# MARKER ASSISTED SELECTION FOR SEED YIELD IN SOYBEAN [*GLYCINE MAX* (L.) MERR.] PLANT ROW YIELD TRIALS

BY

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DISSERTATION

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## ABSTRACT

Quantitative trait loci (QTL) controlling seed yield in soybean [Glycine max (L.) Merr.] have been difficult to confirm among populations. Our objective was to determine whether a method of marker-assisted selection (MAS) for seed yield in elite lines would be applicable to selection in soybean plant row yield trials (PRYTs). Lines from two populations with elite parents were grown in PRYTs in 2008 and tested with markers to identify quantitative trait loci (QTL) associated with seed yield. The first population was tested with 53 single nucleotide polymorphism (SNP) markers and the second population with 26 SNP markers. *F*-tests were conducted to determine which loci were significantly associated with seed yield in the PRYTs. Lines from each population were then selected from the PRYTs to form five groups from each population: high and low seed yield phenotypes, high and low seed yield genotypes, and random. The five groups from each population were planted at 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. Even with the limited marker coverage, the genotypic selection method used in this study successfully identified lines in PRYTs that would not have been selected due to poor seed yield performance in 2008.

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## TABLE OF CONTENTS

# INTRODUCTION

Soybean [*Glycine max* (L.) Merr.] is a very important oilseed crop (Wilcox, 2004) and in 2001 accounted for 35% of the total oilseed production of the world (Wilcox, 2004). The United States ranked number one in world soybean production in 2007 (FAO, 2010a). From 1961 to 2008, soybean seed yields in the United States increased from 1690 kg/ha$^{-1}$ to 2666 kg/ha$^{-1}$ (FAO, 2010b). While much of this increase is explained by genetic improvement in soybean varieties, some may also be explained by changes in cultural practices including the use of herbicides and fertilizer (Luedders, 1977). Luedders (1977) reported that one major improvement in soybean over time is a reduction of lodging. Reduced lodging results in more harvestable seed by improving ease of mechanical harvest.

Projections of human population growth indicate there may be in excess of 9 billion people by 2050 (U.S. Census Bureau, 2010). It has been suggested that an increasing world population, along with the increasing rate of population growth, requires a second green revolution (Pardue, 2010). At a 2008 conference of food security, United Nations secretary-general Ban Ki-moon indicated that food production must increase 50% by the year 2030 to meet the demand of a growing population (Ki-moon, 2008).

Marker-assisted selection (MAS) has been arguably the most important plant breeding tool developed in the last 20 years. Marker-assisted selection increases the heritability of selectable traits, and increases the rate of genetic gain, by decreasing the variance of the selected trait. The ability to select only lines with a desired trait phenotype promotes a more efficient use of plant breeding resources and is thus a desirable method of selection. Genetic markers have been developed for many commercially important traits and are being used in soybean breeding programs. Genetic markers useful for the selection of plants with resistance to phytophthora

(Hegstad et al., 1997, Salamath and Bhattacharyya, 1998), soybean cyst nematode (Concibido et al., 1996; Coryell et al., 1999), brown stem rot (Bachman et al., 2001), and more recently, soybean rust (Hyten et al., 2007), have been developed.

Plant row yield trials in a soybean breeding program are typically grown at a single location in a single replicate experiment in relatively short, single row plots (Hegstad et al., 1999; Streit et al., 2001; Cooper, 1990). This allows the breeder to observe lines from many populations and allow for the selection of lines from populations with an above average probability of being superior (Orf et al., 2004). Selections may be made visually, by seed yield data, or a combination of both. Selections that are made from the plant row yield trials are then evaluated at multiple locations and selection is imposed in subsequent generations until the line is either discarded or released as a breeding line or a commercial cultivar. A breeding program that combines both MAS to select plants for line derivation together with selection based on plant row yield trials can make more breeding progress than programs that do not use these methods.

Unfortunately, plant row yield trials have a low predictive value for seed yield. This is partially due to the lack of replications, which results in the confounding of location and genotype and increased errors in the seed yield estimates. Hegstad et al. (1999) reported the broad sense heritability of seed yield from plant row yield trials of five populations at 0.55, 0.49, 0.44, 0.63, and 0.29. They also reported correlation coefficients of seed yield from plant row yield trials with two subsequent years of yield testing from five populations, which averaged 0.17. Only one of the five correlation coefficients was significant at the 0.05 level. Streit et al. (2001) reported the broad sense heritability of four populations at 0.35, 0.61, 0.63, and 0.50. They reported the correlation coefficient between seed yield from plant row yield trials and one

subsequent year of yield testing was 0.41 averaged across four populations. All four coefficients were significant at the 0.05 probability level.

Traits such as seed yield that are difficult or expensive to phenotype and have low correlations between years are prime candidates for MAS. The use of molecular markers to select for seed yield could increase genetic gain through the elimination of lines lacking a beneficial allelic profile for seed yield. Unfortunately, the identification of molecular markers associated with major seed yield genes has been difficult in elite by elite populations (Reyna and Sneller, 2001; Sebastian et al., 2010).

A considerable amount of work has been done to identify quantitative trait loci (QTL) associated with seed yield. In the following discussions, when a marker is identified it is followed in parentheses by the chromosome number and position in Centimorgans (cM).

Orf et al. (1999a) conducted a study to identify seed yield QTL in soybean. They studied $F_7$ derived recombinant inbred lines (RILs) from the two populations 'Minsoy' x 'Archer' and 'Noir 1' x Archer. The lines were evaluated in three environments for several traits, including seed yield. The RILs were characterized for more than 400 molecular markers. Quantitative trait loci for seed yield were identified in association with Satt277 (6, 107.6 cM), B172_2 (unknown), Satt561 (16, 71.4 cM), and Satt507 (1, 64.5 cM). The beneficial alleles associated with Satt277 and B172_2 were derived from Noir 1 and those of Satt561 and Satt507 from Archer. The authors concluded that the beneficial alleles from Archer were likely already common in northern germplasm but not in southern germplasm.

Reyna and Sneller (2001) reported the results of introgressing three seed yield QTL identified in the cultivar Archer by Orf et al. (1999b) into southern germplasm. To test these QTL in southern germplasm, near isogenic line (NIL) populations were developed from the

crosses of Archer x ‘Asgrow A5403’ and Archer x ‘Pioneer 9641’. The NIL populations were developed from $F_6$ plants that were heterozygous for the markers Satt144 (13, 102.1 cM), Satt002 (1, 64.5 cM), and Sct_33/SoyHSP176 (unknown). $F_{7:8}$ lines homozygous for either the Archer or southern alleles were then selected to form the populations. The families were yield tested at two locations with two replications in 1998 and two locations with three replications in 1999. The seed yield data indicated the alleles from Archer did not contribute to seed yield in combination with southern germplasm. It was hypothesized that the Archer alleles were superior to the alleles of the other northern parent in the original study from Orf et al. (1999b), but may not be superior to the southern alleles in the southern environment. The authors commented that it may be difficult to successfully exploit beneficial alleles for complex traits in genetic backgrounds that are different than where they were originally mapped.

A study from Yuan et al. (2002) identified QTL for seed yield in a population of 100 RILs from the cross ‘Essex’ x ‘Forrest’ and a population of 94 RILs from the cross ‘Flyer’ x ‘Hartwig’. The Essex x Forrest RILs were evaluated in two environments each in 1997 and 1998. The Flyer x Hartwig RILs were evaluated in two environments each in 1998 and 1999. A total of 135 polymorphic SSR markers were used to screen the Essex x Forrest RILs. Nine polymorphic simple sequence repeat (SSR) markers were used to screen the Flyer x Hartwig RILs. Markers Satt337 (9, 47.4 cM) (high yield allele from Essex), Satt167 (9, 45.7 cM), which is linked to Satt337 (high yield allele from Essex) and Satt294 (4, 78.7 cM) (high yield allele from Forrest) were found to be significantly associated with yield in the Essex x Forrest population. Two markers were significantly associated with seed yield in the Flyer x Hartwig RILs. These markers are Satt337 (9, 47.4 cM) (high yield allele from Flyer), and Satt539 (9, 2.8 cM) (high

yield allele from Hartwig). The seed yield QTL that mapped to Satt337 is common to both of the populations and is identical by descent in Flyer from Essex.

More recent studies of seed yield QTL have concentrated on the detection of positive QTL alleles from both *Glycine max* and *Glycine soja* plant introductions. Plant introductions often carry undesirable alleles that can be detrimental to breeding programs. However, exotic germplasm may contribute beneficial alleles that have been lost or were never present in the North American germplasm pool. An example of where exotic germplasm has played an important role in breeding programs has been in providing new disease resistance alleles, such as those that contribute to soybean cyst nematode resistance (Concibido et al., 1996).

Concibido et al. (2003) published a study involving the identification of a beneficial seed yield allele from *G. soja* PI 407305. Alleles beneficial to seed yield were identified by growing $BC_2F_1$ lines in three locations in 1996 and seven locations in 1997. Lines carrying the allele from PI 407305 at AFLP locus U3944 showed an average 9.4% seed yield increase across years and locations. $BC_2$ lines of Asgrow germplasm were then developed in order to test the PI 407305 allele in other backgrounds. The following lines were used as recurrent parents: AG4501, AG2401, QP4459, QR4459, QR4544, and QR4604. Three of the populations showed a positive yield response: AG4501 ($P < 0.0006$), AG2401 ($P < 0.1057$), and QP4459 ($P < 0.0119$). QR4459 ($P < 0.7148$), QR4544 ($P < 0.6541$) and QR4606 ($P < 0.5210$) each showed a negative seed yield response.

A study published in 2004 by Kabelka et al. involved the identification of seed yield QTL in a population containing exotic alleles from PI 68508 and FC 04007B. 'BSR101' was used as the elite parent in the population. One hundred and sixty seven $F_5$-derived lines were developed with the single-seed descent method. The lines were grouped into sets by maturity and evaluated

in six locations each in 2000 and 2001. A total of 145 polymorphic SSR markers were used to screen the lines for allelic profiles. A total of 15 seed yield QTL were reported. For nine of the 15 QTL, the yield increasing allele was from PI 68508 or FC 04007B. These QTL were mapped with Satt363 (6, 98.1 cM), Satt358 (10, 5.4 cM), Satt225 (5, 95.2 cM), Satt394 (18, 43.4 cM), Satt544 (9, 43.3 cM), Satt168 (14, 55.2 cM), Satt186 (17, 105.4 cM), Satt142 (12, 86.5 cM), and Satt308 (7, 130.8 cM). The seed yield increasing allele for the remaining QTL were from BSR101 and these QTL were mapped by the markers Satt383 (1, 56.6 cM), Satt191 (18, 96.6 cM), Satt387 (3, 53.3 cM), Satt339 (3, 75.9 cM), Satt547 (1, 67.8 cM), Satt440 (20, 112.7 cM). On average, the exotic alleles accounted for an average increase in seed yield of 2.9%, while the BSR101 alleles accounted for an average increase in seed yield of 3.3%.

In 2004, Wang et al. reported data from a seed yield QTL study in $BC_2F_4$-derived lines where 'IA2008' was used as the recurrent parent and *G. soja* 'PI 468916' was used as an exotic donor parent. To produce the lines for study, five random $F_{2:3}$ lines were crossed with IA2008 to produce $BC_1F_1$ plants. These were again crossed with IA2008 to obtain $BC_2F_1$ seed. Five $BC_2F_1$ plants that traced to different $F_2$ plants were inbred to $F_4$ using the single-seed descent method. Each $F_4$ plant was then threshed to form $BC_2F_4$ lines. The $BC_2F_4$ lines and the two parents of the populations were grown in tests with two replicates in Lincoln, NE and Urbana, IL in both 1999 and 2000. Each line was screened for 302 polymorphic SSR markers and QTL were mapped by composite interval mapping (CIM). Four seed yield QTL regions were reported with the CIM method: Satt137 (9, 37.0 cM), Satt134 (6, 112.8 cM), Satt575 (15, 3.3), and Satt567 (7, 33.5 cM). Each of these QTL were derived from IA2008. The authors noted that the CIM method was unable to detect significant seed yield QTL from PI 468916. This may have been due to the

lack of QTL alleles from PI 468916 that could increase the yield of IA2008 or their inability to detect such positive QTL.

A study published by Smalley et al. (2004) took a slightly different approach to the detection of seed yield QTL. The authors identified seed yield QTL by studying allele frequency changes for markers in three recurrent selection populations. The populations were designed as follows: population AP10 originated from 40 PI parents, AP12 originated with 40 elite and 40 PI parents, and AP14 was formed with 40 elite parents. All parents were selected based upon their seed yield performance in maturity groups I to IV. Recurrent selection for seed yield was performed among $F_4$ lines for four cycles. The cycle four populations and each set of founders were screened with 184 SSR markers that were polymorphic among the founders. Alleles with no selection pressure applied to them should have the same frequency in both the cycle four lines and the founders. If the allele frequency is different in the cycle four lines compared to the founder lines, then it is hypothesized that the alleles were selected because of their beneficial influence on seed yield over time. This approach was first described by Sebastian et al. (1995) as "Breeding Bias". Smalley et al. (2004) assumed migration was not a concern due to the attention to detail when intermating lines for the next cycle. In addition, the self-pollinated nature of soybean helps reduce undesirable out-crossing. The effect of mutation was also considered negligible because there were only four cycles of recurrent selection. The authors did have concerns about genetic drift and to account for drift, they devised a simulation to create a probability density function (PDF). The simulation was repeated 10,000 times to provide an estimated PDF for allele frequencies of cycle four lines under the null hypothesis of no selection. A *P*-value of 0.05 was used as the significance level to declare that allele changes were not due to drift over time, but were due to selection. With this methodology, the authors identified a

number of seed yield QTL in their populations. Among the three populations, the authors identified a total of 60 SSR markers that significantly deviated from the expected ratio. Of the deviated markers, 15 were unique to the PI parents, 9 were unique to the elite parents, and 36 were common between both the PI and elite parents. This list of significantly deviated markers is too extensive to fully give here. However, nine of the deviated markers map to regions where yield QTL were previously mapped. The large number of identified QTL in this study is likely due to the large number of parents used to form the populations. The large number of parents would have contributed more alleles that are segregating and can be detected.

In 2007, Guzman et al. reported mapping exotic seed yield QTL alleles in three backcross populations. In the development of the three backcross populations, lines were developed and tested for seed yield and those lines with the greatest seed yield were crossed back to the recurrent parent. $BC_3F_2$–derived lines were developed for study from a population developed using PI 68658 as a donor parent and 'Lawrence' as a recurrent parent. In addition, $BC_2F_5$–derived lines were also evaluated in the study from a population developed using PI 407720 as a donor parent and 'Beeson 80' as a recurrent parent. A third population used a selected line from the cross PI 391583 and PI 297544 as the donor parent and 'Kenwood' as the recurrent parent. Lines in the yield tests were $BC_1F_5$ derived. The Beeson 80 and Kenwood populations were evaluated at three locations in 2003 and four locations in 2004. The Lawrence population was evaluated at four locations in 2003 and three locations in 2004. Lines from each population were evaluated with polymorphic SSR markers: 45 in the Beeson 80 population, 84 in the Kenwood population, and 30 in the Lawrence population. A total of 13 QTL significant for seed yield were detected: three in the Beeson 80 population and five each in the other two. Quantitative trait loci for seed yield were mapped with the markers Satt046 (9, 45.6cM), Satt215 (16, 44.8 cM), and

Satt547 (16, 67.7 cM) in the Beeson 80 population. Quantitative trait loci for seed yield were mapped with Satt399 (4, 76.2 cM), Satt557 (6, 112.2 cM), Satt405 (16, 11.7 cM), Satt313 (19, 34.5 cM), and Satt477 (10, 82.1 cM) in the Kenwood population. In the Lawrence population, QTL were mapped with Satt300 (5, 30.9 cM), Satt474 (14, 75.3 cM), Satt640 (6, 30.5 cM), Satt622 (16, 42.4 cM), and Satt445 (10, 20.4 cM). The alleles beneficial to seed yield were derived from the PI parent in eight of the 13 QTL identified. The authors noted that all of these QTL mapped to regions that seed yield QTL were previously identified.

Most of the published yield QTL mapping studies are from populations segregating for exotic alleles. This is in contrast to initial studies focused on identifying the QTL in elite populations. One major drawback of mapping QTL in elite populations is the limited allelic diversity available in the modern elite germplasm pool (Concibido et al., 2003; Carter et al., 2004; Kabelka et al., 2004; Smalley et al., 2004; Guzman et al., 2007) resulting in many regions of the genome being fixed among elite parents. This reduces the number of polymorphisms which, in turn, reduces the ability to detect allelic affects. Studies were more successful in identifying seed yield QTL in populations segregating for exotic alleles. With the exception of studies publish by Reyna and Sneller (2001) and Concibido et al., (2003), little work has been published on confirming exotic alleles beneficial for seed yield among populations.

The primary source of germplasm in modern breeding programs of North America are elite, commercial cultivars (Kabelka et al., 2004). Limited progress has been made in improving elite populations through the use of mapped QTL controlling seed yield (Reyna and Sneller, 2001; Sebastian et al., 2010). Previous work in elite populations showed that seed yield QTL can be detected, but it was difficult to confirm these QTL in other populations (Reyna and Sneller, 2001). With this in mind, Sebastian et al. (2010) describes a method for implementing the use of

seed yield QTL within elite populations. The authors used a method known as Context-Specific Marker Assisted Selection, which is designed to detect QTL alleles beneficial to seed yield within a set of highly inbred $F_{7:8}$ lines that were derived from elite cultivars. The $F_{7:8}$ lines are derived from an elite cultivar and grown in plant row yield trials to collect seed yield data. The $F_{7:8}$ lines were screened with SSR markers at loci that were polymorphic in the parents of the original population. *F*-tests were then performed to determine which loci were significant for seed yield. The allele with the greatest seed yield mean at each significant locus was considered to be beneficial to seed yield. Lines with the most alleles beneficial to seed yield were then selected to resynthesize a new version of the original elite cultivar with a greater seed yield. In their study, the seed yields of the reselected lines were greater than the original five elite cultivars by an average of 3.1%. While all the resynthesized cultivars had a higher seed yield mean than the original cultivar, only three of the five differences were significant at the 0.05 probability level.

The purpose of our study was to determine whether the methodology explained by Sebastian et al. (2010) could be used in addition to phenotypic selection for seed yield in plant row yield trials of lines developed from biparental crosses. While Sebastian et al. (2010) made selections within highly inbred cultivars that were segregating for only a small proportion of their genomes, in this study the yield QTL will be mapped and selections will be made among $F_4$-derived lines in populations developed from biparental crosses.

Plant row yield trials were grown in 2008. Selections were made from these and grown in an eight location confirmation study in 2009. The data from the confirmation study indicated that we were able to use genotypic selection to mitigate Type II errors in the plant row yield trial selections.

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# MARKER ASSISTED SELECTION FOR SEED YIELD IN SOYBEAN [*Glycine max* (L.) Merr.] PLANT ROW YIELD TRIALS

## INTRODUCTION

Plant row yield trials (PRYTs) are commonly used by soybean breeders to select lines superior for seed yield early in the product development cycle (Hegstad et al., 1999; Streit et al., 2001). Plant row yield trials are typically grown as single replicate experiments with a relatively small plot size (Hegstad et al., 1999; Streit et al., 2001; Orf et al., 2004). The lack of replicates and small plot size is due to the limited number of seed that can be obtained from a soybean plant.

Unfortunately, the lack of multiple replicates not only results in large errors in the estimates of seed yield but also the confounding of genotype and environment. This can limit the predictability of seed yield data obtained from the experiment and thus reduce the effectiveness of selection from such experiments. This may result in the genotypes with the best potential seed yield not being selected due to poor performance in the PRYT.

### Usefulness of Quantitative Trait Loci for Predicting Seed Yield

Several studies identifying quantitative trait loci (QTL) controlling seed yield in soybean have been published. Many involve the identification of seed yield QTL from plant introductions (Concibido et al., 2003; Kabelka et al., 2004; Smalley et al., 2004; Wang et al., 2004; Guzman et al., 2007). Concibido et al., (2003) reported identifying and introgressing an exotic allele into six elite cultivars, three of which resulted in an increase in seed yield ($P<0.0006$, $P<0.1057$, and $P<0.0119$). A third resulted in an increase in seed yield, but was not statistically significant. Guzman, et al., (2007) reported QTLs from exotic germplasm in

previously identified regions. This indicates exotic germplasm may contribute alleles beneficial to seed yield in some elite backgrounds.

Unfortunately, confirmation of seed yield QTL among elite populations has been difficult (Reyna, et al., 2001; Sebastian, et al., 2010). The apparent lack of major QTLs for seed yield among elite soybean populations may be due to the limited number of founders of modern elite germplasm. It has been reported that 26 ancestors account for nearly 90% of the alleles found in the modern soybean germplasm pool (Carter, et al., 2004). This may have resulted in the fixation of any major seed yield QTL during early cycles of plant breeding (Bernardo, 2008).

## Context Specific Marker Assisted Selection

A method for detecting and leveraging seed yield QTL that are context specific in elite populations was introduced by Sebsatian, et al. (2010). With context specific QTL, it is expected that the QTL will be detected in some populations and not others. One possible benefit of this method may be the ability to increase the effectiveness of selection in PRYTs by including beneficial allelic combinations, in addition to seed yield phenotype, as selection criteria.

Sebastian et al. (2010) describes a method to reselect lines with an allelic combination beneficial for seed yield from highly inbred $F_7$ lines. Their study involved deriving sub-lines from nine elite cultivars and determining seed yield of the sub-lines in PRYTs. Simple sequence repeat markers were analyzed to determine alleles beneficial to seed yield. Sub-lines were then selected that had an allelic profile that was predicted to have a greater seed yield than the mother line. Seed yield gains up to 5.8% were achieved with this procedure.

## Study Objective

A marker assisted selection (MAS) program for seed yield would be of great benefit to plant breeders. If realized, it would increase the efficiency of breeding programs by allowing the breeder to select lines with the greatest genetic potential for seed yield. This would increase the heritability of the trait by decreasing the number of lines with limited genetic potential in a breeding program.

