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Title<br>QUANTITATIVE GENETIC ANALYSIS OF 16 MAIZE POPULATIONS<br>ADAPTED TO THE NORTHERN U.S. CORN BELT<br>By<br>TONETTE PACHO LAUDE

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#### Abstract

Genetic diversity is essential for genome sequencing and a key contributor to increase frequency of favorable alleles for maize improvement. The objectives of this study were to determine the genetic components, assess the genetic diversity, and propose the heterotic grouping of a large sample of short-season maize populations based on multiple traits. Sixteen maize populations were included in a diallel mating design that followed Gardner-Eberhart Analysis (GEAN) II to estimate variety $\left(v_{i}\right)$ and heterosis $\left(h_{i j}\right)$ genetic effects. The general combining ability $\left(g_{i}\right)$ estimates were also determined and used to classify the populations based on their genetic diversity. Data were generated in partially balanced single lattice experiments across North Dakota (ND) locations in 2010, 2011, and 2012. Combined analyses of variance showed significant differences among genotypes. Heterosis effects explained the most among diallel entries sum of squares for grain yield, while $v_{i}$ effects had greater influence on grain quality traits. The $g_{i}$ effects agreed with the genetic effect that had larger contribution to the total among diallel entries sum of squares for various traits. Three groups were formed based on the genetic distances (GD) of the $g_{i}$ estimates. Four heterotic groups were established based on $s_{i j}$ estimates for grain yield. Close correspondence was observed between the groups formed using GD and $s_{i j}$. The heterotic grouping among populations agreed with their genetic background information and heterotic group's specific and general combining ability (HSGCA) estimates. The EARLYGEM 21 populations having exotic background were assigned to a unique heterotic group. The heterotic groups established among these populations will increase breeding efficiency to improve and develop genetically broad-based populations. Inter-population recurrent selection programs can be employed for population crosses with high grain yield and above average grain quality formed by parental populations belonging to different heterotic


groups. Intra-population recurrent selection programs can also be established for the parental populations identified with desirable grain quality traits. These populations will serve as unique germplasm sources of short-season diverse inbred lines to produce the next generation of diverse northern U.S. hybrids. New heterotic patterns have been established as a source of new commercially viable single-cross and population hybrids.

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## DISSERTATION ORGANIZATION

This dissertation is divided into four chapters with two chapters, 2 and 3, each comprising one manuscript. Chapter 1 includes general introduction followed by literature review. The literature review includes a general review on maize production and demand in North Dakota, grain quality traits for genetic improvement, and concepts on genetics of quantitative traits with emphasis on pre-breeding, genetic variance components, heterosis and genetic diversity. Chapter 2 examines the genetic components for grain yield and grain quality traits, and provides a preliminary assessment of useful heterotic groups and patterns from a large sample of maize populations adapted to the northern U.S. Corn Belt. Chapter 3 evaluates the genetic diversity of the 16 maize populations to establish heterotic groups among them. The manuscripts were written in journal form and will be submitted for publication. A chapter on general conclusions follows chapter 3. Appendices to the dissertation containing description of the maize populations used in the diallel analysis, analysis of variance for agronomic traits and individual means for all traits across environments follow the general conclusions.

## CHAPTER 1. INTRODUCTION

Maize (Zea mays L.) is the principal source of energy in many feed rations. Earlier efforts in maize genetic improvement have been oriented toward high grain yield instead of grain quality. In North Dakota (ND), there has been a significant increase in maize area planted and harvested for the past 20 years according to USDA (NASS 2013). Fig. 1 shows that the area planted for maize in hectares increased by more than three fold since 1993. Consequently, the grain harvested $\left(\mathrm{Mg} \mathrm{ha}^{-1}\right)$ increased by more than four fold in the same period. Improvement in maize genotypes has played an important role in the increase in production.


Fig. 1. North Dakota maize production based on grain harvested and area planted from 1993 to 2012 (NASS, 2013).

Maize has shown a variety of uses. In U.S., maize is primarily utilized for feed, food, seed, industrial use, alcohol for fuel use, and for the export market. Fig. 2 shows the distribution of maize uses for the last 20 years. Large demands for maize are attributed to feed, food, seed,


Fig. 2. U.S. maize utilization from 1993 to 2012 (ERS 2013).
industrial use, and alcohol for fuel. Alcohol produced from maize is mainly ethanol, which is currently in significant demand. In 2012, the ND Corn Growers Association (NDCGA) and ND Corn Utilization Council (NDCUC) reported that the increase in maize production has allowed ND to become one of the faster growing U.S. ethanol producer and exporter sectors (Wilson 2012). In addition, the growth of the ethanol industry has been accompanied by an increase in its by-products that are utilized as protein and energy sources for livestock. In relation to protein quality, normal maize kernel is deficient in essential amino acids (lysine, tryptophan, methionine) that are required to meet the nutritional requirements of monogastric animals and also humans (Scott et al. 2004; Pollak and Scott 2005). Because of the deficiencies in essential amino acids, maize protein is not properly utilized. Synthetic amino acids or other protein sources are supplemented to compensate for these deficiencies, but with additional cost (Pollak
and Scott 2005). Therefore, improvement of grain quality is necessary to address the growing demand for feed, ethanol, and its by-product uses. Selection of maize genotypes with higher levels of starch, protein, oil, and amino acids is a potential strategy to improve maize grain and protein quality.

The maize breeding program of the North Dakota State University (NDSU) has introduced and adapted several genotypes from exotic germplasm. Choice of germplasm and maximization of its genetic improvement are vital in a breeding program (Hallauer and Carena 2009). The use of genetically diverse germplasm pools provides potential sources to increase frequency of favorable alleles for maize improvement. Knowledge on population structure and genetic effects involved in quantitative traits can be determined using mating designs. The diallel mating design has been effective in evaluating parents for their general and specific combining ability (Sprague and Tatum 1942). A fixed set of populations for diallel analyses can provide estimates of genetic components and basis for preliminary assessment of heterotic patterns. Moreover, genetic parameter estimates for quantitative traits in a set of genotypes were used to group genotypes based on their genetic similarities (Hanson and Casas 1968; Camussi et al. 1985). In addition, information on heterosis examines the genetic divergence between genotypes (Camussi et al. 1985, Betran et al. 2003). This information is useful in classifying genotypes to heterotic groups. This provides ease and efficiency in planning crosses for a breeding program. The objectives of this study were to (1) determine the genetic components for grain yield and grain quality traits from a set of populations; and (2) assess the genetic diversity and heterotic grouping of a large sample of maize populations adapted to the northern U.S. Corn Belt based on grain yield, agronomic traits, and grain quality traits (starch, oil, protein, density, lysine, methionine, and cysteine). This study also determined appropriate breeding strategies for the
improvement of elite maize populations as source of new early maturing inbred lines for the northern U.S. Corn Belt.

## Literature Review

## Maize

## Domestication and genetic improvement

Maize is one of the crops highly influenced by man. Maize can be traced back to its nearest relative teosinte (Galinat 1988; Boyer and Hannah 2001; Hallauer and Carena 2009) in southern Mexico (Matsuoka et al. 2002). Based on the calculated genetic distance between modern maize and Balsas teosinte, domestication may have happened about 9,000 years ago. This finding is consistent with the archaeological record that maize domestication happened more than 6,300 years ago (Smith 2001).

Modern maize has greatly improved since its domestication. Selection and intermating of superior individuals were the key activities in breeding. Early cultivation of maize prompted farmers and breeders to use open-pollinated cultivars, since maize is a cross-pollinated crop (Hallauer 1987). Among the open-pollinated cultivars, the Corn Belt Dents dominated the U.S. maize germplasm. This race was a product of crosses between Southern Dents and Northern Flints. Reports suggest that the cross to create Corn Belt Dents happened when Southern Dents were replanted by early Northern Flints due to poor stands (Hallauer 1987; Goodman and Brown 1988). Later, the first inbred lines were developed using landrace open-pollinated cultivars as germplasm sources (Hallauer and Carena 2009). The introduction of the inbred-hybrid concept by Shull (1908) made a huge impact on maize yields in the U.S. and worldwide. In the 1930s, double-cross hybrids were developed. These replaced the use of open-pollinated cultivars in the
U.S. This phenomenon improved maize productivity in terms of higher grain yield, better crop stand, and more uniform maturity as compared with open-pollinated cultivars. In the 1960s, when pest control methods and production techniques became available, single-cross hybrids were used on a commercial scale (Hallauer 1987; Hallauer and Carena 2009). Since then, singlecross hybrids have been extensively used in the U.S. and in other temperate countries worldwide. However, complex hybrids and improved open-pollinated cultivars are still being used in developing countries due to economic constraints and environmental stresses (Hallauer and Carena 2009).

## Maize production and demand in ND

The adaptation of maize plants encompasses a wide range of environments, from tropical to temperate ones. North Dakota is characterized to have short-growing environments. The maize growth and production in ND are specifically influenced by temperature, rainfall, and radiation (Ransom et al. 2004). Despite these challenging climatic conditions, maize production has significantly increased over the years (Fig. 1). Area planted for maize has increased by $362 \%$ during the past 20 years. In addition, productivity (grain yield in $\mathrm{Mg} \mathrm{ha}^{-1}$ ) has increased by $457 \%$ in the past 20 years, with an average of $7.38 \mathrm{Mg} \mathrm{ha}^{-1}$ in 2012. The growing interest of ND farmers on maize production is primarily due to the higher profitability of maize over other crops. Ransom et al. (2004) added that the availability of early maturing maize hybrids and more favorable growing environments for maize relative to other cereals also contributed to increase in maize production. At present, the NDSU maize breeding program is the most northern public program in North America (Carena et al. 2009), moving maize north to cooler seasons and west to drier environments. Most of the inbred lines from maize hybrids available to farmers were
developed elsewhere; as a result, industry maize hybrids still have several challenges to adapt to ND environments.

In terms of utilization, majority of maize produced in ND is used for feed and ethanol, with increasing demand in ethanol (Wilson 2012). Fig. 2 shows that feed, food, and ethanol are the major uses of maize in the U.S., and there has been an increasing demand for ethanol in the past 20 years. In addition, as the oil industry is progressing in western ND, more maize is produced for ethanol in the area. Carena (2011) explained that ethanol plants were first established in places where cheap energy sources are available such as coal and oil in western ND. As a consequence to the rapid expansion of the ethanol industry, the production of its byproducts also increased (Klopfenstein et al. 2008). Ethanol by-products such as dried distiller grains with solubles (DDGS) are utilized in the livestock industry as protein and energy sources (Taheripour et al. 2010). Since most of the maize grain produced is used for food, feed, and ethanol, it is necessary to improve grain quality (Scott et al. 2006).

## Grain quality

## Kernel composition

The maize kernel is basically composed of starch, protein, and oil. Upon its physiological maturity, the grain accumulates 70 to $75 \%$ starch, 8 to $10 \%$ protein, and 4 to $5 \%$ oil (Boyer and Hannah 2001). The primary structures of the kernel are endosperm and embryo. Most of the starch is found on the endosperm, and the embryo contains high amounts of protein and oil. Reports suggested that protein and oil concentrations are negatively correlated with starch (Dado 1999; Scott et al. 2006). The primary carbon source for starch and oil biosynthesis in developing maize kernel is sucrose, and the nitrogen coming from amino acids is used for protein synthesis (Dochlert 1990).

Starch processed from wet-milling of dent maize usually yields $66 \%$ starch on a dryweight basis. Other maize types such as waxy and high-amylose maize yield $90 \%$ and $60-70 \%$, respectively (White 2001). The basic starch structure consists of two major polymers, the amylose and amylopectin (Liu 2005). Amylose is a linear polymer with anhydroglucose units linked by $\alpha-D-(1 \rightarrow 4)$ bonds and few branching that can occur at carbon 6 position by $\alpha-D-(1 \rightarrow$ 6) glucosidic bonds. On the other hand, amylopectin is a high molecular weight polymer due to anhydroglucose units linked by $\alpha-D-(1 \rightarrow 4)$ bonds with periodic side branches of anhydroglucose units at carbon 6 position by $\alpha-D-(1 \rightarrow 6)$ glucosidic bonds (Nelson and Pan 1995; Fergason 2001; White 2001). Starch synthesis in maize occurs in amyloplasts (Nelson and Pan 1995), and is initiated at the basal endosperm cells during late kernel development. Starch accumulation happens during kernel maturation, which specifically starts at 7 to 10 days after pollination and peaks up at 30 to 35 days after pollination (White 2001). Improvement in starch biosynthesis has a great influence in grain yield, since starch is the principal storage reserve of maize and other cereals. Moreover, starch granule properties also have effects on eating and cooking qualities of maize used for food, and production of industrial polymers (Pollak and Scott 2005; Jeon et al. 2010). On the other hand, fermented starch is converted to ethanol, an important biofuel source. Ethanol from maize can be produced using wet-mill (33\%) or dry-grind (67\%) methods (Bothast and Schlicher 2005; Bothast 2005). Maize hybrids have been developed with high extractable starch (HES) and high fermentable starch content (HFC) for wet-mill and dry-grind ethanol production, respectively (Bothast 2005).

Storage proteins have been classified based on their extraction and solubility. The different classes are albumins (water soluble), globulins (soluble in saline solution), zein or prolamins (soluble in alcohol), and glutenins (alkali soluble) (Shewry et al. 1995; Vasal 2001;

Shewry and Halford 2002). A normal maize endosperm typically has 3\% albumins, 3\% globulins, $60 \%$ zein, and $34 \%$ glutenins, while protein found in the embryo contains more than $60 \%$ albumins and only 5 to $10 \%$ zein (Vasal 2001). Zein is the major class of storage protein accumulated in the developing endosperm of maize. However, it is limited in essential amino acids lysine and tryptophan (Larkins et al. 1976; Vasal 2001), which are important amino acids in the diets of monogastric animals. Other limiting essential amino acids in livestock diets are methionine and cysteine. These are usually limiting in legume protein sources (Shewry et al. 1995). The discovery of opaque 2 and floury 2 maize mutants allowed the reduction in zein and increase in non-zein proteins that consequently increased lysine and tryptophan (Mertz et al. 1964; Nelson et al. 1965). Using the traditional backcross method, elite maize genotypes were converted to opaque2. The promotion and commercial acceptance of these genotypes became difficult due to the soft and chalky kernel appearance of opaque2 (Vasal et al. 1984; Vasal 2000). Later, Prasanna et al. (2001) reported that selection for opaque 2 genotypes with modified genetic background was found to be effective in improving the negative attributes of the opaque phenotype. Maize improved for limiting amino acids i.e. lysine and tryptophan is beneficial to livestock industry, since livestock feed can be produced at a lower cost (Pollak and Scott 2005). It is also beneficial to dairy cattle (Dado 1999).

Storage lipids or oil in a normal maize kernel is generally $4 \%$ based on seed dry weight (Baud and Lepiniec 2010). On the average, the amount of oil found in the whole kernel is distributed as follows: $>80 \%$ in the embryo, $12 \%$ in aleurone, and $5 \%$ in endosperm (Lambert 2001). The use of oil is determined by the fatty acid composition (Saoussem et al. 2009). According to Poneleit and Davis (1972), three factors affect the fatty acid distribution and final oil content: 1) the duration of synthesis which vary across maize genotypes. Some inbred lines
accumulated linoleic acid longer than other inbred lines; 2) the time of synthesis. If the fatty acid is accumulated early, it will later be metabolized. Therefore, a decrease in fatty acid content will be observed in later stages of kernel development. Ideally, oil stored in the kernel is later used as energy source for germination, respiration, and other metabolic processes; 3) genotypic variation. Different genotypes vary in time and rate of fatty acid synthesis, affecting the final oil content. Saoussem et al. (2009) also observed genotypic variation among maize kernels with varying amounts of linoleic acid. The Illinois long-term selection for high and low kernel oil and protein concentrations using the Burr's White variety successfully improved grain quality (Wassom et al. 2008). The Illinois High Oil strain (IHO) increased oil concentration from 47 to $193 \mathrm{mg} \mathrm{g}^{-1}$ after 90 cycles of ear-to-row selection, and the Illinois Low Oil strain (ILO) decreased oil concentration to less than $10 \mathrm{mg} \mathrm{g}^{-1}$ after 87 cycles of selection. According to Lambert (2001), high oil maize is utilized for livestock feeds. For the food industry, alteration of maize fatty acid composition provided healthier vegetable oil by selecting for maize genotypes with higher levels of oleic acid and lower levels of saturated fatty acids (Pollak and Scott 2005).

## Grain quality improvement

Several maize kernel mutants have been discovered since the early 1900s (Boyer and Hannah 2001). Table 1 provides the list of genes affecting the grain quality of maize and description on their major effects on kernel composition. The long-term selection experiments at the University of Illinois (Wassom et al. 2008) showed successful improvement in oil and protein concentration using the available genetic variation in Burr's White. The IHO strain was allowed to undergo 90 selection cycles to achieve $19.3 \%$ oil content. Bletsos and Goulas (1999) used mass selection to improve grain yield and protein concentration for a genetically narrowbased maize population. The experiment was conducted for three cycles, but no measurable

Table 1. Genes affecting maize kernel storage compounds composition ${ }^{\text {a }}$.

| Gene | Symbol | Chromosome | Mature kernel phenotype | Major changes in kernel composition ${ }^{\text {b }}$ |
| :---: | :---: | :---: | :---: | :---: |
| Carbohydrate |  |  |  |  |
| amylose extender 1 | ael | 5 | tarnished, glassy | increase in amylose and loosely branched polysaccharide |
| brittle1 | bt1 | 5 | collapsed, angular, translucent, brittle | increase in sugar, decrease in starch content |
| brittle-2 | $b t 2$ | 4 | collapsed | increase in sugar, decrease in starch content |
| dull1 | du1 | 10 | tarnished, sometimes shrunken or dented | increase in amylase |
| miniature seed1 | mn1 | 2 | small, slightly defective | none |
| shrunken1 | sh1 | 9 | collapsed with smooth indentation of crown | increase in sugar, decrease in starch content |
| shrunken-2 | sh2 | 3 | collapsed, angular, brittle | increase in sugar, decrease in starch content |
| shrunken-4 | sh4 | 5 | shrunken, floury | increase in sugar, decrease in starch content |
| soft starch1 | h1 |  | soft, opaque |  |
| sugary1 | su1 | 4 | wrinkled, translucent | increase in sugar, decrease in starch content |
| sugary-2 | su2 | 6 | glassy, translucent to opaque | increase in sugar, decrease in starch content |
| waxy1 | wxl | 9 | opaque | $\sim 100 \%$ amylopectin |
| Protein |  |  |  |  |
| floury1 | fl1 | 2 | opaque, soft, floury | general reduction in zein |
| floury2 | $f l 2$ | 4 | opaque, soft | general reduction in zein, altered amino acid content |
| floury3 | fl3 | - | opaque, soft | general reduction in zein, and increase in lysine |
| opaque 1 | o1 | 4 | opaque, soft, floury |  |
| opaque2 | o2 | 7 | opaque | decrease in the accumulation of 22$\mathrm{kDa} \alpha$-zeins, and altered amino acid content |
| opaque 5 | o5 | 7 | opaque, lighter yellow, not floury | none |
| opaque 6 | o6 |  | crumpled, opaque, floury | general reduction in zein |
| opaque7 | o7 | 10 | opaque, floury | decrease in the accumulation of 22$\mathrm{kDa} \alpha$-zeins, and increase in lysine |
| defective endospermB30 | De-B30 | 7 |  | general reduction in zein |
| mucronate1 | Mc1 |  | opaque | general reduction in zein, and increase in methionine |
| Oil |  |  |  |  |
| linoleic acid1 | $\ln 1$ |  | normal | lower oleic acid to linoleic acid ratio |
| ${ }^{\text {a }}$ Adapted from Boyer and Hannah (2001) and modifications from Neuffer et al. (1997). ${ }^{\mathrm{b}}$ Information was obtained from Motto et al. (2011), except for linoleic acid1 (Neuffer et al. 1997). |  |  |  |  |

differences among cycles were observed. More cycles of selection were necessary to observe significant differences. With the advancements in molecular biology, more researchers try to commercially manipulate important genes to improve grain quality by identifying genes that affect composition, development, and structure of the maize kernel focusing on the pathways involved in the biosynthesis of starch, storage proteins, and lipids (Balconi et al. 2007; Motto et al. 2009).

## Determination of grain quality

The chemical and physical laboratory analyses to determine grain quality have been routinely used by many laboratories worldwide. However, these analyses are labor intensive and time consuming. Only a limited number of samples can be done in a single run (Montes et al. 2006; Burgers 2009). Breeders require fast, efficient, cost-effective, and non-destructive methods that can handle large number of samples per day. Therefore, an alternative method that can work for breeding purposes is the use of near-infrared spectroscopy (NIRS). This method has been used as early as in the 1960s to determine moisture content from seed extracts. A multivariate calibration approach was used (Hart et al. 1962). In the early 1980s, NIR was first recognized by the American Association of Cereal Chemist (AACC) as an analytical procedure to determine protein content in wheat, as cited by Agelet and Hurburgh (2010). Nowadays, more laboratories are using NIRS due to its accuracy, rapid screening and results, non-destructive nature, and affordability (Burgers 2009; Montes et al. 2006; Berardo et al. 2009). The NIR that passes through a sample can be absorbed, reflected, or transmitted. NIR measurements can be done using transmittance taken at lower wavelengths ( $<1,800 \mathrm{~nm}$ ), and diffuse reflectance measurements at higher wavelengths (1,200 to 2,500 nm) (Agelet and Hurburgh 2010). Moreover, transmittance measurements require fixed pathlength, and reflectance measurements
are more flexible, but are affected by the sample physical characteristics. Whole grain samples of maize can be analyzed using NIRS to predict their moisture, protein, oil, starch, density (Orman and Schumann 1991; Berardo et al. 2009; Montes et al. 2006), and some essential amino acids (Pollak and Scott 2005).

## Genetics of quantitative traits

Maize breeding for quantitative traits involves the following phases: pre-breeding, genetic improvement, and development and testing of inbred lines for hybrid use (Hallauer and Carena 2009). Understanding the concepts of pre-breeding, genetic variance components, and genetic diversity and heterosis are necessary to learn more about the germplasm and come up with strategies for genetic improvement.

## Pre-breeding

The concept of pre-breeding is gaining more interest to breeders. This allows breeders to increase frequency of favorable alleles from the diverse maize germplasm pools. Pre-breeding involves long-term efforts on germplasm introduction, adaptation, evolution, and improvement for breeding purposes (Hallauer and Carena 2009). Nass and Paterniani (2000) suggested that pre-breeding links germplasm resources and breeding programs. Germplasm used in prebreeding are unadapted materials, which includes exotic, semi-exotic, and even adapted materials not subjected to any type of selection for improvement. Hallauer and Miranda (1988) defined exotics as any germplasm that does not have immediate use unless selected for adaptation in a particular area.

Pre-breeding has been an important concept in the development of single-cross hybrids (Hallauer and Carena 2009). It is useful in generating new base populations and identifying heterotic patterns for hybrid programs (Nass and Pateriani 2000). The use of germplasm
collections allows breeders to create new heterotic patterns between populations for reciprocal recurrent selection, and develop inbred lines and hybrids based on combining ability (Crossa et al. 1990). Moreover, intra-population recurrent selection programs can also be used for populations used for developing superior open-pollinated varieties.

The limited germplasm pool used in the U.S. encouraged the importance of pre-breeding in many breeding programs (Hallauer and Carena 2009). Researchers showed the potential in using exotic germplasm for different breeding goals. RuMing et al. (1998) evaluated the genetic variability in exotic $\times$ adapted maize germplasm for resistance to maize weevil (Sitophilus zeamais). The breeding crosses showed highly significant differences for maize weevil resistance, which were useful in developing maize weevil resistant hybrids or cultivars. Nass and Coors (2003) introgressed Latin American germplasm from the Germplasm Enhancement of Maize (GEM) national program to their adapted silage germplasm. Their results suggest that several GEM breeding crosses showed potential for yield and silage quality improvement. Ng et al. (1997) used 62 exotic lines to evaluate thermal properties of starch. Using differential scanning calorimetry, significant differences among the 62 exotic lines were observed for gelatinization values (i.e. gelatinization onset, range, peak height index, and enthalpy). The existing variation was sufficient enough to be used for further breeding activities. Sharma and Carena (2012) incorporated tropical and temperate elite exotic germplasm to increase the genetic diversity of early maturing maize. They found that exotic incorporations could be useful sources to identify early maturing maize genotypes with better adaptation, yield, drought tolerance, disease resistance, and grain quality.

The NDSU maize breeding program gives strong emphasis on germplasm adaptation to maximize genetic improvement of adapted germplasm, and to develop elite and unique cultivars
(Carena 2011). This breeding program integrates pre-breeding with cultivar development to keep up with the changing climatic patterns and market demands. Maize for ethanol is becoming a popular demand in ND particularly in the western part of the state. Western ND is characterized to have a short-season drought environment. Most of the hybrids available from the industry have been bred elsewhere, and they are late-maturing with below average grain quality, drought and cold tolerance, and rate of dry down (Carena et al. 2009; Carena 2011). Local pre-breeding can provide genetically broad-based cultivars that have adaptive advantages over adverse environments supplementing industry needs for stable cultivars in the northern U.S. Therefore, adapted exotic germplasm can be used to maximize genetic improvement, and provide unique and quality cultivars for ND.

## Genetic variance components

Information on genetic variances and heritabilities is essential in all phases of crop improvement (Dudley and Moll 1969). Fisher (1919) first attempted to partition the genetic variance into additive genetic variance, dominance genetic variance and epistatic variance. The total additive genetic variance is described as the sum of the additive genetic variances contributed by individual loci (Dudley and Moll 1969). The additive genetic variance for a single locus can be determined by the gene frequency and average effect of gene substitution. Falconer and Mackay (1996) emphasized that additive genetic variance can also arise from genes with varying levels of dominance or epistasis. The additive variance can also be fixed and used to predict response to selection (Robinson and Comstock 1955). The dominance genetic variance, on the other hand, is the result of within-locus variance after subtracting the additive genetic variance from the total within-locus variance. Unlike additive genetic variance, the dominance genetic variance cannot be fixed because its occurrence, direction and magnitude may be
dependent on the scale used to represent the variable expression of a trait. The epistatic variance may exist when the genotype refers to more than one locus (Falconer and Mackay 1996). This was partitioned into different types based on the possible interactions between additive and dominant genetic variance (Cockerham 1954; Kempthorne 1955). Epistatic variance refers to the non-additive genetic variance among loci, contrary to dominance genetic variance that is due to non-additive genetic variance within a locus (Hallauer and Miranda 1988). Only the additive types of epistasis can be fixed, however it is believed that epistasis plays a role in determining hybrid vigor (Mather and Jinks 1971; Hallauer and Miranda 1988).

