1a	4.60	.	8.50	2.24	W	0.0003	SAS	B
Wooster, OH 2011	Gm01_1494600_C_T	1	D1a	5.52	.	4.73	2.44	E	0.009	SAS	A
Knoxville, TN 2010	Gm01_1045893_G_A	1	D1a	5.88	2.63	5.45	1.18	E	.	R/qtl	C
Knoxville, TN 2010	Gm01_2747136_A_C	1	D1a	11.28	.	7.32	1.30	W	0.0008	SAS	C
Belleville, IL 2011 Knoxville, TN 2010-11	Gm01_29787876_G_A	1	D1a	59.29	.	10.02	0.92	E	<.0001	SAS	B
Belleville, IL 2011 Knoxville, TN 2010-11	Gm01_29787876_G_A	1	D1a	59.29	.	8.08	1.00	E	<.0001	SAS	B
Plymouth, NC 2011	Gm01_47115450_G_T	1	D1a	70.15	.	5.61	0.24	E	0.0008	SAS	D
Knoxville, TN 2010	Gm01_54171147_G_T	1	D1a	118.27	.	4.91	1.81	E	0.0082	SAS	D
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm02_707483_A_G	2	D1b	5.25	3.07	6.7	2.48	E	.	R/qtl	A
Portageville, MO 2011	Gm02_6820177_A_C	2	D1b	38.07	3.25	4.31	1.80	W	.	R/qtl	C
Knoxville, TN 2010	Gm02_6821311_A_C	2	D1b	38.24	2.35	4.35	1.18	E	.	R/qtl	C
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm02_12770553_A_G	2	D1b	46.15	.	6.29	1.69	W	0.0022	SAS	B
Belleville, IL 2011	Gm02_42469280_A_C	2	D1b	105.17	2.65	4.07	1.16	W	.	R/qtl	B
Knoxville, TN 2010	Gm02_44803277_C_T	2	D1b	107.06	.	6.11	0.51	W	0.0026	SAS	C
Belleville, IL 2011	Gm02_44803277_C_T	2	D1b	114.09	2.83	4.66	2.10	W	.	R/qtl	B
Knoxville, TN 2010	Gm02_47790307_C_T	2	D1b	121.66	.	6.04	3.39	E	0.0028	SAS	A
Wooster, OH 2011 Knoxville, TN 2010-11	Gm02_49126947_T_C	2	D1b	127.25	.	5.31	3.44	E	0.0051	SAS	A
Wooster, OH 2011 Knoxville, TN 2010-11	Gm02_49126947_T_C	2	D1b	127.25	.	5.07	5.82	E	0.0071	SAS	A
Portageville, MO 2011 Knoxville, TN 2010-11	Gm02_49746270_A_G	2	D1b	146.54	.	5.40	1.19	W	0.0046	SAS	C
Wooster, OH 2011	Gm02_47790307_C_T	2	D1b	150.38	2.56	5.7	3.26	E	.	R/qtl	A
Portageville, MO 2011	Gm03_838582_T_C	3	N	4.68	.	4.82	2.34	W	0.0089	SAS	C
Wooster, OH 2011	Gm03_2151432_A_G	3	N	14.00	3.21	8.3	4.33	E	.	R/qtl	A
Belleville, IL 2011 Knoxville, TN 2010-11	Gm03_5264953_A_G	3	N	19.43	.	5.58	0.36	E	0.001	SAS	B
Portageville, MO 2011	Gm03_21003884_A_G	3	N	44.15	.	6.76	0.37	E	0.0012	SAS	C
Plymouth, NC 2011	Gm03_39552601_T_C	3	N	87.68	.	5.54	3.81	E	0.0045	SAS	D
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm03_39559139_G_A	3	N	93.64	2.78	7.38	3.09	E	.	R/qtl	D
Wooster, OH 2011 Knoxville, TN 2010-11	Gm03_47386481_A_C	3	N	120.71	.	5.67	5.81	E	0.004	SAS	A
Plymouth, NC 2011	Gm04_8845668_G_T	4	C1	63.93	.	4.84	0.28	E	0.0081	SAS	D
Knoxville, TN 2010	Gm04_8247949_C_T	4	C1	65.87	.	6.79	0.97	W	0.0014	SAS	D
Knoxville, TN 2010	Gm04_48782140_G_T	4	C1	152.98	2.48	6.4	2.13	E	.	R/qtl	A
Wooster, OH 2011	Gm04_48993297_T_G	4	C1	154.16	2.78	5.2	3.18	E	.	R/qtl	A
Knoxville, TN 2010	Gm05_1128604_A_G	5	A1	3.24	.	4.95	0.52	W	0.0024	SAS	C
Belleville, IL 2011 Knoxville, TN 2010-11	Gm05_3485480_T_C	5	A1	19.73	2.66	5.86	1.61	W	.	R/qtl	B
Wooster, OH 2011 Knoxville, TN 2010-11	Gm05_33176582_G_A	5	A1	33.77	3.44	7.8	2.56	W	.	R/qtl	A
Belleville, IL 2011 Knoxville, TN 2010-11	Gm05_30953466_G_T	5	A1	39.76	.	7.68	1.60	W	0.0005	SAS	B
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm05_31399360_G_A	5	A1	41.55	.	5.71	0.99	W	0.0007	SAS	D
Portageville, MO 2011	Gm05_34850619_C_T	5	A1	72.38	.	5.71	0.27	W	0.0007	SAS	C