The purpose of my study was to determine whether the methodology described by Sebastian et al. (2010) can be used to increase the effectiveness of selection in PRYTs by allowing us to select lines superior in seed yield based upon predicted beneficial allelic combinations in addition to seed yield phenotype.

## MATERIALS AND METHODS

### Population Development

Two single cross populations were developed in 2006 by Pioneer Hi-Bred International, Inc. (Pioneer) by crossing pairs of elite Pioneer cultivars possessing desirable agronomic characteristics. Population 34 was developed at Dallas Center, IA and population 35 was developed at Ivesdale, IL. All parents were of Maturity Group III.

The $F_1$ seeds of the single crosses were planted in November 2006 at the Pioneer nursery in Salinas, Puerto Rico. The $F_1$ plants were confirmed as hybrids for Population 34 by flower color and those of Population 35 by genetic marker analysis. The $F_2$ seeds of each population were advanced using the bulk method and planted in February 2007 at the Pioneer nursery in Salinas. The $F_3$ seed of each population was advanced using the bulk method and planted in May 2007 at the Pioneer Research Center in Ivesdale, IL. Each plant was harvested individually but not threshed. This resulted in harvesting 531 $F_3$ plants in Population 34 and 654 $F_3$ plants in Population 35. This was not considered to be an adequate number of plants to detect seed yield QTL with small effects in PRYTs. To increase the number of plants for PRYTs, one three seeded pod was collected from each plant and used to form a resynthesized bulk of each population. The $F_4$ seeds were planted in December 2007 at the Pioneer nursery in Pergamino, Argentina. Leaf tissue was collected from each $F_4$ plant for QTL marker analysis. The $F_4$ plants of each population were harvested and threshed individually.

### Plant Row Yield Trials

In the spring of 2008, the $F_{4:5}$ lines with sufficient seed from each population were divided and planted in PRYTs at one of three diverse locations for seed yield and maturity

classification. Each population was grown in a separate experiment and the lines within each population were divided into experiments of 63 entries for Population 34 and 69 entries for Population 35. Each experiment was planted as an augmented design. The two parents of each population were replicated three times within each experiment to form an error estimate for each experiment. The seed from each plant in Argentina was returned to Ivesdale, IL where they were packaged for planting in the PRYT experiments. Each population was divided into three equal sets for the three locations to be planted. As the experiments were packaged, lines with insufficient seed were not included for planting. This resulted in differing numbers of lines for each location. For Population 34, 486 lines were planted at Hedrick, IA, 384 lines were planted at Ivesdale, IL, and 502 lines were planted at Napoleon, OH. For Population 35, 552 lines were planted at Hedrick, IA, 506 lines were planted at Ivesdale, IL, and 552 lines were planted at Napoleon, OH. Hedrick, IA was planted on May 19, Ivesdale, IL was planted on June 14, and Napoleon, OH was planted on May 22. Each plot was a single row 1.5 m long with a row spacing of 0.9 m. The seeding rate was 30 seeds $m^{-1}$ of row.

During the growing season, the Napoleon, OH location experienced flooding. As a result, the lines planted there were harvested but the data were not included in any seed yield analysis. Maturity was recorded as the date when 95% of the pods in each plot reached mature color (R8) (Fehr and Caviness, 1977). Lines were harvested individually with a self propelled combine. Seed yield data were collected and expressed on a 13% moisture basis. Least squares (LS) means for seed yield were calculated using the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). Line was considered to be a fixed effect. Days from planting to maturity was used a covariate in the analysis.

## Single Nucleotide Polymorphism Marker Analysis

During the summer of 2008, marker analysis was performed at the Pioneer Research Center at Dallas Center, IA on the $F_4$ leaf tissue samples obtained from each plant of both populations grown in Argentina. This analysis was done to identify markers associated with seed yield. Markers used in this analysis were selected by first testing the parents of the populations with 982 Pioneer single nucleotide polymorphism (SNP) markers. All markers identified as polymorphic in this screen were then used to test the lines in the populations. This resulted in the selection of 53 polymorphic markers for Population 34 and 26 polymorphic markers for Population 35. Assuming that each marker is able to detect a QTL within 15 cM, it is estimated that these markers provided 45% detection coverage of the genome for Population 34 and 21% detection coverage in Population 35. The marker analyses were completed using a 5μL reaction format TaqMan SNP marker detection assay (Applied Biosystems, 2004).

Significance of each locus for seed yield was determined with *F*-tests using the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). The analysis was performed as described by Sebastian et al. (2010) except that days to maturity was used a covariate in the analysis. Associations between markers and seed yield were declared significant using a *P*-value of 0.25. This threshold was chosen because previous reports suggested that a relatively low stringency should be used in identifying loci significant for seed yield (Bernardo, 2008). Allelic effects were determined for each significant locus with the LSMEANS option of the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). For significant loci, the allele in the homozygous state with the greater mean was considered to be the allele most beneficial to seed yield. The allele in the homozygous state with the lesser mean was considered to be the allele that was either neutral or deleterious to

seed yield. Lines homozygous for the beneficial allele at all or most of the significant loci are considered to have the most desirable genotype for seed yield.

In order to identify whether our QTL were in regions where yield QTL were previously identified, we estimated the positions of our QTL on the soybean map from Choi et al (2007). This was done with markers that have known positions on both the Pioneer and consensus maps. The positions of the Pioneer QTL on the soybean consensus map were then estimated by using the FORECAST function in Microsoft Office Excel 2007 (Microsoft Corporation, 2006).

## Selection of Lines for Further Study

Five groups of 11 lines each were formed from each population for further study. The five groups formed were phenotypic high, phenotypic low, genotypic high, genotypic low, and random. The phenotypic high group is composed of lines that had the greatest seed yield in the PRYT. The phenotypic low group is composed of lines with the least seed yield in the PRYT. The genotypic high group is composed of lines that were homozygous for the beneficial allele at all or most of the significant loci identified. The genotypic low group is composed of lines that were homozygous for the neutral/deleterious allele at all or most of the significant loci identified. Lines heterozygous at any significant locus were not considered for selection in either the genotypic high or low group. The random group represents lines that were selected by assigning random numbers to each line and selecting the 11 lines with the lowest numbers. Lines were allowed to reside in multiple groups. For example, a line may exist in both the phenotypic high and genotypic high groups. Although the PRYT seed yield data from Napoleon, OH were not used in the phenotypic selections, lines harvested from this environment were considered for inclusion in the genotypic high, genotypic low, and random groups. In Population 34, five of the

11 lines in the genotypic high group possessed the beneficial allele for all nine markers significant for yield. The remaining lines possessed favorable alleles for eight of the nine markers. Five of the 11 lines in the genotypic low group lacked the beneficial allele for at all nine markers. The remaining lines lacked the beneficial allele for eight of the nine markers. In Population 35, all lines of the genotypic high group possessed the beneficial allele for all significant markers and all lines of the genotypic low group lacked the beneficial allele for all markers. After forming the five groups for Population 35, five lines existed in two groups. As a result, two additional genotypic high lines were selected to fill the extra space in the experiment. This resulted in 13 lines in the genotypic high group.

The selected $F_{4:6}$ lines were sent to the Pioneer nursery in Viluco, Chile for seed increase. This was done to ensure an adequate seed supply for wide area testing in 2009 and to obtain seed from the same source environment for each line. Each line was harvested individually and returned to Ivesdale, IL where it was packaged for testing in 2009.

## Germination Testing of the Selected Genotypes

A warm germination test was performed on each of the selected $F_{4:7}$ lines by the Pioneer germination laboratory in Johnston, IA. The testing was done by growing each selected line in a randomized complete block in four replications of 50 seeds each as described by Meis et al. (2003) except that the 2008 editions of Rules for Testing Seeds (AOSA, 2008) and 2006 edition of the Seedling Evaluation Handbook (AOSA, 2006) were used as references. Germination percentage was determined by counting the number of seeds that germinated, dividing by the 50 seeds tested, and multiplying by 100.

Data were analyzed using the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). Groups and lines nested in groups were considered fixed effects. Replication was considered a random effect. *F*-tests were used to evaluate the significance of fixed effects. The LSMEANS option of the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008) was used to calculate the mean for each group. Single degree of freedom linear contrasts were used to determine significant differences between the genotypic high group and the other groups for each trait.

## Field Testing of Selected Genotypes

The selected $F_{4:7}$ lines from each population were grown in separate experiments at eight diverse locations in 2009. Each experiment was a randomized complete block design in a 5 x 12 row-column configuration. The row-column configurations were obtained from the OPTEX procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). Elite checks were used to bring the number of entries in each experiment to 60. Each location was grown as a single replication. Population 34 was grown at locations near Metamora, IL; Gilman, IL; Pesotum, IL; Anna, OH; Napoleon, OH; Atlantic, IA; Abington, IA; and Washington, IA. Metamora, IL, was planted on May 30; Gilman, IL was planted on May 27; Pesotum, IL, was planted on June 1; Anna, OH was planted on May 22; Napoleon, OH, was planted on May 25; Atlantic, IA, was planted on May 20; Abington, IA, was planted on June 1; and Washington, IA was planted on May 23. Population 35 was grown at the same locations as Population 34 except that Emery, IL, which was planted on June 7, replaced Gilman, IL. The plots were two rows 3.7 m in length spaced 0.76 m apart within the plot and between adjacent plots. The seeding rate was 30 seeds $m^{-1}$ of row.

Maturity was recorded as the date when 95% of the pods in each plot reached mature color (R8) (Fehr and Caviness, 1977). Plant height was measured at maturity in centimeters from the soil surface to the terminal node. Lodging was scored at maturity using a scale of 1 (all plants erect) to 5 (all plants prostrate). The plots were harvested with a two-row self-propelled combine. The seed yield was expressed in kg $ha^{-1}$ on a 13% moisture basis. Seed size was recorded from the harvested seed and expressed as weight in grams of 100 seeds.

Data were analyzed using the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008). Groups and lines nested in groups were considered fixed effects. Environments, rows nested in environments, columns nested in environments, and the interaction between environment and group were considered random effects. *F*-tests were used to evaluate the significance of fixed effects. The LSMEANS option of the MIXED procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008) was used to calculate the mean of each trait for each group. Single degree of freedom linear contrasts were used to determine significant differences between the genotypic high group and the other groups for each trait. Phenotypic correlations among the traits measured in the study were computed based on the line means averaged across environments with the CORR procedure of the SAS statistical software package (release 9.2) (SAS Institute, 2008).

## RESULTS AND DISCUSSION

The QTL analysis of the PRYTs resulted in nine SNP markers identified as significant ($P$<0.25) in Population 34 and three SNP markers in Population 35 (Tables 1 and 2). In Population 34, two significant markers on chromosome 17 (77.2 cM and 77.7 cM) and two on chromosome 18 (102.1 cM and 103.5 cM) are closely linked and likely map the same QTL. In addition, the two significant markers on chromosome 16 are within 21.6 cM of each other and may also map the same QTL. Therefore, we likely mapped six or seven unique QTL in this population. For Population 35, the location of the two significant SNP markers on chromosome 16 are in close proximity (42.8 cM and 49.4 cM). Therefore, we likely mapped two unique QTL controlling seed yield in this population. The frequency distributions of seed yield for lines homozygous for either the paternal or maternal parent allele for the significant QTL show bimodal distributions in Population 34 (Figures 1-9). The paternal alleles for the significant QTL in Population 35 show bimodal distributions (Figures 10-13) but only QTL S14 shows a bimodal distribution of the maternal allele (Figure 10). These bimodal peaks are due to the two environments in the study. None of the QTL were significant for a QTL by location interaction at the 0.05 significance level.

QTL significant for seed yield were identified in each population in regions that had been previously associated with seed yield. In Population 34, S39 and S40 on chromosome 16 map within 8.3 cM and 6.9 cM, respectively, of the marker G815_1, which Specht et al. (2001) used to map a seed yield QTL. S39 maps to within 2.6 cM of Satt406 that Sebastian et al. (2010) used to map a seed yield QTL. In addition, a seed yield QTL was identified by Cregan et al. (1999) with Satt191 on chromosome 18 and this marker maps to within 9.8 cM of marker S47 and 10.6 cM of marker S46, which we used to map a seed yield QTL in Population 34. A seed yield QTL

was mapped in Population 35 with the marker S14 and this maps 9.4 cM from Satt339, which was used to map a seed yield QTL by Kabelka et al. (2004).

There were significant ($P$<0.01) seed yield differences among the groups of selected lines in both populations based on the 2009 seed yield tests (Table 3). In both populations, the phenotypic high group had the greatest average seed yield followed by the genotypic high group. The difference between the phenotypic high and genotypic high groups was significant ($P$<0.05) for Population 35 but not for Population 34 (Table 4). In Population 35, the phenotypic high group mean was 90 kg/ha$^{-1}$ greater in seed yield than the mean of the genotypic high group (Table 3). The genotypic high group in Population 34 was not significantly different from the random group which is at least partially the result of the line with the highest seed yield in the confirmation study of Population 34 being a random selection (Tables 4 and 5). The genotypic high group in Population 35 had significantly ($P$<0.01) greater seed yield than the random group (Table 4). The line with the greatest seed yield in the 2009 test of Population 35 was a line in the genotypic high group (Table 5). This indicates that selection based on genotype alone was successful in identifying lines with superior seed yield in this population.

Single degree of freedom contrasts showed the genotypic high group in both populations was significantly ($P$<0.01) greater in seed yield than both the phenotypic low and genotypic low groups (Table 4). There was a difference of 242 kg/ha$^{-1}$ in Population 34 and 163 kg/ha$^{-1}$ in Population 35 between the genotypic high and genotypic low groups (Table 3). This indicates we were able to induce a seed yield shift with very few QTL in each population. Seed yield was significantly ($P$<0.01) correlated with seed size and height in both populations and with maturity, emergence and lodging in Population 35 (Tables 6 and 7). Correlation of seed yield between 2008 and 2009 for all lines was significant ($P$<0.05) only in population 35, which had a

coefficient of 0.28, indicating the PRYT seed yield data of 2008 had a low predictive value of seed yield in 2009.

There were significant ($P<0.01$) differences among the groups for maturity in both populations in the 2009 tests (Table 3). Population 34 shows the largest differences with the genotypic high group being the latest in maturity at 2 days later than the random group (Table 3). However, the correlation between maturity and seed yield in Population 34 was not significant (Table 6). The maturity differences among the groups in Population 35 are less pronounced with the phenotypic high group having the latest maturity and the genotypic high group having a maturity equal to the random group (Table 3). Analysis of data from the PRYTs indicated that none of the markers associated with seed yield were significant for maturity in 2008. Maturity was significantly ($P<0.01$) correlated with seed size, height, and lodging in both populations and with seed yield and emergence in Population 35 (Tables 6 and 7).

There were significant ($P<0.01$) differences among the groups of Population 34 for lodging (Table 3). Although statistically significant, the differences in lodging among the groups have little practical value. There was no significant difference among groups in Population 35 for lodging (Table 3). Lodging was significantly ($P<0.01$) correlated with maturity and height in both populations and with seed yield and seed size in Population 35 (Tables 6 and 7).

There were significant ($P<0.01$) differences among the groups of both populations for height (Table 3). The mean heights of the phenotypic low and genotypic low groups were shorter than the other three groups in both populations (Table 3). The Genotypic High group was significantly ($P<0.01$) greater in height than the Random group with a 6 cm difference in Population 34 (Tables 3 and 4). The Genotypic High group was 1 cm greater in height than the Phenotypic High group in Population 35, but this difference was not significant at the 0.05 level

(Tables 3 and 4). The genotypic high group in Population 35 was not significantly different in height when compared to the Phenotypic High and Random groups (Table 4). Height was significantly ($P$<0.01) correlated with seed yield, maturity, and lodging in both populations and with germination in Population 35 (Tables 6 and 7). Height was negatively and significantly ($P$<0.01) correlated with seed size both populations (Tables 6 and 7).

There were significant ($P$<0.05 and $P$<0.01, respectively) differences among the groups of both populations for germination (Table 3). Even though there are significant differences among the groups, there is no clear pattern between the populations. There also are no clear patterns between the populations for correlations of germination with the other measured traits (Tables 6 and 7). There are significant differences ($P$<0.01) among the groups in Population 34 for seed size but not for Population 35 (Table 5). The means of the groups are very similar indicating little meaningful difference among the groups. Seed size was significantly ($P$<0.01) correlated with seed yield, and height in both populations and with lodging in Population 35 (Tables 6 and 7). Seed size was negatively and significantly ($P$<0.01) correlated with maturity in both populations (Tables 6 and 7).

The fact that the phenotypic high group had a greater mean seed yield in both populations indicates that we were unable to account for all the components of seed yield in these populations with the QTL identified. This is likely either the result of our inability to detect all loci controlling seed yield or a QTL by environment effect where the identified QTL were not as important to seed yield in the 2009 environments as in 2008. Detecting seed yield QTL is especially difficult with non-replicated PRYT tests. More QTL controlling seed yield could have potentially been detected with a lower stringency level in our QTL analysis of seed yield data from PRYTs. Bernardo (2008) recommended using alpha levels from 0.20 to 0.40 when

selecting for QTL involved in complex traits because highly stringent significance levels may lead to an unrealistic expectation of QTL effects. An alpha level of 0.25 was used in this study. Using an alpha level of 0.40 would have added seven more loci in Population 34 and an additional three loci in Population 35. At this low stringency level, some of these additional QTL will likely be false positives. However, according to Bernardo (2008), the benefits of identifying additional QTL with minor effects is greater than the drawbacks associated with a higher incidence of false positives. Identifying plants that carry the positive alleles for all of these QTL will also be difficult. In Population 34, if the six unique QTL originally detected were added to the seven additional QTL, only one out of every 46,482 plants in a single seed descent $F_4$ population would carry all 13 positive alleles in a beneficial homozygous state. A marker based recurrent selection program would be needed to combine all of these positive alleles into a single plant. As with any population, the breeder must choose between testing more plants of fewer populations or fewer plants of more populations.

Despite extremely limited genomic coverage, the methods implemented in this study resulted in selection of superior lines based upon genotype alone for seed yield. In both populations, the genotypic high group had a greater seed yield mean than the random group. In Population 34, the genotypic high group was not statistically different from the phenotypic high group at the 0.05 significance level. In Population 35, the genotypic high group was within 90 $kg/ha^{-1}$ of the phenotypic high group. Two of the top ten lines for seed yield in 2009 were selected based on genotype alone, including the line with the greatest seed yield in Population 35 (Table 5). It is unlikely that these lines would have been selected because of their poor seed yield phenotype in PRYTs. Knowledge of beneficial allelic combinations gives us a greater level

of information for selecting lines that may be superior. Using the methodology in this study, we increased our selection effectiveness from PRYTs by including genotype as a selection criteria.

## TABLES AND FIGURES

Table 1. Position and seed yield means of selected loci from Population 34 grown in plant row yield trials in 2008.

| Marker | Chromosome | cM | Locus *P*-value | Beneficial Allele Mean (kg ha$^{-1}$) | Neutral/Deleterious Allele Mean (kg ha$^{-1}$) |
|---|---|---|---|---|---|
| S1 | Unmapped† | | 0.1540 | 3265 | 3239 |
| S39 | 16 | 77.4 | 0.0545 | 3326 | 3171 |
| S40 | 16 | 99.0 | 0.2252 | 3272 | 3198 |
| S41 | 17 | 16.2 | 0.2220 | 3265 | 3192 |
| S42 | 17 | 77.2 | 0.0019 | 3279 | 3178 |
| S43 | 17 | 77.7 | 0.0004 | 3286 | 3171 |
| S46 | 18 | 102.1 | 0.0851 | 3292 | 3165 |
| S47 | 18 | 103.5 | 0.0955 | 3292 | 3178 |
| S48 | 19 | 13.7 | 0.1622 | 3272 | 3192 |

†Chromosome and position based on Pioneer soybean map.

Table 2. Position and seed yield means of selected loci from Population 35 grown in plan row yield trials in 2008.

| Marker | Chromosome | cM | Locus *P*-value | Beneficial Allele Mean (kg ha$^{-1}$) | Neutral/Deleterious Allele Mean (kg ha$^{-1}$) |
|---|---|---|---|---|---|
| S14 | 3† | 92.8 | 0.2412 | 3328 | 3295 |
| S69 | 16 | 42.9 | 0.0115 | 3343 | 3281 |
| S70 | 16 | 49.5 | 0.0092 | 3336 | 3271 |

†Chromosome and position based on Pioneer soybean map.