Some scientists believe that additive genetic variance is the principal contributor to the total genetic variance in some crops (Robinson and Harvey 1955; Lonnquist 1967; Hallauer 1968; Sprague and Eberhart 1977; Betran and Hallauer 1996; Garay et al. 1996; Lamkey and Edwards 1999; Malik et al. 2004); in flint and dent heterotic groups developed in the 30 years hybrid breeding efforts of the University of Hohenheim (Fischer et al. 2008); in yield among the 18 maize populations (Naspolini Filho et al. 1981); and in the quality protein maize (QPM) inbred lines (Hohls et al. 1996). According to Falconer and Mackay (1996), additive genetic variance is the primary cause of resemblance between relatives, and determinant of the observable genetic properties of populations. In contrast, several researchers suggested that dominance genetic effects were important in the inheritance of yield among six maize inbred lines (Gamble 1962); in BSSS germplasm (Holthaus and Lamkey 1995); and in BSCB1(R)C13 (Wardyn et al. 2007). The increase in dominance genetic effects in BSCB1(R)C13 was speculated to be caused by drift and linkage disequilibrium. The role of epistasis in the expression of quantitative traits, like yield, is not yet conclusive. Eberhart et al. (1966), Chi et al. (1969) and Wright et al. (1971) suggested the minor importance of epistasis to random-mating
populations. However, epistasis showed more influence for quantitative traits like yield (Jinks 1954; Hayman 1957; 1958; Lamkey et al. 1995; Ceballos et al. 1998); in grain yield and its components using 294 recombinant inbred lines from Yuyu22 population (Ma et al. 2007); and in several other quantitative traits in both selected and unselected maize populations (Stuber and Moll 1971). On the other hand, Todorovic et al. (1997) noted the primary importance of dominant and epistatic genetic effects in grain yield of the hybrids studied. Moll et al. (1965), Brncic (1954), and Vetukhiv (1954) suggested that the importance of epistasis becomes more evident with more diverse parents of the crosses.

## Estimation of genetic variance components

Appropriate mating and environmental designs are important to estimate the genetic variance components of populations. Diallel analyses have been used to evaluate general and specific combining ability (Sprague and Tatum 1942). The differences of general combining ability (GCA) are attributed to additive variance and additive x additive interactions in the base population, while the differences of specific combining ability (SCA) show the existence of nonadditive genetic variance (Falconer and Mackay 1996). Knowledge of the combining ability of the populations used in a breeding program is important in creating a superior germplasm for developing composite cultivars and their hybrids for direct commercial use, as well as classifying populations into heterotic groups for further improvement.

The two basic approaches of diallel analyses involving homozygous parents are Hayman's (1954) and Griffing's (1956) approaches. The diallel analysis of Hayman (1954) uses a full diallel set consisting of parents, $\mathrm{F}_{1} \mathrm{~S}$ and reciprocals. This approach also follows a fixed model (Model I) in which the parents are considered as the population on which inferences are to be made. Similarly, Kempthorne (1956) used homozygous parents for diallel analysis, and
generated similar results with Hayman's (1954) approach when epistasis is ignored.
Kempthorne's (1956) approach considers a random model (Model II), wherein the parents are assumed to be randomly sampled from a larger population. Griffing's (1956) approach is based on Models I and II, where four methods of diallel analysis are proposed to include: parents, $\mathrm{F}_{1}$ 's and reciprocals (Method 1), parents and $\mathrm{F}_{1}$ 's only (Method 2), $\mathrm{F}_{1}$ 's and reciprocals (Method 3), and $F_{1}$ 's only (Method 4). The choice among the four methods to be used would depend on the type of experimental materials and the breeding objectives.

A model proposed by Gardner and Eberhart (1966) called Gardner-Eberhart Analysis (GEAN) is suitable not only for homozygous parents i.e. inbred lines and pure line cultivars, but also for random mating varieties in Hardy-Weinberg equilibrium. It provides estimates for genetic effects and heterosis. Deviation for the model provides a test for linkage and epistasis. The model aids the breeder in selecting breeding materials, and in designing breeding strategies that will increase the probability of creating better inbred lines or improved cultivars. It can estimate more genetic parameters with additional types of populations. GEAN I requires parents, crosses, and their inbred progenies. It provides information on additive and dominance genetic effects, heterosis and inbreeding depression. The GEAN II is evaluated using parents and their crosses. The variation among all populations is then partitioned into varieties (parents) and midparent heterosis, which is subdivided into average, variety, and specific heterosis. However, additive and dominance genetic effects cannot be estimated separately in GEAN II, since the genetic effects are confounded in the "variety" parameter. For GEAN III, the sources of variation are parents, parents vs. crosses, and crosses (Gardner and Eberhart 1966; Zhang et al. 2005). It provides estimates of variety and GCA effects, the latter of which is estimated similar to Griffing's Method 4, Model 1 (Zhang et al. 2005). In addition, both GEAN II and GEAN III
provide estimates of average heterosis and SCA effects (Gardner and Eberhart 1966; Murray et al. 2003; Zhang et al. 2005).

Several researchers have been successful in the use of GEAN for estimating variety, heterosis, GCA, and SCA effects in variety diallel crosses. Misevic et al. (1989) did a six parent population diallel using GEAN II to determine heterotic patterns among high oil populations and to identify superior high oil populations for use in recurrent selection programs. Variety effects explained most of the among diallel entries sum of squares for oil percentage, grain yield, and moisture. The additive genetic effects seemed to be more important than non-additive in terms of oil percentage due to a low fraction of heterosis effects to the total among diallel entries sum of squares. Araujo and Miranda Filho (2001) observed similar pattern for grain yield. However, Santos et al. (1994) reported greater influence of heterosis effects over variety effects on grain yield using 28-parent diallel. Using GEAN III, Melani and Carena (2005) indicated the predominance of additive gene effects as noted by larger sum of squares observed in GCA than SCA in 10 northern maize populations evaluated for multiple traits. Moreover, Osorno and Carena (2008) studied the genetic relationships among maize populations for grain quality using GEAN III. Their results also revealed the importance of GCA over SCA in most of the traits except for protein and starch contents. Additionally, Jumbo and Carena (2008) also noted larger contribution of GCA compared to SCA effects for most traits evaluated among the diallel entries. They also identified significant maternal and reciprocal effects on ear height. Jampatong et al. (2010) performed a diallel mating design on 10 improved maize populations (incorporated with exotic germplasm) to evaluate their breeding potential for hybrid breeding programs. Highly significant differences due to GCA and SCA effects for yield were observed. Greatest GCA and variety effects were observed on KS23(S)C5 over other populations. Development of crosses
from the population with Suwan1 and its derivatives were recommended for hybrid breeding programs. Diallel studies, therefore, have shown useful information for estimating genetic effects, and for identifying appropriate breeding and selection strategies for future breeding activities.

## Heterosis and genetic diversity

Heterosis is the superior performance of offspring compared with their parents. Exploitation of heterosis by breeders contributed to the significant yield increase of crops, especially in maize. Heterotic groups and heterotic patterns generate vital information in hybrid breeding. A heterotic group is defined as a group of related or unrelated genotypes from the same or different populations that display similar combining ability or heterosis when crossed with genotypes from other genetically distinct germplasm groups. Heterotic pattern is based on a cross between known genotypes that expresses high level of heterosis (Melchinger and Gumber 1998; Carena and Hallauer 2001). According to Reif et al. (2005), the performance of a hybrid population increases with the divergence of the parent populations. Hence, when establishing heterotic patterns, the two populations should be composed of genetically distinct germplasm.

Genetic diversity between two populations, on the other hand, refers to the difference in genotypic compositions for the populations. This difference can be brought about by geographical isolation accompanied by favorable genetic drift and selection in different environments. Moll et al. (1962) studied six maize varieties from three geographical regions to determine the relationship of genetic diversity and heterosis in variety crosses. The results of their study indicated that heterosis was greater with increased genetic diversity. However, a later study by Moll et al. (1965) indicated that the direct relationship between heterosis and genetic diversity is only true to a restricted range of genetic divergence. Extremely divergent crosses
resulted in a decrease in heterosis. It was noted that there is an optimum degree of genetic divergence, beyond which crosses may experience incompability such as those caused by cytological irregularities. Similarly, Prasad and Singh (1986) found that higher heterosis for grain yield in maize was observed from crosses with moderate parental diversity than from crosses with extreme parental diversity. Moreover, they emphasized that high per se performance (not only genetic diversity) should also be considered when selecting parents for hybridization.

In maize hybrid breeding, information on the genetic relationship of inbred lines is useful in planning crosses for hybrid and line development, assigning lines to heterotic groups and identifying of inbreds for plant variety protection. Methods used in assessing genetic similarity (or distance) between lines, populations or races, may be based on analysis of pedigree data (Melchinger et al. 1991; Mohammadi and Prasanna 2003), morphological data (Osorno and Carena 2008; Badu-Apraku et al. 2006), genetic parameter estimates (Camussi et al. 1985), heterosis data (Badu-Apraku et al. 2013a; 2013b), biochemical data or molecular marker data (Mohammadi and Prasanna 2003; Melchinger et al. 1991; Betran et al. 2003). The genetic relationships between genotypes can be presented in cluster analysis or principal coordinate analysis. The cluster analysis is commonly used, since it identifies groups that show high internal homogeneity (within groups) and high external heterogeneity (between groups) (Mohammadi and Prasanna 2003). Among the methods for cluster analysis, the UPGMA (Unweighted Paired Group Method using Arithmetic averages) method is the most common, followed by the Ward's minimum variance method (Mohammadi and Prasanna 2003; Padilla et al. 2007; Badu-Apraku et al. 2006). Mohammadi and Prasanna (2003) stated that molecular marker data provide more reliable differentiation of genotypes, since these are less affected by environmental effects. However, when genotypes are to be assigned to heterotic groups, it becomes challenging
(Melchinger and Gumber 1998). Several researchers suggested that field experiments are still needed to validate heterotic relationships among the genotypes that were characterized based on molecular markers (Melchinger and Gumber 1998; Barata and Carena 2006). These experiments are essential in identifying heterotic patterns and/or specific heterotic combinations.

Conventional hybrids are produced from inbred lines through single-cross, three-way cross, or double-cross combinations. Alternatively, heterosis can also be exploited through genetically broad-based germplasm upon hybridization of elite populations to develop population hybrids (Carena 2005; Carena and Wicks 2006). Improved maize germplasm through recurrent selection reduced the mean differences between population hybrids and single-cross hybrids. As a result, population hybrids identified by Carena (2005) were comparable with commercial hybrids for grain yield and agronomic performance. Carena (2007) suggested that extensive testing of population hybrids is an effective approach to further select and improve germplasm resources with high mean performance, useful genetic variability, and excellent combining ability.

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## CHAPTER 2. DIALLEL ANALYSIS AMONG 16 MAIZE POPULATIONS ADAPTED TO THE NORTHERN U.S. CORN BELT


#### Abstract

Genetically diverse germplasm is needed to increase frequency of favorable alleles of economically important traits in maize improvement. The objectives of this study were to determine the genetic components involved in grain yield and grain quality traits, and provide preliminary assessment of useful heterotic groups and patterns from a large sample of maize populations adapted to the northern U.S. Corn Belt. Sixteen populations were used in diallel mating design following Gardner-Eberhart Analysis (GEAN) II to estimate variety ( $v_{i}$ ) and heterosis $\left(h_{i j}\right)$ genetic effects for grain yield and grain quality traits. Specific heterosis $\left(s_{i j}\right)$ and predicted means of population crosses for grain yield were used to evaluate the heterotic relationships among the populations. Data for grain yield and grain quality traits were generated in partially balanced single lattice experiments across North Dakota (ND) locations in 2010, 2011, and 2012. Analyses of variance showed significant differences among genotypes. Heterosis effects explained most of the differences among diallel entries for grain yield, while $v_{i}$ effects had greater influence on grain quality traits. NDL, EARLYGEM 21c, NDSCD(FSCS)C2, NDSS, and NDSM(M-FS)C9 were identified as elite populations for grain quality improvement. NDSS x NDBS22(R-T1)C9 and NDBS1011 x EARLYGEM 21c showed high $s_{i j}$ effects for grain yield with good grain quality. NDSS and EARLYGEM 21c represent stiff stalk synthetic (SSS) group, and NDBS1011 fall under non-SSS group. Further studies need to validate the heterotic group of NDBS22(R-T1)C9. Recurrent and pedigree selection programs will be established for selected populations and population crosses to integrate pre-breeding with cultivar development.


## Introduction

Pre-breeding allows plant breeders to increase frequency of favorable alleles from genetically diverse germplasm. This concept encompasses germplasm introduction, adaptation, evolution, and improvement for breeding purposes (Hallauer and Carena 2009). The North Dakota State University (NDSU) maize breeding program puts a strong emphasis on germplasm adaptation, germplasm improvement, and development of not only unique cultivars (Carena 2011), but also development of applied breeding methodologies for fast screening of genetically complex traits. Recurrent selection has been one of the most important breeding methodologies used to improve maize populations in order to serve as diverse sources of unique cultivars that meet the growing demands in the northern U.S. Corn Belt. Improved populations from recurrent selection programs are characterized to be heterogeneous and heterozygous in terms of allele frequencies. These make them useful sources to increase the frequency of favorable alleles for developing high yielding cultivars with above average grain quality for the northern U.S. Corn Belt.

Mating designs have been widely used to examine the genetic components of the set of genotypes in terms of the genetic effects involved in quantitative traits. These designs allow screening of large population samples. The diallel analysis for a fixed set of populations can provide estimates for genetic effects and a basis for the preliminary assessment of heterotic groups. The heterotic groups can be assumed based on their combining ability with other populations. Consequently, alternative heterotic patterns among population crosses can also be identified. Gardner and Eberhart (1966) proposed a model to estimate genetic effects from a diallel cross of a fixed set of random-mating populations with arbitrary gene frequencies at all
loci assuming diploid inheritance and no epistasis. The GEAN I is a complete model, which consists of parents, selfed parents, crosses, selfed crosses, and random mated crosses. This analysis gives information on inbreeding depression, heterosis, and additive and dominance genetic effects. A modification of GEAN I was also presented as GEAN II and III, which only include parents and crosses. GEAN II provides estimates for the effects of $v_{i}$ and $h_{i j}$ and its components [average $(\bar{h})$, variety $\left(h_{i}\right)$, and specific heterosis $\left(s_{i j}\right)$ ]. Since GEAN II does not include selfing for parents and crosses, additive and dominance genetic effects are confounded in $v_{i}$ effects. GEAN III uses the same set of genotypes as GEAN II, and it provides estimates for general combining ability $\left(g_{i}\right)$ and specific combining ability effects observed in crosses. Estimation of effects for GEAN III is similar to Griffing's method 4, Model I (1956). Relative to GEAN III, the GEAN II provides more information in terms of the number of genetic effects estimated. The overall heterosis is subdivided to $\bar{h}, h_{i}$, and $s_{i j}$, which provide detailed explanation on the cause of heterosis. These heterosis parameters are attributed to the differences in gene frequencies in parents $i$ and $j$, and to dominance. As explained by Gardner and Eberhart (1966), the $\bar{h}$ contributed by the parents used in crosses is the difference between the mean performance of all crosses and all parents. The $h_{i}$ is the mean heterosis contributed by parent $i$ in its crosses measured as the deviation from $\bar{h}$. The $s_{i j}$ is the heterosis observed when parents $i$ and $j$ are mated. Furthermore, genetic effects for GEAN III can be derived from GEAN II. The $g_{i}$ effects are equal to $h_{i}$ and half of the $v_{i}$ effects, and specific combining ability effects are equivalent to $s_{i j}$. Several researchers have used GEAN II for assessing genetic effects for yield (Santos et al. 1994), plant height and earliness (Araujo and Miranda Filho 2001), and oil content (Misevic et al. 1989).

Grain quality is becoming an important concern for maize growers in ND as ethanol plants are planning to pay premiums on high quality maize. In addition to the fact that maize is the primary energy source in many feed rations for livestock, the demand for maize grain has greatly increased due to higher demand for ethanol (Wilson 2012). Ethanol plants have been established in areas where there are cheap energy sources available i.e. coal and oil in western ND (Carena 2011). The growth in the ethanol industry accompanies increased production of dried-distiller grains with solubles, which are utilized by livestock as protein and energy sources (Taheripour et al. 2010; Klopfenstein et al. 2008). Thus, breeding for improved grain quality is desirable to maximize the nutritional and industrial potential of maize, and consequently, provide added value. A normal maize kernel typically has $70-75 \%$ starch, $8-10 \%$ protein, and $4-5 \%$ oil at physiological maturity (Boyer and Hannah 2001). Additionally, the amounts of essential amino acids, lysine, tryptophan, and methionine, are limited in the normal maize kernel (Larkins et al. 1976; Vasal 2001; Pollak and Scott 2005). Lysine, tryptophan, methionine together with cysteine are among the essential amino acids limiting in the diets of monogastric animals (Shewry et al. 1995). Deficiencies in these essential amino acids lead to poor utilization of maize protein.

Pollak and Scott (2005) explained that the deficiencies can be corrected with dietary supplementation using other protein sources or synthetic amino acids, but these supplements require additional cost. Selection of maize genotypes with higher levels of starch, protein, oil, and amino acids is necessary to improve grain and protein quality, at little or no added cost. However, a large and diverse sample of genotypes is needed for initial screening. The genetic diversity available from the populations improved through recurrent selection is a potential source to increase frequency of favorable alleles for grain quality. The objectives of the study were to determine the genetic components for grain yield and grain quality traits, and provide a
preliminary assessment of useful heterotic groups and patterns from a large sample of maize populations adapted to the northern U.S. Corn Belt.

## Materials and Methods

Plant materials

The 16 maize populations used in this study have been improved and adapted to ND environmental conditions. Six populations were developed at NDSU [NDBS1011, NDL, NDSS, NDSAB(MER-FS)C15, NDSCD(FS-CS)C2, and NDSM(M-FS)C9]. Even though NDBS1011 was developed at NDSU, the cross was made between two populations of Iowa origin (BS10 and BS11), and was adapted to ND short-seasons. The remaining 10 populations originated from different areas prior to their adaptation and improvement at NDSU. Three populations were from Iowa origin [NDBS11(FR-M)C3, NDBS21(R-T)C9, and NDBS22(R-T1)C9]. One population derived from Ohio, Leaming(S-FS)C6, was adapted to and improved under Iowa conditions prior to adaptation to and improvement under ND conditions. NDBSK(HI-M)C3 was developed at the Nebraska Agricultural Experiment Station and was later improved under Iowa and ND conditions. NDCG(FS)C1 originated from two synthetic populations developed at the University of Guelph, Canada, and later was adapted to and improved under ND. NDSHLC(M-FS)C5 represents a highland tropical maize population from Mexico. This population was adapted to and improved under ND conditions, too. Three populations, EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c, are temperate maize populations created in ND with EarlyGEM lines developed from South American breeding crosses and selected for different traits. These 16 populations were chosen to represent a large part of the diversity present in the NDSU maize
breeding program. Detailed description on the development of each population is presented in Appendix A.

## Development of test materials

Each population was increased and intercrossed following the diallel mating design in two breeding nurseries: 1) the 2009 Fargo, ND summer breeding nursery, and 2) the 2010-2011 Salta, Argentina winter breeding nursery. Additional crossing was conducted in the winter nursery because of the 2009 ND cool and wet growing season that led to a small population size to represent each population. Two-paired rows consisting of 30 plants each were grown to obtain seeds for the population cross. The crosses were made by using each male parent to pollinate only one ear shoot. This procedure allowed as many gametes as possible to be represented within the population cross. Used tassels were broken to ensure that these would not be used to cross another ear shoot. The pollinated ears from four rows were harvested, dried, and shelled individually, and balanced bulks were created and kept in cold storage for future experimentation. The procedure was followed for each of the 120 population crosses.

Four rows of 30 plants each were grown to increase the parental populations per se, too. The crossing procedure followed was based on the method described by Melani and Carena (2005). Pollinated ears from the four rows representing each population were harvested, dried, and shelled individually, and balanced bulks were created and kept in cold storage for future experimentation. The procedure was followed for each of the 16 parental populations.

## Experimental design

The experiment consisting of 16 parental populations, 120 population crosses and 8 checks (four industry single-cross hybrids and four improved population hybrids) was arranged and randomized in a $12 \times 12$ partially balanced lattice design with two replicates across four ND
locations (Larimore, Thompson, Prosper, and Casselton) in 2010, 2011, and 2012. Seeds generated from the 2009 Fargo breeding nursery were used for evaluation in 2010 trials, and seeds from the 2010-2011 Salta breeding nursery were used in 2011 and 2012 trials. Each location by year combination represented one environment; therefore, 12 environments were used to evaluate the experiment. Experimental units consisted of 7 m row plots spaced 0.76 m between rows. Standard cultural management practices for maize trials were followed.

## Traits studied

Grain yield data (adjusted to $155 \mathrm{~g} \mathrm{~kg}^{-1}$ grain moisture and expressed in $\mathrm{Mg}_{\mathrm{ha}}{ }^{-1}$ ) were gathered in all environments except for Casselton in 2011. Plots were machine harvested for all environments. Grain quality traits were determined using 500 g kernel samples from each plot in 11 environments. Concentration of protein, oil, starch, lysine, methionine, and cysteine were measured using a near-infrared spectroscopy (NIRS) grain analyzer (OmegAnalyzer G) to determine quantitatively the relative proportion of each component in maize kernels for all entries. The calibration for OmegAnalyzer G was provided by the Iowa Grain Quality Initiative Lab at the Iowa State University. A second NIRS grain analyzer (FOSS Infratec 1241) was used, in cooperation with Monsanto, to determine extractable starch (HES) and fermentable starch (HFC) in maize kernels for all entries. Data for HES and HFC were obtained from all locations in 2010 and 2012.

## Statistical analyses

Analyses of variance (ANOVA) were conducted for all traits within and among environments. Genotypes were considered as fixed effects, and environments and replications were considered as random effects. ANOVA for each environment were performed using SAS version 9.3 PROC MIXED procedure with method=REML (restricted maximum likelihood)
option (SAS Institute Inc. 2010; Littell et al. 2006). Test for homogeneity of error variances was conducted using the $\mathrm{F}_{\text {max }}$ test (Tabachnick and Fidell 2001) before combining data across environments. When the difference in error variances for each trait across environments was less than 10 times of the smallest error variance, then combined analysis for those environments was performed. Least-squares means from each environment were used for combined analyses of variance using PROC GLM procedure from SAS version 9.3 (SAS Institute Inc. 2010). Genetic and environmental effects were partitioned following GEAN II based on the genetic model presented below (Gardner and Eberhart 1966):

$$
Y_{i j}=\mu_{v}+\frac{1}{2}\left(v_{i}+v_{j}\right)+\gamma\left(\bar{h}+h_{i}+h_{j}+s_{i j}\right),
$$

where $\mu_{v}$ is the mean of all parental populations, $v_{i}$ is the variety effect, and heterosis $\left(h_{i j}\right)$ effects are partitioned to $\bar{h}$ (average heterosis), $h_{i}$ (variety heterosis), and $s_{i j}$ (specific heterosis). The coefficient, $\gamma$, is equal to 0 when $i=j$, and $\gamma=1$ when $i \neq j$. Checks were removed from the data set prior to analysis. Additionally, general combining ability estimate $\left(g_{i}\right)$ defined as the variety effect in crosses was calculated following the formula, $g_{i}=\frac{1}{2} v_{i}+h_{i}$ to determine the performance of parental populations in population crosses (Gardner and Eberhart 1966). The analysis was done using the DIALLEL-SAS05 program developed by Zhang et al. (2005) with modifications to extend the linear matrix for a 16-parent diallel. The Student's $t$ test of significance was used to test the null hypothesis that the estimates for $v_{i}$ and heterosis effects were equal to zero. Predicted population cross mean for grain yield was calculated following the GEAN II model that showed significant sources of variation. Since $v_{i}, \bar{h}, h_{i}$, and $s_{i j}$ effects were significant sources of variation for grain yield (Table 2), these genetic effects were included in the model to calculate the predicted mean for each population cross. Additionally, other sources of variation due to genotypes (G) and genotype by environment interaction (GxE) such as checks
and 'checks vs. others' and their interactions with environment were also generated. The combined error mean squares were computed by pooling individual environment error mean squares weighted by their corresponding error degrees of freedom.

## Results and Discussion

Highly significant differences $(\mathrm{P}<0.01)$ were found in the GxE interaction source of variation for grain yield and grain quality traits (starch, HFC, HES, oil, protein, lysine, methionine, and cysteine) (Table 2). Fig. 3 on the means from each genotypic class (parental populations, population crosses, checks, and overall entries) plotted across location and years for grain yield, starch, oil, and protein showed interaction based on magnitude. The ranks of each genotypic class were similar across traits, but differences in grain yield and starch seem to be more evident across locations and years. For instance, Larimore obtained the highest grain yield in 2011, but had low grain yield in 2010 and 2012 relative to other locations. In general, low grain yield was observed in 2012 due to drought. Similarly, Santos et al. (1994) also found interactions based on magnitude in their diallel study consisting of 28 maize populations. The results were expected since distinct locations, in terms of geographical distance, climate, and soil, were used in the study.