Table 3.89 Continued.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADD. EFFECT[†]	FAV. ALLELE	P-VALUE	PROGRAM	GROUP
Portageville, MO 2011 Knoxville, TN 2010-11	Gm06_10864751_A_G	6	C2	24.86	.	5.61	2.83	W	0.0042	SAS	C
Portageville, MO 2011	Gm06_16723946_G_A	6	C2	32.46	3.72	5.57	2.64	W	.	R/qtl	C
Knoxville, TN 2010	Gm06_17617727_G_T	6	C2	55.04	2.82	3.42	3.70	W	.	R/qtl	B
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm06_20996124_T_C	6	C2	58.54	.	9.03	7.90	W	0.0002	SAS	B
Belleville, IL 2011	Gm06_20996124_T_C	6	C2	58.54	.	10.63	4.03	W	<.0001	SAS	B
Belleville, IL 2011 Knoxville, TN 2010-11	Gm06_20996124_T_C	6	C2	60.21	5.56	10.48	5.26	W	.	R/qtl	B
Belleville, IL 2011	Gm06_20996124_T_C	6	C2	62.03	3.92	6.23	3.22	W	.	R/qtl	B
Belleville, IL 2011	Gm06_27540819_T_G	6	C2	66.24	.	10.29	4.48	W	<.0001	SAS	B
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm07_149664_T_C	7	M	1.34	.	11.29	5.43	W	<.0001	SAS	D
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm07_4008483_C_T	7	M	5.19	2.92	8.64	1.86	W	.	R/qtl	D
Portageville, MO 2011	Gm07_4837493_A_G	7	M	11.06	.	5.71	2.04	E	0.0007	SAS	C
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm07_16814628_C_T	7	M	38.47	.	5.41	0.83	W	0.0051	SAS	C
Belleville, IL 2011	Gm07_17460956_C_A	7	M	39.95	.	14.85	1.90	W	<.0001	SAS	B
Knoxville, TN 2010	Gm07_18539902_T_G	7	M	42.42	.	5.69	3.04	W	0.0039	SAS	D
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm07_16144523_C_A	7	M	51.90	3.65	6.67	1.87	W	.	R/qtl	B
Belleville, IL 2011	Gm07_17362808_A_G	7	M	55.95	5.31	8.20	2.04	W	.	R/qtl	B
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm07_18539902_T_G	7	M	61.37	3.52	8.83	2.67	W	.	R/qtl	D
Belleville, IL 2011	Gm08_15866777_G_A	8	A2	22.31	.	7.09	0.35	E	0.0001	SAS	B
Plymouth, NC 2011	Gm09_457853_A_G	9	K	5.23	.	6.06	4.10	E	0.0027	SAS	D
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm09_2634593_G_A	9	K	5.62	3.02	7.87	3.09	E	.	R/qtl	D
Plymouth, NC 2011	Gm09_3394608_G_A	9	K	7.76	.	4.53	1.20	E	0.0037	SAS	D
Knoxville, TN 2010	Gm09_6967374_C_T	9	K	15.94	.	4.64	0.88	E	0.0106	SAS	A
Portageville, MO 2011	Gm09_18969901_T_C	9	K	28.52	2.32	3.81	2.77	W	.	R/qtl	C
Belleville, IL 2011 Knoxville, TN 2010-11	Gm09_12463468_C_T	9	K	31.76	.	9.79	0.02	W	<.0001	SAS	B
Belleville, IL 2011	Gm09_12463468_C_T	9	K	31.76	.	7.11	0.45	W	<.0001	SAS	B
Portageville, MO 2011 Knoxville, TN 2010-11	Gm09_34191288_T_C	9	K	78.24	.	6.88	3.47	W	0.0013	SAS	C
Belleville, IL 2011	Gm10_571698_A_G	10	O	1.30	.	6.48	0.14	E	0.0016	SAS	B
Wooster, OH 2011 Knoxville, TN 2010-11	Gm10_47585270_T_G	10	O	108.89	.	5.35	2.27	E	0.0049	SAS	A
Plymouth, NC 2011	Gm10_48428720_T_C	10	O	110.82	.	5.46	0.11	E	0.001	SAS	D
Knoxville, TN 2010 Knoxville, TN 2010-11	Gm11_4453218_T_C	11	B1	16.23	.	5.66	2.88	E	0.004	SAS	D
Wooster, OH 2011 Knoxville, TN 2010-11	Gm11_5773052_G_A	11	B1	20.42	.	6.53	3.80	E	0.0018	SAS	A
Belleville, IL 2011 Knoxville, TN 2010-11	Gm11_7323949_A_G	11	B1	26.24	.	6.83	0.28	E	0.0001	SAS	B
Portageville, MO 2011 Knoxville, TN 2010-11	Gm11_7445495_G_A	11	B1	26.72	.	5.97	0.67	E	0.0026	SAS	C
Plymouth, NC 2011	Gm11_36807939_C_A	11	B1	84.22	.	5.95	1.25	E	0.0027	SAS	D
Knoxville, TN 2010	Gm12_1594873_A_G	12	H	3.64	.	5.34	0.62	W	0.0055	SAS	C
Belleville, IL 2011 Knoxville, TN 2010-11	Gm12_7135310_A_G	12	H	36.25	3.71	6.22	2.28	W	.	R/qtl	B
Portageville, MO 2011 Knoxville, TN 2010-11	Gm12_39962521_A_G	12	H	91.44	.	6.07	1.54	E	0.0004	SAS	C
Plymouth, NC 2011 Knoxville, TN 2010-11	Gm13_11355266_T_C	13	F	35.49	.	6.73	1.34	E	0.0002	SAS	D
Wooster, OH 2011	Gm13_27348409_A_G	13	F	150.28	.	6.07	4.13	E	0.0006	SAS	A
Knoxville, TN 2010	Gm13_27092408_C_T	13	F	150.77	2.75	6.18	2.21	E	.	R/qtl	D
Plymouth, NC 2011	Gm13_29895148_C_T	13	F	154.76	.	4.73	2.54	W	0.0098	SAS	D