Table 3. Agronomic performance of the five groups studied from two populations grown at eight diverse locations in 2009.

| | | Population | | | |
|---|---|---|---|---|---|
| | | 34 | | 35 | |
| Trait | Group | Mean | Range | Mean | Range |
| Seed Yield | genotypic high | 4001** | 3801 - 4181 | 4150** | 4046 – 4388 |
| (kg $ha^{-1}$) | phenotypic high | 4029 | 3895 - 4257 | 4240 | 4132 – 4363 |
| | genotypic low | 3759 | 3236 - 4052** | 3987 | 3878 – 4228* |
| | phenotypic low | 3326 | 3034 - 3559** | 3887 | 3423 – 4302** |
| | random | 3944 | 3218 - 4285** | 4013 | 3635 – 4246** |
| Maturity | genotypic high | 130** | 129 - 133** | 126** | 123 - 129** |
| (d) † | phenotypic high | 129 | 125 - 132** | 127 | 123- 131** |
| | genotypic low | 127 | 125 - 128 | 125 | 124 - 128 |
| | phenotypic low | 127 | 123 - 130** | 124 | 121 - 129** |
| | random | 128 | 122 - 133** | 126 | 122 - 129** |
| Lodging | genotypic high | 2.0** | 1.0 - 2.8** | 1.5 | 1.1 – 1.9** |
| (score) ‡ | phenotypic high | 2.0 | 1.8 - 2.4 | 1.7 | 1.3 – 2.0 |
| | genotypic low | 1.6 | 1.3 – 2.0** | 1.5 | 1.2 – 1.8** |
| | phenotypic low | 1.5 | 1.3 - 2.1** | 1.5 | 1.3 – 1.8* |
| | random | 2.0 | 1.3 - 2.4** | 1.6 | 1.3 – 1.8 |

Table 3. Continued.

| | | Population | | | |
|---|---|---|---|---|---|
| | | 34 | | 35 | |
| Trait | Group | Mean | Range | Mean | Range |
| Height | genotypic high | 103** | 98 – 108** | 91** | 87 – 98** |
| (cm) | phenotypic high | 102 | 96 – 107** | 92 | 88 – 95** |
| | genotypic low | 96 | 88 – 103** | 90 | 84 – 98** |
| | phenotypic low | 93 | 87 – 102** | 87 | 83 – 94** |
| | random | 97 | 81 – 106** | 92 | 84 – 100** |
| Germination | genotypic high | 88* | 77 – 91** | 83** | 77 – 88 |
| (%) | phenotypic high | 87 | 75 – 91** | 84 | 80 – 88 |
| | genotypic low | 86 | 81 – 93** | 83 | 74 – 89** |
| | phenotypic low | 87 | 82 – 92* | 79 | 71 – 89** |
| | random | 89 | 82 – 95** | 81 | 69 – 86** |
| Seed Size | genotypic high | 17.3** | 16.2 – 18.3** | 18.1 | 16.8 – 19.2** |
| (g per 100) | phenotypic high | 17.9 | 16.2 – 18.5** | 18.3 | 17.1 – 19.6** |
| | genotypic low | 17.8 | 16.2 – 18.9** | 18.2 | 17.3 – 19.0** |
| | phenotypic low | 17.0 | 16.0 – 18.0** | 18.0 | 16.2 – 19.3** |
| | random | 18.2 | 16.7 – 20.4** | 18.1 | 16.9 – 19.1** |

*,** Differences among the means of the groups or means of the lines within each group were significant at the 0.05 and 0.01 probability levels, respectively.

† Days after planting.

‡ Lodging score = 1.0 (all plants erect) to 5.0 (all plants prostrate).

Table 4. Single degree of freedom linear contrasts of genotypic high group versus other groups.

| | Population | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | 34 | | | | 35 | | | |
| Trait | PH† | GL | PL | RA | PH | GL | PL | RA |
| Seed Yield | ns‡ | ** | ** | ns | * | ** | ** | ** |
| Maturity | ** | ** | ** | ** | ** | * | ** | ns |
| Lodging | ns | ** | ** | ns | -§ | - | - | - |
| Height | ns | ** | ** | ** | ns | ** | ** | ns |
| Germination | ns | * | ns | ns | ns | ns | ** | ns |
| Seed Size | ** | * | ns | ** | - | - | - | - |

*,** Differences among the means of the groups or means of the lines within each group were significant at the 0.05 and 0.01 probability levels, respectively.

† PH=phenotypic high, GL=genotypic low, PL=phenotypic low, RA=random.

‡ Differences were not significant at the 0.05 probability level.

§ A dash sign indicates the contrast was not performed due to lack of significance among the groups for the trait.

Table 5. Seed yield of selected lines grown in plant row yield trials (PRYTs) in 2008 and eight diverse environments in 2009.

| Population | 2009 Seed Yield Rank | Line | Group† | 2008 PRYTs (kg ha$^{-1}$)‡ | 2009 Yield Test (kg ha$^{-1}$)§ |
|---|---|---|---|---|---|
| 34 | | | | | |
| | 1 | 34-1140 | RA | 1775 | 4285¶ |
| | 2 | 34-1157 | PH | 4340 | 4257 |
| | 3 | 34-1730 | GH | 1211 | 4181 |
| | 4 | 34-0692 | GH | 2005 | 4181 |
| | 5 | 34-0679 | RA | 1444 | 4131 |
| | 6 | 34-0724 | GH/PH | 3701 | 4129 |
| | 7 | 34-0754 | PH | 3792 | 4124 |
| | 8 | 34-1340 | PH | 4698 | 4097 |
| | 9 | 34-1118 | PH | 3305 | 4073 |
| | 10 | 34-0467 | RA | 3045 | 4055 |
| | 11 | 34-0873 | GL | 2889 | 4052 |
| | 12 | 34-1029 | RA | 2562 | 4052 |
| | 13 | 34-1847 | RA | 709 | 4045 |
| | 14 | 34-1058 | GH | 2115 | 4038 |
| | 15 | 34-1716 | GL | 1340 | 4019 |
| | 16 | 34-0947 | PH | 3483 | 4018 |
| | 17 | 34-1757 | GH | 3059 | 4008 |
| | 18 | 34-1779 | RA | 2729 | 4008 |
| | 19 | 34-1046 | GH | 3147 | 3999 |
| | 20 | 34-1288 | GL | 2472 | 3979 |
| | 21 | 34-0662 | PH | 4538 | 3967 |
| | 22 | 34-1055 | GH | 2255 | 3960 |
| | 23 | 34-1333 | RA | 1171 | 3957 |
| | 24 | 34-1242 | GL | 3071 | 3953 |
| | 25 | 34-0626 | PH | 3789 | 3949 |
| | 26 | 34-1806 | GL | 2622 | 3947 |
| | 27 | 34-1627 | GH | 3457 | 3944 |
| | 28 | 34-1032 | RA | 1011 | 3926 |
| | 29 | 34-0518 | PH | 4543 | 3911 |
| | 30 | 34-1440 | PH | 4324 | 3902 |
| | 31 | 34-0761 | RA | 1779 | 3899 |

Table 5. Continued.

| Population | 2009 Seed Yield Rank | Line | Group† | 2008 PRYTs (kg ha$^{-1}$)‡ | 2009 Yield Test (kg ha$^{-1}$)§ |
|---|---|---|---|---|---|
| | 32 | 34-0506 | PH | 4569 | 3895 |
| | 33 | 34-1553 | GH | 3652 | 3895 |
| | 34 | 34-0777 | GH | 1158 | 3879 |
| | 35 | 34-1625 | RA | 3551 | 3810 |
| | 36 | 34-0414 | GH | 1773 | 3801 |
| | 37 | 34-1897 | GL | 1118 | 3775 |
| | 38 | 34-0450 | GL | 2614 | 3758 |
| | 39 | 34-0485 | GL | 3886 | 3702 |
| | 40 | 34-0503 | GL | 2991 | 3626 |
| | 41 | 34-1426 | PL | 2817 | 3559 |
| | 42 | 34-0778 | PL | 2192 | 3472 |
| | 43 | 34-1256 | PL | 1932 | 3471 |
| | 44 | 34-0378 | PL | 2400 | 3466 |
| | 45 | 34-1486 | PL | 2339 | 3425 |
| | 46 | 34-0351 | GL | 1512 | 3307 |
| | 47 | 34-1654 | PL | 2665 | 3298 |
| | 48 | 34-0538 | PL | 2406 | 3268 |
| | 49 | 34-1808 | PL | 1619 | 3252 |
| | 50 | 34-0760 | GL | 1067 | 3236 |
| | 51 | 34-1666 | RA | 3400 | 3218 |
| | 52 | 34-0405 | PL | 1896 | 3198 |
| | 53 | 34-1609 | PL | 2507 | 3138 |
| | 54 | 34-0297 | PL | 2742 | 3034 |
| 35 | | | | | |
| | 1 | 35-2455 | GH | 1658 | 4388# |
| | 2 | 35-3018 | PH | 5726 | 4371 |
| | 3 | 35-2701 | PH | 5692 | 4363 |
| | 4 | 35-2684 | PH | 6079 | 4345 |
| | 5 | 35-2972 | GH | 3999 | 4312 |
| | 6 | 35-3545 | PH | 3716 | 4311 |
| | 7 | 35-2328 | PL | 1443 | 4302 |
| | 8 | 35-2323 | PH | 3639 | 4287 |

Table 5. Continued.

| Population | 2009 Seed Yield Rank | Line | Group† | 2008 PRYTs (kg ha$^{-1}$)‡ | 2009 Yield Test (kg ha$^{-1}$)§ |
|---|---|---|---|---|---|
| | 9 | 35-2589 | RA | 1370 | 4246 |
| | 10 | 35-2808 | RA | 3461 | 4238 |
| | 11 | 35-3388 | GL | 3873 | 4228 |
| | 12 | 35-2366 | PL | 1117 | 4219 |
| | 13 | 35-2235 | PH | 4647 | 4218 |
| | 14 | 35-2485 | GL | 3091 | 4196 |
| | 15 | 35-2690 | PH | 4255 | 4184 |
| | 16 | 35-2343 | GH/RA | 1491 | 4180 |
| | 17 | 35-2152 | GH | 2989 | 4179 |
| | 18 | 35-3049 | GH | 3763 | 4162 |
| | 19 | 35-3927 | PH | 4615 | 4146 |
| | 20 | 35-3544 | PH | 3420 | 4141 |
| | 21 | 35-3993 | PH | 2721 | 4136 |
| | 22 | 35-3707 | RA | 2890 | 4134 |
| | 23 | 35-2592 | GH/PH | 3662 | 4132 |
| | 24 | 35-2213 | PL | 2460 | 4127 |
| | 25 | 35-3787 | GH | 2882 | 4125 |
| | 26 | 35-2344 | PL | 1508 | 4122 |
| | 27 | 35-2820 | GH | 3775 | 4110 |
| | 28 | 35-3190 | GH | 2815 | 4100 |
| | 29 | 35-2039 | GH | 2439 | 4096 |
| | 30 | 35-2646 | GH | 2269 | 4063 |
| | 31 | 35-3071 | GH/RA | 2781 | 4053 |
| | 32 | 35-2671 | GH | 2835 | 4046 |
| | 33 | 35-3980 | RA | 2001 | 4046 |
| | 34 | 35-1983 | GL | 2339 | 4038 |
| | 35 | 35-3731 | GL | 3733 | 3996 |
| | 36 | 35-2450 | GL | 1786 | 3995 |
| | 37 | 35-3536 | RA | 1734 | 3977 |
| | 38 | 35-3497 | RA | 2127 | 3964 |
| | 39 | 35-2184 | GL | 1232 | 3941 |
| | 40 | 35-3478 | GL | 3055 | 3932 |
| | 41 | 35-3801 | GL | 2992 | 3889 |

Table 5. Continued.

| Population | 2009 Seed Yield Rank | Line | Group† | 2008 PRYTs (kg ha$^{-1}$)‡ | 2009 Yield Test (kg ha$^{-1}$)§ |
|---|---|---|---|---|---|
| | 42 | 35-2062 | GL | 1913 | 3883 |
| | 43 | 35-2244 | GL | 2134 | 3881 |
| | 44 | 35-3253 | GL | 2353 | 3878 |
| | 45 | 35-2474 | RA | 3015 | 3861 |
| | 46 | 35-2874 | PL | 3281 | 3851 |
| | 47 | 35-2951 | PL | 3209 | 3831 |
| | 48 | 35-3726 | PL | 2815 | 3814 |
| | 49 | 35-2728 | RA | 4145 | 3812 |
| | 50 | 35-3757 | PL | 2307 | 3736 |
| | 51 | 35-2270 | PL | 2902 | 3695 |
| | 52 | 35-2845 | PL/RA | 3142 | 3635 |
| | 53 | 35-2666 | PL | 2003 | 3423 |

†GH=genotypic high, PH=phenotypic high, GL=genotypic low, PL=phenotypic low, RA=random.

‡LS Mean calculated on single replication PRYT.

§LS Mean calculated using eight replications at diverse locations.

¶ LSD (α=0.05) Of Population 34 in 2009 = 232.0 kg/ha$^{-1}$

#LSD (α=0.05) Of Population 35 in 2009 = 197.2 kg/ha$^{-1}$

Table 6. Phenotypic correlation coefficients of Population 34 grown at eight diverse locations in 2009.

| Trait | Maturity | Seed Size | Emergence | Height | Lodging (score)† |
|---|---|---|---|---|---|
| Seed Yield (kg ha$^{-1}$) | 0.06 | 0.47** | -0.02 | 0.16** | 0.10 |
| Maturity (d)‡ | | -0.28** | -0.05 | 0.35** | 0.40** |
| Seed Size (g per 100) | | | 0.01 | -0.41** | 0.00 |
| Germination (%) | | | | 0.02 | 0.02 |
| Height (cm) | | | | | 0.67** |

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

† Lodging score = 1.0 (all plants erect) to 5.0 (all plants prostrate).

‡ Days after planting.

Table 7. Phenotypic correlation coefficients of Population 35 grown at eight diverse locations in 2009.

| Trait | Maturity | Seed Size | Emergence | Height | Lodging (score)† |
|---|---|---|---|---|---|
| Seed Yield (kg ha$^{-1}$) | 0.32** | 0.38** | 0.19** | 0.34** | 0.26** |
| Maturity (d)‡ | | -0.21** | 0.14* | 0.38** | 0.46** |
| Seed Size (g per 100) | | | -0.09 | -0.40** | 0.16* |
| Germination (%) | | | | 0.17** | -0.09 |
| Height (cm) | | | | | 0.38** |

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

† Lodging score = 1.0 (all plants erect) to 5.0 (all plants prostrate).

‡Days after planting.

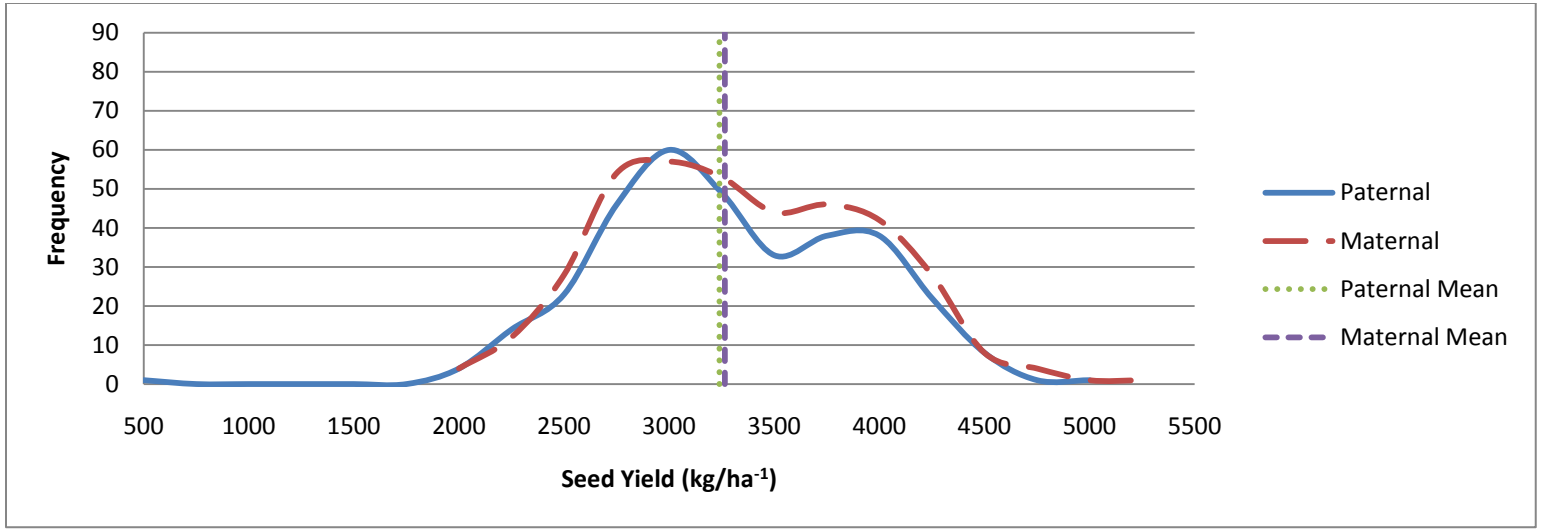


Figure 1. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S1 in Population 34 at two plant row yield trial locations in 2008.

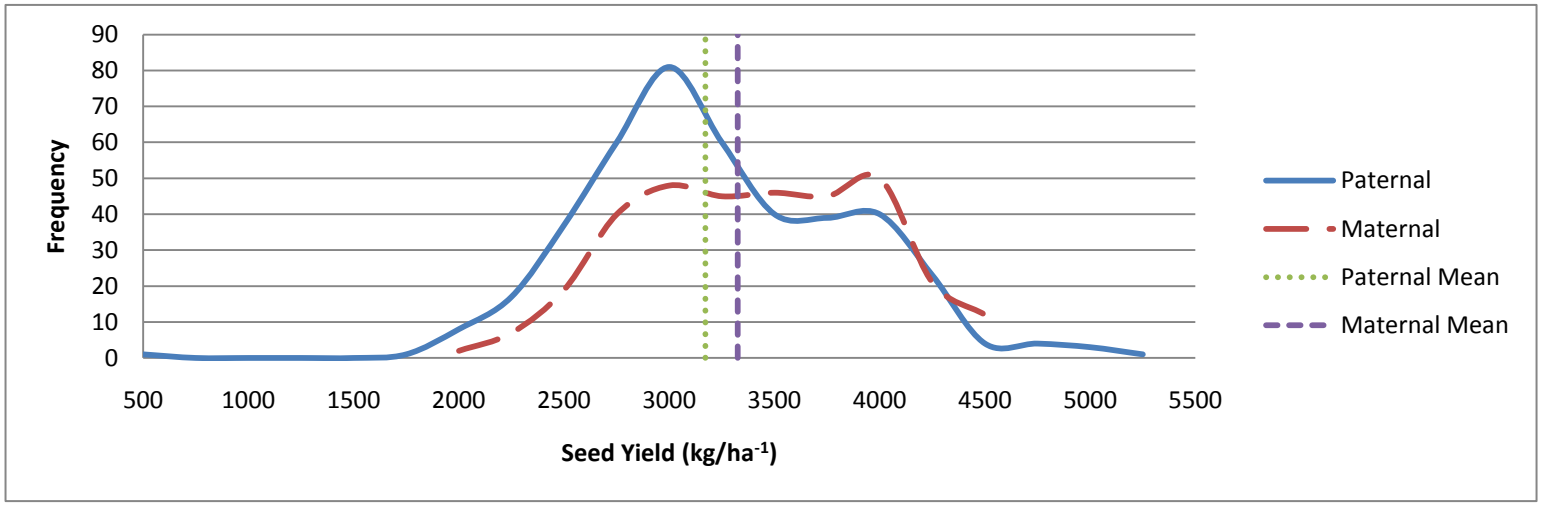


Figure 2. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S39 in Population 34 at two plant row yield trial locations in 2008.

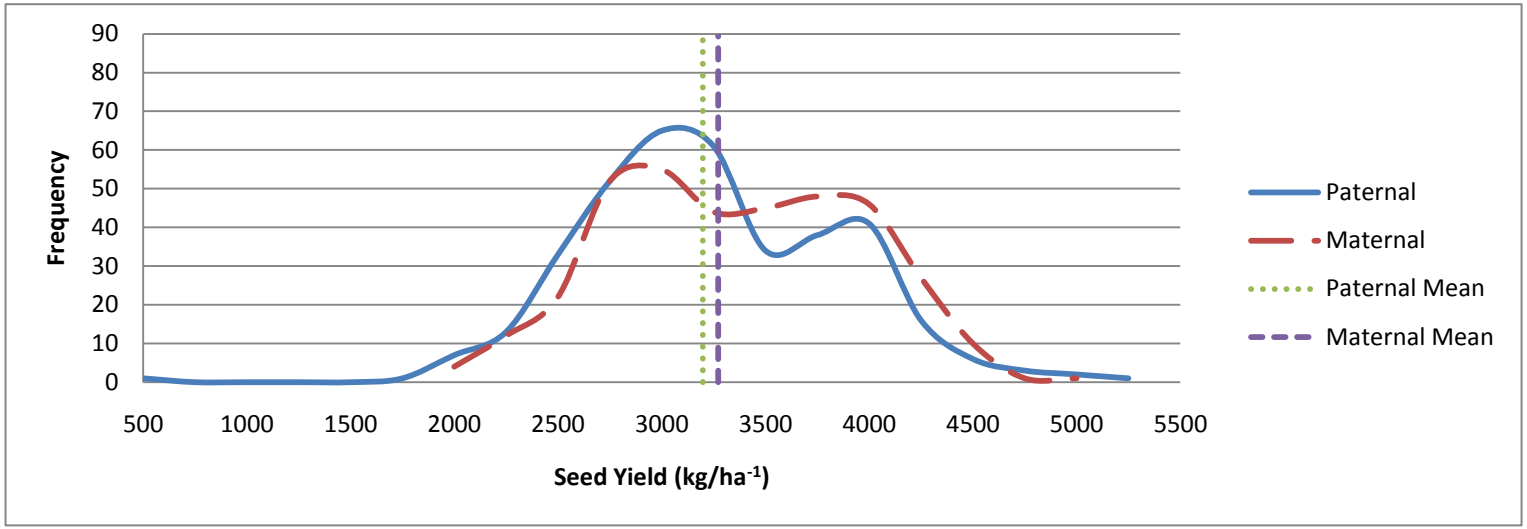


Figure 3. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S40 in Population 34 at two plant row yield trial locations in 2008.