The main effects (genotypes, varieties, heterosis, and checks) had highly significant ( $\mathrm{P}<0.01$ ) differences for all traits (Table 2). The significant differences among genotypes and genotypic classes allow us to discriminate the 16 populations for their genetic effects and performance per se. The mean squares for checks vs. others (parental populations and population crosses) were also highly significant $(\mathrm{P}<0.01)$ for grain yield, starch, HES, oil, protein, methionine, and cysteine, and significant $(\mathrm{P}<0.05)$ for lysine. Our results are in agreement with

Table 2. Combined analyses of variance (GEAN II) for 16 adapted maize populations in the northern U.S. Corn Belt, their crosses, and checks for grain yield $\left(\mathrm{Mg} \mathrm{ha}^{-1}\right)$, and percentage of grain quality traits (starch, HFC, HES, oil, protein, lysine, methionine, and cysteine).

| Source of variation | Grain yield |  | Starch |  | df | $\begin{gathered} \hline \text { HFC } \\ \hline \text { MS } \\ \hline \end{gathered}$ | $\begin{gathered} \hline \text { HES } \\ \hline \text { MS } \\ \hline \end{gathered}$ | Oil |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | MS | Df | MS |  |  |  | df | MS |
| Environments (E) | 10 | $163.9^{* *}$ | 10 | $113.1{ }^{\text {** }}$ | 7 | $1719.96{ }^{* *}$ | $354.35^{* *}$ | 10 | $9.54 * *$ |
| Genotypes (G) | 143 | 10.6 ** | 143 | 3.0 ** | 143 | $1.42{ }^{* *}$ | 8.12** | 143 | 0.27 ** |
| Variety ( $v_{i}$ ) | 15 | 20.9 ** | 15 | $17.8{ }^{* *}$ | 15 | $9.77^{* *}$ | $51.98 * *$ | 15 | 1.85** |
| Heterosis ( $h_{i j}$ ) | 120 | $4.8{ }^{* *}$ | 120 | $0.2{ }^{* *}$ | 120 | 0.46 ** | $0.97 * *$ | 120 | $0.05^{* *}$ |
| Average heterosis ( $\bar{h}$ ) | 1 | 281.0************ | 1 | $6.2^{* *}$ | 1 | 0.02 | $11.49^{* *}$ | , | 0.43*** |
| Variety heterosis ( $h_{i}$ ) | 15 | 2.8** | 15 | $0.3{ }^{*}$ | 15 | 0.20 | 1.26 ** | 15 | 0.07** |
| Specific heterosis ( $s_{i j}$ ) | 104 | $2.5{ }^{* *}$ | 104 | $0.2{ }^{*}$ | 104 | $0.50{ }^{* *}$ | 0.83*************) | 104 | 0.04** |
| Checks (C) | 7 | $31.7{ }^{* *}$ | 7 | 11.0 ** | 7 | $1.47{ }^{* *}$ | $26.51{ }^{* *}$ | 7 | 0.65 ** |
| C vs. others | 1 | 353.7** | 1 | $57.1{ }^{* *}$ | 1 | 0.83 | 82.38** | 1 | 0.79 ** |
| GxE | 1422 | 1.0** | 1429 | 0.2 ** | 994 | 0.40 ** | 0.61 ** | 1429 | 0.02** |
| $v_{i} \mathrm{x}$ E | 150 | $1.7{ }^{* *}$ | 150 | $0.4^{* *}$ | 105 | $0.43{ }^{*}$ | 0.92 ** | 150 | 0.04** |
| $h_{i j} \times \mathrm{E}$ | 1200 | 0.5 | 1200 | $0.1{ }^{* *}$ | 840 | 0.28 | 0.34 | 1200 | 0.01 |
| $\bar{h} \times \mathrm{E}$ | 10 | 0.0 | 10 | 0.2 | 7 | 0.57 | $1.37{ }^{* *}$ | 10 | 0.02 |
| $h_{i} \mathrm{xE}$ | 150 | 0.6 | 150 | 0.2 ** | 105 | 0.25 | 0.29 | 150 | 0.01 |
| $s_{i j} \times \mathrm{E}$ | 1040 | 0.6 | 1040 | $0.1{ }^{*}$ | 728 | 0.28 | 0.33 | 1040 | 0.01 |
| CxE | 70 |  | 70 | 0.2 *** | 49 | 0.32 | $0.69{ }^{* *}$ | 70 | 0.02** |
| C vs. others x E | 10 | 13.3 ** | 10 | 0.8 ** | 7 | $1.15{ }^{* *}$ | $2.94{ }^{* *}$ | 10 | 0.04** |
| Pooled error | 1285 | 0.6 | 1306 | 0.1 | 888 | 0.34 | 0.39 | 1306 | 0.01 |
| CV (\%) |  | 21.1 |  | 0.6 |  | 1.3 | 1.3 |  | 3.1 |

and ${ }^{* *}$ indicate significance at $\alpha$ level of 0.05 and 0.01 , respectively.

Table 2 (continued). Combined analyses of variance (GEAN II) for 16 adapted maize populations in northern U. S. Corn Belt, their crosses, and checks for grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ), and percentage of grain quality traits (starch, HFC, HES, oil, protein, lysine, methionine, and cysteine).

| Source of variation | Protein |  | Lysine ${ }^{\text {a }}$ |  | Methionine |  | Cysteine ${ }^{\text {b }}$ |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | MS | df | MS | df | MS | df | MS |
| Environments (E) | 10 | 141.5***********) | 10 | $741.0{ }^{\text {** }}$ | 10 | $444.2^{* *}$ | 8 | 494.4**********) |
| Genotypes (G) | 143 | $2.5{ }^{* *}$ | 143 | $6.4 * *$ | 143 | 10.0 ** | 143 | $5.2{ }^{* *}$ |
| Variety ( $v_{i}$ ) | 15 | 12.0 ** | 15 | $48.2{ }^{* *}$ | 15 | $52.7{ }^{* *}$ | 15 | $19.9 *$ |
| Heterosis ( $h_{i j}$ ) | 120 | 0.3 ** | 120 | $0.8{ }^{* *}$ | 120 | $1.5 * *$ | 120 | $1.0{ }^{* *}$ |
| Average heterosis ( $\bar{h}$ ) | 1 | 8.6** | 1 | 11.6** | 1 | $30.7{ }^{* *}$ | 1 | 19.1** |
| Variety heterosis ( $h_{i}$ ) | 15 | $0.4 * *$ | 15 | $0.9{ }^{*}$ | 15 | $1.9{ }^{* *}$ | 15 | 0.7 |
| Specific heterosis ( $s_{i j}$ ) | 104 | $0.2^{* *}$ | 104 | 0.7 | 104 | $1.1{ }^{* *}$ | 104 | $0.9{ }^{* *}$ |
| Checks (C) | 7 | 9.8 ** | 7 | $11.6{ }^{* *}$ | 7 | $32.1{ }^{* *}$ | 7 | 21.4** |
| C vs. others | 1 | 74.3 ** | 1 | 15.0 * | 1 | 276.6** | 1 | $185 .{ }^{* *}$ |
| GxE | 1428 | $0.2^{* *}$ | 1429 | $0.7{ }^{* *}$ | 1415 | 0.9 ** | 1132 | 0.6 ** |
| $v_{i} \mathrm{xE}$ | 150 | $0.4 * *$ | 150 | 1.0 ** | 150 | $1.4 * *$ | 120 | 0.8 ** |
| $h_{i j} \times \mathrm{E}$ | 1200 | $0.1{ }^{* *}$ | 1200 | 0.5 | 1200 | $0.6{ }^{*}$ | 960 | 0.3 |
| $\bar{h} \times \mathrm{E}$ | 10 | 0.1 | 10 | 0.2 | 10 | 0.4 | 8 | 0.2 |
| $h_{i} \times \mathrm{E}$ | 150 | $0.2^{* *}$ | 150 | 0.5 | 150 | 0.6 | 120 | 0.4 |
| $s_{i j} \times \mathrm{E}$ | 1040 | $0.1{ }^{* *}$ | 1040 | 0.5 | 1040 | $0.6{ }^{*}$ | 832 | 0.3 |
| CxE | 70 | $0.2^{* *}$ | 70 | 0.9 ** | 69 | 0.9 ** | 55 | 0.5 |
| C vs. others x E | 10 | 0.8 ** | 10 | 1.6 ** | 10 | $1.7{ }^{* *}$ | 8 | 0.6 |
| Pooled error | 1300 | 0.1 | 1306 | 0.5 | 1235 | 0.6 | 1016 | 0.4 |
| CV (\%) |  | 3.8 |  | 2.7 |  | 3.9 |  | 3.3 |

[^0]

Fig. 3. Mean performance of parents, crosses, checks, and overall maize entries for (a) grain yield, (b) starch, (c) protein, and (d) oil across locations and years.
researchers who observed similar patterns of significance for same sources of variation for grain yield (Araujo and Miranda Filho 2001; Santos et al. 1994) and oil content (Misevic et al. 1989).

The contribution of $v_{i}$ and $h_{i j}$ effects was assessed from the total sum of squares among diallel entries. The $h_{i j}$ effects for grain yield accounted for $65 \%$ of the total among diallel entries sum of squares, as opposed to $35 \%$ due to $v_{i}$ effects. These results agree with the proportions found by Santos et al. (1994). In contrast, Araujo and Miranda Filho (2001) and Misevic et al. (1989) found that $v_{i}$ effects were more important than $h_{i j}$ effects for the among diallel entries sum of squares due to grain yield. Within the overall $h_{i j}$ effects, $\bar{h}$ explained $31 \%$ of the among diallel entries sum of squares, and $s_{i j}$ and $h_{i}$ explained $29 \%$ and $5 \%$, respectively. The larger proportion of the $\bar{h}$ for grain yield explains the superiority of population crosses over parental populations
as shown in Fig. 3a. The predominance of $h_{i j}$ effects over $v_{i}$ effects suggests that the sum of squares due to grain yield among diallel entries is mostly due to non-additive genetic effects. Previous studies suggest that dominance genetic effects were important for the inheritance of grain yield (Gamble 1962; Holthaus and Lamkey 1995; Wardyn et al. 2007). However, this assumption did not agree with studies using similar populations. Melani and Carena (2005) and Jumbo and Carena (2008) suggested that additive genetic effects had large contribution on the sum of squares due to grain yield among diallel entries of a significantly smaller set of genotypes.

The proportion of $v_{i}$ effects to the total among diallel entries sum of squares was higher than $h_{i j}$ effects for all grain quality traits. The $v_{i}$ effects ranged from 71 to $90 \%$ of the among diallel entries sum of squares, while $h_{i j}$ effects ranged from 10 to $29 \%$. The largest contribution of $v_{i}$ effects to the among diallel entries sum of squares was due to starch ( $90 \%$ ), and the smallest contribution was due to cysteine (71\%). For $h_{i j}$ effects, the largest contribution to the among diallel entries sum of squares was due to cysteine (29\%), and the smallest contribution was $10 \%$ for starch. Misevic et al. (1989) also found similar proportions of $v_{i}$ and $h_{i j}$ effects for oil concentration. Since $h_{i j}$ effects were not dominant over $v_{i}$ effects, it can be assumed that additive genetic effects were the most important source of variation explaining grain quality traits. Theoretically, however, additive and dominance genetic effects are confounded by $v_{i}$ effects using GEAN II (Gardner and Eberhart 1966). Previous studies discussed the genetic effects responsible for the differences of some grain quality traits. Wattoo et al. (2009) found that protein and oil contents were controlled by partial dominance with additive gene action. Similarly, Osorno and Carena (2008) suggested that general combining ability effects were more important for oil, however, they also noted that specific combining ability effects were
predominant for protein and starch. Medici et al. (2009) noted the significance of general combining ability over specific combining ability effects for lysine content in their diallel analysis using advanced lines of maize.

The estimates for $v_{i}, h_{i}, \bar{h}$, and mean of all parental populations for grain yield and grain quality traits are presented in Table 3. The $v_{i}$ effects for grain yield was highest for NDL and NDBSK(HI-M)C3, and lowest for EARLYGEM 21b. Only NDL, NDBSK(HI-M)C3, and NDBS1011 had positive and significant $v_{i}$ effects ( $\mathrm{P}<0.05$ ), while EARLYGEM 21 b and NDSHLC(M-FS)C5 had negative and significant $v_{i}$ effects $(\mathrm{P}<0.05)$. The $v_{i}$ effects agree with the mean grain yield of parental populations. Grain yield for parental populations ranged from 2.1 to $4.6 \mathrm{Mg} \mathrm{ha}^{-1}$, with EARLYGEM 21b having the lowest grain yield and NDBSK(HI-M)C3 the highest. High grain yield for NDL, NDBSK(HI-M)C3, and NDBS1011 can be explained by the choice of germplasm and efforts in recurrent selection. NDL, a Lancaster version created for ND conditions, was developed from 8 elite short-season inbred lines known to have good combining ability for grain yield. NDBSK(HI-M)C3 and NDBS1011 had undergone at least 13 cycles of recurrent selection from their base populations. On the other hand, the low yield for EARLYGEM 21b and NDSHLC(M-FS)C5 may be due to the fact that they largely represent the most exotic germplasm and may need additional improvement. These populations may contain a low frequency of desirable alleles that resulted to low grain yield.

For grain quality traits, the highest $v_{i}$ effects for starch content was observed in NDL $(\mathrm{P}<0.01)$, and the lowest $v_{i}$ effects was observed in NDSS $(\mathrm{P}<0.01)$. EARLYGEM 21c and EARLYGEM 21b also had positive and significant $v_{i}$ effects for starch at $\mathrm{P}<0.01$ and $\mathrm{P}<0.05$, respectively. Significant and negative $v_{i}$ effects were found for NDSS, NDSCD(FS-CS)C2,

Table 3. Estimates for variety $\left(v_{i}\right)$, variety heterosis $\left(h_{i}\right)$, average heterosis $(\bar{h})$, and general combining ability $\left(g_{i}\right)$ effects from GEAN II and mean, maximum, and minimum values for grain yield and grain quality traits (starch, HFC, HES, oil, protein, lysine,
methionine, and cysteine) for 16-parent diallel in maize.

${ }^{*}$ and ${ }^{* *}$ indicate that the estimates are significantly different from zero at $\alpha$ level of 0.05 and 0.01 , respectively.
${ }^{a}$ Mean, maximum, and minimum values among parental populations.

Table 3 (continued). Estimates for variety $\left(v_{i}\right)$, variety heterosis $\left(h_{i}\right)$, average heterosis ( $\bar{h}$ ), and general combining ability $\left(g_{i}\right)$ effects from GEAN II and mean, maximum, and minimum values for grain yield and grain quality traits (starch, HFC, HES, oil, protein, lysine, methionine, and cysteine) for 16-parent diallel in maize.

| Populations | Protein |  |  | Lysine ${ }^{\text {b }}$ |  |  | Methionine |  |  | Cysteine |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | $v_{i}$ | $h_{i}$ | $g_{i}$ | $v_{i}$ | $h_{i}$ | $g_{i}$ | $v_{i}$ | $h_{i}$ | $g_{i}$ | $v_{i}$ | $h_{i}$ | $g_{i}$ |
| NDSS | $0.7 *$ | 0.1 | 0.5 | 2.0 ** | -0.2 | 0.8 | 1.1 | 0.2 | 0.8 | 0.8 | 0.1 | 0.5 |
| NDCG(FS)C1 | -0.1 | 0.2 | 0.1 | 0.1 | 0.3 | 0.3 | -0.2 | 0.4 | 0.3 | -0.2 | 0.2 | 0.2 |
| NDL | -0.9 ** | 0.1 | -0.4 | -0.3 | 0.2 | 0.0 | -1.0 | 0.1 | -0.4 | -1.2 | 0.0 | -0.6 |
| NDBSK(HI-M)C3 | -0.4 | 0.0 | -0.2 | -0.4 | 0.1 | 0.0 | -0.5 | 0.3 | 0.0 | -0.1 | 0.2 | 0.1 |
| NDBS11(FR-M)C3 | 0.4 | -0.1 | 0.1 | 0.7 | -0.1 | 0.3 | $1.4{ }^{*}$ | -0.2 | 0.5 | 0.4 | -0.0 | 0.2 |
| NDBS1011 | -0.4 | 0.1 | -0.1 | -0.7 | 0.1 | -0.2 | -0.3 | 0.2 | 0.1 | 0.0 | 0.1 | 0.0 |
| Leaming(S-FS)C6 | -0.2 | -0.2 | -0.3 | 1.3 | -0.2 | 0.5 | -0.1 | -0.4 | -0.4 | -0.4 | -0.2 | -0.5 |
| NDBS22(R-T1)C9 | 0.5 | -0.2 | 0.1 | 0.1 | -0.0 | 0.0 | 0.6 | -0.2 | 0.1 | 0.9 | -0.2 | 0.2 |
| NDSAB(MER-FS)C15 | 0.2 | -0.1 | 0.0 | 1.2 | -0.4 | 0.2 | 0.5 | -0.3 | 0.0 | -0.2 | -0.1 | -0.2 |
| - $\mathrm{NDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ | $0.7{ }^{*}$ | 0.0 | 0.4 | 0.1 | 0.1 | 0.1 | $1.5 * *$ | -0.1 | 0.7 | 1.2 | -0.2 | 0.4 |
| $\pm \quad \mathrm{NDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | 0.1 | -0.1 | 0.0 | -0.4 | -0.0 | -0.2 | 0.3 | -0.2 | 0.0 | 0.2 | -0.1 | 0.0 |
| NDSCD(FS-CS)C2 | 0.5 | 0.1 | 0.3 | $1.5 *$ | -0.1 | 0.7 | 0.7 | 0.2 | 0.6 | 0.3 | 0.3 | 0.5 |
| NDSHLC(M-FS)C5 | 0.1 | 0.1 | 0.1 | -0.6 | 0.1 | -0.2 | 0.5 | 0.1 | 0.4 | 0.6 | 0.0 | 0.3 |
| EARLYGEM 21a | -0.3 | 0.1 | -0.1 | -1.4 | 0.0 | -0.7 | -1.5** | 0.2 | -0.6 | -0.6 | -0.0 | -0.3 |
| EARLYGEM 21b | -0.3 | -0.1 | -0.2 | -1.4** | -0.0 | -0.7 | -1.3** | -0.1 | -0.8 | -0.8 | 0.0 | -0.4 |
| EARLYGEM 21c | -0.6 | 0.0 | -0.3 | $-1.8{ }^{*}$ | 0.0 | -0.9 | $-1.7{ }^{* *}$ | -0.2 | -1.0 | -0.9 | -0.0 | -0.5 |
| $\bar{h}$ |  | -0.23** |  |  | -0.27 |  |  | -0.45** |  |  | $-0.39^{*}$ |  |
| Mean |  | 11.53 |  |  | 0.30 |  |  | 0.25 |  |  | 0.24 |  |
| Maximum |  | 12.26 |  |  | 0.32 |  |  | 0.27 |  |  | 0.25 |  |
| Minimum |  | 10.61 |  |  | 0.28 |  |  | 0.23 |  |  | 0.23 |  |

${ }^{\mathrm{b}}$ The estimates for lysine, methionine, and cysteine were multiplied by 100 .

NDBS11(FR-M)C3, and NDSM(M-FS)C9. Mean starch content (\%) for the parental populations ranged from 68.0 to $70.2 \%$, with NDL and NDSS having the highest and lowest percentages, respectively. Starch is a function of grain yield, which explains the high starch content for NDL. However, for EARLYGEM 21b and EARLYGEM 21c, their exotic background and traits selected may explain their high $v_{i}$ effects for starch only. EARLYGEM 21 b and EARLYGEM 21c have similar genetic background, and EARLYGEM 21b was specifically selected for high test weight.

HFC and HES are important starch components for ethanol production. The $v_{i}$ effects for HFC were not significantly different from zero. The mean HFC (\%) among parental populations ranged from 47.1 to $48.9 \%$, with EARLYGEM 21c and NDBSK(HI-M)C3 having the highest and lowest percentages, respectively. For HES, the three EARLYGEM 21 populations showed positive and highly significant $v_{i}$ effects ( $\mathrm{P}<0.01$ ). In contrast, $\operatorname{NDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ had the lowest $v_{i}$ effects for HES. The mean HES (\%) for parental populations varied from 58.4 to $62.1 \%$, with EARLYGEM 21c and NDSM(M-FS)C9 having the highest and lowest percentages, respectively. Considering the $v_{i}$ effects for starch content and HES, NDL and EARLYGEM 21c can be good candidates to improve starch for ethanol use. Besides, a $3.6 \%$ range in HES among populations shows there is enough genetic diversity in these 16 maize populations to make a significant economic impact.

Three parental populations showed significant and positive $v_{i}$ estimates for oil content (Table 3). NDSCD(FS-CS)C2 gave the highest $v_{i}$ effects, followed by NDSHLC(M-FS)C5 and NDBS11(FR-M)C3, while NDL gave lowest $v_{i}$ effects. The mean oil (\%) for parental populations varied from 4.08 to $4.83 \%$, with NDSCD(FS-CS)C2 having the highest and NDL the lowest percentages. The high $v_{i}$ effects and population mean of NDSCD(FS-CS)C2 make it a
good candidate for developing cultivars with high oil content. Negative correlations were observed between oil and starch contents. Parental populations with high oil content had low starch content, and vice versa. Dado (1999) and Scott et al. (2006) reported that oil and protein concentrations were negatively correlated with starch.

NDSS and NDSM(M-FS)C9 showed the highest $v_{i}$ effects for protein content, and NDL had the lowest $v_{i}$ effects. The mean protein (\%) ranged from 10.6 to $12.3 \%$, with NDSS and NDL having the highest and lowest percentages, respectively. Negative correlations between protein and starch contents were also evident. NDSS showed highest protein and lowest starch contents, while NDL showed lowest protein and highest starch contents, which could make an excellent complementation for hybrid and reciprocal recurrent selection programs.

The $v_{i}$ effects for lysine were highest and significant $(\mathrm{P}<0.01)$ for NDSS, and lowest for EARLYGEM 21c ( P <0.01). NDSCD(FS-CS)C2 also showed positive and significant $v_{i}$ effects for this trait. The mean lysine (\%) ranged from 0.28 to $0.32 \%$. NDSS showed the highest mean lysine content, while EARLYGEM 21c had the lowest. In terms of methionine content, NDSM(M-FS)C9 showed the highest and significant $v_{i}$ effects ( $\mathrm{P}<0.01$ ), while EARLYGEM 21c had the lowest $v_{i}$ effects and was significantly different from zero $(\mathrm{P}<0.01)$. The mean methionine (\%) ranged from 0.23 to $0.27 \%$, which agrees with $v_{i}$ effects. For cysteine, $v_{i}$ effects were not significantly different from zero. Mean cysteine (\%) among parent populations ranged from 0.23 to $0.25 \%$. Lysine and methionine were negatively correlated with starch. NDSM(MFS)C9 had high lysine and methionine contents, but low starch content. In contrast, EARLYGEM 21c showed high starch content, but low lysine and methionine contents. To improve protein and amino acids for food and feeds, NDSS and NDSM(M-FS)C9 are good candidates.

The $\bar{h}$ effect is the difference between the means of all population crosses and all parental populations. Positive and significant $\bar{h}$ effects (Table 3) were found in grain yield ( $\mathrm{P}<0.01$ ), and starch and oil contents $(\mathrm{P}<0.05)$. The positive estimates indicate that dominance for grain yield, starch and oil contents is towards high value for these traits. This is contrary to the result obtained for oil content by Misevic et al. (1989). Since $v_{i}$ effects had large sum of squares for starch and oil among diallel entries, it is assumed that these traits are controlled by partial dominance with additive gene action. Results for oil content are similar to Wattoo et al. (2009). On the other hand, negative and significant $\bar{h}$ effects were observed for protein, methionine ( $\mathrm{P}<0.01$ ), and cysteine $(\mathrm{P}<0.05)$ contents. The negative estimates for protein, methionine, and cysteine contents suggest that dominance is towards low value for these traits. High extractable starch and lysine contents for $\bar{h}$ effects were not significantly different from zero, although $\bar{h}$ from the ANOVA showed significance for HES and lysine contents.

Only grain yield had $h_{i}$ effects that were significantly different from zero (Table 3). NDBS21(R-T)C9 was the only parental population that showed positive and significant $h_{i}$ effect ( $\mathrm{P}<0.01$ ). NDBS21(R-T)C9 was initially developed through reciprocal recurrent selection and was selected for grain yield, grain moisture, and resistance to root and stalk lodging. Additive and dominance genetic effects are expected to be accumulated in advanced cycles of reciprocal recurrent selection (Comstock et al. 1949). Accumulation of dominance genetic effects may explain the positive $h_{i}$ effect of NDBS21(R-T)C9 for grain yield. Grain quality traits did not show $h_{i}$ effects significantly different from zero, although $h_{i}$ from the ANOVA showed significance for starch, HES, oil, protein, lysine, and methionine contents.

Effects for $g_{i}$ were calculated from the estimates for $v_{i}$ and $h_{i}$ effects. NDBS21(R-T)C9 showed the highest $g_{i}$ effect (Table 3) for grain yield, since it also had the highest $h_{i}$ effect. It also
confirms previous estimations on this population (Melani and Carena, 2005). The predominance of $h_{i j}$ over $v_{i}$ effects in the total sum squares among the diallel entries for grain yield explained the agreement between $h_{i}$ and $g_{i}$ effects. The trends of parental populations for $g_{i}$ effects were similar with $v_{i}$ effects for all grain quality traits. This agreement is explained by the larger proportion of $v_{i}$ against $h_{i j}$ effects to the total among diallel entries sum of squares for grain quality traits. Similar results were also observed by Misevic et al. (1989) for oil content.

The $s_{i j}$ effects and predicted means for grain yield of the population crosses are presented in Table 4. Predicted means were calculated based on GEAN II model. The predicted population cross means for grain yield ranged from 2.4 to $5.9 \mathrm{Mg} \mathrm{ha}^{-1}$. NDBS21(R-T)C9 x EARLYGEM 21b had the highest grain yield, and EARLYGEM 21a x EARLYGEM 21c had the lowest yield. Two population crosses [NDSS x NDBS22(R-T1)C9 and NDBS1011 x EARLYGEM 21c] showed positive $s_{i j}$ effects and were significantly different from zero ( $\mathrm{P}<0.05$ ), with predicted means of $5.6 \mathrm{Mg}_{\mathrm{ha}}{ }^{-1}$ for both population crosses. NDBS21(R-T)C9 x EARLYGEM 21 b showed also a positive $s_{i j}$ effect, but was not significantly different from zero. On the other hand, three population crosses between EARLYGEM 21 populations (EARLYGEM 21a x EARLYGEM 21b, EARLYGEM 21a x EARLYGEM 21b, and EARLYGEM 21b x EARLYGEM 21c) had negative $s_{i j}$ effects and significantly different from zero ( $\mathrm{P}<0.01$ ), which was expected due to their common origin. This confirms the accuracy of the model.

The $s_{i j}$ and mean cross performance are dependent on the relatedness between populations. This is in agreement with the negative $s_{i j}$ effects and low grain yield of the three EARLYGEM 21 population crosses, which share the same genetic background. The $s_{i j}$ is equivalent to specific combining ability (Gardner and Eberhart 1966). High specific combining ability can be observed from a cross between germplasm belonging to two distinct heterotic

Table 4. Predicted means (above the diagonal) and specific heterosis (below the diagonal) for grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) for all maize population crosses.

${ }^{5}$ The following are the parental populations listed in the order: NDSS, NDCG(FS)C1, NDL, NDBSK(HI-M)C3, NDBS11(FR-M)C3, NDBS1011, Leaming(S-FS)C6, NDBS22(R-T1)C9, NDSAB(MER-FS)C15, NDSM(M-FS)C9, NDBS21(R-T)C9, NDSCD(FS-
$\left.{ }_{*}^{C S}\right)$ C2, NDSHLC(M-FS)C5, EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c.