Table 3.89 Continued.

ENVIRONMENT	MARKERS	CHR	MLG	LOC (cM)	LOD	R^2 (%)	ADD. EFFECT†	FAV. ALLELE	P-VALUE	PROGRAM	GROUP
Knoxville, TN 2010-11											
Portageville, MO 2011	Gm13_32183364_A_C	13	F	162.13	.	6.32	0.02	E	0.0019	SAS	C
Portageville, MO 2011	Gm13_34751493_C_A	13	F	165.33	3.17	5.02	1.16	W	.	R/qtl	C
Portageville, MO 2011	Gm13_34946643_T_C	13	F	180.68	.	7.28	2.9	E	0.0009	SAS	C
Knoxville, TN 2010-11											
Wooster, OH 2011	Gm14_49107190_G_A	14	B2	102.52	.	5.97	6.14	W	0.003	SAS	A
Knoxville, TN 2010-11											
Plymouth, NC 2011	Gm15_48028533_G_A	15	E	72.40	2.77	6.49	1.86	W	.	R/qtl	D
Knoxville, TN 2010	Gm15_43797502_G_T	15	E	72.68	.	6.38	1.88	W	0.002	SAS	A
Knoxville, TN 2010-11											
Belleville, IL 2011	Gm15_49231503_C_T	15	E	89.13	.	7.60	0.98	W	<.0001	SAS	B
Knoxville, TN 2010-11											
Plymouth, NC 2011	Gm16_1339719_T_C	16	J	6.55	.	5.39	1.81	W	0.0011	SAS	D
Knoxville, TN 2010-11											
Portageville, MO 2011	Gm16_5735654_A_G	16	J	8.95	3.71	4.61	1.8	W	.	R/qtl	C
Portageville, MO 2011	Gm16_6262227_C_T	16	J	10.66	3.18	5.25	3.09	E	.	R/qtl	C
Portageville, MO 2011	Gm16_6233586_A_G	16	J	14.23	.	8.39	3.13	E	0.0003	SAS	C
Knoxville, TN 2010-11											
Portageville, MO 2011	Gm16_6496577_A_C	16	J	14.86	.	7.62	0.42	E	0.0005	SAS	C
Belleville, IL 2011	Gm17_13240263_C_T	17	D2	30.29	.	6.86	1.22	E	0.0002	SAS	B
Knoxville, TN 2010-11											
Plymouth, NC 2011	Gm17_12822621_A_G	17	D2	35.12	2.56	4.86	1.09	E	.	R/qtl	D
Plymouth, NC 2011	Gm17_32687336_C_T	17	D2	49.59	2.47	5.71	2.92	E	.	R/qtl	D
Knoxville, TN 2010-11											
Portageville, MO 2011	Gm18_265662_T_C	18	G	1.19	.	5.71	0.96	E	0.0007	SAS	C
Knoxville, TN 2010-11											
Wooster, OH 2011	Gm18_8772679_T_C	18	D2	33.67	.	6.88	2.83	W	0.0002	SAS	A
Plymouth, NC 2011	Gm18_15660496_T_G	18	G	44.64	.	4.92	0.85	E	0.0025	SAS	D
Knoxville, TN 2010-11											
Belleville, IL 2011	Gm18_23913313_A_G	18	G	54.72	.	7.42	0.38	E	<.0001	SAS	B
Knoxville, TN 2010	Gm18_57988264_A_G	18	G	78.75	2.79	6.57	2.44	E	.	R/qtl	D
Knoxville, TN 2010	Gm18_58055444_T_C	18	G	112.85	.	4.72	2.72	E	0.0034	SAS	D
Knoxville, TN 2010-11											
Belleville, IL 2011	Gm19_2404683_A_G	19	L	25.12	.	6.39	0.87	W	0.0017	SAS	B
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	70.65	3.25	8.25	5.04	W	.	R/qtl	A