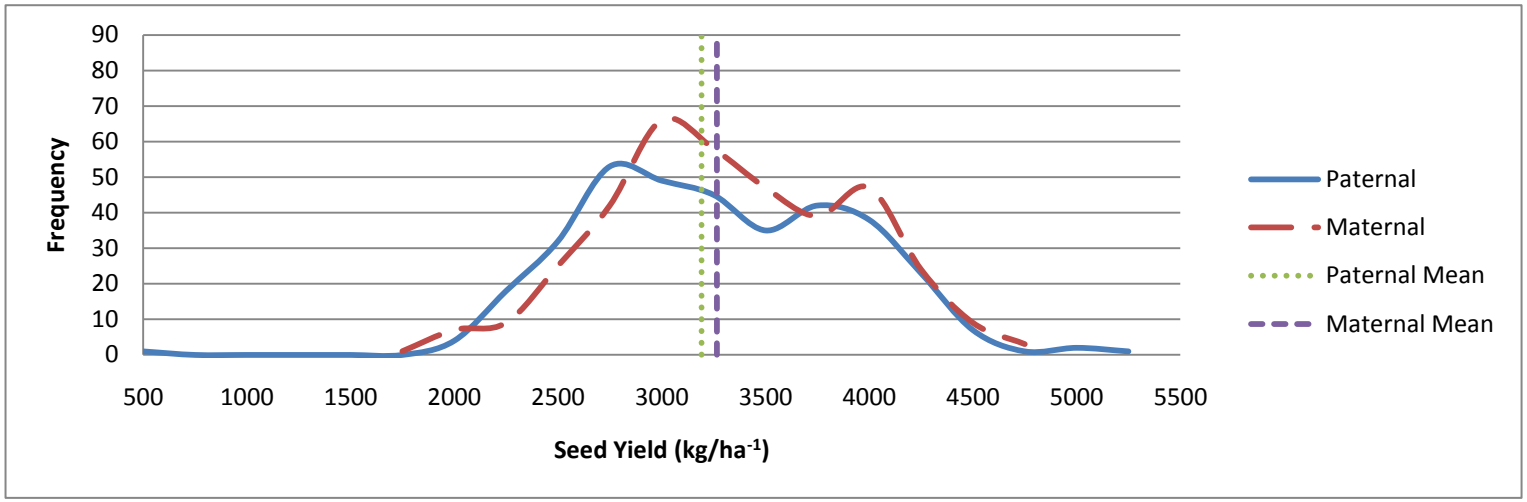


Figure 4. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S41 in Population 34 at two plant row yield trial locations in 2008.

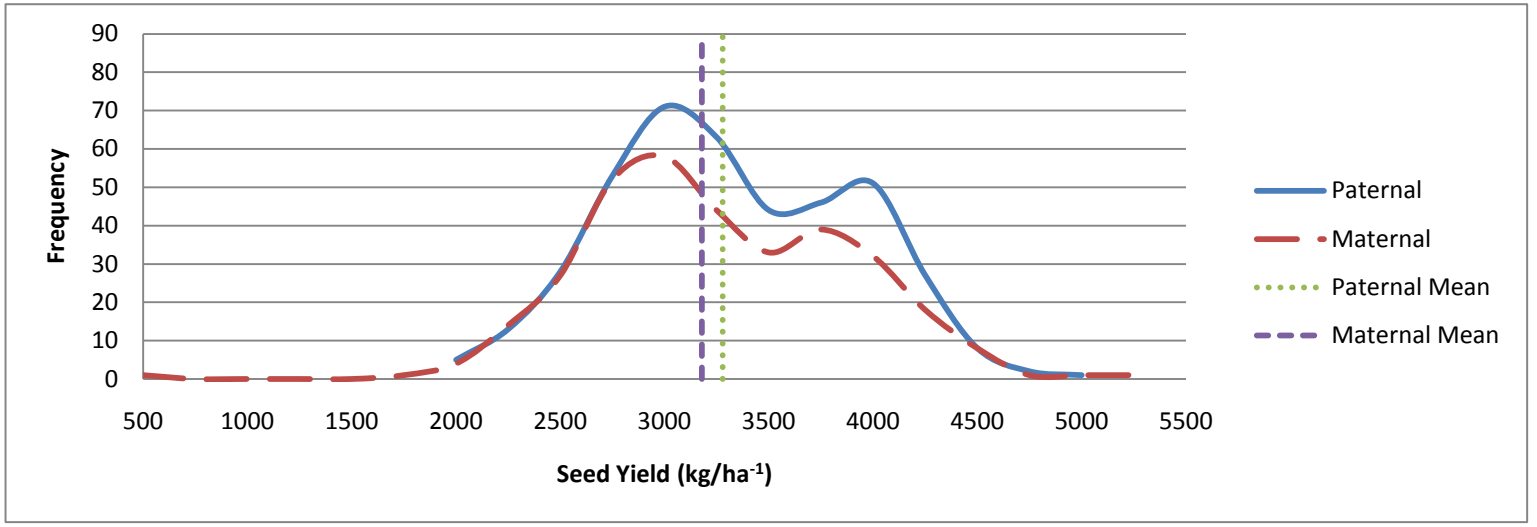


Figure 5. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S42 in Population 34 at two plant row yield trial locations in 2008.

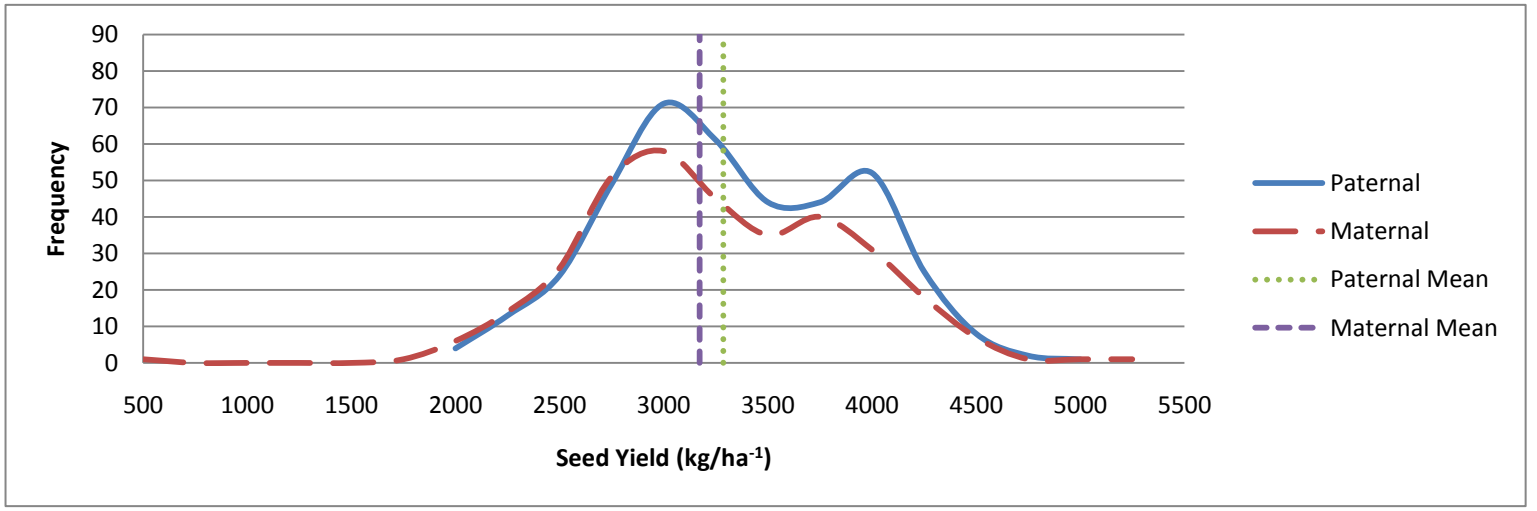


Figure 6. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S43 in Population 34 at two plant row yield trial locations in 2008.

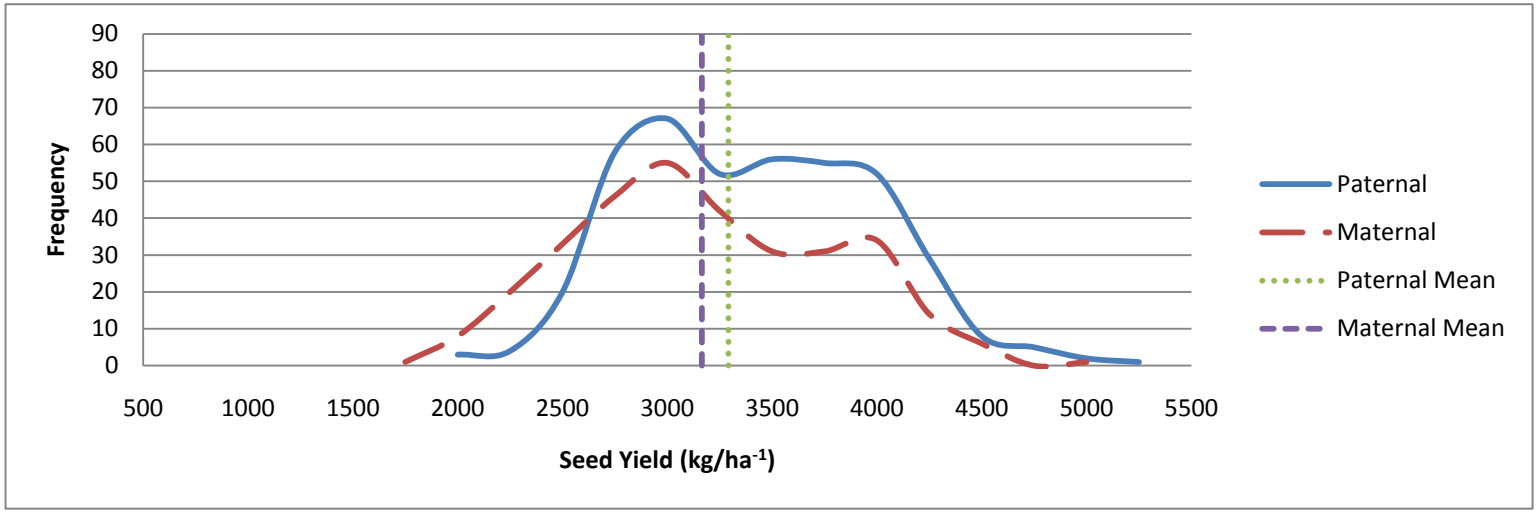


Figure 7. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S46 in Population 34 at two plant row yield trial locations in 2008.

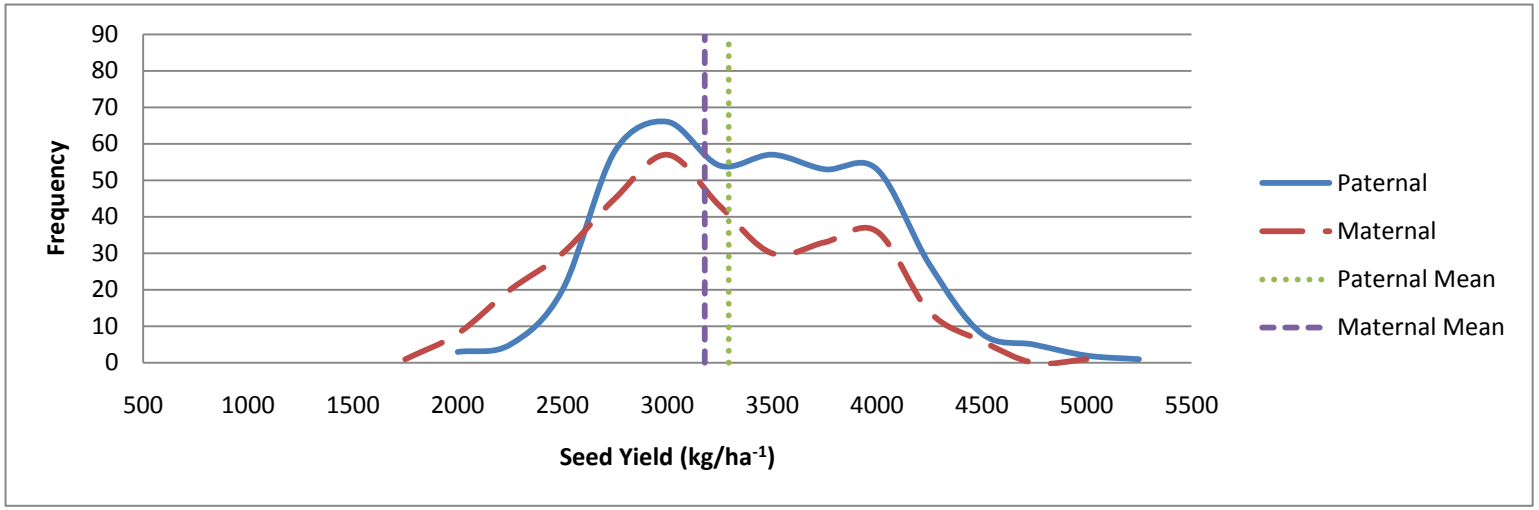


Figure 8. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S47 in Population 34 at two plant row yield trial locations in 2008.

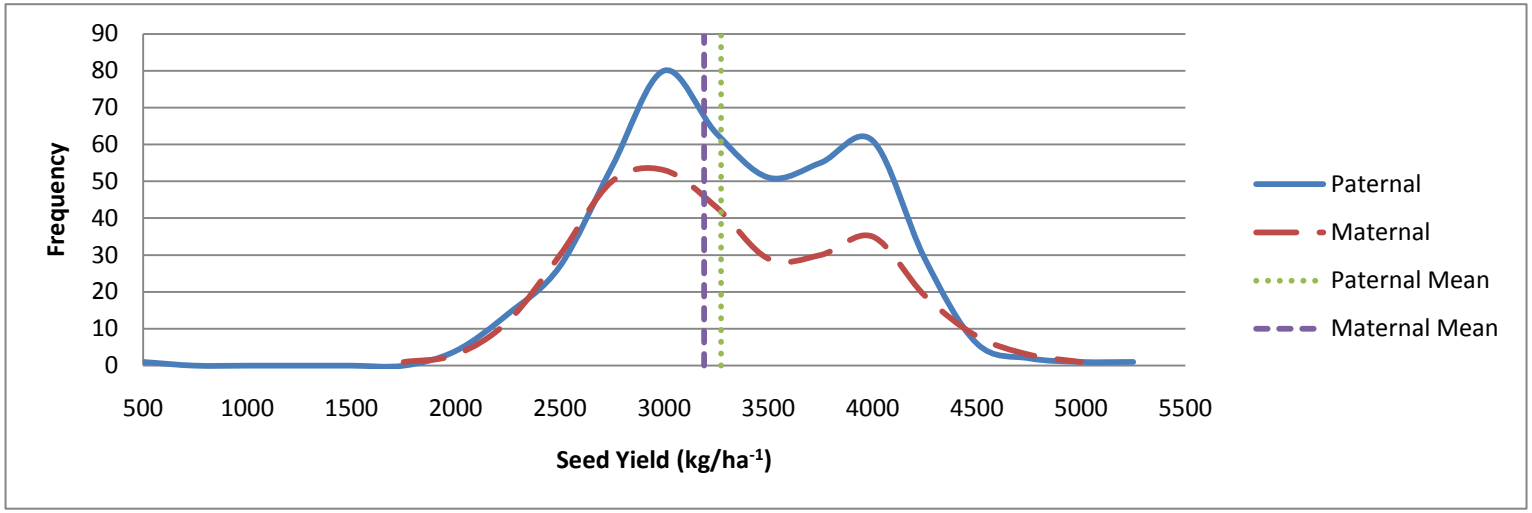


Figure 9. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S48 in Population 34 at two plant row yield trial locations in 2008.

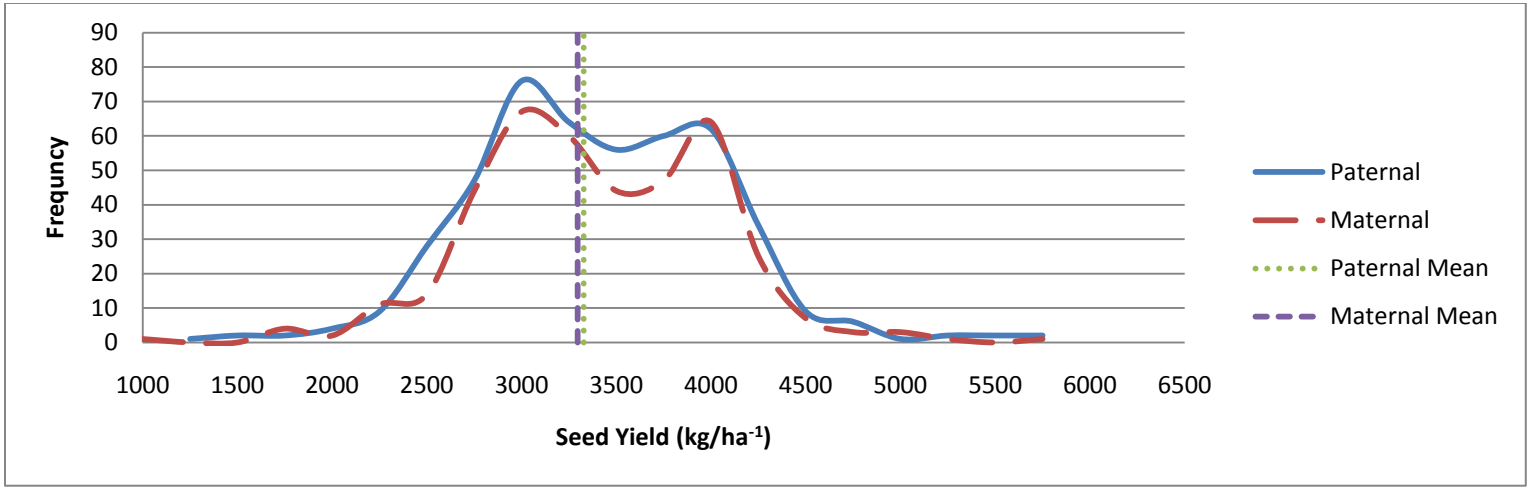


Figure 10. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S14 in Population 35 at two plant row yield trial locations in 2008.

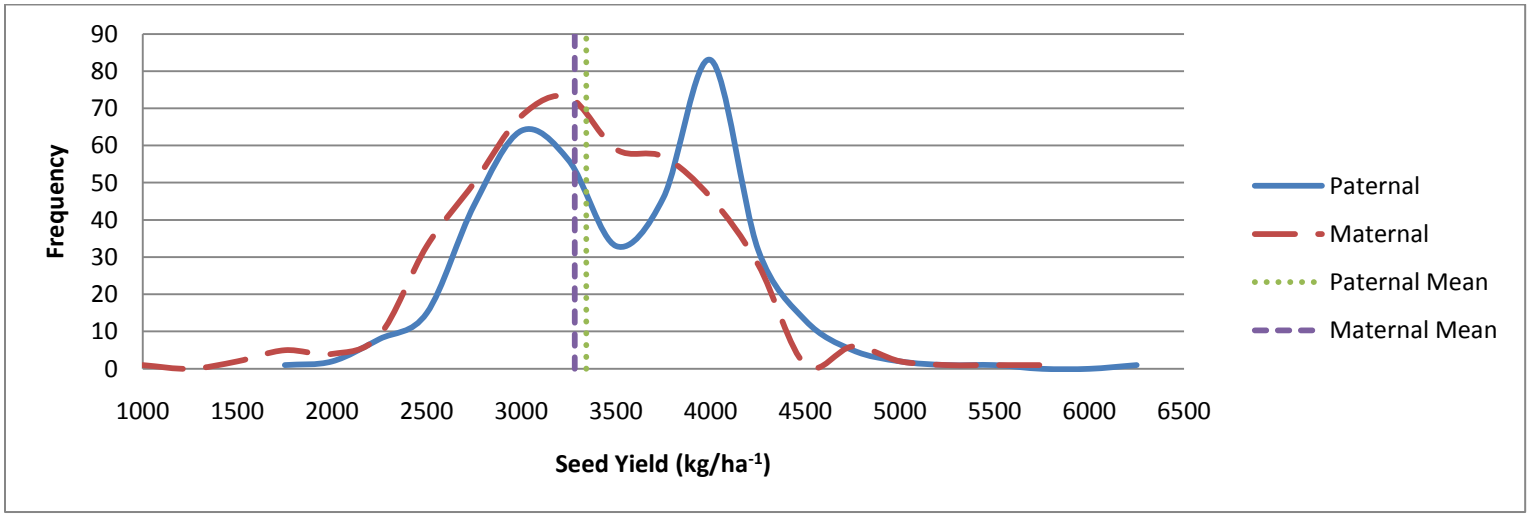


Figure 11. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S69 in Population 35 at two plant row yield trial locations in 2008.

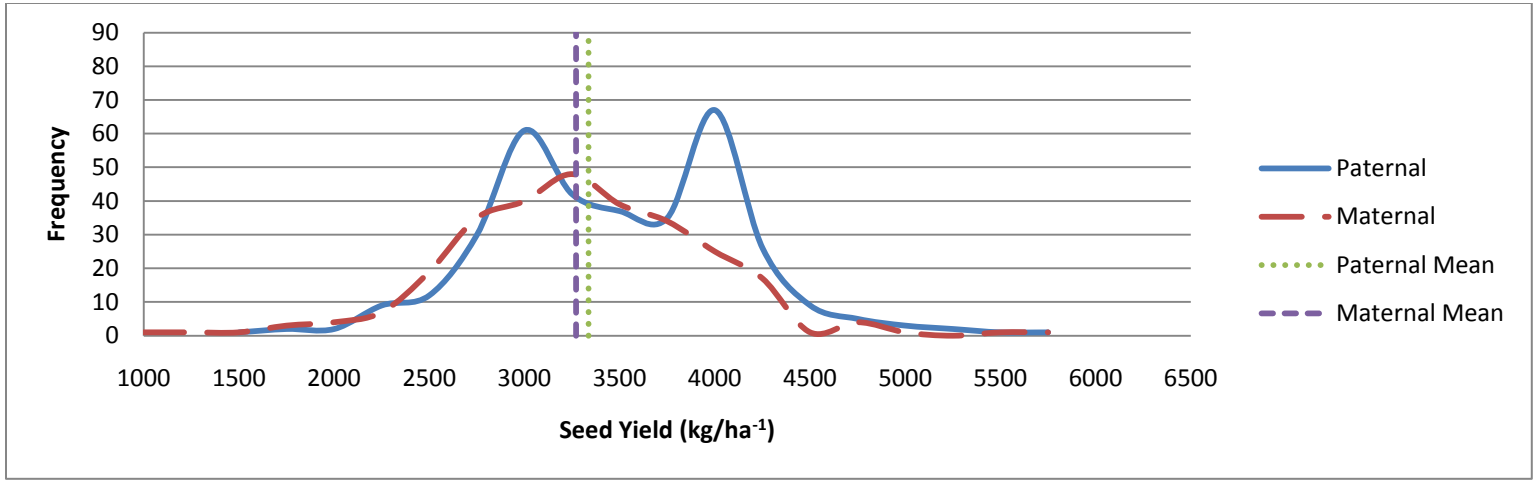


Figure 12. Frequency distribution of seed yields for lines homozygous for either the maternal or paternal allele at the quantitative trait locus S70 in Population 35 at two plant row yield trial locations in 2008.