* and ${ }^{* *}$ indicate that the estimates are significantly different from zero at $\alpha$ level of 0.05 and 0.01 , respectively.
groups. The population crosses with high $s_{i j}$ and predicted means for grain yield mostly followed the popular heterotic pattern, BSSS x Lancaster or non-SSS, except for NDSS x NDBS22(RT1)C9. Earlier versions of NDBS21(R-T)C9 belonged to non-SSS (Carena et al. 2008), consequently from the cross between NDBS21(R-T)C9 and EARLYGEM 21b, EARLYGEM 21b may behave like BSSS. Since EARLYGEM 21b and EARLYGEM 21c are genetically related, it seems appropriate to classify EARLYGEM 21c under SSS group. For the cross between NDBS 1011 and EARLYGEM 21c, NDBS1011 may belong to non-SSS, although Carena et al. (2008) suggested that NDBS1011 may belong to an alternative heterotic group. On the other hand, a deviation from the traditional heterotic pattern is observed for NDSS x NDBS22(R-T1)C9. NDSS is a synthetic population composed of germplasm belonging to BSSS, and earlier versions of NDBS22(R-T1)C9 were reported to possibly belong to SSS group (Carena et al. 2008). Melani and Carena (2005) stated that NDBS22(R)C7 has high proportion of non-BSSS in their background. It can be assumed that NDBS22(R-T1)C9 may have behaved as non-SSS when crossed with NDSS, since NDSS was derived from BSSS background. Further studies may need to be conducted to confirm the heterotic group of this particular parental population.

Recurrent selection programs can be established from selected populations and population crosses. Table 5 presents a summary of parental populations and population crosses having favorable mean performance and genetic estimates for grain yield and grain quality traits.

## Summary

Sixteen populations were used in a diallel mating design following GEAN II to determine the genetic components and heterotic responses for grain yield and grain quality traits.

Table 5. Summary of parental populations and population crosses with favorable per se performance and genetic estimates for grain yield and grain quality traits.

| Populations | Favorable traits |
| :--- | :--- |
| Parental populations |  |
| NDSS | Protein and lysine |
| NDL | Grain yield and starch |
| NDBSK(HI-M)C3 | Grain yield |
| NDBS11(FR-M)C3 | Oil |
| NDBS1011 | Grain yield |
| NDSM(M-FS)C9 | Protein and methionine |
| NDBS21(R-T)C9 | Grain yield |
| NDSCD(FS-CS)C2 | Oil and lysine |
| NDSHLC(M-FS)C5 | Oil |
| EARLYGEM 21a | HES |
| EARLYGEM 21b | Starch and HES |
| EARLYGEM 21c | Starch and HES |
|  |  |
| Population crosses |  |
| NDSS x NDBS22(R-T1)C9 | Grain yield, protein, lysine, and methionine |
| NDBS1011 x EARLYGEM 21c | Grain yield, starch, and HES |
| NDBS21(R-T)C9 x EARLYGEM 21b | Grain yield |

The GEAN II was effective in showing the genetic effects that had a large contribution to the total among diallel entries sum of squares for different traits. Heterosis effects had greater influence on the among diallel entries sum of squares for grain yield, while $v_{i}$ effects for grain quality traits. Grain yield, starch, and oil contents accounted for positive and significant $\bar{h}$ effects, suggesting the presence of non-additive effects. The dominance was towards higher mean performance of populations for grain yield, starch, and oil contents. Since $v_{i}$ effects were more dominant than $h_{i j}$ effects for starch and oil contents, these traits could be controlled by partial dominance with additive gene action. On the other hand, protein, methionine, and cysteine contents showed significance for negative $\bar{h}$ effects, suggesting that dominance was in the direction of low mean performance for protein, methionine, and cysteine contents.

Based on the effects of $v_{i}$ and $g_{i}$, the following populations can be considered as candidates for grain quality improvement: NDL and EARLYGEM 21c for starch, NDSCD(FS-

CS)C2 for oil, and NDSS and NDSM(M-FS)C9 for protein and amino acids. High $s_{i j}$ effects for grain yield were observed between distinct populations. NDSS x NDBS22(R-T1)C9 and NDBS1011 x EARLYGEM 21c can be good candidates as population hybrids with good grain quality traits. Although, NDBS21(R-T)C9 x EARLYGEM 21b showed the highest grain yield, only an average level for grain quality traits was observed (data not shown). NDSS, EARLYGEM 21c, and EARLYGEM 21b can be categorized under SSS group, and NDBS1011 may belong to non-SSS group. Further studies are needed to confirm the heterotic group of NDBS22(R-T1)C9.

Population selection for breeding purposes should consider overall trait performance, genetic estimates and diversity, high population mean, and heterosis observed in crosses. Intrapopulation recurrent selection programs could be established for the parental populations identified with desirable grain quality traits. Inter-population recurrent selection programs can be established for the selected population crosses with high grain yield and favorable grain quality. Recurrent selection programs will integrate pre-breeding with cultivar development by improving populations that will allow the release of the next generation of NDSU maize inbred lines and hybrids.

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## CHAPTER 3. GENETIC DIVERSITY AND HETEROTIC GROUPING OF 16 MAIZE POPULATIONS ADAPTED TO THE NORTHERN U.S. CORN BELT


#### Abstract

Understanding the genetic relationships among genetically broad-based populations is a good starting point for breeding programs. These utilize germplasm introduction and adaptation to broaden the genetic resources available for genetic improvement. A diallel of 16 maize populations adapted to the northern U.S. Corn Belt was used to estimate genetic parameters. These were used to assess the genetic diversity of the populations and assign them to heterotic groups. Using the general combining ability $\left(g_{i}\right)$ estimates, 19 agronomic and grain quality traits showed a large contribution on the variability of the first two principal components (PC). All the traits were used to characterize the genetic similarities among the populations. The cluster analysis formed three groups and a singleton based on genetic distances (GD) of $g_{i}$ estimates. The specific heterosis $\left(s_{i j}\right)$ estimates for grain yield were used to assign the 16 populations to heterotic groups, since there was a highly significant correlation between GD and $s_{i j}$. Four heterotic groups were established. There was a good agreement with the groups formed using GD. Generally, the heterotic grouping agreed with genetic background information and heterotic group's specific and general combining ability (HSGCA) estimates. The EARLYGEM 21 populations with exotic background were assigned to a unique heterotic group. They showed high heterosis when crossed with populations from other heterotic groups. The heterotic groupings among the 16 populations validated former heterotic groups, and new heterotic patterns were created. These will increase breeding efficiency to develop new cultivars for the northern U.S. Corn Belt.


## Introduction

Genetic diversity is vital in plant breeding. The use of genetically diverse germplasm allows the identification of promising transgressive segregants and the exploration of useful gene combinations for future breeding activities. The genetic diversity of a set of genotypes can be determined by their inherent genetic variability, difference in allele frequencies, presence of heterosis when used in crosses, and their variable response to the environment expressed in the phenotype. Classifying variable genotypes in homogeneous groups based on their genetic relationships and similarities increase the efficiency in planning crosses for a breeding program.

Genetic diversity studies determine the variation among individuals or groups of individuals using a specific method or combination of methods to analyze multivariate datasets (Mohammadi and Prasanna 2003). Diverse datasets have been used to analyze genetic diversity in crop plants, among which are pedigree data, morphological data (Badu-Apraku et al. 2006), genetic parameter estimates (Camussi et al. 1985), heterosis data (Badu-Apraku et al. 2013a; 2013b), biochemical data, and molecular marker data (Melchinger et al. 1991; Betran et al. 2003; Mohammadi and Prasanna 2003). Molecular marker data provide a more reliable differentiation of genotypes (Mohammadi and Prasanna 2003), since these data are less affected by environmental effects. Molecular marker data classified a set of germplasm based on genetic similarities, however Melchinger and Gumber (1998) emphasized that it has been challenging to predict heterotic relationships based on these data. Additionally, researchers agreed that field experiments are still needed to validate groupings of germplasm based on molecular marker data (Melchinger and Gumber 1998; Barata and Carena 2006).

Several methods are available to analyze multivariate datasets. The commonly used methods for genetic diversity studies are cluster analysis, principal component analysis (PCA),
principal coordinate analysis, and multidimensional scaling (Mohammadi and Prasanna 2003). Cluster analysis allows the identification of groups that show high internal homogeneity (within groups) and high external heterogeneity (between groups). Hierarchical clustering methods are usually performed for genetic diversity study in crop plants. Among these, the UPGMA (Unweighted Paired Group Method using Arithmetic averages) method has been the most common for agronomic and morphological data, followed by the Ward's minimum variance method (Mohammadi and Prasanna 2003; Padilla et al. 2007; Badu-Apraku et al. 2006).

Germplasm introduction and adaptation have been common strategies to broaden genetic resources available for breeding purposes. Genetic diversity between populations can be brought about by geographical isolation accompanied with favorable genetic drift and selection in different environments (Moll et al. 1962). Crosses between maize populations from different origins showed heterosis, and greater heterosis was reported from crosses between divergent parents (Moll et al. 1962). Reif et al. (2005) also observed that hybrid performance was higher when parents are genetically diverse. However, the direct relationship between heterosis and genetic diversity is only true to a restricted range of genetic divergence. Extremely divergent crosses resulted in a decrease in heterosis (Moll et al. 1965). Prasad and Singh (1986) also found that greater heterosis for grain yield in maize was observed from crosses with moderate parental diversity over crosses with extreme parental diversity.

Exploitation of heterosis by breeders contributed to the significant yield increase of crops, especially in maize. Heterotic groups and heterotic patterns generate vital information in hybrid breeding. Genotypes belonging to a heterotic group display similar combining ability or heterosis when crossed with other genotypes from genetically distinct germplasm groups. A heterotic pattern is a cross between known genotypes that expresses high levels of heterosis
(Melchinger and Gumber 1998; Carena and Hallauer 2001a). Useful heterotic patterns can, therefore, be established from genetically diverse germplasm. A more strategic breeding plan is to classify genotypes based on heterotic groups. Inbred lines are then often developed from crosses within heterotic groups. Promising hybrids are expected from crosses of inbred lines developed between different heterotic groups.

Extensive information can be generated from diallel studies. These provide useful information to understand the genetic relationships within a set of genotypes. GD from diallel progeny data can be obtained for plant populations (Hanson and Casas 1968; Camussi et al. 1985). Camussi et al. (1985) showed a general method for estimating genetic distances of quantitative traits using a diallel mating design based on Gardner and Eberhart (1966) Analysis (GEAN) II. Their results suggested that variety $\left(v_{i}\right)$ effects reflect the genetic differences shown by the populations in their phenotypes. The heterosis $\left(h_{i j}\right)$ effects provided the basis of genetic divergence between populations, which can be due to differences in allele frequencies between populations. Badu-Apraku et al. (2013a; 2013b) classified inbred lines according to heterotic groups based on combining ability effects and molecular marker data. They used the heterotic group's specific and general combining ability (HSGCA) proposed by Fan et al. (2009). BaduApraku et al. (2013a) found close correspondence between the heterotic groups identified by HSGCA and molecular marker data. On the other hand, Betran et al. (2003) classified tropical maize inbred lines according to their GD measured by molecular marker data, and identified the correlation between the GD, hybrid performance, heterosis, and specific combining ability (SCA). They observed a strong positive correlation between GD and SCA. Genetic parameter estimates from diallel studies have been useful in classifying genotypes into groups according to
their genetic similarities. Grouping of populations into heterotic groups is then based on heterosis.

The objective of this study is to assess the genetic diversity of the 16 maize populations adapted to the northern U.S. Corn Belt and establish heterotic groups among them for future breeding activities.

## Materials and Methods

## Genetic materials

Sixteen maize populations improved and adapted to North Dakota (ND) environmental conditions were used in a diallel study. The list of the populations is presented in Table 6. The 16 populations were chosen to represent as much genetic diversity that exists in the North Dakota State University (NDSU) maize germplasm. Seeds for population crosses and parental populations were generated from two breeding nurseries: 1) the 2009 Fargo, ND summer breeding nursery, and 2) the 2010-2011 Salta, Argentina winter breeding nursery. Additional seed increase was conducted in the winter nursery due to the 2009 ND cool and wet growing season that led to small population size for each population. The crossing procedure for population crosses and parental populations was described by Laude and Carena (2013).

## Experimental design

The experiment consisted of 16 parental populations, 120 population crosses, and 8 checks (four industry single-cross hybrids and four improved population hybrids). The experiment was laid out and randomized in a $12 \times 12$ partially balanced lattice design with two replicates across four ND locations (Larimore, Thompson, Prosper, and Casselton) in 2010,

Table 6. Origin and reference for 16 maize populations evaluated in 12 northern U.S. Corn Belt environments.

| Population | Origin | Reference |
| :---: | :---: | :---: |
| NDSS | North Dakota State Univ. | Carena 2013 |
| NDCG(FS)C1 | Univ. of Guelph, Canada | Melani and Carena 2005; <br> Lee et al. 2006; Carena 2013 |
| NDL | North Dakota State Univ. | Carena 2013 |
| NDBSK(HI-M)C3 | Nebraska Agric. Exp. Stn. | Carena et al. 2008 |
| NDBS11(FR-M)C3 | Iowa State Univ. | Hallauer 1967; Carena et al. 2008 |
| NDBS1011 | Iowa State Univ. | Carena et al. 2008 |
| Leaming(S-FS)C6 | Iowa State Univ. | Carena and Hallauer 2001b; <br> Melani and Carena 2005; Carena 2013 |
| NDBS22(R-T1)C9 | Iowa State Univ. | Hallauer et al. 2000; Laude and Carena 2013 |
| NDSAB(MER-FS)C15 | North Dakota State Univ. | Cross 1983; <br> Carena and Wanner 2005 |
| NDSM(M-FS)C9 | North Dakota State Univ. | Cross and Wanner 1991; Melani and Carena 2005; Carena 2013 |
| NDBS21(R-T)C9 | Iowa State Univ. | Hallauer et al. 2000; <br> Laude and Carena 2013 |
| NDSCD(FS-CS)C2 | North Dakota State Univ. | Cross 1982; Cross 1988; Melani and Carena 2005; Sezegen and Carena 2009 |
| NDSHLC(M-FS)C5 | CIMMYT, Mexico | Eagles and Lothrop 1994; <br> Eno and Carena 2008; <br> Laude and Carena 2013 |
| EARLYGEM 21a | South America | Carena et al. 2009; <br> Laude and Carena 2013 |
| EARLYGEM 21b | South America | Carena et al. 2009; <br> Laude and Carena 2013 |
| EARLYGEM 21c | South America | Carena et al. 2009; <br> Laude and Carena 2013 |

2011, and 2012. Seeds generated from the 2009 Fargo breeding nursery were used for evaluation in 2010 trials, and seeds from the 2010-2011 Salta breeding nursery were used in 2011 and 2012 trials. A total of 12 environments (location by year combination) were used for evaluation. Experimental units were single-row plots, each at 7 m long with row spacing of 0.76 m . The
experiment in each environment was planted with 50 seeds, and later was thinned to desired stand. Standard cultural management practices for maize trials were followed.

## Traits studied

Agronomic data gathered from all environments were stand (number of plants in each experimental unit before harvest adjusted to number of plants $\mathrm{ha}^{-1}$ ), and stalk lodging (\%). Grain yield (adjusted to $155 \mathrm{~g} \mathrm{~kg}^{-1}$ grain moisture, expressed in $\mathrm{Mg} \mathrm{ha}^{-1}$ ), and grain moisture ( $\mathrm{g} \mathrm{kg}^{-1}$ ) were gathered for all locations except at Casselton in 2011, and test weight $\left(\mathrm{kg} \mathrm{hL}^{-1}\right)$ were obtained from all locations except at Casselton in 2011 and 2012. Root lodging (\%), ear and plant heights (cm) were obtained from all locations except at Prosper in 2010, due to severe lodging caused by storms that affected the area. Dropped ears (\%) were not observed in 2010 for all locations, and data were analyzed only for all locations in 2011 and 2012. Days to silking (the number of days from germination to time when $50 \%$ of the plants within an experimental unit have emerged their silks) and days to anthesis (the number of days when $50 \%$ of the plants within an experimental unit started to shed their pollen) were gathered from Prosper and Casselton for three years, except in 2012 at Casselton. Plots were machine harvested for all environments.

Grain quality traits were determined using 500 g of kernels sampled from each experimental unit in 11 environments. Near-infrared spectroscopy (NIRS) grain analyzer (OmegAnalyzer G) was used to determine the relative concentrations of protein, oil, starch, lysine, methionine, and cysteine in maize kernels for all entries. The calibration for OmegAnalyzer G was provided by the Iowa Grain Quality Initiative Lab at the Iowa State University. A second NIRS grain analyzer (FOSS Infratec 1241) was used to determine extractable starch (HES) and fermentable starch (HFC) in maize kernels for all entries. The

FOSS Infratec 1241 was provided with proprietary calibration in cooperation with Monsanto. Data for HES and HFC were obtained only from all locations in 2010 and 2012.

## Statistical analyses

Analyses of variance (ANOVA) were conducted for all traits within and among environments. Genotypes were considered as fixed effects, and environments and replications were considered as random effects. ANOVA for each environment were performed using SAS version 9.3 PROC MIXED procedure with method=REML (restricted maximum likelihood) option (SAS Institute Inc. 2010; Littell et al. 2006). Test for homogeneity of error variances was conducted using the $\mathrm{F}_{\text {max }}$ test (Tabachnick and Fidell 2001) before combining data across environments. Least-squares means from each environment were used for combined analyses of variance using PROC GLM procedure from SAS version 9.3 (SAS Institute Inc. 2010). Genetic and environmental effects were partitioned following GEAN II (Gardner and Eberhart 1966). The genetic model provides estimates for variety $\left(v_{i}\right)$ and heterosis $\left(h_{i j}\right)$ effects. The $h_{i j}$ effects were partitioned to average heterosis $(\bar{h})$, variety heterosis $\left(h_{i}\right)$, and $s_{i j}$. Checks were removed from the data set prior to analysis. Additionally, $g_{i}$ estimate was calculated following the formula, $g_{i}=\frac{1}{2} v_{i}+h_{i}$ to determine the performance of parental populations in population crosses (Gardner and Eberhart 1966). The analysis was performed using the DIALLEL-SAS05 program developed by Zhang et al. (2005) with modifications to extend the linear matrix for a 16-parent diallel. The $v_{i}$ and $h_{i j}$ effects were tested for significance using the student's $t$ test. In addition, other sources of variation due to genotypes and genotype by environment interaction (GxE) such as checks and 'checks vs. others' and their interactions with environment were also generated. The combined error mean squares were computed by pooling individual environment error mean squares weighted by their corresponding error degrees of freedom.

The estimates of $g_{i}$ effects were used for PCA and cluster analysis. The $g_{i}$ effects were chosen to perform the analysis, since they agreed with the source of variation that explained the most sum of squares in the genetic model (Laude and Carena 2013). The $g_{i}$ estimates for each trait were standardized to general coefficients by taking the observed value and dividing it by the range of that trait (Milligan and Cooper 1988). The PCA was performed on the standardized $g_{i}$ estimates for each trait to determine which group of traits accounted for most of the variation in the dataset. A simple correlation analysis between the PC scores and each trait was conducted to identify the contribution of each trait to the PC axis. For the cluster analysis, the GD between parental populations was calculated from standardized $g_{i}$ estimates as Euclidean distances. This was used to construct a rectangular dissimilarity matrix. The cluster analysis was done using the UPGMA method (Sneath and Sokal 1973). Cophenetic matrix as implied by the dendrogram was computed using ultrametric distance method (Sokal 1986). To determine whether groups created using the cluster analysis represent the relationships observed among the parental populations, the dissimilarity and cophenetic matrices were compared to generate cophenetic correlation coefficient using Mantel statistics (Mantel 1967). The PCA and cluster analysis were performed using NTSYSpc version 2.1 (Rohlf 2000).

Percentage heterosis of population crosses was determined for grain yield. Percentage heterosis based on the high-parent (HPH) was computed using the formula:
$\frac{\left(F_{1}-H P\right)}{H P} \times 100$, where $\mathrm{F}_{1}$ refers to the mean grain yield of the population cross and HP is the mean grain yield of the parental population with higher performance.

The HSGCA computation proposed by Fan et al. (2009) was performed for grain yield. The HSCGA combined the $g_{i}$ and SCA estimates, wherein the latter is equivalent to $s_{i j}$. The formula used for this study was $H S G C A=\frac{1}{2}\left(g_{i}+g_{j}\right)+s_{i j}$, where $g_{i}$ is the general combining
ability estimate of the $i^{\text {th }}$ population and $s_{i j}$ is the specific heterosis observed when population $i$ is mated to population $j$.

Pearson correlation coefficients ( $r$ ) between GD and grain yield of $\mathrm{F}_{1}, \mathrm{HPH}, s_{i j}$, and HSGCA were computed from means across environments. The statistical computations were performed using SAS version 9.3 (SAS Institute Inc. 2010). Heterotic groups were established by constructing a dendrogram on the heterosis parameter that was highly correlated with GD.

## Results and Discussion

The combined analyses of variance showed significant differences among genotypes $(\mathrm{P}<0.01)$ for the genotype by environment interaction $(\mathrm{GxE})$ source of variation in all traits studied except for dropped ears (data not shown). The source of variation due to genotypes was also highly significant $(\mathrm{P}<0.01)$ for all traits. Fig. 4 shows the proportion of sum of squares due to $v_{i}$ and $h_{i j}$ effects over the total among diallel entries sum of squares contributing to the differences of the traits studied. The $v_{i}$ effects contributed most of the among diallel entries sum of squares for grain moisture, test weight, stalk lodging, ear height, plant height, days to silking, days to tasseling, and grain quality traits (protein, oil, starch, lysine, methionine, cysteine, HFC, and HES). The largest proportion of sum of squares due to $v_{i}$ effects was observed for grain moisture having $94 \%$. Heterosis effects contributed most of the among diallel entries sum of squares for grain yield, stand, root lodging, and dropped ears. Largest proportion of sum of squares due to $h_{i j}$ effects was observed for dropped ears followed by grain yield and stand at 79 , 64 , and $63 \%$, respectively. Our results suggest that $g_{i}$ effects agreed with the genetic effect that had larger contribution to the total among diallel entries sum of squares for a particular trait (Laude and Carena 2013). For example, the parental population, NDBS21(R-T)C9, showed the


Fig. 4. Proportion of sum of squares due to variety $\left(v_{i}\right)$ and heterosis $\left(h_{i j}\right)$ effects over the total among diallel entries sum of squares for the agronomic traits [grain yield (GY), grain moisture (MSTR), test weight (TWT), stand, stalk lodging (PSL), root lodging (PRL), dropped ears (PDE), days to silking (DS), days to anthesis (DA), ear height (EH), plant height (PH)], and grain quality traits [protein, oil, starch, lysine (LYS), methionine (MET), cysteine (CYS), high fermentable starch (HFC), and high extractable starch (HES)] across environments in the 16parent maize population diallel.
highest $h_{i}$ effect for grain yield, consequently it also had the highest $g_{i}$ effect. In terms of grain quality traits, parental populations showed similar trends for their $v_{i}$ and $g_{i}$ effects. These results prompted us to use $g_{i}$ effects to estimate GD for all traits to assess the genetic relationships among the parental populations.

The results of PCA suggest that five PC axis described the majority of the variability among the 19 traits studied. The cumulative percent of the variability accounted for by the five PC axis was $88.8 \%$ (Table 7). The majority of the variability was explained by PC 1 and PC 2,

Table 7. Eigenvectors of the first five principal components (PC 1, PC 2, PC 3, PC 4, and PC 5) axes for 16 maize populations evaluated in 12 northern U.S. Corn Belt environments.

| Trait | PC 1 | PC 2 | PC 3 | PC 4 | PC 5 |
| :--- | ---: | ---: | ---: | ---: | ---: |
| Grain yield | 0.04 | 0.82 | 0.25 | 0.33 | 0.18 |
| Grain moisture | -0.34 | 0.37 | -0.12 | -0.76 | 0.19 |
| Test weight | 0.74 | -0.28 | 0.20 | 0.44 | -0.09 |
| Stand | -0.04 | 0.79 | 0.38 | 0.19 | 0.35 |
| Stalk lodging | 0.42 | -0.75 | -0.18 | 0.08 | -0.07 |
| Root lodging | -0.43 | -0.81 | -0.22 | 0.14 | -0.03 |
| Dropped ears | -0.67 | -0.04 | -0.33 | 0.45 | -0.17 |
| Ear height | -0.72 | -0.30 | -0.47 | 0.17 | 0.21 |
| Plant height | -0.82 | 0.14 | -0.26 | 0.30 | 0.27 |
| Days to silking | -0.68 | 0.36 | -0.53 | -0.12 | -0.05 |
| Days to anthesis | -0.52 | 0.37 | -0.63 | -0.13 | -0.05 |
| Protein | -0.70 | -0.42 | 0.45 | -0.19 | -0.13 |
| Oil | -0.21 | -0.56 | 0.09 | 0.16 | 0.71 |
| Starch | 0.82 | 0.41 | -0.37 | -0.04 | -0.07 |
| Lysine | -0.89 | 0.10 | 0.19 | 0.25 | -0.04 |
| Methionine | -0.89 | -0.07 | 0.33 | -0.21 | -0.07 |
| Cysteine | -0.78 | -0.24 | 0.36 | -0.34 | -0.11 |
| HFC | 0.53 | -0.44 | -0.09 | -0.37 | 0.42 |
| HES | 0.90 | -0.08 | -0.27 | -0.17 | 0.08 |
| Proportion of variance |  |  |  |  |  |
| accounted for by PC | 41.47 | 21.30 | 11.16 | 9.13 | 5.74 |
| Cumulative proportion |  |  |  |  |  |
| of variance accounted |  |  |  |  |  |
| for by PC | 41.47 | 62.77 | 73.93 | 83.06 | 88.80 |

${ }^{\text {a }}$ The absolute magnitude of the eigenvector coefficients (values in italicized) are equal to or
greater than 0.3 .
which accounted for 41.4 and $21.3 \%$, respectively. The eigenvectors indicated the relative importance of each trait within each PC axis. The absolute magnitude of the eigenvector coefficients that is equal to or greater than 0.3 was used as a cut-off point (Badu-Apraku et al. 2006). PC 1 appeared to have large loadings for 16 traits. The loadings for these traits also had opposite signs of the eigenvector coefficients. This reflected the negative correlation between traits. Test weight, stalk lodging, starch, HFC, and HES were negatively correlated with grain moisture, root lodging, dropped ears, ear and plant heights, days to silking and anthesis, protein, and amino acids (lysine, methionine, and cysteine). Previous studies reported the negative
correlation between starch and protein on maize kernels (Dado 1999; Scott et al. 2006).
However, the use of large samples of genotypes can reduce this effect. For PC 2, 12 traits showed large loadings, among which were grain yield, grain moisture, stand, stalk lodging, root lodging, ear height, days to silking and anthesis, protein, oil, starch, and HFC. The negative correlation between grain yield and stalk and root lodging may be explained by the yield losses due to lodged plants. Our purpose of doing PCA was to identify group of traits that accounted for the most variation in the dataset. Since PC 1 and PC 2 showed the majority of the variability, the groups of traits that showed large loadings for each PC were considered for cluster analysis. All the 19 traits showed large loadings for PC 1 and PC 2. The result was positive, since maximum number of variables was considered to characterize the parental populations. This is expected to improve the accuracy of grouping the populations.