Knoxville, TN 2010-11											
Wooster, OH 2011	Gm19_44937486_T_C	19	L	70.75	3.75	7.2	3.17	W	.	R/qtl	A
Wooster, OH 2011	Gm19_45198812_C_A	19	L	72.00	3.28	9.5	2.40	W	.	R/qtl	A
Plymouth, NC 2011	Gm19_39246602_T_C	19	L	73.68	.	5.66	3.38	E	0.0009	SAS	D
Knoxville, TN 2010	Gm19_44937486_T_C	19	L	76.71	.	8.17	5.75	W	<0.0001	SAS	A
Wooster, OH 2011	Gm19_44955912_T_G	19	L	76.84	.	7.98	4.22	W	<0.0001	SAS	A
Knoxville, TN 2010-11											
Wooster, OH 2011	Gm19_44964042_C_T	19	L	76.91	.	8.12	3.21	W	<0.0001	SAS	A
Knoxville, TN 2010	Gm19_45062248_T_C	19	L	77.05	.	6.10	2.56	W	0.0005	SAS	B
Knoxville, TN 2010	Gm19_46733772_T_C	19	L	84.11	2.87	6.10	1.85	W	.	R/qtl	C
Belleville, IL 2011	Gm20_800671_A_G	20	I	1.83	.	7.78	1.18	W	<.0001	SAS	B
Knoxville, TN 2010-11											
Plymouth, NC 2011	Gm20_41827386_T_C	20	I	43.53	.	5.15	0.82	E	0.0016	SAS	D
Knoxville, TN 2010	Gm20_43890641_G_T	20	I	54.79	.	6.70	2.67	W	0.0015	SAS	C
Knoxville, TN 2010-11											
Portageville, MO 2011	Gm20_46574547_T_C	20	I	65.04	.	8.90	1.72	W	0.0001	SAS	C

†ADD. EFFECT = Additive effect refers to the quantitative change in yield that is associated with either (E) Essex 15-86-1 or (W) Williams 82-11-43-1; FAV. ALLELE = favorable allele MLG = molecular linkage group; CHR = chromosome; LOC = map position

Vita

Benjamin David Fallen was born on August 8, 1984 in Stovall, Virginia. In 2002, he graduated from Halifax County High School in South Boston, VA. He then went to Virginia Polytechnic Institute and State University in Blacksburg, VA and earned a Bachelor of Science in Crop and Soil Environmental Sciences in 2006. From April 2006 to July 2007 he worked as an agricultural specialist for the Soybean Breeding and Genetics program at Virginia Tech.

In July of 2007 he enrolled at the University of Tennessee and began soybean breeding research under Dr. Vincent Pantalone. In September of 2008 he began working full time as a Research Associate II and finished his Master of Science degree in August of 2009. He continued his education at the University of Tennessee by pursuing a PhD. in Plant Science with a concentration in soybean breeding. Benjamin hopes to begin a career in plant breeding after the successful completion of his studies.