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# APPENDIX A

ANALYSIS OF VARIANCE FOR AGRONOMIC TRAITS AMONG ENVIRONMENTS

The additive model for all traits for the combined analysis across environments in 2009 was:

$$Y_{ijklm} = \mu+E_i+R_{(i)j}+C_{(i)k}+G_l+L_{(l)m}+EG_{im}+\beta(M_{ijklm}-M_{.....})+e_{(ijklm)}$$

where:

$Y_{ijklm}$ = observed value of the $m^{th}$ line in the $l^{th}$ group in the $k^{th}$ column of the $j^{th}$ row of the $i^{th}$ environment

$\mu$ = overall mean

$E_i$ = effect of the $i^{th}$ environment, NID$(0,\sigma^2_i)$

$R_{(i)j}$ = effect of the $j^{th}$ row within the $i^{th}$ environment, NID$(0,\sigma^2_j)$

$C_{(i)k}$ = effect of the $k^{th}$ column within the $i^{th}$ environment, NID$(0,\sigma^2_k)$

$G_l$ = effect of the $l^{th}$ group

$L_{(l)m}$ = effect of the $m^{th}$ line within the $l^{th}$ group

$EG_{im}$ = effect of the interaction between the $i^{th}$ environment and the $m^{th}$ group, NID$(0,\sigma^2_{im})$

$\beta(M_{ijklm}-M_{.....})$ = maturity covariate

$e_{(ijklm)}$ = residual of the $m^{th}$ line in the $l^{th}$ group in the $k^{th}$ column of the $j^{th}$ row of the $i^{th}$ environment

Table A1. Analysis of variance and expected mean squares for combined environments for all traits

| Source of Variation | Expected Mean Squares |
|---|---|
| Environment | $\sigma^2_e+rgl\sigma^2_{C(E)}+cgl\sigma^2_{R(E)}+rcgl\sigma^2_E$ |
| Row/Environment | $\sigma^2_e+cgl\sigma^2_{R(E)}$ |
| Column/Environment | $\sigma^2_e+rgl\sigma^2_{C(E)}$ |
| Group | $\sigma^2_e+rcl\sigma^2_{EG}+ercl\Phi_G$ |
| Line/Group | $\sigma^2_e+erc\Phi_{L(G)}$ |
| Genotypic High/Group | $\sigma^2_e+ercGlPhPlRa\Phi_{Gh(G)}$ |
| Genotypic Low/Group | $\sigma^2_e+ercGhPhPlRa\Phi_{Gl(G)}$ |
| Phenotypic High/Group | $\sigma^2_e+ercGhGlPlRa\Phi_{Ph(G)}$ |
| Phenotypic Low/Group | $\sigma^2_e+ercGhGlPlRa\Phi_{Pl(G)}$ |
| Random/Group | $\sigma^2_e+ercGhGlPhPl\Phi_{Ra(G)}$ |
| Environment x Group | $\sigma^2_e+rcl\sigma^2_{EG}$ |
| Maturity Covariate | $\sigma^2_e+\Phi_{MAT}$ |
| Error | $\sigma^2_e$ |

Table A2. Analysis of variance for yield across eight diverse environments in 2009 for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Environment | 7 | 1271.22** | 7 | 1023.81** |
| Row/Environment | 32 | 35.44** | 32 | 20.90** |
| Column/Environment | 88 | 38.18** | 88 | 29.31** |
| Group | 4 | 745.16** | 4 | 150.48** |
| Line/Group | 50 | 59.51** | 52 | 20.29** |
| Genotypic High/Group | 10 | 13.37 | 12 | 8.19 |
| Genotypic Low/Group | 10 | 111.54** | 10 | 18.78* |
| Phenotypic High/Group | 10 | 15.83 | 10 | 12.20 |
| Phenotypic Low/Group | 10 | 33.88** | 10 | 34.79** |
| Random/Group | 10 | 110.25** | 10 | 44.43** |
| Environment x Group | 28 | 17.67 | 28 | 14.07 |
| Maturity Covariate | 1 | 12.45 | 1 | 10.56 |
| Error | 224 | 12.27 | 242 | 9.22 |
| C.V. | | 6.2 | | 5.0 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table A3. Analysis of variance for lodging across seven diverse environments in 2009 for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Environment | 6 | 72.30** | 6 | 23.16** |
| Row/Environment | 28 | 1.10** | 28 | 0.58 |
| Column/Environment | 77 | 0.83** | 77 | 0.67* |
| Group | 4 | 8.91** | 4 | 1.21 |
| Line/Group | 50 | 1.72** | 52 | 0.84** |
| Genotypic High/Group | 10 | 3.71** | 12 | 1.05* |
| Genotypic Low/Group | 10 | 1.00* | 10 | 0.79 |
| Phenotypic High/Group | 10 | 0.58 | 10 | 0.81 |
| Phenotypic Low/Group | 10 | 1.80** | 10 | 0.73 |
| Random/Group | 10 | 1.85** | 10 | 0.74 |
| Environment x Group | 24 | 0.71* | 24 | 0.50 |
| Error | 194 | 0.43 | 207 | 0.47 |
| C.V. | | 8.9 | | 8.6 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table A4. Analysis of variance for height across seven diverse environments in 2009 for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Environment | 6 | 863.91** | 6 | 614.35** |
| Row/Environment | 28 | 4.61* | 28 | 4.24** |
| Column/Environment | 77 | 6.30** | 77 | 3.87** |
| Group | 4 | 105.21** | 4 | 30.93** |
| Line/Group | 50 | 16.45** | 52 | 11.06** |
| Genotypic High/Group | 10 | 8.57** | 12 | 9.00** |
| Genotypic Low/Group | 10 | 9.93** | 10 | 16.73** |
| Phenotypic High/Group | 10 | 10.78** | 10 | 3.56* |
| Phenotypic Low/Group | 10 | 13.87** | 10 | 10.67** |
| Random/Group | 10 | 41.20** | 10 | 13.20** |
| Environment x Group | 24 | 7.09** | 24 | 1.47 |
| Error | 194 | 2.94 | 207 | 1.58 |
| C.V. | | 4.4 | | 3.5 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table A5. Analysis of variance for seed size across four diverse environments in 2009 for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Environment | 3 | 48.24** | 3 | 75.92** |
| Row/Environment | 16 | 0.27 | 16 | 0.35 |
| Column/Environment | 44 | 0.37 | 44 | 0.66* |
| Group | 4 | 6.08** | 4 | 0.42 |
| Line/Group | 50 | 1.52** | 52 | 1.32** |
| Genotypic High/Group | 10 | 1.15** | 12 | 1.76** |
| Genotypic Low/Group | 10 | 0.87** | 10 | 0.73 |
| Phenotypic High/Group | 10 | 1.58** | 10 | 1.37** |
| Phenotypic Low/Group | 10 | 1.13** | 10 | 1.33** |
| Random/Group | 10 | 3.10** | 10 | 1.29** |
| Environment x Group | 12 | 0.53 | 12 | 0.28 |
| Error | 84 | 0.32 | 94 | 0.42 |
| C.V. | | 3.2 | | 3.4 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table A6. Analysis of variance for maturity across six diverse environments in 2009 for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Environment | 5 | 2084.26** | 5 | 1677.12** |
| Row/Environment | 24 | 3.97** | 24 | 4.27** |
| Column/Environment | 66 | 2.47* | 66 | 5.21** |
| Group | 4 | 87.84** | 4 | 37.31** |
| Line/Group | 50 | 24.82** | 52 | 17.61** |
| Genotypic High/Group | 10 | 19.81** | 12 | 13.78** |
| Genotypic Low/Group | 10 | 3.35* | 10 | 5.09** |
| Phenotypic High/Group | 10 | 17.97** | 10 | 14.90** |
| Phenotypic Low/Group | 10 | 19.73** | 10 | 38.90** |
| Random/Group | 10 | 47.28** | 10 | 17.59** |
| Environment x Group | 20 | 3.89* | 20 | 1.99 |
| Error | 160 | 1.63 | 170 | 1.46 |
| C.V. | | 1.0 | | 1.0 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

## APPENDIX B

ANALYSIS OF VARIANCE FOR GERMINATION

The additive model for germination was:

$$Y_{ijk} = \mu + R_i + G_j + L_{(j)k} + e_{(ijk)}$$

where:

$Y_{ijk}$ = observed value of the $k^{th}$ line in the $j^{th}$ group in the $i^{th}$ replication

$\mu$ = overall mean

$R_i$ = effect of the $i^{th}$ replication, NID$(0,\sigma^2_i)$

$G_j$ = effect of the $j^{th}$ group

$L_{(j)k}$ = effect of the $k^{th}$ line within the $j^{th}$ group

$e_{(ijk)}$ = residual of the $k^{th}$ line in the $j^{th}$ group in the $i^{th}$ replication

Table B1. Analysis of variance and expected mean squares for germination

| Source of Variation | Expected Mean Squares |
|---|---|
| Replications | $\sigma^2_e+gl\sigma^2_R$ |
| Group | $\sigma^2_e+rl\ \Phi_G$ |
| Line/Group | $\sigma^2_e+r\ \Phi_{L(G)}$ |
| Genotypic High/Group | $\sigma^2_e+rGlPhPlRa\Phi_{Gh(G)}$ |
| Genotypic Low/Group | $\sigma^2_e+rGhPhPlRa\Phi_{Gl(G)}$ |
| Phenotypic High/Group | $\sigma^2_e+rGhGlPlRa\Phi_{Ph(G)}$ |
| Phenotypic Low/Group | $\sigma^2_e+rGhGlPlRa\Phi_{Pl(G)}$ |
| Random/Group | $\sigma^2_e+rGhGlPhPl\Phi_{Ra(G)}$ |
| Error | $\sigma^2_e$ |

Table B2. Analysis of variance for germination for Population 34 and 35.

| | Population | | | |
|---|---|---|---|---|
| | 34 | | 35 | |
| Source of Variation | df | Mean Square | df | Mean Square |
| Replications | 3 | 13.3 | 3 | 279.42** |
| Group | 4 | 58.30* | 4 | 158.58** |
| Line/Group | 50 | 61.24** | 52 | 81.93** |
| Genotypic High/Group | 10 | 74.80** | 12 | 30.23 |
| Genotypic Low/Group | 10 | 58.29** | 10 | 91.00** |
| Phenotypic High/Group | 10 | 85.45** | 10 | 26.96 |
| Phenotypic Low/Group | 10 | 40.67* | 10 | 133.76** |
| Random/Group | 10 | 47.00** | 10 | 138.02** |
| Error | 162 | 18.59 | 168 | 33.19 |
| C.V. | | 4.9 | | 7.0 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

## APPENDIX C

ANALYSIS OF VARIANCE FOR AGRONOMIC TRAITS AT INDIVIDUAL ENVIRONMENTS

The additive model for all traits at individual environments in 2009 was:

$$Y_{ij} = \mu + G_i + L_{(i)j} + e_{(ij)}$$

where:

$Y_{ij}$ = observed value of the $j^{th}$ line of the $i^{th}$ group

$\mu$ = overall mean

$G_l$ = effect of the $i^{th}$ group

$L_{(i)j}$ = effect of the $j^{th}$ line within the $i^{th}$ group

$e_{(ij)}$ = residual of the $j^{th}$ line in the $i^{th}$ group

Table C1. Analysis of variance and expected mean squares for individual environments for all traits.

| Source of Variation | Expected Mean Squares |
|---|---|
| Group | $\sigma^2_e + l\Phi_G$ |
| Line/Group | $\sigma^2_e + \Phi_{L(G)}$ |
| Check/Group | $\sigma^2_e + GhGlPhPlRa\Phi_{Gh(G)}$ |
| Genotypic High/Group | $\sigma^2_e + ChGlPhPlRa\Phi_{Gh(G)}$ |
| Genotypic Low/Group | $\sigma^2_e + ChGhPhPlRa\Phi_{Gl(G)}$ |
| Phenotypic High/Group | $\sigma^2_e + ChGhGlPlRa\Phi_{Ph(G)}$ |
| Phenotypic Low/Group | $\sigma^2_e + ChGhGlPlRa\Phi_{Pl(G)}$ |
| Random/Group | $\sigma^2_e + ChGhGlPhPl\Phi_{Ra(G)}$ |
| Error | $\sigma^2_e$ |

Table C2. Analysis of variance mean squares for seed yield at individual locations in 2009 for Population 34.

| | | Location | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Source of Variation | df | Metamora, IL | Anna, OH | Napoleon, OH | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Pesotum, IL |
| Group | 5 | 83.77 | 69.69 | 236.22 | 259.28 | 309.76* | 369.73 | 242.91** | 154.15** |
| Line/Group | 53 | 34.50 | 13.22 | 18.83 | 30.86 | 38.72 | 48.77 | 17.93 | 14.81 |
| Check/Group | 3 | 11.08 | 14.17 | 8.47 | 44.92 | 2.68 | 78.04 | 7.79 | 38.61* |
| Genotypic High/Group | 10 | 42.99 | 10.75 | 8.54 | 23.54 | 16.12 | 117.81 | 15.88 | 9.03 |
| Genotypic Low/Group | 10 | 72.59 | 15.52 | 25.97 | 34.16 | 54.43 | 22.21 | 27.39 | 16.64 |
| Phenotypic High/Group | 10 | 38.06 | 10.85 | 16.50 | 28.45 | 64.53 | 6.45 | 13.15 | 13.22 |
| Phenotypic Low/Group | 10 | 9.81 | 11.21 | 15.23 | 33.49 | 7.44 | 84.30 | 14.21 | 15.64 |
| Random/Group | 10 | 16.09 | 17.27 | 30.88 | 30.44 | 58.77 | 18.66 | 22.05 | 12.40 |
| Error | 2 | 21.22 | 17.33 | 24.91 | 16.21 | 5.05 | 24.20 | 2.21 | 1.12 |
| C.V. | | 9.4 | 7.7 | 8.5 | 5.8 | 4.2 | 8.1 | 2.6 | 1.6 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table C3. Analysis of variance mean squares for lodging at individual locations in 2009 for Population 34.

| | | Location | | | | | |
|---|---|---|---|---|---|---|---|
| Source of Variation | df | Metamora, IL | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Pesotum, IL |
| Group | 5 | 1.10 | 8.00 | 4.68 | 2.51 | 0.04 | 1.27 |
| Line/Group | 53 | 0.81 | 2.77 | 1.14 | 0.76 | 0.08 | 0.35 |
| Check/Group | 3 | 1.78 | 14.74 | 2.78 | 4.00 | 0.00 | 0.78 |
| Genotypic High/Group | 10 | 0.80 | 2.67 | 1.62 | 0.69 | 0.16 | 0.46 |
| Genotypic Low/Group | 10 | 0.89 | 1.07 | 1.25 | 0.60 | 0.09 | 0.09 |
| Phenotypic High/Group | 10 | 0.85 | 1.07 | 0.47 | 0.27 | 0.09 | 0.22 |
| Phenotypic Low/Group | 10 | 0.47 | 2.80 | 0.85 | 0.56 | 0.00 | 0.27 |
| Random/Group | 10 | 0.76 | 2.62 | 0.96 | 0.67 | 0.09 | 0.56 |
| Error | 2 | 0.00 | 0.00 | 0.25 | 0.00 | 0.00 | 0.50 |
| C.V. | | 0.0 | 0.0 | 6.9 | 0.0 | 0.0 | 8.8 |

Table C4. Analysis of variance mean squares for height at individual locations in 2009 for Population 34.

| | | Location | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Source of Variation | df | Metamora, IL | Napoleon, OH | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Pesotum, IL |
| Group | 5 | 29.35* | 80.75* | 19.75 | 36.43 | 30.85** | 33.05 | 32.63 |
| Line/Group | 53 | 6.71 | 12.59 | 9.45 | 9.30 | 6.64* | 6.34 | 7.50 |
| Check/Group | 3 | 33.61** | 31.44* | 13.44 | 36.00 | 24.78* | 12.78 | 36.11 |
| Genotypic High/Group | 10 | 2.36 | 10.49 | 5.36 | 2.26 | 4.22 | 4.89 | 3.29 |
| Genotypic Low/Group | 10 | 3.09 | 9.82 | 5.47 | 2.56 | 2.16 | 3.96 | 4.85 |
| Phenotypic High/Group | 10 | 3.87 | 8.27 | 7.89 | 1.76 | 2.26 | 11.42 | 4.00 |
| Phenotypic Low/Group | 10 | 4.29 | 5.65 | 8.05 | 12.84 | 5.02* | 3.89 | 2.87 |
| Random/Group | 10 | 11.87 | 23.05* | 19.27 | 19.42 | 14.09* | 5.62 | 13.89 |
| Error | 2 | 1.25 | 2.25 | 2.5 | 5.0 | 0.25 | 8.50 | 13.25 |
| C.V. | | 2.9 | 3.4 | 3.6 | 6.2 | 1.4 | 8.4 | 10.2 |

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Table C5. Analysis of variance mean squares for seed size at individual locations in 2009 for Population 34.

| | | Location | | | |
|---|---|---|---|---|---|
| Source of Variation | df | Metamora, IL | Napoleon, OH | Gillman, IL | Pesotum, IL |
| Group | 5 | 2.22 | 2.14 | 6.89 | 1.86 |
| Line/Group | 53 | 0.75 | 0.77 | 1.96 | 1.31 |
| Check/Group | 3 | 3.60 | 1.34 | 18.07 | 3.27 |
| Genotypic High/Group | 10 | 0.38 | 0.50 | 0.70 | 1.71 |
| Genotypic Low/Group | 10 | 0.56 | 1.46 | 0.68 | 0.82 |
| Phenotypic High/Group | 10 | 0.65 | 0.45 | 0.81 | 1.17 |
| Phenotypic Low/Group | 10 | 0.56 | 0.66 | 0.86 | 0.45 |
| Random/Group | 10 | 1.00 | 0.96 | 1.79 | 1.79 |
| Error | 2 | 0.20 | 2.41 | 17.64 | 0.43 |
| C.V. | | 2.6 | 9.3 | 23.46 | 3.5 |

Table C6. Analysis of variance mean squares for maturity at individual locations in 2009 for Population 34.

| | | Location | | | | | |
|---|---|---|---|---|---|---|---|
| Source of Variation | df | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
| Group | 5 | 21.37 | 20.18 | 51.61 | 33.63** | 23.46* | 25.51 |
| Line/Group | 53 | 9.48 | 6.70 | 13.64 | 10.39* | 7.62* | 10.07 |
| Check/Group | 3 | 46.28 | 26.94 | 79.11 | 64.78** | 48.94** | 40.50 |
| Genotypic High/Group | 10 | 7.42 | 1.20 | 11.56 | 6.07* | 2.02 | 4.47 |
| Genotypic Low/Group | 10 | 2.22 | 3.67 | 3.22 | 2.13 | 3.27 | 2.09 |
| Phenotypic High/Group | 10 | 8.27 | 6.26 | 6.66 | 4.06 | 3.02 | 5.69 |
| Phenotypic Low/Group | 10 | 9.05 | 5.49 | 8.69 | 8.27* | 5.76* | 11.36 |
| Random/Group | 10 | 9.42 | 10.80 | 18.46 | 14.96* | 11.62* | 17.60 |
| Error | 2 | 0.00 | 0.00 | 0.00 | 0.25 | 0.25 | 0.00 |
| C.V. | | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.0 |

*,** Significant at the 0.05 or 0.01 probability levels, respectively

Table C7. Analysis of variance mean squares for yield at individual locations in 2009 for Population 35.

| | | Location | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Source of Variation | df | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
| Group | 5 | 61.78 | 52.32 | 58.28 | 41.08* | 10.83 | 38.63 | 34.71 | 65.35 |
| Line/Group | 56 | 20.76 | 29.82 | 9.93 | 22.57* | 14.14 | 22.95 | 8.74 | 15.44 |
| Check/Group | 4 | 24.50 | 38.21 | 11.82 | 56.00* | 5.45 | 12.13 | 11.54 | 9.91 |
| Genotypic High/Group | 12 | 15.07 | 19.46 | 8.18 | 10.86 | 12.44 | 16.35 | 5.15 | 19.70 |
| Genotypic Low/Group | 10 | 24.51 | 27.11 | 11.46 | 30.73* | 20.98 | 28.93 | 8.51 | 13.60 |
| Phenotypic High/Group | 10 | 14.53 | 37.23 | 4.09 | 20.46* | 11.26 | 29.57 | 3.45 | 17.18 |
| Phenotypic Low/Group | 10 | 23.29 | 36.95 | 18.42 | 29.41* | 11.56 | 12.08 | 7.80 | 15.93 |
| Random/Group | 10 | 26.04 | 27.05 | 7.08 | 11.67 | 18.27 | 33.46 | 18.40 | 12.17 |
| Error | 2 | 6.05 | 36.57 | 8.90 | 0.94 | 6.51 | 5.93 | 16.47 | 31.77 |
| C.V. | | 3.8 | 10.2 | 4.8 | 1.6 | 5.1 | 4.1 | 7.0 | 8.8 |

* Significant at the 0.05 and 0.01 probability level

Table C8. Analysis of variance mean squares for lodging at individual locations in 2009 for Population 35.