The GD values based on $g_{i}$ estimates of the 19 traits are presented Table 8. The GD values ranged from 0.38 (between EARLYGEM 21a and EARLYGEM 21b) to 3.30 [between NDSCD(FS-CS)C2 and EARLYGEM 21c]. The three cross combinations with the least GD values were shown by the population crosses between EARLYGEM 21 populations. This is expected, since they all share similar genetic background. The NDSCD(FS-CS)C2 and EARLYGEM 21c showed the largest GD value, and NDSCD(FS-CS)C2 and EARLYGEM 21b also showed large GD value of 2.83 . These results confirmed the divergence between NDSCD(FS-CS)C2 and EARLYGEM 21 populations. Additionally, a large GD value (2.93) was observed between NDSS and EARLYGEM 21c. Preliminary heterotic grouping reported by Laude and Carena (2013) suggest that NDSS and EARLYGEM 21c behaved as a stiff-stalk synthetic heterotic group (SSS). However, our results suggest that EARLYGEM 21 populations may belong to a unique group. The GD value between NDBS22(R-T1)C9 and NDBS21(R-T)C9

Table 8. Dissimilarity matrix of the 16 maize populations constructed based on Euclidean distances of the general combining ability estimates for agronomic and grain quality traits.

| Population code ${ }^{\text {a }}$ | P1 | P2 | P3 | P4 | P5 | P6 | P7 | P8 | P9 | P10 | P11 | P12 | P13 | P14 | P15 | P16 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| P1 | 0.00 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| P2 | 1.48 | 0.00 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| P3 | 2.12 | 2.05 | 0.00 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| P4 | 1.67 | 1.61 | 1.26 | 0.00 |  |  |  |  |  |  |  |  |  |  |  |  |
| P5 | 1.06 | 1.53 | 1.48 | 1.45 | 0.00 |  |  |  |  |  |  |  |  |  |  |  |
| P6 | 1.53 | 1.84 | 1.16 | 1.34 | 0.91 | 0.00 |  |  |  |  |  |  |  |  |  |  |
| P7 | 1.73 | 1.40 | 1.42 | 1.33 | 1.30 | 1.43 | 0.00 |  |  |  |  |  |  |  |  |  |
| P8 | 1.32 | 1.48 | 1.30 | 0.83 | 1.11 | 1.09 | 1.36 | 0.00 |  |  |  |  |  |  |  |  |
| P9 | 1.40 | 1.10 | 1.37 | 1.29 | 1.23 | 1.09 | 1.19 | 1.05 | 0.00 |  |  |  |  |  |  |  |
| P10 | 1.11 | 1.36 | 2.04 | 1.47 | 1.39 | 1.78 | 1.63 | 1.29 | 1.49 | 0.00 |  |  |  |  |  |  |
| P11 | 1.81 | 1.39 | 1.57 | 1.38 | 1.37 | 1.64 | 1.30 | 1.41 | 1.60 | 1.55 | 0.00 |  |  |  |  |  |
| P12 | 1.50 | 2.21 | 2.78 | 2.46 | 1.97 | 1.98 | 2.22 | 2.24 | 1.91 | 1.91 | 2.69 | 0.00 |  |  |  |  |
| P13 | 1.57 | 1.96 | 2.08 | 1.65 | 1.39 | 1.65 | 1.73 | 1.49 | 1.75 | 1.38 | 1.66 | 2.06 | 0.00 |  |  |  |
| P14 | 2.35 | 1.89 | 1.84 | 1.78 | 2.06 | 2.00 | 1.78 | 1.90 | 1.77 | 1.70 | 1.62 | 2.66 | 1.81 | 0.00 |  |  |
| P15 | 2.53 | 1.96 | 1.96 | 1.92 | 2.26 | 2.17 | 1.92 | 2.08 | 1.86 | 1.92 | 1.76 | 2.83 | 2.03 | 0.38 | 0.00 |  |
| P16 | 2.93 | 2.31 | 2.19 | 2.12 | 2.63 | 2.55 | 2.19 | 2.38 | 2.25 | 2.25 | 2.00 | 3.30 | 2.32 | 0.77 | 0.59 | 0.00 |

${ }^{a}$ The following are the parental populations listed in the order: NDSS, NDCG(FS)C1, NDL, NDBSK(HI-M)C3, NDBS11(FR-M)C3, NDBS1011, Leaming(S-FS)C6, NDBS22(R-T1)C9, NDSAB(MER-FS)C15, NDSM(M-FS)C9, NDBS21(R-T)C9, NDSCD(FS-
CS)C2, NDSHLC(M-FS)C5, EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c.
was 1.41. These two populations represented different heterotic groups. Former versions of NDBS22(R-T1)C9 belonged to the SSS group, while NDBS21(R-T)C9 belonged to the non-SSS group according to previous reports (Carena et al. 2008). High grain yield was observed between BS21(R)C7 x BS22(R)C7 (Melani and Carena 2005), which was expected as the two populations were improved through reciprocal recurrent selection for seven cycles (Hallauer et al. 2000). On the other hand, a relatively small GD value (0.91) was observed between NDBS11(FR-M)C3 and NDBS1011 suggesting that the two populations are related. NDBS1011 was developed from the cross between $\mathrm{BS} 10(\mathrm{FR}) \mathrm{C} 13$ and $\mathrm{BS} 11(\mathrm{FR}) \mathrm{C} 13$, with the latter being an earlier version of NDBS11(FR-M)C3 (Carena et al. 2008).

The dendrogram using the UPGMA method is shown in Fig. 5. The cophenetic correlation coefficient, $r_{c}$, based on Mantel statistics was 0.83 . Similar $r_{c}$ was also obtained by Osorno and Carena (2008). Sokal (1986) suggested that $r_{c}>0.85$ has a high cophenetic correlation. Our results suggest that there was a good correlation between the dissimilarity matrix and cophenetic matrix obtained by the dendrogram. The hierarchic classification generated by the UPGMA method represented well the relationship implied by the dissimilarity matrix among the 16 populations. Permutation test was performed to test the null hypothesis that a set of genetic variants will not affect the outcome. After 5,000 permutations, the clusters found had strong consistency at $\mathrm{P}=0.0004$. Osorno and Carena (2008) explained that when the matrix was shuffled at random by 5,000 times, similar grouping cannot be obtained by chance at $\mathrm{P}=0.0004$. When the cut-off point for the dendrogram was set at 1.49 , three groups and a singleton [NDSCD(FS-CS)C2] were observed. The cut-off point was set based on our knowledge of the genetic backgrounds of the populations studied and the preliminary results. The group 1 contained three populations, NDSS, NDSM(M-FS)C9, and NDSHLC(M-FS)C5. The NDSS and


Fig. 5. Dendrogram of genetic relationships among 16 maize populations adapted to the northern U.S. Corn Belt. Three main clusters (group 1 to group 3) were formed. The UPGMA (Unweighted Paired Group Method using Arithmetic averages) method was used based on general combining ability estimates of agronomic and grain quality traits.

NDSM(M-FS)C9 showed similar response for grain quality traits. Both of these two populations showed high protein contents and low starch contents (Laude and Carena 2013). However, Osorno and Carena (2008) reported that an earlier version of NDSM(M-FS)C9 was grouped together with the earlier versions of NDSAB(MER-FS)C15. Therefore, a larger sample of genotypes provided more details. Although NDSHLC(M-FS)C5 was classified under group 1, it was slightly divergent from the other two populations. The genetic divergence of NDSHLC(MFS)C5 can be explained by its genetic background and geographical origin. NDSHLC(M-FS)C5 is an exotic germplasm, which originated from four highland white dent populations from Mexico (Eno and Carena 2008).

The group 2 included nine populations. This group can be subdivided into two subgroups and one singleton, NDBS21(R-T)C9. The sub-group 1 had NDCG(FS)C1, NDSAB(MER-FS)C15, and Leaming(S-FS)C6. This result is contrary to the earlier grouping made by Osorno and Carena (2008). They classified the earlier versions of NDSAB(MERFS)C15 and Leaming(S-FS)C6 and parental populations of NDCG(FS)C1 into three different groups. Additional cycles of recurrent selection might have contributed to a change in allele frequencies, which caused the variation in group assignments of these populations. Moreover, the different locations and years of evaluation may also affect the phenotypic response of the populations. The sub-group 2 contained NDL, NDBSK(HI-M)C3, NDBS22(R-T1)C9, NDBS11(FR-M)C3, and NDBS1011. The close resemblance of NDBS11(FR-M)C3 and NDBS1011 placed them in the same group. Additionally, NDBSK(HI-M)C3, NDBS22(RT1)C9, NDBS11(FR-M)C3, and NDBS1011 were initially developed at the Iowa State University before they got adapted and further improved at ND. Their geographic origin may explain the genetic similarities among these populations. Divergence of NDBS21(R-T)C9 from
other populations in group 2 can be explained by its relationship with NDBS22(R-T1)C9. The heterosis for grain yield observed between these two populations may have contributed to their genetic divergence between each other. Previous studies, however, reported some degree of relatedness between BS21(R)C7 and BS22(R)C7 (Melani and Carena 2005; Hallauer et al. 2000).

Group 3 contained EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c. This is expected as these three populations have similar genetic background. Their small GD values reflected the close resemblance among these populations. Additionally, the uniqueness of this group can be attributed to the fact that EARLYGEM 21 is an exotic germplasm derived from South America.

NDSCD(FS-CS)C2 did not belong to any of the three groups. It was the most divergent population, since it was widely separated from the other 15 populations. Osorno and Carena (2008) also had a similar observation. The earlier version of NDSCD(FS-CS)C2 was also grouped separately from the 10 populations they studied.

Grain yield was used to evaluate the heterotic relationships among the 16 populations. Heterosis between genotypes was best measured by grain yield. Additionally, Froyer et al. (1988) stated that yield was the best trait to accurately estimate genetic diversity. The means and HPH for grain yield of the population crosses are presented in Table 9. Means for grain yield ranged from 2.2 (EARLYGEM 21b x EARLYGEM 21c) to $5.9 \mathrm{Mg} \mathrm{ha}^{-1}$ [NDBS21(R-T)C9 x EARLYGEM 21b]. The poor grain yield of EARLYGEM 21b x EARLYGEM 21c was expected, since the two populations are genetically related, hence, the lack of heterosis. The high grain yield observed for NDBS21(R-T)C9 x EARLYGEM 21b can be explained by the divergence between the two populations. NDBS21(R-T)C9 had $3.5 \mathrm{Mg} \mathrm{ha}^{-1}$, while EARLYGEM

Table 9. Mean grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) for the 16 parental populations (diagonal), their crosses (above the diagonal), and percentage of high-parent heterosis (below the diagonal).

${ }^{9}$ The following are the parental populations listed in the order: NDSS, NDCG(FS)C1, NDL, NDBSK(HI-M)C3, NDBS11(FR-M)C3, NDBS1011, Leaming(S-FS)C6, NDBS22(R-T1)C9, NDSAB(MER-FS)C15, NDSM(M-FS)C9, NDBS21(R-T)C9, NDSCD(FS-
CS)C2, NDSHLC(M-FS)C5, EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c.

21b had only $2.1 \mathrm{Mg} \mathrm{ha}^{-1}$, the lowest mean grain yield among the parental populations. Moreover, the geographical origin of the two populations contributed to the high grain yield of the cross (Moll et al. 1962; Moll et al. 1965; Reif et al. 2005). In terms of HPH, NDSHLC(MFS)C5 x EARLYGEM 21b had the highest HPH (93.7\%), while EARLYGEM 21a x EARLYGEM 21c had the lowest HPH (-15.4\%). High HPH of NDSHLC(M-FS)C5 x

EARLYGEM 21b can be explained by the divergence between the two populations and the low parental population means, although mean grain yield for the cross was only $4.7 \mathrm{Mg} \mathrm{ha}^{-1}$. The two populations originated from different exotic germplasm sources. This result agrees with Prasad and Singh (1986), wherein they observed that higher grain yield was obtained from crosses between parents with moderate genetic diversity. Additionally, the HPH of top-yielding population cross [NDBS21(R-T)C9 x EARLYGEM 21b] was $69.4 \%$. The difference in parental performance caused the heterosis observed in the cross. On the other hand, the three

EARLYGEM 21 populations showed low and negative heterosis for the crosses between them. Their pedigrees and low frequency of desirable alleles may have resulted in low grain yield of the parental populations and population crosses.

The estimates for $s_{i j}$ effects and HSGCA of the population crosses for grain yield are presented in Table 10. The $s_{i j}$ effects ranged from -1.76 (EARLYGEM 21a x EARLYGEM 21c) to $0.97 \mathrm{Mg} \mathrm{ha}^{-1}$ (NDBS $1011 \times$ EARLYGEM 21c). The negative $s_{i j}$ effect for EARLYGEM 21a x EARLYGEM 21c agreed with its mean grain yield and HPH. EARLYGEM 21a x EARLYGEM 21c obtained the least value for the three heterosis parameters among all the population crosses. However, the uniqueness of the EARLYGEM 21 populations over the other 13 populations seems to increase the frequency of favorable alleles when crossed with populations from different groups. NDBS1011 x EARLYGEM 21c showed the largest $s_{i j}$ effect and high mean

Table 10. Estimates for specific heterosis (above the diagonal) and heterotic group's specific and general combining ability (below the diagonal) for grain yield $\left(\mathrm{Mg} \mathrm{ha}^{-1}\right)$ for all maize population crosses.

| Population <br> code $^{\text {a }}$ | P 1 | P 2 | P 3 | P 4 | P 5 | P 6 | P 7 | P 8 | P 9 | P 10 | P 11 | P 12 | P 13 | P14 | P15 | P16 |
| :--- | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: | ---: |
| P1 |  | -0.66 | 0.26 | 0.05 | 0.58 | -0.05 | -0.56 | 0.79 | 0.11 | -0.02 | -0.47 | 0.00 | -0.46 | 0.21 | 0.37 | -0.15 |
| P2 | -0.49 |  | -0.56 | -0.58 | 0.23 | 0.03 | 0.15 | 0.46 | 0.34 | -0.22 | -0.06 | 0.11 | -0.18 | 0.46 | -0.02 | 0.49 |
| P3 | 0.45 | -0.27 |  | 0.08 | 0.06 | 0.28 | -0.50 | -0.01 | -0.24 | -0.40 | -0.19 | 0.28 | -0.02 | 0.52 | 0.15 | 0.29 |
| P4 | 0.20 | -0.34 | 0.35 |  | -0.51 | 0.47 | -0.10 | -0.32 | -0.18 | 0.32 | -0.09 | -0.17 | -0.09 | 0.31 | 0.23 | 0.58 |
| P5 | 0.72 | 0.47 | 0.32 | -0.30 |  | -1.05 | 0.36 | 0.23 | 0.17 | -0.26 | -0.42 | 0.50 | -0.76 | 0.29 | 0.56 | 0.02 |
| P6 | 0.07 | 0.24 | 0.51 | 0.66 | -0.87 |  | 0.16 | 0.10 | -0.62 | 0.05 | -0.66 | -0.01 | -0.18 | 0.39 | 0.13 | 0.97 |
| P7 | -0.46 | 0.34 | -0.28 | 0.08 | 0.53 | 0.30 |  | 0.10 | -0.08 | 0.25 | 0.17 | -0.53 | -0.25 | 0.60 | 0.33 | -0.09 |
| P8 | 0.85 | 0.62 | 0.17 | -0.18 | 0.36 | 0.20 | 0.19 |  | 0.00 | -0.75 | -0.36 | -0.63 | -0.10 | 0.16 | 0.29 | 0.04 |
| P9 | 0.15 | 0.47 | -0.09 | -0.07 | 0.27 | -0.54 | -0.02 | 0.02 |  | -0.11 | 0.26 | -0.17 | 0.02 | 0.14 | 0.13 | 0.24 |
| P10 | -0.15 | -0.27 | -0.42 | 0.26 | -0.33 | -0.05 | 0.14 | -0.90 | -0.29 |  | 0.65 | -0.04 | 0.27 | 0.21 | -0.42 | 0.49 |
| P11 | -0.05 | 0.46 | 0.35 | 0.41 | 0.07 | -0.20 | 0.62 | 0.05 | 0.63 | 0.85 |  | 0.13 | 0.28 | 0.03 | 0.57 | 0.16 |
| P12 | -0.24 | -0.03 | 0.15 | -0.34 | 0.32 | -0.21 | -0.74 | -0.88 | -0.46 | -0.49 | 0.23 |  | 0.26 | -0.23 | 0.26 | 0.25 |
| P13 | -0.73 | -0.35 | -0.17 | -0.28 | -0.96 | -0.40 | -0.49 | -0.38 | -0.29 | -0.21 | 0.36 | -0.32 |  | 0.27 | 0.73 | 0.20 |
| P14 | 0.10 | 0.45 | 0.53 | 0.28 | 0.25 | 0.33 | 0.51 | 0.04 | -0.01 | -0.11 | 0.26 | -0.65 | -0.18 |  | -1.60 | -1.76 |
| P15 | 0.35 | 0.06 | 0.24 | 0.28 | 0.60 | 0.14 | 0.33 | 0.26 | 0.06 | -0.65 | 0.89 | -0.08 | 0.37 | -1.80 |  | -1.71 |
| P16 | -0.24 | 0.50 | 0.32 | 0.56 | -0.01 | 0.92 | -0.15 | -0.06 | 0.11 | 0.18 | 0.42 | -0.16 | -0.23 | -2.03 | -1.90 |  |

${ }^{9}$ The following are the parental populations listed in the order: NDSS, NDCG(FS)C1, NDL, NDBSK(HI-M)C3, NDBS11(FR-M)C3, NDBS1011, Leaming(S-FS)C6, NDBS22(R-T1)C9, NDSAB(MER-FS)C15, NDSM(M-FS)C9, NDBS21(R-T)C9, NDSCD(FS-
CS)C2, NDSHLC(M-FS)C5, EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c

Table 11. Correlation between genetic distance (GD) with mean grain yield of the population crosses ( $\mathrm{F}_{1}$ ), high-parent heterosis (HPH), specific heterosis ( $s_{i j}$ ), and heterotic group's specific and general combining ability (HSGCA) values.

| Parameter | GD | $\mathrm{F}_{1}$ | HPH | $s_{i j}$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~F}_{1}$ | 0.05 |  |  |  |
| HPH | $0.20^{* a}$ | $0.45^{* *}$ |  |  |
| $s_{i j}$ | $0.39^{* *}$ | $0.71^{* *}$ | $0.58^{* *}$ |  |
| HSGCA | $0.19^{*}$ | $0.95^{* *}$ | $0.55^{* *}$ | $0.89^{* *}$ |
| $a^{*}$ |  |  |  |  |

$\mathrm{a}^{*}$ and ${ }^{* *}$ indicate that the coefficients are significantly different from zero at $\alpha$ level of 0.05 and 0.01 , respectively.
grain yield ( $5.6 \mathrm{Mg} \mathrm{ha}^{-1}$ ). Similar mean grain yield was also obtained by NDSS x NDBS22(RT1)C9, which had the second largest $s_{i j}$ estimate ( $0.79 \mathrm{Mg} \mathrm{ha}^{-1}$ ). For HSGCA, the estimates ranged from - 2.03 (EARLYGEM 21a x EARLYGEM 21c) to $0.92 \mathrm{Mg} \mathrm{ha}^{-1}$ (NDBS1011 x EARLYGEM 21c). The same population crosses were identified to have the smallest and largest estimates for $s_{i j}$ effects and HSGCA. Additionally, NDSS x NDBS22(R-T1)C9 also obtained the third largest HSGCA estimate ( $0.85 \mathrm{Mg} \mathrm{ha}^{-1}$ ). The similarity in estimates between $s_{i j}$ effects and HSGCA can be attributed to the large contribution (50\%) of $s_{i j}$ effect in calculating HSGCA.

A positive correlation was observed between GD and grain yield based on $\mathrm{F}_{1}, \mathrm{HPH}, s_{i j}$, and HSGCA (Table 11). The GD was significantly correlated ( $\mathrm{P}<0.05$ ) with HPH and HSGCA. The correlation between GD and $s_{i j}$ was highly significant ( $\mathrm{P}<0.01$ ). Betran et al. (2003) also observed strongest correlation between GD and SCA. The results suggest that the groups formed by GD using the UPGMA method can be validated by $s_{i j}$ to assign the 16 populations to heterotic groups. Among the heterosis parameters measured for grain yield, the highest correlation was observed between $\mathrm{F}_{1}$ and HSGCA with $r=0.95$. This indicates that HSGCA among parental populations can predict population cross performance for this set of genotypes. The top-yielding population cross, NDBS21(R-T)C9 x EARLYGEM 21b, obtained the second largest HSGCA estimate $\left(0.89 \mathrm{Mg} \mathrm{ha}^{-1}\right)$. Additionally, a high correlation of 0.89 was observed between $s_{i j}$ and

HSGCA. This relationship can also be used to confirm the heterotic relationships among the 16 populations. Moreover, Badu-Apraku et al. (2013a) showed that the groups formed using HSGCA agreed with grouping they generated using microsatellite markers.

A second dendrogram was constructed to assess the heterotic relationships among the 16 populations. The estimates for $s_{i j}$ effects for grain yield were used to construct the dissimilarity matrix. Fig. 6 shows four possible heterotic groups at the cut-off point of -0.09 . Heterotic group (HG) 1 contained NDSS, NDCG(FS)C1, NDSHLC(M-FS)C5, and NDBSK(HI-M)C3. The grouping formed using GD classified NDSS and NDSHLC(M-FS)C5 to group 1, and NDCG(FS)C1 and NDBSK(HI-M)C3 to group 2 (Fig. 5). Although NDSS and NDSHLC(MFS)C5 were initially grouped separately from NDCG(FS)C1 and NDBSK(HI-M)C3, small and negative HSGCA estimates were observed among the crosses formed by the populations belonging to HG 1 (Table 10). If we look at NDCG(FS)C1, its HSGCA estimates with NDSS, NDSHLC(M-FS)C5, and NDBSK(HI-M)C3 were $-0.49,-0.35$, and $-0.34 \mathrm{Mg} \mathrm{ha}^{-1}$. This suggests that the populations belonging to HG 1 have similar combining ability for grain yield. On the other hand, HG 2 included three populations, NDBS11(FR-M)C3, NDBS1011, and NDBS21(RT)C9. Earlier grouping based on GD classified NDBS11(FR-M)C3 and NDBS1011 under the same sub-group of group 2 (Fig. 5). The high degree of relatedness between these two populations reflected similarity in their heterotic response with other populations. Moreover, NDBS11(FR-M)C3 x NDBS21(R-T)C9 and NDBS1011 x NDBS21(R-T)C9 had small HSGCA estimates of 0.07 and $-0.20 \mathrm{Mg} \mathrm{ha}^{-1}$ (Table 10). The lack of heterosis for grain yield between these populations allowed NDBS21(R-T)C9 to be classified under HG 2. The HG 3 was the largest group containing NDL, NDSAB(MER-FS)C15, NDBS22(R-T1)C9, NDSM(M-FS)C9, Leaming(S-FS)C6, and NDSCD(FS-CS)C2. Based on GD, these populations were classified


Fig. 6. Dendrogram of genetic relationships among 16 maize populations adapted to the northern U.S. Corn Belt based on specific heterosis estimates for grain yield. Four main clusters (HG 1 to HG 4) were formed using the UPGMA method.
under group 2 except for NDSCD(FS-CS)C2 and NDSM(M-FS)C9 (Fig. 5). The HSGCA estimates of population crosses with NDSCD(FS-CS)C2 ranged from -0.88 [NDBS22(R-T1)C9 x NDSCD(FS-CS)C2] to $0.15 \mathrm{Mg}_{\mathrm{ha}}{ }^{-1}$ [NDL x NDSCD(FS-CS)C2] (Table 10). This result suggests that NDSCD(FS-CS)C2 has similar heterotic response with other five populations under HG 3. On the other hand, NDSM(M-FS)C9 was initially grouped with NDSS due to their similar response to grain quality traits. However, this current grouping agreed with Osorno and Carena (2008), wherein they classified NDSM(M)C7 and earlier versions of NDSAB(MER-FS)C15 together. The last group, HG 4, contained EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c. These three populations were very different from the other 13 populations, and so a unique group was formed among them. This result is consistent with the previous grouping based on GD. Furthermore, the crosses among EARLYGEM 21 populations showed negative heterotic responses based on $s_{i j}$ effects and HSGCA, suggesting lack of heterosis. The heterotic groupings established among the 16 populations validated former heterotic groups. New heterotic patterns were also created from population crosses, NDBS21(R-T)C9 x EARLYGEM 21b, NDBS1011 x EARLYGEM 21c, and NDSS x NDBS22(R-T1)C9. These results are expected to increase breeding efficiency to develop new cultivars for the northern U.S. Corn Belt.

## Summary

The population diallel including 16 short-season maize populations provided sufficient information to assess the genetic diversity and establish heterotic groups among them. The genetic parameter estimates based on $g_{i}$ effects from phenotypic data were used for the genetic diversity study. Laude and Carena (2013) showed a good correlation between $g_{i}$ and the genetic
effect showing larger contribution to the total among diallel entries sum of squares. All the traits evaluated from the 16 parental populations were important to explain the variability in PC 1 and PC 2. A total of 19 traits were used to characterize the genetic differences phenotypically expressed by the populations. The cluster analysis based on GD formed three major groups. The populations included in each group were classified based on similarities in phenotypic response, pedigree information, geographic origin, and results of previous studies. Group 1 contained NDSS, NDSM(M-FS)C9, and NDSHLC(M-FS)C5. Both NDSS and NDSM(M-FS)C9 had favorable protein and amino acid contents (data not shown). Group 2 mostly contained populations developed at the Iowa State University. Group 3 was divergent with the other two groups. This group included exotic populations from South America. On the other hand, NDSCD(FS-CS)C2 was not classified to any groups. This population was previously reported as a divergent population within NDSU germplasm (Osorno and Carena 2008).

The heterotic relationships among the 16 populations were determined by the mean performance of population crosses, HPH, $s_{i j}$, and HSGCA for grain yield. Similar results were obtained from the different parameters. High heterosis was observed from population crosses formed from different groups, i.e. NDBS21(R-T)C9 x EARLYGEM 21b and NDBS1011 x EARLYGEM 21c. Both NDBS21(R-T)C9 and NDBS1011 belong to group 2, while EARLYGEM 21b and EARLYGEM 21c are under group 3. Additionally, EARLYGEM 21 populations seemed to increase the frequency of favorable alleles when crossed with populations from different groups.

The highly significant correlation between GD and $s_{i j}$ prompted the use of $s_{i j}$ as a basis to assign the 16 populations to heterotic groups. Four heterotic groups (HG 1 to HG 4) were established. The heterotic groups had good agreement with the groups formed using GD. The
populations belonging to each HG agree with their HSGCA estimates and genetic background. The introduction and adaptation of exotic germplasm formed a unique group that provides utility in population improvement and inbred line development. The heterotic groupings among the 16 populations not only validated former heterotic groups, but also created new heterotic patterns. These results are expected to increase efficiency in breeding. Intra- and inter-population recurrent selection programs can be employed for population improvement according to these results as well as developing the next generation of low and high cost cultivars.

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## CHAPTER 4. GENERAL CONCLUSIONS

The $v_{i}$ and $h_{i j}$ effects were significant sources of variation among the 16 short-season populations used in the diallel mating design for 19 traits. Heterosis effects had a greater contribution to the total sum of squares for grain yield among diallel entries, while $v_{i}$ effects had a greater influence for grain quality traits. Grain yield, starch, and oil contents showed significant and positive $\bar{h}$ effects, indicating the presence of non-additive genetic effects. The dominance was in the direction of high mean performance of populations for grain yield, starch, and oil contents. The predominance of $v_{i}$ effects on starch and oil contents suggest that these traits could be controlled by partial dominance with additive gene action. On the other hand, the negative $\bar{h}$ effects were significant for protein, including methionine and cysteine amino acids, which indicate that dominance was towards a low population mean for this set of traits.

The following populations were selected for grain quality improvement based on their $v_{i}$ and $g_{i}$ effects: NDL and EARLYGEM 21c for starch, NDSCD(FS-CS)C2 for oil content, and NDSS and NDSM(M-FS)C9 for protein and amino acid contents. The population crosses, NDSS x NDBS22(R-T1)C9 and NDBS1011 x EARLYGEM 21c, had high $s_{i j}$ for grain yield with good protein and starch contents, respectively. The knowledge generated on genetic and heterotic relationships is important to devise appropriate breeding strategies in population improvement for desirable quantitative traits.

The $g_{i}$ effects agreed with the genetic effect that had larger contribution to the total among diallel entries sum of squares for a particular trait. The $g_{i}$ effects on multiple traits were then used to measure the GD between populations. Three major groups were formed. The populations were classified based on similarities in phenotypic response, pedigree information, geographic origin, and results of previous studies. Similar response to grain quality traits
classified NDSS and NDSM(M-FS)C9 to group 1. Most of the populations belonging to group 2 were developed at the Iowa State University. Group 3 was divergent from the other two groups, since it included the exotic populations from South America. On the other hand, NDSCD(FSCS)C2 was not classified to any of the groups. This population was previously reported as a unique divergent population within the NDSU germplasm, and continues to be a unique source of short-season cultivars.

The heterotic relationships among the 16 populations were determined by estimates for grain yield. High heterosis was observed from population crosses formed from different groups, i.e. NDBS21(R-T)C9 x EARLYGEM 21b and NDBS1011 x EARLYGEM 21c. Moreover, EARLYGEM 21 populations seemed to increase the frequency of favorable alleles when crossed with populations from different groups. The highly significant correlation between GD and $s_{i j}$ allowed the use of $s_{i j}$ in assigning the 16 populations to heterotic groups. Four heterotic groups (HG 1 to HG 4) were established. The heterotic groups had good agreement with the groups formed using GD, except for group 1. The populations belonging to each HG agree with HSGCA estimates and genetic background information. The three EARLYGEM 21 populations formed a unique HG. Therefore, the introduction and adaptation of exotic germplasm offered remarkable potential in population improvement and inbred line development.

The establishment of heterotic groups among these populations is expected to increase breeding efficiency especially in planning for breeding crosses and integrating them with inbred line development and testcrossing for hybrid evaluation. New heterotic patterns were created from population crosses, NDBS21(R-T)C9 x EARLYGEM 21b, NDBS1011 x EARLYGEM 21c, and NDSS x NDBS22(R-T1)C9. Inter-population recurrent selection programs can be established independently for two population crosses for grain quality improvement, NDSS x

NDBS22(R-T1)C9 and NDBS1011 x EARLYGEM 21c. NDSS and NDBS22(R-T1)C9 belong to HG 1 and HG 3, respectively, and NDBS1011 and EARLYGEM21c belong to HG 2 and HG 4, respectively. Inter-population recurrent selection programs can be employed for populations belonging to different heterotic groups. Intra-population recurrent selection programs can be established for the parental populations selected for good grain quality traits. Segregating populations for inbred line development may also be developed from populations belonging to same heterotic group. The predominant genetic effect/s influencing a trait should also be considered in choosing the appropriate breeding strategy. The knowledge generated in this dissertation will successfully integrate germplasm improvement with inbred line development. Therefore, the NDSU maize breeding program will continue to serve as a unique genetic provider of genetically diverse inbred lines. This study will increase the chances of identifying unique and diverse outstanding inbred lines for the northern U.S. industry.

## APPENDIX A. MAIZE POPULATIONS USED IN THE DIALLEL ANALYSIS

NDL was developed from eight early maturing elite inbred lines from the Lancaster heterotic group. The list of the lines used is presented in Table A1. Paired-crosses of the different inbred lines were produced in the 2005, 2006, and 2007 Fargo, ND breeding nurseries. They were intercrossed the following season to develop NDL. This was followed by one generation of recombination.

NDSS was developed from seven elite inbred lines from the BSSS heterotic group and the synthetic population BSSS. The list of inbred lines used is presented in Table A1. Pairedcrosses of the different germplasms were done in the 2005, 2006, and 2007 Fargo, ND breeding nurseries. They were intercrossed the following season to form NDSS. One generation of recombination followed.

NDSAB(MER-FS)C15 originated from NDSAB, which was developed from the cross between two synthetic populations, NDSA and NDSB (Cross 1983). Table A1 presents the list of inbred lines used in NDSA and NDSB to create NDSAB. NDSAB(MER-FS)C15 was developed from 12 cycles of modified ear to row selection followed by three cycles of full-sib recurrent selection (Carena and Wanner 2005). A rank-summation index selected $33 \%$ of the half-sib families evaluated per each cycle of modified ear to row selection. The families were selected based on the traits weighted as $40 \%$ for grain yield, and $20 \%$ each for grain moisture, root lodging, and stalk lodging. A heritability index with similar group of traits was used to select $8 \%$ of the full-sib families evaluated per each cycle of full-sib recurrent selection conducted in multilocation trials. Bulk-entry method was used to recombine selected families for each cycle of selection. The population was allowed to random mate for three more generations.

NDSAB(MER-FS)C15 has a yellow dent endosperm with high grain yield and test weight, low
grain moisture content at harvest, early maturing (AES 200) and comparable lodging resistance with some commercial hybrids. The earlier version was reported to differ with the traditional heterotic groups, BSSS and Lancaster (Carena and Wanner 2005).

NDSCD(FS-CS)C2 was derived from the cross between two synthetic populations, NDSC and NDSD (Cross 1982). The list of inbred lines used to develop NDSCD from the populations, NDSC and NDSD, is presented in Table A1. One cycle of full-sib family selection between $\operatorname{NDSC}(\mathrm{FS}) \mathrm{C} 1$ and $\operatorname{NDSD}(\mathrm{FS}) \mathrm{C} 1$ was conducted to create the base population (Cross 1988). A rank summation index was used to select 20 full-sib families evaluated in multilocation trials for grain yield, grain moisture at harvest, and root and stalk lodging. Selected families were recombined to create NDSCD. Ten cycles of mass selection for grain yield and standability were used to develop NDSCD(M)C10 (Melani and Carena 2005). Full-sib families were developed for divergent recurrent selection for cold tolerance. For this study, cold susceptible type, NDSCD(FS-CS)C2, was created after two cycles of recurrent selection (Sezegen and Carena 2009).

NDSM(M-FS)C9 originated from NDSM, which was developed by intercrossing 13 elite inbred lines with AES100 to AES300 maturity (Cross and Wanner 1991). The list of inbred lines used to create NDSM is presented in Table A1. The lines were selected based on their combining ability for stalk breakage resistance and grain yield. Three generations of random mating were used to create the base population. Then, the population went through seven cycles of mass selection to create NDSM(M)C7 (Melani and Carena 2005). To further improve the population, two cycles of full-sib recurrent selection was conducted to create NDSM(M-FS)C9. The population was maintained by random mating for three generations.

NDCG(FS)C1 was derived from two synthetic populations, CG-Stiff Stalk (CGSS) and CG-Lancaster (CGL) developed at the University of Guelph, Canada (Lee et al. 2006). CGSS was synthesized using 18 elite inbred lines from the BSSS heterotic group and CO263, an early maturing inbred line developed at Ottawa, Canada. CGSS was improved using five cycles of $\mathrm{S}_{1-}$ $\mathrm{S}_{2}$ recurrent selection to create $\operatorname{CGSS}\left(\mathrm{S}_{1}-\mathrm{S}_{2}\right) \mathrm{C} 5$ (Melani and Carena 2005). CGL was synthesized using 26 elite inbred lines from the Lancaster heterotic group and OX553, an early maturing CGL inbred line (Lee et al. 2006). CGL was also improved using five cycles of $S_{1}-S_{2}$ recurrent selection to create $\operatorname{CGL}\left(\mathrm{S}_{1}-\mathrm{S}_{2}\right) \mathrm{C} 5$. Both populations have maturity rating of AES 200 (Melani and Carena 2005). The cross between $\operatorname{CGSS}\left(\mathrm{S}_{1}-\mathrm{S}_{2}\right) \mathrm{C} 5$ and $\mathrm{CGL}\left(\mathrm{S}_{1}-\mathrm{S}_{2}\right) \mathrm{C} 5$ was done in the 2002 NDSU winter nursery due to the lack of heterosis in the cross. Full-sib families from the population hybrid were generated in the 2003 Fargo, ND breeding nursery. Selected families were chosen from multi-location trials and then recombined to create $\operatorname{NDCG}(\mathrm{FS}) \mathrm{C} 1$. The population was maintained by random mating for several generations.

The following populations, NDBSK(HI-M)C3, NDBS1011, and NDBS11(FR-M)C3, were coded after adaptation was initiated at ND (Carena et al. 2008). The original codes, BS and K , as well as selection methods, were kept the same to recognize the previous germplasm improvement and breeding efforts at the Iowa State University and Nebraska Agriculture Experiment Station. These three populations are early maturing versions of BSK(HI)C11, BS10(FR)C13 x BS11(FR)C13, and BS11(FR)C13, respectively. Without exceptions, all populations were significantly improved for earliness with stratified mass selection (Carena et al. 2008).

BSK was derived from Krug Yellow Dent, an open-pollinated variety developed at the Nebraska Agriculture Experiment Station. NDBSK(HI-M)C3 was developed using first stratified
mass selection for adaptation and half-sib recurrent selection. BSK was improved for stalk strength in Iowa after 11 cycles of half-sib recurrent selection. The adapted version of BSK(HIM)C11 for early silk emergence was improved using three cycles of stratified mass selection in ND to develop NDBSK(HI-M)C3. The population was allowed to random mate for another generation. Carena et al. (2008) suggested that NDBSK(HI-M)C3 could fall under BSSS heterotic group.

NDBS11(FR-M)C3 was derived from a prolific genetically broad-based maize population, BS11 or 'Pioneer Two-Ear Composite’ (Hallauer 1967; Carena et al. 2008). Germplasm improvement for BS11 was conducted using reciprocal full-sib recurrent selection with BS10 as tester, another prolific maize population designated as 'Iowa Two-Ear Synthetic.' Reciprocal recurrent selection for 13 cycles was carried out to improve grain yield, grain moisture at harvest, and root and stalk lodging. An improved version of BS11(FR)C13 for early silk emergence was developed using three cycles of stratified mass selection in ND to develop NDBS11(FR-M)C3. The population was maintained by another generation of random mating. Carena et al. (2008) suggested that NDBS11(FR-M)C3 shared the same heterotic group as BS21(R-T)C8, LEAMING(S-FS)C6, and CGL(S1-S2)C5.

The cross between BS10(FR)C13 and BS11(FR)C13 was made in the 2000 Fargo, ND breeding nursery to create NDBS1011 (Carena et al. 2008). NDBS1011 was improved for early silk emergence after four cycles of stratified mass selection. The population was allowed to have another generation of random mating. Carena et al. (2008) suggested that NDBS1011 might belong to an alternative heterotic group different from the traditional heterotic groups, BSSS and Lancaster.

NDBS21(R-T)C9 was derived from BS21(R)C7, which was developed at the Iowa State University. The population originated from the cross between BS5 and BS20. Seven cycles of reciprocal recurrent selection with $\mathrm{BS} 22(\mathrm{R}) \mathrm{C} 7$ as tester were used to improve $\mathrm{BS} 21(\mathrm{R}) \mathrm{C} 7$ for grain yield, grain moisture, and resistance to root and stalk lodging (Hallauer et al. 2000). This population has a maturity rating of AES 500-600, and was selected for earliness in ND before further improvement. To further improve the population, two cycles of half-sib recurrent selection with SSS industry sister line tester, LH145 x LH146, was done to develop NDBS21(RT)C9. The improved population was allowed to random mate for another generation.

NDBS22(R-T1)C9 is an improved and adapted version of BS22(R)C7, which was developed at the Iowa State University. BS22 was developed using 16 early maturing lines listed in Table A1. Reciprocal recurrent selection was used to create BS22(R)C7 after seven cycles of selection with BS21(R)C7 as tester. The population was improved for grain yield, grain moisture, and resistance to root and stalk lodging (Hallauer et al. 2000). This population has a maturity rating of AES 500-600, and was selected for earliness in ND before further improvement. Similar procedure with NDBS21(R-T)C9 was used to develop NDBS22(R-T1)C9, with a non-SSS industry sister line tester, LH176 x LH177. The population was maintained by random mating it for another generation.

Leaming(S-FS)C6 was improved from Leaming(S)C4 developed at the Iowa State University (Carena and Hallauer 2001). Leaming(S)C4 was developed using three cycles of $\mathrm{S}_{1^{-}}$ $S_{2}$ recurrent selection and one cycle of half-sib selection with tester. This population has a maturity rating of AES 500, and was selected for earliness in ND before further improvement. Full-sib families for full-sib family selection of Leaming(S)C4 were generated in the 2002 NDSU winter nursery. Selected families from multi-location trials were chosen and recombined.

Two cycles of full-sib family selection were conducted to create Leaming(S-FS)C6. The improved population was allowed to random mate for one generation. Leaming is characterized to have yellow dent endosperm, good yield potential and feed value (Melani and Carena 2005).

NDSHLC(M-FS)C5 was derived from four tropical highland white dent populations developed at CIMMYT, Mexico. A mixture of seeds from Pop.800(FR)C5, Pop.85(FR)C4 (Eagles and Lothrop 1994), Pop.902(FR)C2, and Pop.903(FR)C2 was grown in an isolated field to form a new composite coded as NDSHLC(M)C1 (Eno and Carena 2008). Three more cycles of stratified mass selection for earliness and standability were conducted to improve the population that was coded as NDSHLC(M)C4. Full-sib families were produced for full-sib family selection. Selected families from multi-location trials were chosen and recombined to form NDSHLC(M-FS)C5. The population was maintained by random mating for one generation.

EARLYGEM 21a, EARLYGEM 21b, and EARLYGEM 21c were derived from
AR16026:S17-66-1-B, an $S_{3}$ line from the Germplasm Enhancement of Maize (GEM) USDAbased program. AR16026:S17-66-1-B was screened for adaptation to the northern U.S. Corn Belt, and was crossed to ND2000, an early maturing elite inbred line (Carena et al. 2009). The $\mathrm{F}_{1}$ plants were backcrossed to ND2000. $\mathrm{F}_{1}$ s were planted side by side with ND2000 and laterflowering plants were discarded. Ears from each $\mathrm{BC}_{1}$ plant were harvested separately. Further screening for earliness, seedling vigor, and uniformity was done at $\mathrm{BC}_{1}: \mathrm{S}_{0}$ generation. $\mathrm{BC}_{1}: \mathrm{S}_{1}$ lines were crossed to a non-SS industry tester and hybrids were evaluated in multi-location trials the following season. Top lines were selected based on high grain yield and test weight, and low grain moisture at harvest. Lines selected for high grain yield were recombined to form EARLYGEM 21a. The lines selected for high test weight were recombined to form EARLYGEM 21b, and those selected for low grain moisture at harvest were recombined to form

EARLYGEM 21c. Each of the three populations was allowed to random mate for one
generation.

Table A1. Populations used in the 16-parent maize diallel mating design and their improvement methods and genetic backgrounds (modified from Carena 2013).

| Populations ${ }^{\text {a }}$ | Genetic background |
| :---: | :---: |
| NDSS Syn 2 | A632, A641, ND278, BSSS, B37, ND2000, CG102, B73 |
| NDCG(FS)C1 Syn 4 | CGSS (A632, A634, A635, A664, A665, A669, B14A, B37, B73, CH586-12, CH591-23, CH591-36, CM105, CM174, H84, MS153, N28, SD24, CO263), and CGL (A619, A661, A662, A663, A666, A667, A668, CH24, CH661- 17, CH663-8, CH6717, CH671-28, H99, Mo17Ht, MS71, Oh545, Oh551, Pa762, SD23, SDp310, Va26, Va35, W117HHt, W153RHt, W406, W64AHt, OX553) |
| NDL Syn 2 | ND291, Mo17,OH43, B100, ND290, CG44, CG63, A619 |
| NDBSK(HI-M)C3 Syn 2 | BSK(HI)C11 |
| NDBS11(FR-M)C3 Syn 2 | BS11(FR)C13 |
| NDBS1011 Syn 2 | BS10(FR)C13 and BS11(FR)C13 |
| Leaming(S-FS)C6 Syn 2 | Leaming open-pollinated variety |
| NDBS22(R-T1)C9 Syn 2 | A619, A632, B55, B68, C123, Ch9, CM37, (CMV3 x B14)B14 sel, M14, Mo17, MS214, Pa884P, SD10, SD15, Va43, W153R |
| [NDSAB(MER-FS)C15 | A90, MS1334, ND376, ND474, ND478, NDB8, SD10, W153R, |
| Syn2]Syn 2 | CO303, CV3, MS142, ND33, ND405, ND363, Zapalote Chico |
| [NDSM(M-FS)C9 | A654, A664, CM105, CM153, ND101, ND245, ND247, ND250, |
| Syn2]Syn 2 | ND363, ND468, ND8Rf, Pa363, W59E |
| NDBS21(R-T)C9 Syn 2 | BS5 (A625, A458, A554, A575, A619, B8, Ch9, F2, F7, F47, F49, F52, F431, Mt42, ND203, WD, WH, WJ, W9, W59M, W97A, W75, W153R), and BS20 (B14A, B53, B57, B64, B67, B69, A73, N6, N28, R101, HD2286, 38-11) |
| NDSCD(FS-CS)C2 | A556(2), CG1, CG5, CO303, MS93, ND474(2), ND478, ND480, ND481, NDB8, W153R(2), A554, A654, A90, MS141, ND203, ND363, ND364, ND376, SD5, SDP2, SDP232, SDP236M, SDP254 |
| NDSHLC(M-FS)C5 Syn 2 | Pop.800(FR)C5, Pop.85(FR)C4, Pop.902(FR)C2, Pop.903(FR)C2 |
| EARLYGEM 21a Syn 2 | Top yielding lines recombined from AR16026:S17-66-1-B, ND2000 |
| EARLYGEM 21b Syn 2 | Top test weight lines recombined from AR16026:S17-66-1-B, ND2000 |
| EARLYGEM 21c Syn 2 | Top grain moisture lines recombined from AR16026:S17-66-1-B, ND2000 |

${ }^{\text {a }}$ Syn $=$ Number of recombinations, FS = intra-population full-sib recurrent selection (RS), $\mathrm{HI}=$ half-sib RS with tester, $\mathrm{M}=$ mass selection, $\mathrm{FR}=$ inter-population full-sib $\mathrm{RS}, \mathrm{S}=$ inbred progeny RS, $\mathrm{R}=$ inter-population half-sib $\mathrm{RS}, \mathrm{T}=$ use of a tester, MER = modified ear-to-row selection, $\mathrm{CS}=$ divergent RS for cold tolerance, in this case, cold susceptibility

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## APPENDIX B. ADDITIONAL TABLES

Table B1. Combined analyses of variance (GEAN II) for 16 adapted maize populations in the northern U.S. Corn Belt, their crosses, and checks for grain moisture $\left(\mathrm{g} \mathrm{kg}^{-1}\right)$, test weight $\left(\mathrm{kg} \mathrm{h}^{-1}\right)$, stand (plants ha ${ }^{-1}$ ), days to silking, days to anthesis, percentage of stalk lodging, root lodging, and dropped ears, ear and plant heights (cm)

| Source of variation | Grain moisture |  | Test weight |  | Stand |  | df | $\begin{gathered} \hline \begin{array}{c} \text { Days to } \\ \text { silking } \end{array} \\ \hline \text { MS } \end{gathered}$ | $\begin{gathered} \hline \begin{array}{c} \text { Days to } \\ \text { anthesis } \end{array} \\ \hline \text { MS } \end{gathered}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | MS | df | MS | df | MS |  |  |  |
| Environments (E) | 9 | $50901.7^{* *}$ | 9 | $790.8{ }^{* *}$ | 11 | $46051437127^{* *}$ | 4 | 5018.0 ** | 4131.6** |
| Genotypes (G) | 143 | $3722.1{ }^{* *}$ | 143 | 35.2 ** | 143 | $177823753^{* *}$ | 143 | $6.6{ }^{* *}$ | $5.2^{* *}$ |
| Variety ( $v_{i}$ ) | 15 | 30049.5** | 15 | 236.7** | 15 | 479454632** | 15 | $39.5 * *$ | $33.5{ }^{* *}$ |
| Heterosis (H) | 120 | $223.8^{* *}$ | 120 | 9.9** | 120 | $101638468^{* *}$ | 120 | 2.5** | $1.7{ }^{* *}$ |
| Average heterosis ( $\bar{h}$ ) | 1 | 19.1 | 1 | 291.8** | 1 | $562490506^{* *}$ | 1 | 49.5** | 30.3** |
| Variety heterosis ( $h_{i}$ ) | 15 | 208.6* | 15 | 19.2** | 15 | 100288959* | 15 | 2.6 * | $1.8{ }^{* *}$ |
| Specific heterosis ( $s_{i j}$ ) | 104 | 227.9** | 104 | 5.9 ** | 104 | 97403467** | 104 | 2.1 ** | $1.4{ }^{* *}$ |
| Checks (C) | 7 | 4508.7** | 7 | 37.6 ** | 7 | $397060526^{* *}$ | 7 | $5.6 * *$ | $4.2^{* *}$ |
| C vs. others | 1 | $12877.0^{* *}$ | 1 | 4.6 | 1 | $3232457214^{* *}$ | 1 | 4.6 | 0.7 |
| GxE | 1279 | 202.1** | 1269 | $6.7^{* *}$ | 1572 | $54482332 * *$ | 572 | 1.3 ** | 0.9 ** |
| $v_{i} \times \mathrm{E}$ | 135 | 717.0** | 135 | $12.8{ }^{* *}$ | 165 | $82291242 * *$ | 60 | $3.4 * *$ | 2.2 ** |
| HxE | 1080 | 111.0 | 1080 | 1.7 | 1320 | 45063242** | 480 | 1.0 ** | $0.7 * *$ |
| $\bar{h} \times \mathrm{E}$ | 9 | 215.7 | 9 | 0.0 | 11 | 30448199 | 4 | 0.8 | 0.4 |
| $h_{i} \times \mathrm{E}$ | 135 | 103.7 | 135 | 3.0 | 165 | 47882156** | 60 | $1.4 * *$ | 0.7 |
| $s_{i j} \times \mathrm{E}$ | 936 | 111.1 * | 936 | 1.6 | 1144 | 44797049 ** | 416 | 1.0 *** | $0.7 * *$ |
| CxE | 63 | $166.6{ }^{*}$ | 63 | 4.5* | 77 | $51549244^{* *}$ | 28 | 1.3 ** | 0.9 * |
| C vs. others x E | 9 | 715.0** | 9 | 80.5** | 11 | 292727129 ** | 4 | 0.9 | 1.2 |
| Pooled error | 1169 | 120.1 | 1078 | 3.1 | 1442 | 34528682 | 602 | 0.7 | 0.5 |
| CV (\%) |  | 6.7 |  | 4.0 |  | 11.6 |  | 1.8 | 1.5 |

and ${ }^{* *}$ indicate significance at $\alpha$ level of 0.05 and 0.01 , respectively.