| | | Location | | | | | |
|---|---|---|---|---|---|---|---|
| Source of Variation | df | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
| Group | 5 | 2.92 | 0.35 | 0.53 | 0.12 | 0.18 | 0.16 |
| Line/Group | 56 | 1.93 | 0.78 | 0.54 | 0.22 | 16.34 | 0.28 |
| Check/Group | 4 | 6.59* | 2.09 | 2.09 | 0.18 | 0.73 | 0.68 |
| Genotypic High/Group | 12 | 1.47 | 0.31 | 0.58 | 0.27 | 0.67 | 0.23 |
| Genotypic Low/Group | 10 | 2.16 | 0.29 | 0.22 | 0.22 | 0.27 | 0.22 |
| Phenotypic High/Group | 10 | 2.29 | 0.42 | 0.22 | 0.22 | 0.22 | 0.26 |
| Phenotypic Low/Group | 10 | 1.47 | 0.29 | 0.49 | 0.22 | 0.26 | 0.27 |
| Random/Group | 10 | 0.49 | 0.49 | 0.56 | 0.16 | 0.27 | 0.26 |
| Error | 2 | 0.25 | 0.25 | 0.25 | 0.50 | 0.25 | 0.5 |
| C.V. | | 7.2 | 6.3 | 6.2 | 8.5 | 5.9 | 8.2 |

* Significant at the 0.05 probability level

Table C9. Analysis of variance mean squares for height at individual locations in 2009 for Population 35.

| | | Location | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Source of Variation | df | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
| Group | 5 | 11.69 | 5.46 | 6.99 | 6.82 | 2.96 | 7.10 | 7.78* |
| Line/Group | 56 | 6.18 | 4.52 | 5.01 | 3.62 | 6.35 | 4.82 | 4.08 |
| Check/Group | 4 | 18.21 | 4.43 | 14.68* | 4.80 | 8.88 | 24.71* | 13.72* |
| Genotypic High/Group | 12 | 5.19 | 5.23 | 2.83 | 1.97 | 7.31 | 5.09 | 1.73 |
| Genotypic Low/Group | 10 | 6.07 | 2.07 | 5.42 | 5.06 | 6.62 | 3.07 | 5.47* |
| Phenotypic High/Group | 10 | 5.07 | 2.27 | 2.76 | 2.47 | 4.07 | 1.42 | 1.89 |
| Phenotypic Low/Group | 10 | 5.25 | 6.62 | 3.82 | 4.96 | 5.67 | 2.66 | 5.27* |
| Random/Group | 10 | 4.67 | 6.27 | 6.76 | 3.47 | 6.86 | 5.06 | 2.66 |
| Error | 2 | 1.00 | 1.00 | 0.50 | 10.25 | 16.25 | 1.00 | 0.25 |
| C.V. | | 2.4 | 3.0 | 2.2 | 9.8 | 11.4 | 3.0 | 1.3 |

* Significant at the 0.05 probability level

Table C10. Analysis of variance mean squares for seed size at individual locations in 2009 for Population 34.

| | | Location | | | |
|---|---|---|---|---|---|
| Source of Variation | df | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
| Group | 5 | 1.04 | 0.43 | 0.84 | 0.73 |
| Line/Group | 56 | 0.90 | 0.69 | 1.17 | 0.90 |
| Check/Group | 4 | 0.81 | 1.25 | 1.81 | 0.88 |
| Genotypic High/Group | 12 | 1.33 | 0.75 | 1.49 | 1.16 |
| Genotypic Low/Group | 10 | 1.08 | 0.24 | 0.62 | 0.25 |
| Phenotypic High/Group | 10 | 0.73 | 0.85 | 0.39 | 0.71 |
| Phenotypic Low/Group | 10 | 0.68 | 0.66 | 1.78 | 1.65 |
| Random/Group | 10 | 0.60 | 0.71 | 1.27 | 0.70 |
| Error | 2 | 0.59 | 0.45 | 0.27 | 0.43 |
| C.V. | | 4.0 | 4.0 | 2.7 | 3.8 |

Table C11. Analysis of variance mean squares for maturity at individual locations in 2009 for Population 34.

| | | Location | | | | | |
|---|---|---|---|---|---|---|---|
| Source of Variation | df | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
| Group | 5 | 82.65 | 8.80 | 19.80* | 11.72 | 15.35 | 10.11 |
| Line/Group | 56 | 7.64 | 7.59 | 12.66* | 7.22 | 7.64 | 9.88 |
| Check/Group | 4 | 27.96 | 20.86 | 34.75* | 41.23* | 34.38* | 44.23 |
| Genotypic High/Group | 12 | 3.94 | 6.42 | 7.97 | 3.58 | 3.40 | 4.69 |
| Genotypic Low/Group | 10 | 5.96 | 3.36 | 3.96 | 4.67 | 2.85 | 5.66 |
| Phenotypic High/Group | 10 | 5.87 | 4.67 | 14.67* | 5.76 | 3.76 | 4.82 |
| Phenotypic Low/Group | 10 | 9.22 | 11.56 | 19.60* | 3.76 | 13.16 | 11.49 |
| Random/Group | 10 | 5.82 | 6.87 | 9.16 | 5.47 | 5.20 | 10.06 |
| Error | 2 | 2.50 | 0.00 | 0.50 | 1.25 | 1.25 | 4.25 |
| C.V. | | 1.2 | 0.0 | 0.5 | 0.9 | 0.9 | 1.8 |

*,** Significant at the 0.05 or 0.01 probability levels, respectively

## APPENDIX D

LINE PERFORMANCE AT EACH LOCATION

Table D1. Seed yield by line at individual locations of Population 34 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 34-0414 | GH† | 3830‡ | 3622 | 2452 | 4159 | 3601 | 4515 | 4347 | 3884 |
| 34-0692 | GH | 4569 | 3924 | -§ | 4650 | 3494 | 4710 | 4172 | 3642 |
| 34-0724 | GH/PH | 4005 | 4320 | 4582 | 4267 | 3548 | 4354 | 4220 | 4092 |
| 34-0777 | GH | 3810 | 4112 | 4132 | 3877 | 3393 | 4253 | 4072 | 3904 |
| 34-1046 | GH | 4562 | 4125 | - | 3937 | 3393 | 4502 | 3991 | 3487 |
| 34-1055 | GH | 3964 | 3783 | 4697 | 4246 | 3830 | 4172 | 3870 | 3709 |
| 34-1058 | GH | 4220 | 3924 | 4697 | 4347 | 3400 | 4891 | 4448 | 3272 |
| 34-1553 | GH | 3480 | 3366 | 4307 | 4569 | 3178 | 4354 | 4388 | 3662 |
| 34-1627 | GH | 4005 | 3769 | 4535 | 3951 | 2331 | 4535 | 3984 | 3756 |
| 34-1730 | GH | 4011 | 4139 | 4663 | 4361 | 4038 | 4535 | 4085 | 3648 |
| 34-1757 | GH | 4300 | 3837 | 4784 | 3904 | 3104 | 4488 | 3910 | 3534 |
| 34-0351 | GL | 3239 | 2553 | 3205 | 3030 | 3118 | 4125 | 3608 | 3454 |
| 34-0450 | GL | 3622 | 3931 | 3944 | 4065 | 2970 | 4408 | 3454 | 3400 |
| 34-0485 | GL | 4193 | 3091 | 3984 | 3675 | 1915 | 4320 | 4112 | 3810 |
| 34-0503 | GL | 3695 | 3413 | 3951 | 3716 | 3333 | 3991 | 3501 | 3312 |
| 34-0760 | GL | 3366 | 3333 | 3682 | 3575 | 3239 | 3924 | 3218 | 2970 |
| 34-0873 | GL | 4428 | 3991 | 4213 | 4172 | 2936 | 4636 | 4435 | 3454 |
| 34-1242 | GL | 4031 | 3501 | 4327 | 4058 | 2298 | 4461 | 3890 | 3541 |
| 34-1288 | GL | 3857 | 3769 | 4139 | 4193 | 3151 | 4656 | 3796 | 3742 |
| 34-1716 | GL | 4361 | 4374 | 3984 | 4119 | 3857 | 4596 | 3830 | 3420 |

Table D1. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 34-1806 | GL | 3561 | 3642 | 4260 | 3924 | 3803 | 4623 | 4052 | 3816 |
| 34-1897 | GL | 3648 | 3212 | 3776 | 3615 | 3312 | 4650 | 3924 | 3837 |
| 34-0506 | PH | 3575 | 3460 | 4596 | 3910 | 3615 | 5019 | 3810 | 3460 |
| 34-0518 | PH | 3904 | 3601 | 4179 | 3689 | 2217 | 4650 | 3884 | 3507 |
| 34-0626 | PH | 4058 | 4300 | 4293 | 3769 | 3259 | 4455 | 4273 | 3709 |
| 34-0662 | PH | 4186 | 2473 | 4273 | 4179 | 3548 | 4670 | 4643 | 3924 |
| 34-0754 | PH | 4233 | 4186 | 4623 | 4206 | 3454 | 4112 | 4670 | 4085 |
| 34-0947 | PH | 4562 | 4132 | 4629 | 3642 | 3467 | 4253 | 4307 | 3655 |
| 34-1118 | PH | 4609 | 3608 | 4596 | 4206 | 3353 | 4468 | 4112 | 3568 |
| 34-1157 | PH | 4388 | 4213 | 4555 | 4320 | 3467 | 4414 | 4488 | 3951 |
| 34-1340 | PH | 4522 | 3790 | 4643 | 4018 | 3763 | 4576 | 4293 | 3863 |
| 34-1440 | PH | 3622 | 3910 | 4374 | 3870 | 3084 | 4670 | 4388 | 3756 |
| 34-0297 | PL | 3064 | 2977 | - | 3077 | 2963 | 3272 | 3185 | 3286 |
| 34-0378 | PL | 3675 | 3165 | 3588 | 3514 | 3144 | 3635 | 3292 | 3514 |
| 34-0405 | PL | 3198 | 3037 | 2916 | 3333 | 2869 | 3843 | 3165 | 3259 |
| 34-0538 | PL | 3124 | 2654 | 3521 | 3487 | 3178 | 3776 | 3205 | 3057 |
| 34-0778 | PL | 3870 | 2916 | 3588 | 3259 | 3091 | 4159 | 3044 | 3669 |
| 34-1256 | PL | 3608 | 2983 | 3937 | 3554 | 3393 | 3830 | 3722 | 3480 |
| 34-1426 | PL | 3245 | - | 3937 | 3124 | 3077 | 4072 | 3507 | 3588 |
| 34-1486 | PL | 3588 | 2735 | 3776 | 3595 | 2889 | 4078 | 3642 | 3467 |

Table D1. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 34-1609 | PL | 2627 | 2869 | 3279 | 2802 | 2688 | 3541 | 3366 | 2956 |
| 34-1654 | PL | 2748 | 3259 | 3003 | 3071 | 2694 | 4018 | 3870 | 3232 |
| 34-1808 | PL | 3138 | 2849 | 1901 | 3104 | 2990 | 3910 | 3521 | 3192 |
| 34-0467 | RA | 3494 | 4596 | 4320 | 3575 | 3373 | 4690 | 4226 | 3776 |
| 34-0679 | RA | 4293 | 4025 | 4703 | 4052 | 3407 | 4334 | 4529 | 3521 |
| 34-0761 | RA | 3863 | 4018 | - | 3722 | 3104 | 4193 | 4441 | 3494 |
| 34-1029 | RA | 3971 | 4072 | 4616 | 3857 | 3642 | 4603 | 4112 | 3588 |
| 34-1032 | RA | 3662 | 3608 | 4267 | 4394 | 3286 | 4623 | 4374 | 3561 |
| 34-1140 | RA | 4065 | 4502 | 4220 | 4246 | 3232 | 4488 | 4522 | 3790 |
| 34-1333 | RA | 4253 | 4065 | 4206 | 3736 | 3393 | 4307 | 4058 | 4293 |
| 34-1625 | RA | 4401 | 3292 | 4085 | 4112 | 2950 | 4354 | 3561 | 3884 |
| 34-1666 | RA | 3360 | 2802 | 3742 | 3306 | 2788 | 3857 | 3373 | 3245 |
| 34-1779 | RA | 4468 | 4119 | 3890 | 4112 | 3487 | 4253 | 4045 | 3890 |
| 34-1847 | RA | 4199 | 4031 | 4260 | 3924 | 3648 | 4482 | 4038 | 3521 |
| CV | | 7 | 4 | 8 | 3 | 10 | 4 | 8 | 9 |
| s | | 471 | 523 | 587 | 404 | 413 | 342 | 285 | 409 |
| SE | | 64 | 71 | 80 | 55 | 56 | 47 | 39 | 56 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Seed yield expressed in kg $ha^{-1}$

§A dash sign indicates data not reported

Table D2. Lodging by line at individual locations of Population 34 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-0414 | GH† | 4.5‡ | 3.0 | 2.5 | 1.0 | 1.5 | 1.5 |
| 34-0692 | GH | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 | 1.5 |
| 34-0724 | GH/PH | 2.5 | 2.5 | 1.5 | 1.0 | 1.0 | 1.5 |
| 34-0777 | GH | 4.0 | 3.0 | 2.5 | 1.5 | 2.0 | 2.5 |
| 34-1046 | GH | 3.0 | 1.5 | 1.5 | 1.0 | 1.5 | 2.0 |
| 34-1055 | GH | 3.0 | 2.0 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1058 | GH | 3.0 | 2.0 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1553 | GH | 4.0 | 3.5 | 2.5 | 1.5 | 2.5 | 2.0 |
| 34-1627 | GH | 3.5 | 2.5 | 2.5 | 1.0 | 1.5 | 1.5 |
| 34-1730 | GH | 3.0 | 2.0 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1757 | GH | 3.5 | 2.5 | 2.0 | 1.0 | 1.0 | 1.5 |
| 34-0351 | GL | 2.5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 34-0450 | GL | 3.0 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 34-0485 | GL | 3.0 | 1.0 | 1.5 | 1.0 | 2.0 | 1.5 |
| 34-0503 | GL | 3.0 | 2.0 | 2.0 | 1.0 | 2.0 | 1.5 |
| 34-0760 | GL | 2.0 | 2.0 | 1.0 | 1.0 | 1.0 | 1.5 |
| 34-0873 | GL | 2.5 | 2.5 | 1.5 | 1.0 | 2.0 | 1.5 |
| 34-1242 | GL | 3.5 | 2.5 | 2.0 | 1.0 | 2.0 | 1.5 |
| 34-1288 | GL | 3.0 | 1.5 | 2.0 | 1.0 | 2.0 | 1.5 |
| 34-1716 | GL | 2.0 | 1.5 | 1.5 | 1.0 | 1.0 | 1.5 |

Table D2. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-1806 | GL | 3.5 | 2.0 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-1897 | GL | 2.5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.5 |
| 34-0506 | PH | 4.5 | 2.5 | 1.5 | 1.0 | 2.0 | 1.5 |
| 34-0518 | PH | 3.0 | 2.0 | 1.5 | 1.5 | 2.0 | 1.5 |
| 34-0626 | PH | 3.0 | 2.0 | 2.0 | 1.0 | 1.5 | 2.0 |
| 34-0662 | PH | 3.0 | 2.0 | 1.5 | 1.0 | 2.0 | 2.0 |
| 34-0754 | PH | 3.5 | 2.0 | 2.0 | 1.0 | 2.0 | 1.5 |
| 34-0947 | PH | 3.5 | 2.0 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1118 | PH | 3.5 | 2.5 | 2.0 | 1.0 | 2.5 | 2.0 |
| 34-1157 | PH | 3.0 | 2.5 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1340 | PH | 3.5 | 2.0 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-1440 | PH | 3.0 | 3.0 | 1.5 | 1.0 | 1.0 | 1.5 |
| 34-0297 | PL | 3.0 | 2.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 34-0378 | PL | 2.0 | 2.0 | 1.5 | 1.0 | 1.5 | 1.0 |
| 34-0405 | PL | 2.0 | 1.0 | 1.5 | 1.0 | 1.5 | 1.0 |
| 34-0538 | PL | 3.0 | 1.5 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-0778 | PL | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 | 1.5 |
| 34-1256 | PL | 4.0 | 2.5 | 2.0 | 1.0 | 2.0 | 1.5 |
| 34-1426 | PL | 3.5 | -§ | 2.0 | 1.0 | 1.0 | 1.5 |
| 34-1486 | PL | 2.0 | 1.5 | 1.5 | 1.0 | 1.0 | 1.5 |
| 34-1609 | PL | 3.0 | 1.5 | 1.0 | 1.0 | 1.5 | 1.0 |

Table D2. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-1654 | PL | 2.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 34-1808 | PL | 1.5 | 1.5 | 1.0 | 1.0 | 1.0 | 1.5 |
| 34-0467 | RA | 2.5 | 2.5 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-0679 | RA | 3.0 | 1.5 | 1.5 | 1.0 | 1.0 | 1.0 |
| 34-0761 | RA | 3.5 | 2.5 | 2.5 | 1.0 | 2.0 | 2.0 |
| 34-1029 | RA | 3.0 | 1.5 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-1032 | RA | 4.5 | 2.5 | 2.0 | 1.0 | 2.5 | 2.0 |
| 34-1140 | RA | 3.5 | 2.0 | 2.0 | 1.0 | 2.0 | 2.0 |
| 34-1333 | RA | 3.0 | 2.0 | 2.0 | 1.5 | 1.5 | 1.5 |
| 34-1625 | RA | 2.5 | 2.0 | 1.5 | 1.0 | 1.5 | 1.5 |
| 34-1666 | RA | 2.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 34-1779 | RA | 2.5 | 2.0 | 2.0 | 1.0 | 1.5 | 1.5 |
| 34-1847 | RA | 1.5 | 1.5 | 1.5 | 1.0 | 1.5 | 2.0 |
| | | | | | | | |
| CV | | 0.0 | 7.0 | 0.0 | 0.0 | 0.0 | 8.9 |
| s | | 1.7 | 1.2 | 0.9 | 0.3 | 0.9 | 0.6 |
| SE | | 0.2 | 0.2 | 0.1 | 0.0 | 0.1 | 0.1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡1 = all plants erect, 5 = all plant prostrate

§A dash sign indicates data not reported

Table D3. Height by line at individual locations of Population 34 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 34-0414 | GH† | 117‡ | 91 | 89 | 84 | 104 | 89 | 104 |
| 34-0692 | GH | 112 | 97 | 94 | 86 | 97 | 94 | 117 |
| 34-0724 | GH/PH | 102 | 97 | 94 | 91 | 102 | 97 | 114 |
| 34-0777 | GH | 117 | 102 | 104 | 99 | 109 | 102 | 132 |
| 34-1046 | GH | 122 | 97 | 89 | 91 | 99 | 97 | 109 |
| 34-1055 | GH | 112 | 102 | 97 | 102 | 107 | 102 | 124 |
| 34-1058 | GH | 117 | 97 | 99 | 99 | 104 | 97 | 117 |
| 34-1553 | GH | 122 | 102 | 102 | 94 | 109 | 99 | 124 |
| 34-1627 | GH | 117 | 97 | 91 | 94 | 104 | 99 | 127 |
| 34-1730 | GH | 117 | 102 | 94 | 97 | 104 | 102 | 124 |
| 34-1757 | GH | 109 | 91 | 89 | 99 | 102 | 89 | 117 |
| 34-0351 | GL | 119 | 81 | 84 | 76 | 94 | 91 | 114 |
| 34-0450 | GL | 109 | 97 | 84 | 86 | 97 | 89 | 107 |
| 34-0485 | GL | 109 | 86 | 84 | 86 | 97 | 89 | 114 |
| 34-0503 | GL | 117 | 86 | 81 | 76 | 99 | 86 | 104 |
| 34-0760 | GL | 104 | 86 | 81 | 81 | 89 | 81 | 99 |
| 34-0873 | GL | 117 | 91 | 89 | 86 | 97 | 97 | 109 |
| 34-1242 | GL | 122 | 91 | 91 | 89 | 94 | 89 | 117 |
| 34-1288 | GL | 112 | 91 | 91 | 89 | 107 | 102 | 124 |
| 34-1716 | GL | 114 | 89 | 86 | 76 | 94 | 91 | 104 |

Table D3. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 34-1806 | GL | 117 | 86 | 89 | 84 | 99 | 84 | 122 |
| 34-1897 | GL | 104 | 86 | 84 | 86 | 94 | 89 | 107 |
| 34-0506 | PH | 109 | 91 | 97 | 84 | 104 | 94 | 127 |
| 34-0518 | PH | 112 | 94 | 91 | 84 | 99 | 84 | 119 |
| 34-0626 | PH | 114 | 102 | 99 | 97 | 104 | 97 | 132 |
| 34-0662 | PH | 107 | 94 | 91 | 102 | 102 | 94 | 119 |
| 34-0754 | PH | 119 | 91 | 99 | 104 | 107 | 99 | 122 |
| 34-0947 | PH | 104 | 102 | 91 | 81 | 94 | 89 | 112 |
| 34-1118 | PH | 114 | 97 | 97 | 91 | 112 | 97 | 130 |
| 34-1157 | PH | 124 | 97 | 99 | 76 | 102 | 102 | 124 |
| 34-1340 | PH | 104 | 97 | 91 | 86 | 99 | 89 | 109 |
| 34-1440 | PH | 117 | 97 | 102 | 89 | 109 | 94 | 117 |
| 34-0297 | PL | 112 | 102 | 89 | 86 | 97 | 86 | 107 |
| 34-0378 | PL | 99 | 91 | 79 | 84 | 84 | 79 | 94 |
| 34-0405 | PL | 104 | 81 | 89 | 89 | 94 | 89 | 99 |
| 34-0538 | PL | 107 | 71 | 81 | 84 | 91 | 86 | 107 |
| 34-0778 | PL | 112 | 91 | 86 | 81 | 94 | 89 | 104 |
| 34-1256 | PL | 124 | 91 | 99 | 91 | 102 | 94 | 117 |
| 34-1426 | PL | 102 | -§ | 81 | 89 | 102 | 86 | 107 |
| 34-1486 | PL | 99 | 76 | 81 | 84 | 91 | 84 | 104 |