Table B1 (continued). Combined analyses of variance (GEAN II) for 16 adapted maize populations in northern U. S. Corn Belt, their crosses, and checks for grain moisture $\left(\mathrm{g} \mathrm{kg}^{-1}\right)$, test weight $\left(\mathrm{kg} \mathrm{hL}^{-1}\right.$ ), stand (plants ha ${ }^{-1}$ ), days to silking, days to anthesis, percentage of stalk lodging, root lodging, and dropped ears, ear and plant heights $(\mathrm{cm})$.

| Source of variation | Stalk lodging |  | Root lodging |  | Dropped ears |  | Ear height |  | Plant |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | df | MS | df | MS | df | MS | df | MS | MS |
| Environments (E) | 6 | $12617.3{ }^{\text {** }}$ | 6 | $408.7{ }^{\text {** }}$ | 6 | 161.0 ** | 10 | $57242.9{ }^{\text {** }}$ | $104805.4{ }^{\text {\% }}$ |
| Genotypes (G) | 143 | 326.6** | 143 | $12.5{ }^{* *}$ | 143 | $5.1{ }^{* *}$ | 143 | $300.9^{* *}$ | 644.1** |
| Variety ( $v_{i}$ ) | 15 | 2057.0** | 15 | $54.1{ }^{* *}$ | 15 | $9.7{ }^{* *}$ | 15 | 2069.2** | 4211.9** |
| Heterosis (H) | 120 | 94.2** | 120 | 7.4 | 120 | $4.6{ }^{*}$ | 120 | 77.9 ** | 192.7** |
| Average heterosis ( $\bar{h}$ ) | 1 | 468.3** | 1 | 6.7 | 1 | 2.1 | 1 | 3159.*** | 10543.8** |
| Variety heterosis ( $h_{i}$ ) | 15 | 92.3** | 15 | 5.0 | 15 | 4.1 | 15 | 61.1** | $136.1^{* *}$ |
| Specific heterosis ( $s_{i j}$ ) | 104 | 90.9** | 104 | 7.7 | 104 | $4.7{ }^{*}$ | 104 | 50.6** | $101.4^{* *}$ |
| Checks (C) | 7 | $257.2^{*}$ | 7 | 8.6 | 7 | 1.6 | 7 | $251.2^{* *}$ | 291.2** |
| C vs. others | 1 | 2759.1** | 1 | 28.0 | 1 | 19.3* | 1 | 877.5* | 3700.4** |
| GxE | 857 | 69.0 ** | 858 | $9.1{ }^{* *}$ | 857 | 3.7 | 1429 | 24.3** | 36.0** |
| $v_{i} \mathrm{x}$ E | 90 | 138.0 ** | 90 | $12.6{ }^{* *}$ | 90 | 4.0 | 150 | $45.7{ }^{* *}$ | $67.7{ }^{* *}$ |
| HxE | 720 | 50.7 | 720 | 9.0** | 720 | 3.5 | 1200 | 18.3 | 27.2 ** |
| $\bar{h} \times \mathrm{E}$ | 6 | 59.2 | 6 | 24.7 ** | 6 | 1.8 | 10 | 0.0 | 0.0 |
| $h_{i} \times \mathrm{E}$ | 90 | 49.9 | 90 | $10.7{ }^{* *}$ | 90 | 3.1 | 150 | 16.8 | 27.6 |
| $s_{i j} \times \mathrm{E}$ | 624 | 50.7 | 624 | 8.6** | 624 | 3.5 | 1040 | 19.0 * | 28.3********** |
| CxE | 42 | 84.5** | 42 | 4.8 | 42 | 2.0 | 70 | 23.4* | 35.8** |
| C vs. others x E | 6 | 39.9 | 6 | 6.9 | 6 | 2.7 | 10 | 154.2** | 272.4 ** |
| Pooled error | 838 | 50.3 | 841 | 7.1 | 837 | 4.0 | 1321 | 16.9 | 23.6 |
| CV (\%) |  | 37.1 |  | 159.9 |  | 119.0 |  | 5.3 | 3.1 |

Table B2. Grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 X EARLYGEM 21 c | Cross | 3.8 | 2.8 | 6.4 | 4.7 | 6.6 | 3.5 | 5.9 | 1.8 | 2.8 | 5.9 | 5.1 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 4.5 | 4.6 | 5.0 | 8.1 | 4.8 | 3.2 | 4.5 | 4.2 | 3.5 | 3.6 | 6.1 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 7.7 | 4.9 | 5.3 | 6.8 | 5.6 | 3.7 | 3.9 | 4.3 | 3.3 | 4.9 | 3.3 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 5.8 | 6.1 | 5.1 | 9.2 | 8.3 | 4.0 | 4.7 | 2.3 | 2.7 | 4.6 | 4.6 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 3.4 | 2.9 | 2.7 | 3.4 | 2.2 | 2.2 | 2.1 |  | 3.1 | 3.4 | 1.6 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 3.9 | 4.3 | 5.1 | 6.3 | 5.1 | 3.7 | 4.9 | 3.2 | 3.5 | 2.8 | 4.3 |
| 7 NDSS XNDL | Cross | 5.8 | 6.3 | 5.7 | 6.5 | 6.5 | 2.6 | 7.0 | 2.6 | 5.3 | 5.1 | 5.2 |
| 8 NDBSK(HIM)C3 X EARLYGEM 21 lb | Cross | 6.9 | 7.1 | 4.3 | 5.6 | 5.7 | 3.4 | 5.5 | 4.8 | 4.7 | 3.8 | 3.6 |
| 9 NDLXEARLYGEM 2 lb | Cross | 6.1 | 4.7 | 6.1 | 6.2 | 6.5 | 4.5 | 5.5 | 2.8 | 3.7 | 4.7 | 4.6 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 5.4 | 5.7 | 5.1 | 3.9 | 4.5 | 4.1 | 5.7 | 3.4 | 4.9 | 3.9 | 4.8 |
| 11 NDBS 11(FR-M)C3 | P arent | 4.9 | 3.6 | 4.1 | 5.5 | 4.1 | 2.8 | 3.6 | 1.8 | 2.3 | 4.1 | 2.7 |
| $12 \mathrm{NDBSK}(\mathrm{HF}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 4.7 | 4.4 | 5.2 | 5.2 | 4.5 | 3.1 | 3.9 | 4.3 | 3.7 | 3.2 | 4.2 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 4.0 | 3.6 | 2.2 | 4.7 | 2.9 | 2.2 | 2.9 | 0.7 | 2.3 | 2.5 | 1.7 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 4.9 | 3.9 | 3.2 | 5.2 | 5.8 | 2.4 | 5.6 | 2.6 | 3.5 | 3.5 | 3.8 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 5.6 | 5.8 | 7.2 | 6.8 | 7.1 | 3.9 | 7.1 | 4.3 | 2.7 | 6.5 | 4.7 |
| 16 Check 4 DKC 43-27 VT3 | Check | 10.9 | 7.4 | 11.4 | 11.8 | 10.3 | 5.8 | 9.9 | 2.8 | 4.9 | 7.6 | 10.2 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 4.6 | 2.9 | 5.1 | 3.5 | 3.5 | 3.1 | 4.3 | 2.3 | 3.3 | 2.7 | 5.4 |
| 18 EARLYGEM 2 lc | P arent | 2.8 | 2.2 | 3.4 | 4.3 | 3.3 | 2.0 | 3.1 |  | 3.0 | 2.5 | 1.7 |
| 19 Leaming(S-FS)C6 | P arent | 3.8 | 2.8 | 2.9 | 5.7 | 2.4 | 3.7 | 4.9 | 1.8 | 3.7 | 2.0 | 2.3 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{T} 1) \mathrm{C} 9$ | Cross | 5.1 | 5.4 | 3.3 | 7.6 | 6.4 | 2.9 | 4.7 | 3.7 | 3.6 | 6.1 | 6.4 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 5.5 | 4.6 | 3.6 | 6.4 | 4.4 | 2.4 | 3.8 | 2.6 | 3.4 | 2.5 | 4.4 |
| 22 NDBS 21 (R-T)C9 X NDSHLC(M-FS)C5 | Cross | 6.4 | 5.0 | 5.6 | 6.8 | 6.6 | 3.3 | 6.3 | 2.7 | 3.1 | 2.7 | 8.1 |
| 23 Check 1P IONEER 39V07 | Check | 7.2 | 6.5 | 11.5 | 11.1 | 8.9 | 3.7 | 9.5 | 3.5 | 6.3 | 6.3 | 7.7 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 5.9 | 5.5 | 8.3 | 8.0 | 6.3 | 3.7 | 5.3 | 2.4 | 3.8 | 4.1 | 4.9 |
| 25 Leaming(S-FS)C6 X NDBS 22(R-T) C9 | Cross | 5.3 | 4.1 | 6.0 | 6.4 | 4.8 | 3.5 | 4.6 | 3.3 | 4.7 | 7.0 | 4.8 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T) C 9 | Cross | 7.2 | 4.3 | 7.0 | 7.5 | 6.7 | 3.1 | 7.3 | 4.8 | 4.2 | 4.1 | 7.1 |
| 27 NDBSK(HI-M)C3 XEARLYGEM 21 a | Cross | 6.6 | 5.4 | 4.8 | 5.1 | 5.3 | 4.1 | 5.8 | 3.6 | 4.0 | 3.2 | 6.4 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 5.0 | 3.3 | 5.8 | 6.3 | 7.0 | 3.1 | 4.8 | 2.2 | 4.0 | 4.2 | 5.3 |
| 29 EARLYGEM 21 a XEARLYGEM 21 c | Cross | 1.9 | 2.9 | 2.2 | 2.1 | 2.8 | 1.5 | 3.1 |  | 3.4 | 2.0 | 2.1 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 6.0 | 3.7 | 6.5 | 5.7 | 5.0 | 4.9 | 4.6 | 2.0 | 3.6 | 4.7 | 6.3 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 3.5 | 5.2 | 2.8 | 6.7 | 4.5 | 3.8 | 4.2 | 2.0 | 3.2 | 2.5 | 2.9 |
| 32 NDBSK(HIM)C3 XEARLYGEM 21 c | Cross | 6.5 | 5.5 | 6.2 | 6.9 | 4.0 | 3.4 | 7.8 | 2.6 | 3.6 | 4.0 | 7.3 |
| 33 NDBS 1011 XEARLYGEM 2 lb | Cross | 6.5 | 5.2 | 4.8 | 4.5 | 6.4 | 4.4 | 5.1 | 2.7 | 4.1 | 4.8 | 5.0 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 21 a | Cross | 3.6 | 3.9 | 2.0 | 6.6 | 2.6 | 4.6 | 3.8 | 1.3 | 2.3 | 4.8 | 4.3 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 7.0 | 4.8 | 5.4 | 7.6 | 4.6 | 2.7 | 7.4 | 2.3 | 3.4 | 3.1 | 6.9 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 5.9 | 3.3 | 4.9 | 6.6 | 4.1 | 3.1 | 4.3 | 2.1 | 4.0 | 3.4 | 3.3 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 5.9 | 5.0 | 5.8 | 8.1 | 5.8 | 4.8 | 4.7 | 2.0 | 3.4 | 3.4 | 4.6 |
| 38 NDCG(FS)C1XEARLYGEM 21 a | Cross | 7.7 | 3.9 | 4.9 | 7.2 | 5.5 | 3.4 | 5.9 | 2.9 | 4.0 | 5.7 | 5.6 |
| 39 EARLYGEM 2 lb XEARLYGEM 21 c | Cross | 3.8 | 1.8 | 2.8 | 2.9 | 2.4 | 2.1 | 3.6 |  |  | 2.1 | 2.0 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 5.1 | 4.9 | 4.6 | 6.6 | 6.2 | 3.8 | 4.4 | 2.9 | 2.8 | 4.9 | 6.0 |

Table B2 (continued). Grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 3.9 | 3.5 | 3.6 | 4.8 | 4.1 | 2.8 | 5.0 | 2.3 | 2.4 | 2.7 | 3.3 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 5.0 | 3.9 | 3.5 | 6.7 | 5.2 | 3.0 | 6.0 | 3.3 | 4.4 | 5.5 | 5.2 |
| 43 NDBSK(HI-M)C3 X NDBS 22(R-T ) C 9 | Cross | 4.8 | 6.5 | 3.9 | 5.6 | 7.9 | 2.6 | 3.7 | 2.9 | 3.5 | 4.3 | 5.7 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 6.1 | 6.3 | 4.9 | 6.6 | 5.5 | 2.7 | 5.6 | 4.1 | 5.4 | 3.4 | 4.9 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 4.9 | 5.1 | 2.9 | 3.9 | 5.5 | 3.6 | 4.2 | 3.2 | 4.8 | 5.9 | 3.6 |
| 46 NDLXNDBS22(R-Tl)C9 | Cross | 5.1 | 5.5 | 5.7 | 5.4 | 5.7 | 2.9 | 6.5 | 3.9 | 3.9 | 4.5 | 6.5 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 4.3 | 5.8 | 3.6 | 5.4 | 3.8 | 2.3 | 3.8 | 2.4 | 2.4 | 3.4 | 4.5 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS)C 15 | Cross | 5.2 | 4.4 | 4.9 | 5.8 | 6.2 | 2.9 | 6.5 | 4.3 | 4.4 | 3.3 | 7.8 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 5.8 | 4.8 | 4.1 | 7.8 | 5.0 | 2.9 | 4.2 | 3.4 | 3.1 | 4.1 | 3.4 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 4.1 | 5.3 | 4.7 | 3.5 | 5.5 | 3.1 | 6.2 | 4.0 | 3.6 | 4.5 | 6.4 |
| 51 NDBS 22(R-T1)C9 | P arent | 4.6 | 2.1 | 2.7 | 3.6 | 3.1 | 1.3 | 4.7 | 1.0 | 2.9 | 3.3 | 2.5 |
| 52 NDSS XNDBS 1011 | Cross | 5.9 | 4.3 | 5.3 | 7.0 | 5.3 | 4.1 | 6.2 | 2.8 | 3.0 | 4.2 | 5.4 |
| 53 NDL | P arent | 8.0 | 4.5 | 6.3 | 5.4 | 4.4 | 2.6 | 5.8 | 1.7 | 4.2 | 3.4 | 3.7 |
| 54 NDBS 1011 Leaming(S-FS)C6 | Cross | 5.8 | 5.3 | 5.5 | 7.8 | 6.2 | 3.6 | 4.7 | 3.1 | 3.3 | 5.2 | 6.0 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 5.9 | 6.0 | 6.6 | 6.9 | 6.6 | 4.5 | 6.1 | 3.0 | 3.2 | 6.1 | 6.2 |
| 56 NDSAB(MER-FS)C15 X NDBS 21 (R-T)C9 | Cross | 6.2 | 5.4 | 5.9 | 6.6 | 7.9 | 2.6 | 5.5 | 3.8 | 5.1 | 5.1 | 8.5 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-Tl)C9 | Cross | 6.4 | 4.6 | 6.2 | 6.8 | 5.6 | 3.6 | 5.6 | 2.4 | 4.2 | 5.4 | 6.4 |
| 58 EARLYGEM 2 lb | P arent | 3.1 | 2.2 | 3.1 | 2.6 | 2.7 | 1.3 | 1.9 |  | 1.7 | 2.2 | 2.5 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 5.1 | 4.2 | 6.0 | 6.0 | 5.1 | 2.1 | 5.6 | 2.3 | 2.8 | 2.6 | 4.7 |
| 60 Check 2 DKC 36-34 VT3 | Check | 11.7 | 7.5 | 10.1 | 11.5 | 11.3 | 3.5 | 6.7 | 7.3 | 6.3 | 8.3 | 10.4 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS ) C 2 | Cross | 4.6 | 5.0 | 3.8 | 4.9 | 4.6 | 3.6 | 5.9 | 1.8 | 3.1 | 4.1 | 4.8 |
| 62 NDBS22(R-T ) C 9 XEARLYGEM 21 c | Cross | 4.4 | 5.3 | 6.0 | 4.3 | 6.1 | 3.0 | 5.2 | 2.2 | 3.7 | 3.7 | 6.2 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 6.2 | 5.0 | 7.0 | 6.9 | 6.0 | 4.0 | 5.8 | 3.4 | 3.8 | 4.5 | 5.5 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 3.1 | 3.1 | 5.5 | 4.1 | 4.2 | 2.6 | 3.8 | 2.2 | 2.5 | 3.9 | 4.0 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 7.3 | 7.2 | 7.4 | 6.4 | 6.3 | 5.0 | 7.6 | 3.1 | 2.3 | 3.8 | 5.2 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 7.1 | 5.6 | 5.0 | 7.2 | 5.1 | 2.8 | 3.7 | 4.9 | 3.0 | 3.6 | 4.2 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 4.2 | 5.1 | 4.2 | 3.3 | 4.6 | 2.2 | 4.6 | 2.5 | 4.4 | 3.0 | 6.3 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 8.6 | 6.9 | 6.7 | 9.5 | 6.1 | 2.5 | 6.3 | 2.9 | 3.8 | 3.8 | 6.2 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 6.5 | 5.2 | 5.8 | 5.4 | 4.8 | 3.5 | 4.6 | 3.7 | 2.0 | 3.9 | 5.4 |
| 70 NDSS X NDBS 11(FR-M)C3 | Cross | 7.6 | 4.9 | 7.9 | 6.4 | 6.8 | 3.4 | 6.6 | 3.1 | 4.1 | 4.6 | 5.9 |
| 71 NDBSK(HIM)C3 | P arent | 7.2 | 5.9 | 7.1 | 6.2 | 5.5 | 1.6 | 5.1 | 1.9 | 2.9 | 2.6 | 4.2 |
| 72 NDSS X NDBS 21 (R-T)C9 | Cross | 7.7 | 5.8 | 4.9 | 6.5 | 6.1 | 3.4 | 5.3 | 3.6 | 2.7 | 3.5 | 6.3 |
| 73 NDSS XEARLYGEM 21 c | Cross | 5.4 | 5.3 | 4.1 | 7.0 | 6.0 | 3.2 | 3.1 | 2.4 | 3.7 | 3.5 | 4.2 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 4.7 | 4.2 | 5.3 | 5.1 | 4.4 | 3.3 | 6.1 | 2.6 | 2.7 | 2.7 | 3.0 |
| 75 NDCG(FS)C1 | P arent | 3.5 | 4.5 | 4.2 | 5.4 | 4.9 | 2.6 | 4.1 | 1.7 | 2.7 | 3.9 | 3.3 |
| 76 NDSAB(MER-FS)C 15 | P arent | 4.3 | 2.4 | 2.7 | 4.0 | 4.2 | 2.5 | 5.2 | 2.5 | 3.4 | 2.9 | 3.8 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 4.8 | 5.5 | 3.2 | 6.8 | 4.3 | 3.0 | 6.2 | 2.1 | 3.8 | 3.4 | 3.4 |
| 78 NDBS 1011 X NDBS21(R-T)C9 | Cross | 6.5 | 6.3 | 5.8 | 5.7 | 5.2 | 3.4 | 6.7 | 2.3 | 3.3 | 3.3 | 6.2 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 2 la | Cross | 4.5 | 5.1 | 4.8 | 5.3 | 4.5 | 3.7 | 4.9 | 2.8 | 3.9 | 6.1 | 4.2 |
| 80 NDBS 21 (R-T) C9 X EARLYGEM 21 a | Cross | 6.2 | 5.0 | 4.8 | 6.7 | 7.0 | 3.1 | 6.6 | 2.7 | 3.9 | 4.8 | 6.3 |

Table B2 (continued). Grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B2 (continued). Grain yield ( $\mathrm{Mg} \mathrm{ha}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 NDLXNDSHLC(M-FS)C5 | Cross | 4.6 | 3.8 | 6.3 | 6.8 | 4.4 | 2.7 | 4.6 | 2.4 | 3.7 | 4.5 | 4.3 |
| 122 NDL X NDSAB (MER-FS)C 15 | Cross | 5.8 | 4.0 | 3.9 | 6.0 | 7.3 | 4.7 | 5.5 | 4.1 | 4.2 | 3.1 | 3.8 |
| 123 NDCG(FS) C 1 X NDB S22(R-T1)C9 | Cross | 5.9 | 5.7 | 8.2 | 6.5 | 5.5 | 3.5 | 7.1 | 1.5 | 4.2 | 5.7 | 6.6 |
| 124 NDCG(FS)C1 ${ }^{\text {P }}$ NDSCD(FS-CS)C2 | Cross | 4.7 | 3.7 | 5.4 | 8.7 | 5.0 | 3.5 | 5.5 | 2.6 | 2.6 | 3.4 | 4.7 |
| $125 \mathrm{CGSS} 21(\mathrm{~S}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGSS}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 6.8 | 5.3 | 5.4 | 4.8 | 5.4 | 3.8 | 5.8 | 2.3 | 4.7 | 4.9 | 4.6 |
| 126 NDCG(FS)C1XNDBS21(R-T)C9 | Cross | 6.4 | 4.8 | 7.4 | 8.4 | 5.0 | 3.7 | 7.1 | 3.0 | 4.9 | 4.7 | 7.0 |
| 127 NDBS 22(R-T1)C9 X NDBS21(R-T)C9 | Cross | 4.3 | 5.0 | 6.1 | 4.8 | 6.5 | 2.4 | 7.0 | 2.2 | 4.8 | 6.9 | 6.8 |
| 128 Leaming(S-FS)C6 XEARLYGEM 2 lb | Cross | 3.9 | 3.6 | 4.8 | 5.9 | 6.6 | 5.2 | 6.6 | 2.9 | 5.6 | 4.9 | 5.3 |
| 129 NDBS 1011 X NDSM(M-FS)C9 | Cross | 4.8 | 4.6 | 4.6 | 6.3 | 6.1 | 3.0 | 5.1 | 3.2 | 2.7 | 4.3 | 5.3 |
| 130 NDLXEARLYGEM 21 c | Cross | 5.9 | 5.0 | 6.6 | 6.5 | 5.6 | 3.8 | 5.6 | 3.6 | 3.5 | 4.1 | 5.3 |
| 131 NDL X NDSCD(FS-CS)C2 | Cross | 4.8 | 6.4 | 5.3 | 4.9 | 5.4 | 3.6 | 6.2 | 2.3 | 3.6 | 3.7 | 5.9 |
| 132 EARLYGEM 21 a | P arent | 3.3 | 2.3 | 4.8 | 3.3 | 2.2 | 1.4 | 1.9 |  | 2.8 | 2.2 | 1.9 |
| 133 NDCG(FS)C1X NDBSK(HI-M)C3 | Cross | 5.0 | 3.8 | 4.6 | 5.9 | 6.6 | 3.3 | 7.1 | 2.4 | 3.6 | 3.1 | 5.3 |
| 134 NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 5.7 | 3.9 | 4.9 | 7.0 | 4.7 | 3.7 | 4.5 | 2.2 | 2.3 | 2.2 | 4.4 |
| 135 NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 6.2 | 4.7 | 6.0 | 5.1 | 3.8 | 3.8 | 4.0 | 3.2 | 2.9 | 4.8 | 3.8 |
| 136 NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 4.0 | 4.5 | 4.1 | 7.0 | 4.5 | 3.4 | 3.6 | 2.4 | 3.5 | 2.3 | 4.4 |
| 137 NDSM(M-FS)C9 X EARLYGEM 21 c | Cross | 6.9 | 5.5 | 6.7 | 6.6 | 5.2 | 2.9 | 4.0 | 1.8 | 3.1 | 3.7 | 4.0 |
| 138 Leaming(S-FS)C6 X EARLYGEM 2 la | Cross | 5.1 | 4.9 | 6.2 | 6.3 | 4.4 | 4.5 | 6.1 | 2.5 | 4.5 | 7.1 | 4.8 |
| 139 NDSS XNDCG(FS)C1 | Cross | 3.6 | 3.7 | 5.2 | 5.0 | 4.1 | 3.8 | 6.1 | 2.0 | 3.8 | 4.9 | 6.0 |
| 140 NDSM(M-FS)C9 X NDSCD(FS-CS)C2 | Cross | 4.3 | 4.7 | 3.8 | 5.7 | 3.8 | 3.1 | 4.4 | 2.1 | 2.5 | 3.9 | 3.0 |
| 141 NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | 6.8 | 5.6 | 5.6 | 8.1 | 5.3 | 3.0 | 5.3 | 2.7 | 2.4 | 5.4 | 5.2 |
| 142 NDCG(FS)C1 ${ }^{\text {d }}$ NDBS 1011 | Cross | 8.2 | 4.5 | 7.1 | 7.0 | 4.5 | 3.1 | 6.0 | 2.8 | 4.8 | 4.2 | 4.4 |
| 143 NDBS 1011 X EARLYGEM 21 a | Cross | 5.8 | 4.8 | 5.5 | 4.8 | 5.6 | 3.3 | 6.8 | 3.3 | 2.9 | 6.5 | 5.1 |
| 144 NDSHLC(M-FS)C5 | Parent | 3.3 | 1.7 | 3.7 | 3.6 | 2.1 | 1.7 | 3.7 | 1.0 | 1.8 | 1.8 | 2.3 |
| Experiment mean |  | 5.5 | 4.8 | 5.4 | 6.1 | 5.3 | 3.3 | 5.4 | 2.8 | 3.6 | 4.2 | 4.9 |
| Mean of parental populations |  | 4.3 | 3.4 | 4.1 | 4.8 | 3.5 | 2.2 | 4.0 | 1.7 | 2.8 | 2.8 | 2.9 |
| Mean of population crosses |  | 5.5 | 4.8 | 5.3 | 6.0 | 5.4 | 3.4 | 5.5 | 2.8 | 3.6 | 4.2 | 5.0 |
| Mean of checks |  | 7.7 | 6.7 | 8.2 | 9.0 | 8.0 | 3.8 | 7.4 | 3.7 | 4.4 | 6.4 | 7.0 |
| LSD (0.05) |  | 2.1 | 2.5 | 2.2 | 2.2 | 2.0 | 1.6 | 2.6 | 1.8 | 1.7 | 2.2 | 2.7 |
| CV |  | 19.5 | 26.4 | 20.5 | 18.4 | 18.8 | 24.6 | 23.7 | 32.5 | 24.4 | 26.5 | 28.1 |
| MSE |  | 1.2 | 1.6 | 1.2 | 1.2 | 1.0 | 0.6 | 1.7 | 0.8 | 0.8 | 1.2 | 1.9 |