Table D3. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 34-1609 | PL | 109 | 81 | 84 | 79 | 91 | 94 | 112 |
| 34-1654 | PL | 109 | 91 | 89 | 74 | 97 | 89 | 104 |
| 34-1808 | PL | 107 | 81 | 84 | 84 | 89 | 89 | 109 |
| 34-0467 | RA | 109 | 102 | 99 | 99 | 102 | 94 | 114 |
| 34-0679 | RA | 109 | 102 | 97 | 91 | 107 | 94 | 114 |
| 34-0761 | RA | 117 | 107 | 99 | 89 | 107 | 97 | 127 |
| 34-1029 | RA | 114 | 86 | 86 | 86 | 89 | 89 | 107 |
| 34-1032 | RA | 127 | 86 | 91 | 102 | 107 | 97 | 119 |
| 34-1140 | RA | 114 | 107 | 91 | 94 | 107 | 94 | 117 |
| 34-1333 | RA | 124 | 102 | 99 | 81 | 99 | 99 | 112 |
| 34-1625 | RA | 104 | 91 | 89 | 89 | 99 | 84 | 119 |
| 34-1666 | RA | 89 | 76 | 71 | 89 | 89 | 69 | 89 |
| 34-1779 | RA | 109 | 91 | 79 | 97 | 84 | 81 | 104 |
| 34-1847 | RA | 97 | 76 | 79 | 97 | 89 | 79 | 89 |
| CV | | 4 | 6 | 1 | 8 | 3 | 10 | 3 |
| s | | 8 | 8 | 7 | 7 | 7 | 7 | 10 |
| SE | | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Plant height in cm from ground to terminal node

§A dash sign indicates data not reported

Table D4. Seed size by line at individual locations of Population 34 in 2009.

| Line | Group | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 34-0414 | GH† | 17.2‡ | 17.2 | 18.8 | 15.4 |
| 34-0692 | GH | 18.9 | 17.2 | 19.7 | 17.0 |
| 34-0724 | GH/PH | 16.6 | 15.4 | 16.4 | 16.2 |
| 34-0777 | GH | 16.9 | 16.3 | 16.9 | 16.7 |
| 34-1046 | GH | 17.5 | 16.3 | 17.9 | 15.9 |
| 34-1055 | GH | 18.3 | 17.2 | 19.7 | 15.3 |
| 34-1058 | GH | 18.7 | 17.2 | 20.7 | 16.6 |
| 34-1553 | GH | 17.1 | 16.3 | 17.5 | 16.5 |
| 34-1627 | GH | 17.9 | 17.2 | 18.8 | 15.7 |
| 34-1730 | GH | 18.7 | 17.2 | 19.1 | 17.4 |
| 34-1757 | GH | 16.9 | 17.2 | 17.8 | 17.1 |
| 34-0351 | GL | 17.3 | 16.3 | 17.9 | 15.8 |
| 34-0450 | GL | 19.6 | 17.2 | 19.5 | 17.7 |
| 34-0485 | GL | 18.3 | 17.2 | 19.6 | 17.4 |
| 34-0503 | GL | 18.0 | 17.2 | 18.5 | 16.7 |
| 34-0760 | GL | 17.8 | 17.2 | 18.7 | 16.1 |
| 34-0873 | GL | 18.7 | 16.3 | 19.3 | 16.6 |
| 34-1242 | GL | 19.6 | 18.1 | 19.9 | -§ |
| 34-1288 | GL | 18.7 | 18.1 | 19.8 | 14.2 |
| 34-1716 | GL | 18.6 | 18.1 | 20.5 | 16.6 |

Table D4. Continued.

| Line | Group | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 34-1806 | GL | 17.2 | 16.3 | 17.5 | 14.9 |
| 34-1897 | GL | 17.6 | 16.3 | 19.5 | 16.8 |
| 34-0506 | PH | 18.9 | 18.1 | 20.1 | 16.7 |
| 34-0518 | PH | 17.0 | 16.3 | 17.8 | 16.2 |
| 34-0626 | PH | 18.7 | 18.1 | 18.9 | 17.7 |
| 34-0662 | PH | 19.3 | 17.2 | 19.5 | - |
| 34-0754 | PH | 18.5 | 17.2 | 19.4 | 18.0 |
| 34-0947 | PH | 17.7 | 17.2 | 19.4 | - |
| 34-1118 | PH | 19.2 | 17.2 | 19.6 | 17.8 |
| 34-1157 | PH | 18.0 | 17.2 | 18.4 | 17.1 |
| 34-1340 | PH | 19.0 | 17.2 | 19.8 | 17.4 |
| 34-1440 | PH | 18.8 | 18.1 | 19.6 | 17.4 |
| 34-0297 | PL | - | 17.2 | 18.5 | 17.2 |
| 34-0378 | PL | 18.1 | 16.3 | 18.3 | 16.9 |
| 34-0405 | PL | 18.5 | 17.2 | 19.4 | 16.9 |
| 34-0538 | PL | 15.6 | 15.4 | 17.6 | 15.7 |
| 34-0778 | PL | 17.9 | 16.3 | 18.3 | 16.5 |
| 34-1256 | PL | 17.1 | 16.3 | 17.6 | 16.4 |
| 34-1426 | PL | 15.9 | 15.4 | 18.1 | 15.5 |
| 34-1486 | PL | 17.3 | 17.2 | 18.4 | 16.4 |
| 34-1609 | PL | 16.5 | 15.4 | 17.7 | 14.5 |

Table D4. Continued.

| Line | Group | Gillman, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 34-1654 | PL | 17.1 | 17.2 | 19.6 | - |
| 34-1808 | PL | 17.2 | 16.3 | 17.9 | 15.8 |
| 34-0467 | RA | 17.8 | 16.3 | 19.4 | 16.1 |
| 34-0679 | RA | 18.7 | 17.2 | 19.7 | - |
| 34-0761 | RA | 17.6 | 17.2 | 18.9 | 16.6 |
| 34-1029 | RA | 19.0 | 17.2 | 18.7 | 17.8 |
| 34-1032 | RA | 19.8 | 18.1 | 19.9 | 16.7 |
| 34-1140 | RA | 18.6 | 17.2 | 18.6 | 16.5 |
| 34-1333 | RA | 17.2 | 16.3 | 17.2 | 16.3 |
| 34-1625 | RA | 18.3 | 17.2 | 18.6 | 17.3 |
| 34-1666 | RA | 18.4 | 16.3 | 18.4 | 16.6 |
| 34-1779 | RA | 21.2 | 19.1 | 20.8 | 18.6 |
| 34-1847 | RA | 21.2 | 19.1 | 22.2 | 18.9 |
| | | | | | |
| CV | | 23.5 | 2.6 | 3.5 | 9.3 |
| s | | 1.1 | 0.8 | 1.1 | 0.9 |
| SE | | 0.2 | 0.1 | 0.2 | 0.1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Seed size expressed in g 100 seed$^{-1}$

§A dash sign indicates data not reported

Table D5. Maturity by line at individual locations of Population 34 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-0414 | GH† | 140‡ | 131 | 142 | 136 | 128 | 123 |
| 34-0692 | GH | 134 | 128 | 133 | 130 | 125 | 117 |
| 34-0724 | GH/PH | 137 | 129 | 134 | 132 | 125 | 121 |
| 34-0777 | GH | 139 | 130 | 141 | 135 | 127 | 123 |
| 34-1046 | GH | 137 | 129 | 135 | 133 | 126 | 120 |
| 34-1055 | GH | 132 | 128 | 135 | 130 | 125 | 121 |
| 34-1058 | GH | 135 | 129 | 138 | 134 | 127 | 122 |
| 34-1553 | GH | 137 | 130 | 141 | 135 | 128 | 122 |
| 34-1627 | GH | 139 | 129 | 140 | 133 | 128 | 119 |
| 34-1730 | GH | 132 | 127 | 133 | 128 | 124 | 117 |
| 34-1757 | GH | 137 | 129 | 137 | 132 | 126 | 121 |
| 34-0351 | GL | 134 | 123 | 131 | 128 | 124 | 117 |
| 34-0450 | GL | 135 | 129 | 133 | 129 | 124 | 118 |
| 34-0485 | GL | 134 | 124 | 132 | 128 | 124 | 120 |
| 34-0503 | GL | 134 | 126 | 133 | 128 | 125 | 118 |
| 34-0760 | GL | 135 | 127 | 132 | 128 | 125 | 117 |
| 34-0873 | GL | 132 | 127 | 132 | 130 | 122 | 116 |
| 34-1242 | GL | 137 | 125 | 134 | 128 | 124 | 117 |
| 34-1288 | GL | 136 | 124 | 132 | 131 | 124 | 115 |
| 34-1716 | GL | 132 | 127 | 131 | 127 | 125 | 118 |

Table D5. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-1806 | GL | 134 | 126 | 136 | 132 | 122 | 117 |
| 34-1897 | GL | 134 | 123 | 129 | 129 | 119 | 115 |
| 34-0506 | PH | 139 | 129 | 139 | 135 | 128 | 121 |
| 34-0518 | PH | 134 | 124 | 132 | 130 | 125 | 116 |
| 34-0626 | PH | 136 | 129 | 138 | 133 | 127 | 118 |
| 34-0662 | PH | 130 | 122 | 132 | 128 | 122 | 115 |
| 34-0754 | PH | 137 | 125 | 138 | 131 | 126 | 118 |
| 34-0947 | PH | 131 | 128 | 133 | 130 | 124 | 120 |
| 34-1118 | PH | 138 | 129 | 138 | 132 | 127 | 119 |
| 34-1157 | PH | 136 | 128 | 135 | 129 | 125 | 117 |
| 34-1340 | PH | 138 | 129 | 136 | 133 | 127 | 123 |
| 34-1440 | PH | 135 | 129 | 137 | 132 | 127 | 120 |
| 34-0297 | PL | 136 | 129 | 136 | 129 | 126 | 121 |
| 34-0378 | PL | 135 | 129 | 136 | 132 | 126 | 118 |
| 34-0405 | PL | 130 | 127 | 131 | 128 | 125 | 116 |
| 34-0538 | PL | 134 | 124 | 133 | 130 | 124 | 117 |
| 34-0778 | PL | 134 | 124 | 131 | 130 | 124 | 118 |
| 34-1256 | PL | 137 | 128 | 135 | 132 | 126 | 121 |
| 34-1426 | PL | 132 | 127 | 133 | 131 | 125 | 119 |
| 34-1486 | PL | 134 | 123 | 129 | 127 | 125 | 117 |

Table D5. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Gillman, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 34-1609 | PL | 128 | 124 | 128 | 124 | 121 | 112 |
| 34-1654 | PL | 129 | 127 | 131 | 125 | 121 | 116 |
| 34-1808 | PL | 130 | 123 | 128 | 125 | 119 | 110 |
| 34-0467 | RA | 134 | 128 | 131 | 128 | 122 | 113 |
| 34-0679 | RA | 136 | 129 | 136 | 135 | 126 | 122 |
| 34-0761 | RA | 138 | 130 | 140 | 134 | 127 | 119 |
| 34-1029 | RA | 131 | 123 | 131 | 128 | 122 | 117 |
| 34-1032 | RA | 137 | 124 | 135 | 131 | 125 | 117 |
| 34-1140 | RA | 130 | 122 | 129 | 127 | 119 | 111 |
| 34-1333 | RA | 138 | 130 | 140 | 136 | 128 | 123 |
| 34-1625 | RA | 136 | 126 | 134 | 133 | 126 | 118 |
| 34-1666 | RA | 132 | 123 | 132 | 127 | 124 | 117 |
| 34-1779 | RA | 135 | 129 | 133 | 129 | 125 | 120 |
| 34-1847 | RA | 130 | 122 | 126 | 124 | 117 | 110 |
| CV | | 0 | 0 | 0 | 1 | 1 | 0 |
| s | | 3 | 3 | 4 | 3 | 3 | 3 |
| SE | | 0 | 0 | 1 | 0 | 0 | 0 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Days after planting

Table D6. Seed yield by line at individual locations of Population 35 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 35-2039 | GH† | 4381‡ | 4381 | 4421 | 4052 | 3178 | 4576 | 4152 | 4112 |
| 35-2152 | GH | 4401 | 4280 | 4381 | 4287 | 3541 | 3642 | 3910 | 4542 |
| 35-2343 | GH/RA | 4099 | 4125 | 4159 | 3964 | 3494 | 4508 | 4179 | 4555 |
| 35-2455 | GH | 4367 | 4549 | 4797 | 4508 | 3575 | 4334 | 4119 | 4522 |
| 35-2592 | GH/PH | 4273 | 4508 | 4280 | 4159 | 3050 | 4502 | 4199 | 4549 |
| 35-2646 | GH | 4092 | 3998 | 4435 | 3689 | 3050 | 4105 | 4031 | 4515 |
| 35-2671 | GH | 4629 | 3581 | 4092 | 4058 | 3669 | 4334 | 3816 | 3904 |
| 35-2820 | GH | 4488 | 3803 | 4320 | 4401 | 3124 | 3951 | 3722 | 4495 |
| 35-2972 | GH | 4770 | 3971 | 4569 | 4300 | 3527 | 4623 | 3884 | 5153 |
| 35-3049 | GH | 4932 | 4273 | 4388 | 3964 | 3239 | 4293 | 4179 | 4623 |
| 35-3071 | GH/RA | 4643 | 3823 | 4374 | 4240 | 3003 | 4260 | 3931 | 4616 |
| 35-3190 | GH | 4603 | 3957 | 4435 | 4031 | 3212 | 4213 | 3984 | 4267 |
| 35-3787 | GH | 4797 | 3843 | 4092 | 4334 | 3527 | 4435 | 4025 | 4267 |
| 35-1983 | GL | 4542 | 3333 | 4119 | -§ | 3662 | 3904 | 3769 | 4421 |
| 35-2062 | GL | 4112 | 4052 | 4099 | 3138 | 3346 | 4058 | 3447 | 4448 |
| 35-2184 | GL | 4589 | 4515 | 4018 | 3917 | 2681 | 4092 | 4031 | 4146 |
| 35-2244 | GL | 4193 | 4273 | 4253 | 3742 | 3454 | 4300 | 3595 | 3971 |
| 35-2450 | GL | 4347 | 4354 | 4730 | 3924 | 3635 | 3144 | 4065 | 4421 |
| 35-2485 | GL | 4703 | 4099 | 4159 | 4394 | 3830 | 4267 | 3931 | 4267 |
| 35-3253 | GL | 4455 | 3964 | 4220 | 3991 | 3366 | 3722 | 3581 | 4166 |

Table D6. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 35-3388 | GL | 4576 | 4031 | 4186 | 4226 | 3218 | 4515 | 3910 | 4226 |
| 35-3478 | GL | 4038 | 4179 | 4125 | 4085 | 3662 | 4078 | 3830 | 4085 |
| 35-3731 | GL | 3615 | 3521 | 4018 | 4455 | 3279 | 3964 | 3910 | 4777 |
| 35-3801 | GL | 3957 | 4260 | 3796 | 3897 | 3413 | 4220 | 3749 | 3910 |
| 35-2235 | PH | 4280 | 4320 | 4428 | 4011 | 3447 | 4448 | 4125 | 4287 |
| 35-2323 | PH | 4670 | 4818 | 4340 | 4300 | 3467 | 4058 | 3904 | 4515 |
| 35-2684 | PH | 5059 | 4025 | 4502 | 4468 | 3373 | 4455 | 4085 | 4031 |
| 35-2690 | PH | 4542 | 3474 | 4172 | 4226 | 3554 | 4764 | 4092 | 4428 |
| 35-2701 | PH | 4764 | 4031 | 4421 | 4293 | 3642 | 4643 | 3951 | 4280 |
| 35-3018 | PH | 4253 | 3682 | 4589 | 4367 | 3776 | 4650 | 4045 | 5086 |
| 35-3544 | PH | 4603 | 4576 | 4616 | 4280 | 3050 | 3608 | 3790 | 4663 |
| 35-3545 | PH | 4589 | 3957 | 4320 | 4435 | 3299 | 4240 | 4186 | 4495 |
| 35-3927 | PH | 4885 | 4529 | 4374 | 3360 | 3507 | 3816 | 3984 | 4414 |
| 35-3993 | PH | 4582 | 4018 | 4529 | 4206 | 3292 | 4475 | 3964 | 4172 |
| 35-2213 | PL | 4112 | 4609 | 4045 | 4105 | 3265 | 4300 | 3682 | 4381 |
| 35-2270 | PL | 4159 | 4025 | 3601 | 3702 | 2923 | 4031 | 3742 | 3910 |
| 35-2328 | PL | 4804 | 3756 | 4307 | 4656 | 3742 | 4616 | 3931 | 4092 |
| 35-2344 | PL | 4589 | 4011 | 4246 | 4441 | 3178 | 4092 | 3964 | 4408 |
| 35-2366 | PL | 4320 | 4146 | 4643 | 4253 | 3554 | 4193 | 3924 | 4388 |
| 35-2666 | PL | 4549 | 3192 | 3642 | 3386 | 3178 | 3910 | 3460 | 3588 |

Table D6. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Anna, OH | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|---|
| 35-2845 | PL/RA | 3575 | 3561 | 4099 | 3924 | 3366 | 4193 | 3648 | 4011 |
| 35-2874 | PL | 4038 | 3944 | 4092 | 3850 | 3252 | 4146 | 3716 | 3736 |
| 35-2951 | PL | 4246 | 3393 | 4139 | 4233 | 3312 | 4058 | 3937 | 4011 |
| 35-3726 | PL | 4199 | 3769 | 4146 | 3716 | 3413 | 3736 | 3433 | 4031 |
| 35-3757 | PL | 4186 | 3373 | 4005 | 4105 | 3037 | 4367 | 3648 | 3870 |
| 35-2474 | RA | 4354 | 4052 | 4025 | 4105 | 3064 | 4025 | 3937 | 4146 |
| 35-2589 | RA | 4549 | 4495 | 4058 | 4112 | 3937 | 4226 | 3648 | 4522 |
| 35-2728 | RA | 3937 | 3736 | 3830 | 3816 | 3218 | 3749 | 3837 | 4562 |
| 35-2808 | RA | 4428 | 3386 | 4179 | 4394 | 3742 | 4435 | 4616 | 4273 |
| 35-3497 | RA | 4576 | 3729 | 4139 | 3548 | 3400 | 3944 | 3897 | 4273 |
| 35-3536 | RA | 4031 | 4025 | 4186 | 4052 | 3601 | 3890 | 3843 | 4220 |
| 35-3707 | RA | 4643 | 3306 | 4172 | 3931 | 3279 | 4488 | 3749 | 4770 |
| 35-3980 | RA | 4414 | 4038 | 3722 | 4139 | 3648 | 3185 | 3615 | 4542 |
| CV | | 4 | 10 | 5 | 2 | 5 | 2 | 7 | 9 |
| s | | 324 | 379 | 249 | 320 | 247 | 326 | 222 | 300 |
| SE | | 45 | 52 | 34 | 44 | 34 | 45 | 31 | 41 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Seed yield expressed in kg $ha^{-1}$

§A dash sign indicates data not reported

Table D7. Lodging by line at individual locations of Population 35 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-2039 | GH† | 2.0‡ | 1.5 | 2.0 | 1.0 | 1.5 | 1.0 |
| 35-2152 | GH | 2.0 | 1.5 | 2.0 | 1.5 | 1.5 | 1.0 |
| 35-2343 | GH/RA | 1.5 | 1.5 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-2455 | GH | 3.5 | 2.0 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-2592 | GH/PH | 1.5 | 1.0 | 1.5 | 1.0 | 1.0 | 1.0 |
| 35-2646 | GH | 2.5 | 1.5 | 1.5 | 1.0 | 1.5 | 1.0 |
| 35-2671 | GH | 2.0 | 1.5 | 1.0 | 1.5 | 1.0 | 1.0 |
| 35-2820 | GH | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-2972 | GH | 2.0 | 1.0 | 1.5 | 1.0 | 1.0 | 1.0 |
| 35-3049 | GH | 1.5 | 1.5 | 1.0 | 1.5 | 1.0 | 1.5 |
| 35-3071 | GH/RA | 2.0 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-3190 | GH | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-3787 | GH | 2.0 | 1.5 | 2.0 | 1.5 | 1.5 | 1.5 |
| 35-1983 | GL | 1.5 | 1.5 | 1.0 | 1.0 | 1.5 | 1.0 |
| 35-2062 | GL | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 |
| 35-2184 | GL | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-2244 | GL | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-2450 | GL | 2.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-2485 | GL | 1.5 | 1.0 | 1.0 | 1.5 | 1.0 | 1.0 |
| 35-3253 | GL | 1.0 | 1.5 | 1.5 | 1.0 | 1.0 | 1.0 |

Table D7. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-3388 | GL | 3.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-3478 | GL | 2.0 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-3731 | GL | 3.0 | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-3801 | GL | 2.0 | 2.0 | 1.5 | 1.5 | 1.5 | 1.0 |
| 35-2235 | PH | 3.0 | 1.5 | 2.0 | 1.5 | 1.0 | 1.0 |
| 35-2323 | PH | 3.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-2684 | PH | 2.0 | 2.0 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-2690 | PH | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 |
| 35-2701 | PH | 3.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.5 |
| 35-3018 | PH | 3.0 | 2.0 | 2.0 | 1.5 | 1.5 | 1.5 |
| 35-3544 | PH | 2.5 | 2.0 | 2.0 | 1.5 | 1.0 | 1.0 |
| 35-3545 | PH | 1.5 | 2.0 | 1.5 | 1.0 | 1.0 | 1.0 |
| 35-3927 | PH | 2.5 | 1.5 | 1.5 | 1.0 | 1.5 | 1.5 |
| 35-3993 | PH | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.5 |
| 35-2213 | PL | 2.5 | 2.0 | 2.0 | 1.5 | 1.0 | 1.5 |
| 35-2270 | PL | 1.5 | 1.5 | 2.0 | 1.5 | 1.0 | 1.5 |
| 35-2328 | PL | 1.5 | 2.0 | 1.0 | 1.0 | 1.5 | 1.0 |
| 35-2344 | PL | 1.0 | 1.5 | 1.0 | 1.5 | 1.0 | 1.0 |
| 35-2366 | PL | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-2666 | PL | 2.0 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |

Table D7. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-2845 | PL/RA | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-2874 | PL | 1.0 | 1.5 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-2951 | PL | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
| 35-3726 | PL | 1.0 | 1.0 | 1.5 | 1.0 | 1.0 | 1.0 |
| 35-3757 | PL | 2.0 | 1.5 | 1.5 | 1.5 | 1.0 | 1.5 |
| 35-2474 | RA | 2.0 | 2.0 | 1.5 | 1.5 | 1.0 | 1.0 |
| 35-2589 | RA | 1.5 | 1.5 | 2.0 | 1.5 | 1.0 | 1.5 |
| 35-2728 | RA | 2.0 | 2.0 | 2.0 | 1.5 | 1.5 | 1.5 |
| 35-2808 | RA | 2.0 | 2.0 | 1.5 | 1.5 | 1.5 | 1.0 |
| 35-3497 | RA | 2.0 | 1.0 | 1.0 | 1.5 | 1.0 | 1.0 |
| 35-3536 | RA | 1.5 | 1.0 | 1.0 | 1.5 | 1.0 | 1.0 |
| 35-3707 | RA | 2.0 | 1.5 | 1.0 | 1.0 | 1.0 | 1.0 |
| 35-3980 | RA | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.0 |
| | | | | | | | |
| CV | | 7.1 | 6.3 | 6.2 | 8.5 | 5.9 | 8.2 |
| s | | 1.4 | 0.7 | 0.7 | 0.5 | 0.5 | 0.5 |
| SE | | 0.2 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡1 = all plants erect, 5 = all plants prostrate

Table D8. Height by line at individual locations of Population 35 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 35-2039 | GH† | 104‡ | 86 | 84 | 81 | 94 | 91 | 99 |
| 35-2152 | GH | 112 | 97 | 89 | 89 | 102 | 91 | 102 |
| 35-2343 | GH/RA | 99 | 86 | 89 | 84 | 86 | 89 | 104 |
| 35-2455 | GH | 114 | 91 | 86 | 91 | 91 | 97 | 109 |
| 35-2592 | GH/PH | 102 | 86 | 81 | 79 | 81 | 84 | 99 |
| 35-2646 | GH | 104 | 81 | 84 | 81 | 97 | 81 | 99 |
| 35-2671 | GH | 97 | 81 | 76 | 86 | 97 | 86 | 102 |
| 35-2820 | GH | 112 | 81 | 86 | 84 | 91 | 84 | 97 |
| 35-2972 | GH | 109 | 86 | 86 | 86 | 99 | 97 | 102 |
| 35-3049 | GH | 112 | 89 | 89 | 86 | 94 | 94 | 102 |
| 35-3071 | GH/RA | 107 | 81 | 79 | 81 | 79 | 79 | 97 |
| 35-3190 | GH | 109 | 76 | 81 | 84 | 86 | 86 | 99 |
| 35-3787 | GH | 99 | 76 | 79 | 81 | 86 | 84 | 102 |
| 35-1983 | GL | 107 | 84 | 81 | 84 | 91 | 89 | 102 |
| 35-2062 | GL | 99 | 81 | 76 | 79 | 91 | 81 | 97 |
| 35-2184 | GL | 99 | 86 | 76 | 76 | 79 | 84 | 97 |
| 35-2244 | GL | 97 | 86 | 74 | 71 | 89 | 89 | 89 |
| 35-2450 | GL | 109 | 94 | 91 | 89 | 104 | 86 | 107 |
| 35-2485 | GL | 109 | 86 | 86 | 89 | 94 | 84 | 107 |
| 35-3253 | GL | 99 | 86 | 84 | 89 | 91 | 86 | 104 |

Table D8. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 35-3388 | GL | 109 | 86 | 89 | 84 | 94 | 89 | 104 |
| 35-3478 | GL | 102 | 84 | 81 | 81 | 84 | 81 | 99 |
| 35-3731 | GL | 109 | 81 | 86 | 84 | 94 | 91 | 107 |
| 35-3801 | GL | 91 | 81 | 76 | 79 | 86 | 76 | 94 |
| 35-2235 | PH | 109 | 89 | 81 | 81 | 89 | 84 | 99 |
| 35-2323 | PH | 109 | 91 | 84 | 86 | 89 | 89 | 104 |
| 35-2684 | PH | 102 | 86 | 79 | 81 | 94 | 84 | 99 |
| 35-2690 | PH | 99 | 81 | 79 | 81 | 94 | 86 | 102 |
| 35-2701 | PH | 109 | 86 | 91 | 89 | 89 | 86 | 109 |
| 35-3018 | PH | 109 | 81 | 89 | 86 | 86 | 91 | 102 |
| 35-3544 | PH | 117 | 91 | 86 | 91 | 99 | 84 | 99 |
| 35-3545 | PH | 109 | 86 | 89 | 89 | 84 | 84 | 102 |
| 35-3927 | PH | 107 | 91 | 84 | 86 | 91 | 89 | 99 |
| 35-3993 | PH | 117 | 91 | 84 | 86 | 94 | 81 | 107 |
| 35-2213 | PL | 107 | 97 | 81 | 89 | 86 | 86 | 102 |
| 35-2270 | PL | 94 | 86 | 79 | 71 | 84 | 84 | 97 |
| 35-2328 | PL | 104 | 76 | 84 | 89 | 104 | 89 | 109 |
| 35-2344 | PL | 102 | 81 | 79 | 81 | 86 | 81 | 97 |
| 35-2366 | PL | 107 | 91 | 91 | 84 | 89 | 81 | 104 |
| 35-2666 | PL | 91 | 76 | 86 | 74 | 84 | 79 | 89 |

Table D8. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|---|---|---|
| 35-2845 | PL/RA | 99 | 81 | 76 | 81 | 84 | 81 | 94 |
| 35-2874 | PL | 109 | 86 | 79 | 84 | 81 | 84 | 99 |
| 35-2951 | PL | 99 | 81 | 79 | 79 | 89 | 86 | 99 |
| 35-3726 | PL | 94 | 81 | 79 | 76 | 86 | 76 | 94 |
| 35-3757 | PL | 102 | 76 | 74 | 81 | 89 | 76 | 91 |
| 35-2474 | RA | 104 | 86 | 99 | 84 | 94 | 89 | 99 |
| 35-2589 | RA | 99 | 94 | 81 | 79 | 91 | 94 | 99 |
| 35-2728 | RA | 104 | 84 | 79 | 86 | 86 | 84 | 102 |
| 35-2808 | RA | 117 | 81 | 89 | 89 | 89 | 86 | 99 |
| 35-3497 | RA | 109 | 102 | 89 | 91 | 99 | 99 | 109 |
| 35-3536 | RA | 104 | 91 | 86 | 81 | 102 | 84 | 99 |
| 35-3707 | RA | 109 | 91 | 89 | 86 | 94 | 89 | 104 |
| 35-3980 | RA | 109 | 86 | 89 | 94 | 91 | 86 | 102 |
| CV | | 2 | 3 | 2 | 10 | 11 | 3 | 1 |
| s | | 6 | 6 | 5 | 5 | 6 | 5 | 5 |
| SE | | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Height in cm from ground to terminal node

Table D9. Seed size by line at individual locations of Population 35 in 2009.

| Line | Group | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 35-2039 | GH† | 19.6‡ | 17.2 | -§ | 16.4 |
| 35-2152 | GH | 19.4 | 17.2 | 19.8 | 18.6 |
| 35-2343 | GH/RA | 18.3 | 15.4 | 18.6 | 17.6 |
| 35-2455 | GH | 19.7 | 18.1 | 20.0 | 18.1 |
| 35-2592 | GH/PH | 17.6 | 15.4 | 18.9 | 16.7 |
| 35-2646 | GH | 16.9 | 16.3 | 17.5 | 16.3 |
| 35-2671 | GH | 19.1 | 17.2 | 18.7 | 16.2 |
| 35-2820 | GH | 19.5 | 17.2 | 19.7 | 18.2 |
| 35-2972 | GH | 18.1 | 16.3 | 18.2 | 17.3 |
| 35-3049 | GH | 19.8 | 16.3 | 20.1 | 19.2 |
| 35-3071 | GH/RA | 19.7 | 15.4 | 17.6 | 16.5 |
| 35-3190 | GH | 21.1 | 17.2 | 21.6 | 16.5 |
| 35-3787 | GH | 20.4 | 17.2 | 20.4 | 18.9 |
| 35-1983 | GL | - | 17.2 | 18.5 | 17.8 |
| 35-2062 | GL | 18.1 | 16.3 | 18.1 | 16.2 |
| 35-2184 | GL | 18.9 | 17.2 | 18.4 | 17.0 |
| 35-2244 | GL | 20.5 | 18.1 | 20.3 | 17.5 |
| 35-2450 | GL | 21.0 | 17.2 | 19.5 | 17.9 |
| 35-2485 | GL | 19.3 | 17.2 | 19.5 | 17.2 |
| 35-3253 | GL | 19.6 | 17.2 | 18.6 | 16.7 |

Table D9. Continued.

| Line | Group | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 35-3388 | GL | 18.6 | 17.2 | 19.5 | 17.1 |
| 35-3478 | GL | 18.4 | 17.2 | 19.6 | 17.1 |
| 35-3731 | GL | 18.2 | 16.3 | 18.9 | 16.7 |
| 35-3801 | GL | 20.4 | 17.2 | 20.5 | 17.3 |
| 35-2235 | PH | 20.2 | 18.1 | 19.9 | 17.3 |
| 35-2323 | PH | 19.0 | 16.3 | 19.5 | 18.9 |
| 35-2684 | PH | 20.0 | 16.3 | 20.0 | 16.0 |
| 35-2690 | PH | 19.7 | 17.2 | 20.2 | 17.5 |
| 35-2701 | PH | 18.5 | 16.3 | 19.1 | 17.8 |
| 35-3018 | PH | 19.1 | 18.1 | 19.9 | 18.5 |
| 35-3544 | PH | 19.5 | 16.3 | 19.2 | 17.4 |
| 35-3545 | PH | 18.9 | 17.2 | 19.3 | 17.4 |
| 35-3927 | PH | 20.6 | 18.1 | 20.7 | 18.6 |
| 35-3993 | PH | 18.7 | 16.3 | 18.6 | 17.6 |
| 35-2213 | PL | 18.1 | 16.3 | 17.9 | 17.5 |
| 35-2270 | PL | 19.0 | 16.3 | 19.8 | 17.2 |
| 35-2328 | PL | 18.7 | 17.2 | 18.2 | 15.9 |
| 35-2344 | PL | 18.1 | 17.2 | 18.8 | 17.1 |
| 35-2366 | PL | 19.5 | 17.2 | 20.0 | 17.0 |
| 35-2666 | PL | 17.0 | 15.4 | 17.5 | 15.3 |

Table D9. Continued.

| Line | Group | Emery, IL | Metamora, IL | Pesotum, IL | Napoleon, OH |
|---|---|---|---|---|---|
| 35-2845 | PL/RA | 19.5 | 17.2 | 19.6 | 17.8 |
| 35-2874 | PL | 19.4 | 16.3 | 20.5 | 14.6 |
| 35-2951 | PL | 18.5 | 18.1 | 18.3 | 16.0 |
| 35-3726 | PL | 19.1 | 18.1 | 19.2 | 18.8 |
| 35-3757 | PL | 19.8 | 17.2 | 22.1 | 18.3 |
| 35-2474 | RA | 18.9 | 17.2 | 18.7 | 18.2 |
| 35-2589 | RA | 19.3 | 18.1 | 19.5 | 17.6 |
| 35-2728 | RA | 19.8 | 17.2 | 20.4 | 18.3 |
| 35-2808 | RA | 19.3 | 17.2 | 18.8 | 16.9 |
| 35-3497 | RA | 17.2 | 16.3 | 17.8 | 16.2 |
| 35-3536 | RA | 19.2 | 17.2 | 21.2 | 18.6 |
| 35-3707 | RA | 19.9 | 16.3 | 19.7 | 16.8 |
| 35-3980 | RA | 19.0 | 17.2 | 17.9 | 16.4 |
| | | | | | |
| CV | | 4.0 | 4.0 | 2.7 | 3.8 |
| s | | 0.9 | 0.8 | 1.0 | 1.0 |
| SE | | 0.1 | 0.1 | 0.1 | 0.1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Seed size expressed in g 100 seed$^{-1}$

§A dash sign indicates data not reported

Table D10. Maturity by line at individual locations of Population 35 in 2009.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-2039 | GH† | 132‡ | 124 | 132 | 122 | 122 | 118 |
| 35-2152 | GH | 134 | 129 | 136 | 126 | 125 | 121 |
| 35-2343 | GH/RA | 134 | 127 | 133 | 124 | 124 | 118 |
| 35-2455 | GH | 135 | 127 | 134 | 123 | 125 | 118 |
| 35-2592 | GH/PH | 129 | 123 | 128 | 122 | 121 | 117 |
| 35-2646 | GH | 132 | 129 | 132 | 125 | 122 | 117 |
| 35-2671 | GH | 132 | 125 | 132 | 120 | 121 | 118 |
| 35-2820 | GH | 131 | 130 | 135 | 123 | 124 | 121 |
| 35-2972 | GH | 131 | 129 | 135 | 123 | 125 | 118 |
| 35-3049 | GH | 132 | 127 | 132 | 126 | 124 | 118 |
| 35-3071 | GH/RA | 129 | 123 | 128 | 124 | 121 | 112 |
| 35-3190 | GH | 130 | 129 | 129 | 121 | 120 | 118 |
| 35-3787 | GH | 129 | 124 | 128 | 121 | 121 | 117 |
| 35-1983 | GL | 131 | 126 | 132 | 120 | 124 | 121 |
| 35-2062 | GL | 130 | 127 | 129 | 127 | 122 | 118 |
| 35-2184 | GL | 130 | 127 | 132 | 122 | 121 | 116 |
| 35-2244 | GL | 129 | 123 | 129 | 123 | 122 | 117 |
| 35-2450 | GL | 128 | 123 | 132 | 120 | 120 | 120 |
| 35-2485 | GL | 134 | 124 | 133 | 121 | 124 | 117 |
| 35-3253 | GL | 130 | 127 | 132 | 120 | 124 | 117 |

Table D10. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-3388 | GL | 136 | 128 | 135 | 120 | 125 | 121 |
| 35-3478 | GL | 130 | 124 | 129 | 120 | 122 | 120 |
| 35-3731 | GL | 134 | 124 | 131 | 121 | 122 | 114 |
| 35-3801 | GL | 131 | 124 | 129 | 123 | 120 | 121 |
| 35-2235 | PH | 134 | 125 | 135 | 126 | 126 | 118 |
| 35-2323 | PH | 132 | 126 | 132 | 121 | 125 | 120 |
| 35-2684 | PH | 136 | 130 | 139 | 126 | 126 | 121 |
| 35-2690 | PH | 134 | 128 | 135 | 125 | 125 | 121 |
| 35-2701 | PH | 136 | 130 | 140 | 128 | 127 | 124 |
| 35-3018 | PH | 135 | 128 | 136 | 125 | 126 | 119 |
| 35-3544 | PH | 132 | 127 | 131 | 123 | 124 | 120 |
| 35-3545 | PH | 136 | 129 | 139 | 121 | 127 | 118 |
| 35-3927 | PH | 134 | 129 | 132 | 121 | 124 | 122 |
| 35-3993 | PH | 130 | 127 | 132 | 124 | 122 | 117 |
| 35-2213 | PL | 136 | 130 | 140 | 126 | 126 | 118 |
| 35-2270 | PL | 128 | 122 | 127 | 122 | 117 | 116 |
| 35-2328 | PL | 134 | 130 | 135 | 121 | 127 | 122 |
| 35-2344 | PL | 131 | 127 | 133 | 122 | 122 | 118 |
| 35-2366 | PL | 134 | 130 | 136 | 125 | 125 | 121 |
| 35-2666 | PL | 127 | 123 | 127 | 120 | 116 | 111 |

Table D10. Continued.

| Line | Group | Atlantic, IA | Hedrick, IA | Washington, IA | Emery, IL | Metamora, IL | Pesotum, IL |
|---|---|---|---|---|---|---|---|
| 35-2845 | PL/RA | 128 | 122 | 128 | 121 | 119 | 112 |
| 35-2874 | PL | 129 | 124 | 128 | 120 | 121 | 117 |
| 35-2951 | PL | 128 | 123 | 127 | 121 | 119 | 116 |
| 35-3726 | PL | 129 | 124 | 131 | 121 | 122 | 120 |
| 35-3757 | PL | 129 | 122 | 129 | 121 | 119 | 117 |
| 35-2474 | RA | 131 | 127 | 132 | 120 | 122 | 117 |
| 35-2589 | RA | 134 | 128 | 134 | 125 | 125 | 120 |
| 35-2728 | RA | 132 | 127 | 132 | 127 | 125 | 120 |
| 35-2808 | RA | 135 | 129 | 136 | 125 | 125 | 120 |
| 35-3497 | RA | 130 | 124 | 132 | 124 | 121 | 118 |
| 35-3536 | RA | 134 | 125 | 133 | 120 | 121 | 117 |
| 35-3707 | RA | 134 | 129 | 135 | 126 | 124 | 118 |
| 35-3980 | RA | 134 | 130 | 138 | 123 | 126 | 122 |
| | | | | | | | |
| CV | | 1 | 0 | 1 | 1 | 1 | 2 |
| s | | 3 | 3 | 3 | 2 | 3 | 3 |
| SE | | 0 | 0 | 0 | 0 | 0 | 0 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

‡Days after planting

## APPENDIX E

MEAN GERMINATION OF EACH LINE

Table E1. Mean germination of each selected line of Population 34.

| Line | Group | Germination (%) |
|---|---|---|
| 34-0414 | GH† | 91 |
| 34-0692 | GH | 89 |
| 34-0777 | GH | 91 |
| 34-1046 | GH | 77 |
| 34-1055 | GH | 91 |
| 34-1058 | GH | 88 |
| 34-1553 | GH | 90 |
| 34-1627 | GH | 91 |
| 34-1730 | GH | 88 |
| 34-1757 | GH | 90 |
| 34-0724 | GH/PH | 84 |
| 34-0351 | GL | 93 |
| 34-0450 | GL | 83 |
| 34-0485 | GL | 82 |
| 34-0503 | GL | 88 |
| 34-0760 | GL | 90 |
| 34-0873 | GL | 88 |
| 34-1242 | GL | 87 |
| 34-1288 | GL | 82 |
| 34-1716 | GL | 81 |
| 34-1806 | GL | 85 |
| 34-1897 | GL | 89 |
| 34-0506 | PH | 87 |
| 34-0518 | PH | 91 |
| 34-0626 | PH | 90 |
| 34-0662 | PH | 88 |
| 34-0754 | PH | 91 |
| 34-0947 | PH | 75 |
| 34-1118 | PH | 86 |
| 34-1157 | PH | 90 |
| 34-1340 | PH | 85 |
| 34-1440 | PH | 90 |
| 34-0297 | PL | 82 |

Table E1. Continued.

| | | |
|---|---|---|
| 34-0378 | PL | 84 |
| 34-0405 | PL | 84 |
| 34-0538 | PL | 90 |
| 34-0778 | PL | 90 |
| 34-1256 | PL | 89 |
| 34-1426 | PL | 90 |
| 34-1486 | PL | 88 |
| 34-1609 | PL | 86 |
| 34-1654 | PL | 87 |
| 34-1808 | PL | 92 |
| 34-0467 | RA | 92 |
| 34-0679 | RA | 88 |
| 34-0761 | RA | 82 |
| 34-1029 | RA | 95 |
| 34-1032 | RA | 88 |
| 34-1140 | RA | 89 |
| 34-1333 | RA | 87 |
| 34-1625 | RA | 91 |
| 34-1666 | RA | 88 |
| 34-1779 | RA | 92 |
| 34-1847 | RA | 90 |
| | | |
| CV | | 5 |
| S | | 5 |
| SE | | 1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random

Table E2. Mean germination of each selected line of Population 35.

| Line | Group | Germination (%) |
|---|---|---|
| 35-2039 | GH† | 83 |
| 35-2152 | GH | 81 |
| 35-2455 | GH | 85 |
| 35-2646 | GH | 88 |
| 35-2671 | GH | 85 |
| 35-2820 | GH | 83 |
| 35-2972 | GH | 82 |
| 35-3049 | GH | 86 |
| 35-3190 | GH | 77 |
| 35-3787 | GH | 81 |
| 35-2592 | GH/PH | 85 |
| 35-2343 | GH/RA | 83 |
| 35-3071 | GH/RA | 82 |
| 35-1983 | GL | 83 |
| 35-2062 | GL | 82 |
| 35-2184 | GL | 86 |
| 35-2244 | GL | 74 |
| 35-2450 | GL | 89 |
| 35-2485 | GL | 88 |
| 35-3253 | GL | 85 |
| 35-3388 | GL | 84 |
| 35-3478 | GL | 81 |
| 35-3731 | GL | 84 |
| 35-3801 | GL | 74 |
| 35-2235 | PH | 83 |
| 35-2323 | PH | 83 |
| 35-2684 | PH | 83 |
| 35-2690 | PH | 88 |
| 35-2701 | PH | 88 |
| 35-3018 | PH | 84 |
| 35-3544 | PH | 83 |
| 35-3545 | PH | 86 |
| 35-3927 | PH | 83 |

Table E2. Continued.

| | | |
|---|---|---|
| 35-3993 | PH | 80 |
| 35-2213 | PL | 75 |
| 35-2270 | PL | 79 |
| 35-2328 | PL | 89 |
| 35-2344 | PL | 78 |
| 35-2366 | PL | 89 |
| 35-2666 | PL | 80 |
| 35-2874 | PL | 82 |
| 35-2951 | PL | 74 |
| 35-3726 | PL | 71 |
| 35-3757 | PL | 77 |
| 35-2845 | PL/RA | 79 |
| 35-2474 | RA | 71 |
| 35-2589 | RA | 86 |
| 35-2728 | RA | 69 |
| 35-2808 | RA | 85 |
| 35-3497 | RA | 82 |
| 35-3536 | RA | 85 |
| 35-3707 | RA | 85 |
| 35-3980 | RA | 85 |
| | | |
| CV | | 7 |
| s | | 7 |
| SE | | 1 |

†GH=genotypic high, GL=genotypic low, PH=phenotypic high, PL=phenotypic low, RA=random