Table B3. Grain moisture ( $\mathrm{g} \mathrm{kg}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21c | Cross | 227.3 | 187.0 | 178.0 | 197.5 | 213.5 | 271.9 | 202.6 | 158.9 | 183.2 | 186.8 | 210.7 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 218.3 | 208.5 | 182.0 | 208.5 | 226.0 | 296.0 | 190.5 | 198.4 | 168.4 | 187.0 | 203.8 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 244.5 | 239.5 | 198.5 | 250.5 | 271.0 | 365.0 | 221.0 | 197.3 | 195.5 | 190.1 | 204.7 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 244.0 | 212.5 | 200.0 | 210.9 | 242.5 | 305.8 | 212.0 | 196.8 | 189.1 | 203.3 | 211.6 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 176.2 | 184.5 | 175.5 | 178.4 | 199.0 | 292.8 | 211.2 |  | 160.6 | 180.2 | 207.6 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 218.1 | 218.5 | 209.0 | 221.5 | 251.0 | 309.2 | 217.0 | 193.6 | 182.9 | 189.7 | 208.9 |
| 7 NDSS XNDL | Cross | 269.2 | 249.0 | 202.0 | 244.0 | 219.0 | 274.0 | 198.0 | 187.1 | 168.7 | 186.1 | 205.7 |
| 8 NDBSK(HI-M)C3 X EARLYGEM 21 b | Cross | 235.3 | 195.5 | 191.0 | 199.0 | 210.5 | 252.1 | 202.4 | 188.9 | 178.9 | 198.7 | 220.4 |
| 9 NDL XEARLYGEM 2 lb | Cross | 246.1 | 219.5 | 199.5 | 216.0 | 216.0 | 210.7 | 189.0 | 164.1 | 163.8 | 186.6 | 207.2 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 246.3 | 210.5 | 187.0 | 209.6 | 210.5 | 277.8 | 200.1 | 183.2 | 161.1 | 187.3 | 198.7 |
| 11 NDBS 11(FR-M)C3 | P arent | 266.6 | 262.0 | 198.0 | 245.0 | 250.5 | 325.4 | 210.0 | 200.5 | 191.3 | 193.4 | 208.4 |
| 12 NDBSK(HI-M)C3 X NDSHLC(M-FS)C5 | Cross | 287.0 | 310.0 | 276.0 | 267.1 | 324.5 | 390.8 | 273.9 | 249.2 | 227.9 | 239.5 | 257.6 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 233.2 | 250.0 | 187.0 | 216.0 | 220.5 | 325.3 | 222.2 | 145.9 | 193.6 | 195.6 | 224.9 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 252.2 | 229.0 | 219.5 | 226.5 | 258.0 | 360.4 | 227.7 | 195.9 | 216.5 | 207.4 | 231.6 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 241.4 | 251.0 | 201.5 | 246.5 | 249.0 | 300.9 | 216.1 | 201.3 | 181.0 | 195.9 | 205.4 |
| 16 Check 4 DKC 43-27 VT3 | Check | 236.4 | 204.5 | 182.5 | 182.5 | 189.0 | 267.2 | 184.2 | 187.7 | 146.6 | 182.7 | 195.4 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 270.1 | 259.5 | 222.0 | 268.5 | 283.0 | 388.7 | 273.3 | 225.4 | 223.2 | 225.1 | 250.4 |
| 18 EARLYGEM 21 c | P arent | 185.1 | 165.5 | 188.0 | 181.6 | 199.0 | 270.7 | 188.7 |  | 169.0 | 183.1 | 202.2 |
| 19 Leaming(S-FS)C6 | P arent | 246.1 | 201.5 | 209.0 | 213.0 | 227.5 | 291.3 | 215.2 | 172.5 | 186.3 | 172.9 | 223.9 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{Tl}) \mathrm{C} 9$ | Cross | 242.7 | 247.5 | 219.0 | 239.0 | 233.5 | 383.6 | 268.5 | 212.3 | 185.4 | 198.6 | 213.1 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 273.5 | 256.0 | 225.0 | 257.0 | 305.0 | 371.6 | 248.2 | 205.1 | 207.8 | 239.0 | 238.5 |
| 22 NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 268.3 | 255.0 | 232.5 | 229.6 | 310.0 | 422.7 | 279.8 | 246.6 | 243.7 | 239.7 | 245.0 |
| 23 Check 1P IONEER 39V07 | Check | 17.1 | 152.5 | 172.0 | 149.0 | 172.0 | 189.9 | 166.6 | 183.9 | 138.3 | 178.7 | 185.7 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 203.9 | 180.5 | 174.0 | 182.6 | 202.5 | 261.7 | 189.0 | 195.1 | 170.5 | 179.4 | 203.4 |
| 25 Leaming(S-FS)C6 X NDBS 22(R-T ) C9 | Cross | 267.3 | 259.5 | 228.5 | 229.5 | 237.5 | 353.5 | 215.1 | 193.3 | 184.1 | 201.8 | 213.0 |
| 26 Leaming(S-FS)C6 XNDBS 21 (R-T)C9 | Cross | 257.9 | 205.5 | 194.0 | 225.5 | 229.5 | 299.2 | 222.0 | 198.8 | 185.5 | 228.0 | 232.2 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 1a | Cross | 236.5 | 219.5 | 209.0 | 211.0 | 234.0 | 334.6 | 239.4 | 191.2 | 184.5 | 199.0 | 207.5 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 248.5 | 244.0 | 211.0 | 223.9 | 240.0 | 300.0 | 217.5 | 179.1 | 191.6 | 189.8 | 211.0 |
| 29 EARLYGEM 2 a X EARLYGEM 21 c | Cross | 194.8 | 186.5 | 174.5 | 166.4 | 212.5 | 233.0 | 190.7 |  | 165.2 | 176.4 | 195.5 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 209.7 | 193.0 | 177.5 | 171.0 | 191.5 | 235.9 | 186.5 | 177.0 | 156.0 | 181.2 | 222.3 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 234.3 | 229.5 | 192.5 | 213.0 | 202.5 | 263.2 | 219.0 | 176.9 | 194.8 | 162.6 | 222.5 |
| 32 NDBS K(HI-M)C3 X EARLYGEM 21 c | Cross | 229.8 | 224.0 | 196.5 | 199.5 | 222.0 | 287.8 | 216.9 | 180.7 | 189.4 | 192.7 | 211.3 |
| 33 NDBS 1011 XEARLYGEM 21 b | Cross | 234.2 | 204.5 | 198.0 | 186.0 | 215.0 | 246.9 | 200.0 | 192.3 | 175.8 | 180.1 | 203.6 |
| 34 NDSCD(FS-CS)C2 X EARLYGEM 2 la | Cross | 215.4 | 22.5 | 169.0 | 19.6 | 196.0 | 238.5 | 229.6 | 165.6 | 186.7 | 182.3 | 200.6 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 210.7 | 205.5 | 198.5 | 195.5 | 215.5 | 273.1 | 212.9 | 182.9 | 173.8 | 189.8 | 205.3 |
| 36 NDSAB(MER-FS)C 15 X NDSHLC(M-FS)C5 | Cross | 266.0 | 216.0 | 204.5 | 245.1 | 272.0 | 370.5 | 271.8 | 214.5 | 220.5 | 185.0 | 229.3 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 231.2 | 265.0 | 198.0 | 214.5 | 213.0 | 246.5 | 204.1 | 193.4 | 182.0 | 181.0 | 199.7 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 202.8 | 204.0 | 196.0 | 192.0 | 207.0 | 27.6 | 185.6 | 181.9 | 170.9 | 187.8 | 199.8 |
| 39 EARLYGEM 2 lb X EARLYGEM 21 c | Cross | 183.4 | 184.0 | 191.5 | 173.5 | 206.0 | 261.1 | 187.0 |  |  | 174.2 | 175.2 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 263.4 | 224.5 | 203.0 | 220.0 | 242.0 | 377.1 | 200.1 | 195.2 | 189.1 | 199.0 | 216.7 |

Table B3 (continued). Grain moisture ( $\mathrm{g} \mathrm{kg}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 254.7 | 215.0 | 191.0 | 210.0 | 272.5 | 305.4 | 242.2 | 215.4 | 215.1 | 188.4 | 243.2 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 190.6 | 201.5 | 183.0 | 169.6 | 208.0 | 194.4 | 187.5 | 182.6 | 161.9 | 177.5 | 195.4 |
| 43 NDBSK(HI-M)C3 X NDBS 22(R-T ) C 9 | Cross | 284.7 | 242.0 | 220.5 | 237.0 | 243.0 | 357.6 | 230.1 | 201.5 | 198.7 | 202.8 | 240.7 |
| 44 NDSS X NDBSK(HI-M)C3 | Cross | 254.2 | 283.5 | 212.5 | 233.0 | 240.5 | 300.8 | 267.4 | 199.3 | 205.4 | 206.4 | 232.9 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 216.6 | 225.0 | 188.5 | 213.0 | 222.0 | 315.3 | 226.6 | 177.6 | 182.3 | 192.4 | 211.7 |
| 46 NDLXNDBS22(R-T1)C9 | Cross | 278.3 | 268.5 | 206.0 | 231.6 | 216.0 | 337.9 | 232.7 | 195.1 | 177.1 | 183.1 | 207.2 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 271.1 | 234.0 | 213.0 | 252.0 | 25.0 | 404.1 | 265.5 | 256.1 | 197.3 | 229.6 | 249.4 |
| 48 NDBS 11(FR-M)C3 X NDSAB(MER-FS)C 15 | Cross | 236.4 | 180.5 | 193.5 | 193.1 | 242.5 | 286.9 | 209.9 | 194.6 | 176.4 | 192.3 | 204.2 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 218.3 | 210.5 | 181.5 | 192.4 | 227.0 | 259.6 | 206.4 | 186.2 | 181.2 | 185.3 | 207.6 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 243.9 | 202.0 | 205.0 | 210.4 | 228.0 | 322.8 | 207.4 | 190.7 | 181.1 | 185.5 | 207.8 |
| 51 NDBS 22(R-T1)C9 | P arent | 274.0 | 251.5 | 220.0 | 237.4 | 248.5 | 297.2 | 234.8 | 167.1 | 201.1 | 206.6 | 22.7 |
| 52 NDSS XNDBS 1011 | Cross | 273.0 | 284.5 | 200.0 | 238.4 | 241.5 | 389.0 | 199.9 | 188.5 | 188.2 | 188.3 | 209.6 |
| 53 NDL | P arent | 254.3 | 260.0 | 203.0 | 240.4 | 255.0 | 302.5 | 244.1 | 165.2 | 174.7 | 188.7 | 213.1 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 248.7 | 286.5 | 201.5 | 236.5 | 237.5 | 306.0 | 198.9 | 200.9 | 181.6 | 200.7 | 219.9 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 290.8 | 292.0 | 232.5 | 262.9 | 256.0 | 367.7 | 24.4 | 205.8 | 210.4 | 202.6 | 240.6 |
| 56 NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 215.8 | 208.0 | 190.5 | 201.9 | 231.0 | 341.9 | 220.3 | 200.1 | 184.0 | 193.7 | 208.4 |
| 57 NDBS 11(FR-M)C3 X NDBS 22 (R-Tl)C9 | Cross | 279.7 | 238.5 | 213.5 | 240.4 | 239.0 | 296.5 | 231.9 | 192.4 | 195.4 | 199.1 | 214.2 |
| 58 EARLYGEM 21 b | P arent | 198.4 | 188.0 | 173.0 | 158.5 | 208.0 | 235.1 | 195.0 |  | 158.3 | 153.0 | 198.2 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 198.2 | 201.0 | 203.5 | 183.9 | 220.5 | 293.2 | 190.8 | 186.3 | 179.4 | 189.4 | 205.4 |
| 60 Check 2 DKC 36-34 VT3 | Check | 203.0 | 183.5 | 178.0 | 180.5 | 181.5 | 251.5 | 188.7 | 180.4 | 136.5 | 171.0 | 187.1 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 237.6 | 227.0 | 216.5 | 232.0 | 222.5 | 288.7 | 230.7 | 186.2 | 206.2 | 209.5 | 207.3 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 223.1 | 199.0 | 204.0 | 206.5 | 232.5 | 224.9 | 206.2 | 187.0 | 191.0 | 183.7 | 204.0 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 262.3 | 237.5 | 203.5 | 238.4 | 233.0 | 323.3 | 237.6 | 197.1 | 185.6 | 195.3 | 213.8 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 276.3 | 269.0 | 251.5 | 270.4 | 279.5 | 403.6 | 278.7 | 230.6 | 205.2 | 220.0 | 249.8 |
| 65 NDBSK(HI-M)C3 X NDB S 21 (R-T)C9 | Cross | 270.0 | 266.0 | 222.0 | 245.4 | 250.0 | 370.6 | 251.8 | 210.3 | 205.2 | 216.9 | 249.8 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 250.4 | 199.5 | 212.0 | 211.5 | 213.5 | 328.6 | 217.7 | 188.4 | 186.6 | 191.0 | 222.0 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 268.0 | 270.5 | 232.5 | 205.4 | 328.5 | 360.3 | 284.7 | 235.9 | 260.9 | 215.8 | 256.3 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 258.5 | 236.0 | 202.0 | 215.0 | 239.5 | 262.5 | 232.0 | 180.7 | 195.5 | 194.9 | 217.0 |
| 69 NDBSK(HIM)C3 X NDBS 11(FR-M)C3 | Cross | 266.4 | 269.5 | 225.0 | 265.4 | 270.5 | 297.1 | 249.2 | 201.9 | 173.4 | 206.8 | 221.4 |
| 70 NDSS XNDBS $11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ | Cross | 282.1 | 275.0 | 197.0 | 215.1 | 226.5 | 311.7 | 208.3 | 202.0 | 181.2 | 192.0 | 207.4 |
| 71 NDBSK(HIM)C3 | P arent | 266.9 | 210.5 | 217.0 | 263.4 | 267.0 | 311.3 | 273.1 | 209.8 | 202.4 | 207.6 | 232.5 |
| 72 NDSS XNDBS21(R-T)C9 | Cross | 245.3 | 233.0 | 205.0 | 217.0 | 223.0 | 314.1 | 240.5 | 206.5 | 189.0 | 199.2 | 218.3 |
| 73 NDSS XEARLYGEM 21 c | Cross | 206.3 | 200.5 | 17.5 | 189.0 | 200.5 | 257.6 | 187.2 | 182.0 | 167.2 | 179.3 | 190.4 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 243.3 | 265.0 | 194.0 | 254.5 | 280.5 | 310.8 | 242.1 | 172.1 | 190.1 | 197.0 | 215.1 |
| 75 NDCG(FS)C1 | P arent | 211.5 | 203.0 | 178.0 | 181.0 | 197.5 | 244.2 | 186.1 | 184.0 | 156.6 | 185.6 | 204.4 |
| 76 NDSAB(MER-FS)C15 | P arent | 237.5 | 200.5 | 186.5 | 209.4 | 227.5 | 288.0 | 204.1 | 183.4 | 174.7 | 186.3 | 203.4 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 237.7 | 210.0 | 234.0 | 222.4 | 215.0 | 255.0 | 205.3 | 192.6 | 174.3 | 181.7 | 203.9 |
| 78 NDBS 1011 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 266.2 | 242.0 | 217.0 | 247.5 | 239.5 | 296.0 | 246.6 | 201.7 | 197.1 | 208.8 | 243.6 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 236.7 | 200.0 | 195.0 | 171.5 | 200.5 | 266.2 | 201.2 | 188.2 | 162.9 | 182.6 | 194.9 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 214.8 | 199.5 | 193.0 | 176.0 | 227.5 | 273.4 | 217.5 | 189.0 | 189.0 | 182.2 | 209.1 |

Table B3 (continued). Grain moisture ( $\mathrm{g} \mathrm{kg}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry | Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 | NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 250.1 | 223.0 | 202.0 | 219.0 | 218.0 | 278.0 | 211.6 | 175.2 | 154.4 | 190.1 | 211.0 |
| 82 | NDBSK(HIM)C3 X Leaming(S-FS)C6 | Cross | 255.9 | 205.5 | 211.5 | 245.6 | 254.5 | 295.6 | 214.7 | 190.3 | 185.8 | 202.8 | 200.5 |
| 83 | NDL X NDBS 21 (R-T)C9 | Cross | 252.7 | 235.5 | 213.0 | 247.0 | 268.0 | 288.2 | 255.6 | 200.6 | 179.9 | 200.4 | 220.1 |
| 84 | NDSM(M-FS) C 9 | P arent | 199.0 | 196.0 | 168.0 | 170.1 | 228.5 | 274.5 | 202.0 | 171.5 | 180.6 | 192.6 | 206.4 |
| 85 | NDSS XNDSAB(MER-FS)C 15 | Cross | 231.0 | 220.0 | 192.0 | 198.0 | 219.5 | 252.4 | 212.8 | 185.3 | 17.4 | 189.5 |  |
| 86 | Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 216.5 | 229.5 | 193.5 | 194.0 | 249.5 | 235.6 | 200.2 | 198.3 | 167.7 | 186.8 | 207.7 |
| 87 | NDCG(FS)C1XNDBS 11(FR-M)C3 | Cross | 249.7 | 225.5 | 196.0 | 219.5 | 197.5 | 270.0 | 193.6 | 181.2 | 168.4 | 181.3 | 194.5 |
| 88 | NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 263.2 | 238.5 | 202.0 | 228.0 | 259.5 | 314.8 | 233.7 | 192.1 | 210.5 | 200.0 | 226.4 |
| 89 | NDBS 1011 | Parent | 266.4 | 290.5 | 222.5 | 282.5 | 264.0 | 402.8 | 271.4 | 194.8 | 188.0 | 195.4 | 201.4 |
| 90 | NDBS 1011 X NDSAB (MER-FS)C 15 | Cross | 243.4 | 264.5 | 196.0 | 222.1 | 227.5 | 326.8 | 204.2 | 204.5 | 183.8 | 187.5 | 213.7 |
| 91 | Check 3 P IONEER 39N99 | Check | 234.0 | 222.5 | 200.5 | 182.0 | 217.5 | 208.0 | 200.2 | 177.9 | 140.6 | 177.3 | 189.0 |
| 92 | NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 266.0 | 228.0 | 215.0 | 237.0 | 271.5 | 309.2 | 224.6 | 235.3 | 219.3 | 213.4 | 244.2 |
| 93 | BS 22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 262.9 | 220.5 | 216.5 | 236.5 | 243.5 | 321.3 | 226.2 | 221.5 | 201.2 | 198.9 | 235.0 |
| 94 | NDL X NDBS 1011 | Cross | 274.1 | 238.5 | 202.5 | 235.6 | 272.5 | 331.9 | 227.3 | 195.6 | 180.5 | 198.6 | 219.0 |
| 95 | NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 237.4 | 228.0 | 191.5 | 236.5 | 240.0 | 329.5 | 209.1 | 172.4 | 190.2 | 188.1 | 219.2 |
| 96 | NDL X NDSM(M-FS)C9 | Cross | 253.2 | 241.5 | 193.5 | 212.6 | 225.5 | 298.3 | 217.0 | 198.6 | 158.3 | 188.8 | 204.4 |
| 97 | NDSS | Parent | 237.2 | 243.5 | 199.0 | 198.5 | 209.5 | 277.7 | 207.0 | 188.6 | 184.1 | 184.9 | 216.8 |
| 98 | NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 264.3 | 253.0 | 219.0 | 224.5 | 237.5 | 308.3 | 214.9 | 177.1 | 184.5 | 190.6 | 213.5 |
| 99 | NDCG(FS)C 1 X NDSHLC(M-FS)C5 | Cross | 24.9 | 200.5 | 210.5 | 218.9 | 249.5 | 322.8 | 212.4 | 206.8 | 204.5 | 212.7 | 219.8 |
| 100 | NDL X NDBSK(HI-M)C3 | Cross | 254.9 | 266.5 | 222.5 | 249.4 | 24.0 | 371.1 | 229.0 | 203.4 | 190.6 | 192.9 | 232.8 |
| 10 | NDBS22(R-T1)C9 XEARLYGEM 2 lb | Cross | 231.2 | 199.5 | 204.5 | 215.4 | 215.0 | 278.6 | 237.1 | 158.1 | 187.7 | 189.8 | 207.3 |
| 102 | NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 294.1 | 296.0 | 250.0 | 271.5 | 268.0 | 377.5 | 281.4 | 237.3 | 229.0 | 214.3 | 275.6 |
| 103 | NDSHLC(M-FS)C5 XEARLYGEM 2 lb | Cross | 266.7 | 219.0 | 219.5 | 214.9 | 252.5 | 319.8 | 210.0 | 195.2 | 202.3 | 205.2 | 218.3 |
| 104 | NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 222.7 | 199.0 | 193.0 | 189.5 | 206.5 | 269.4 | 209.3 | 200.0 | 190.4 | 196.3 | 207.5 |
| 105 | CGL(S-FR2)C1X B S $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 252.6 | 252.0 | 191.5 | 237.4 | 260.5 | 299.0 | 221.0 | 203.3 | 192.8 | 216.7 | 217.9 |
| 106 | NDSAB(MER-FS)C 15 XEARLYGEM 21 c | Cross | 211.8 | 196.5 | 189.0 | 191.1 | 211.5 | 224.1 | 194.6 | 185.3 | 162.2 | 180.9 | 203.9 |
| 107 | NDBS 11(FR-M)C3 X EAR LYGEM 2 la | Cross | 243.1 | 226.5 | 210.0 | 213.9 | 203.0 | 269.7 | 208.4 | 170.7 | 158.8 | 185.5 | 204.0 |
| 108 | NDCG(FS)C1X Leaming(S-FS)C6 | Cross | 242.4 | 183.5 | 181.5 | 197.0 | 200.5 | 255.1 | 195.8 | 184.8 | 161.0 | 183.6 | 198.3 |
| 109 | NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 218.7 | 222.0 | 188.0 | 204.1 | 210.0 | 324.6 | 196.0 | 178.0 | 184.6 | 191.0 | 197.9 |
| 110 | NDBS 21 (R-T)C9 X EARLYGEM 2 lb | Cross | 219.2 | 195.0 | 199.5 | 189.6 | 235.5 | 217.2 | 204.4 | 192.5 | 191.5 | 202.2 | 213.5 |
| 11 | NDSCD(FS-CS)C2 X EARLYGEM 2 lb | Cross | 210.9 | 194.0 | 187.5 | 215.0 | 219.0 | 229.9 | 192.9 | 182.9 | 179.1 | 181.2 | 200.4 |
| 112 | NDSS XEARLYGEM 2 1a | Cross | 218.9 | 220.0 | 178.5 | 189.0 | 203.0 | 260.0 | 200.5 | 189.8 | 175.7 | 189.5 | 208.8 |
| 113 | NDCG(FS)C1XEARLYGEM 21 c | Cross | 222.6 | 199.0 | 169.0 | 184.0 | 197.0 | 249.5 | 186.6 | 174.0 | 157.7 | 177.9 | 200.9 |
| 114 | NDCG(FS)C1XNDL | Cross | 252.5 | 226.5 | 194.0 | 249.1 | 196.5 | 299.9 | 202.9 | 169.7 | 167.0 | 180.4 | 201.6 |
| 115 | NDLXEARLYGEM 21 a | Cross | 234.6 | 204.5 | 190.0 | 209.1 | 225.0 | 264.2 | 187.0 | 184.0 | 175.3 | 180.7 | 200.9 |
| 116 | NDSM(M-FS)C9 XEARLYGEM 2 lb | Cross | 212.2 | 195.0 | 172.0 | 175.1 | 208.5 | 247.8 | 216.8 | 146.4 | 172.5 | 199.4 | 211.6 |
| 117 | NDBS $11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 259.5 | 265.0 | 196.5 | 232.0 | 254.5 | 284.4 | 253.0 | 205.2 | 188.9 | 213.3 | 224.9 |
| 118 | NDBS 1011 XEARLYGEM 21 c | Cross | 264.7 | 215.5 | 201.0 | 207.2 | 198.5 | 309.0 | 213.6 | 183.7 | 187.2 | 189.0 | 199.9 |
| 119 | NDBS 11(FR-M)C3 X EARLYGEM 21 b | Cross | 230.0 | 239.0 | 197.0 | 199.0 | 236.0 | 302.1 | 198.9 | 169.0 | 185.9 | 191.5 | 198.1 |
| 120 | NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 254.4 | 215.5 | 204.5 | 232.1 | 229.0 | 298.0 | 229.3 | 202.7 | 181.5 | 186.7 | 210.4 |

Table B3 (continued). Grain moisture ( $\mathrm{g} \mathrm{kg}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B4. Test weight $\left(\mathrm{kg} \mathrm{hL}^{-1}\right)$ adjusted means of 16 maize populations, 120 crosses, and 8 checks across 10 environments. Entry Pedigree

| Entry Pedigree | Type | 20 |  |  |  | 2011 |  |  | 2012 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21 c | Cross | 64.2 | 68.9 | 69.3 | 65.6 | 70.2 | 59.3 | 65.8 |  | 69.6 | 68.4 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 65.3 | 67.7 | 71.0 | 65.0 | 67.3 | 58.4 | 67.3 | 59.6 | 62.0 | 65.8 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 65.1 | 64.3 | 68.8 | 61.2 | 65.9 | 59.4 | 58.9 | 64.0 | 69.4 | 66.8 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 65.1 | 66.4 | 70.6 | 66.6 | 66.8 | 60.8 | 64.8 | 57.6 | 65.4 | 63.1 |
| 5 EARLYGEM 2 la XEARLYGEM 2 lb | Cross | 70.5 | 72.9 | 74.4 | 68.8 | 71.8 | 60.6 | 56.8 | 71.6 | 70.3 | 66.7 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 65.3 | 66.0 | 68.6 | 66.1 | 64.6 | 59.1 | 65.5 | 65.6 | 53.4 | 65.1 |
| 7 NDSS XNDL | Cross | 62.9 | 64.4 | 68.1 | 62.6 | 68.5 | 59.6 | 64.1 | 68.3 | 66.6 | 67.0 |
| 8 NDBSK(HI-M)C3 XEARLYGEM 2 lb | Cross | 64.6 | 69.6 | 69.9 | 66.6 | 70.4 | 60.9 | 67.1 | 69.9 | 65.4 | 59.9 |
| 9 NDL XEARLYGEM 21 b | Cross | 65.2 | 68.8 | 69.0 | 64.5 | 69.4 | 63.8 | 67.5 | 70.3 | 68.4 | 67.3 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21c | Cross | 64.0 | 67.4 | 69.7 | 62.3 | 66.8 | 62.5 | 66.4 | 69.6 | 69.6 | 67.7 |
| 11 NDBS 11(FR-M)C3 | P arent | 62.8 | 65.2 | 68.6 | 60.2 | 63.4 | 58.9 | 59.6 |  | 65.2 | 65.3 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 67.1 | 65.1 | 65.3 | 64.2 | 64.6 | 59.6 | 61.8 | 65.7 | 63.6 | 64.0 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 64.0 | 62.3 | 70.4 | 62.8 | 63.6 | 58.8 | 62.1 | 53.0 | 52.4 |  |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 65.7 | 64.9 | 68.4 | 64.4 | 67.3 | 58.8 | 67.2 | 69.8 | 60.3 | 64.7 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 64.4 | 63.4 | 69.2 | 60.7 | 64.3 | 59.4 | 62.6 | 65.7 | 66.4 | 63.8 |
| 16 Check 4 DKC 43-27 VT3 | Check | 63.3 | 66.3 | 68.6 | 64.3 | 69.6 | 59.6 | 65.7 | 67.9 | 67.2 | 66.9 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 64.4 | 65.4 | 65.7 | 59.8 | 63.3 | 58.1 | 59.5 | 63.5 |  | 61.4 |
| 18 EARLYGEM 2 lc | P arent | 68.9 | 74.5 | 72.0 | 70.4 | 73.9 | 63.6 | 70.4 | 56.8 | 53.4 |  |
| 19 Leaming(S-FS)C6 | P arent | 61.3 | 66.7 | 65.4 | 60.9 | 60.2 | 60.6 | 63.7 | 67.7 |  | 61.3 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{Tl}) \mathrm{C} 9$ | Cross | 65.6 | 64.6 | 66.1 | 63.3 | 66.4 | 58.6 | 59.2 | 68.9 | 68.4 | 67.0 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 62.4 | 63.3 | 66.5 | 62.4 | 65.1 | 59.8 | 63.0 | 66.9 | 57.6 | 61.8 |
| 22 NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 67.2 | 65.1 | 68.3 | 62.6 | 64.8 | 62.8 | 62.7 | 63.5 | 65.5 | 66.6 |
| 23 Check 1P IONEER 39V07 | Check | 66.0 | 70.2 | 69.5 | 67.4 | 72.3 | 62.1 | 66.2 | 69.9 | 67.6 | 68.1 |
| $24 \mathrm{NDCG}(\mathrm{FS}) \mathrm{C} 1 \mathrm{XNDSAB}(\mathrm{MER-FS}) \mathrm{C} 15$ | Cross | 66.7 | 70.0 | 70.1 | 65.8 | 71.4 | 62.8 | 68.5 | 67.2 | 65.6 | 66.6 |
| 25 Leaming(S-FS)C6 XNDBS22(R-T ) C9 | Cross | 63.9 | 66.6 | 66.0 | 59.0 | 65.4 | 58.4 | 62.6 | 68.9 | 67.9 | 67.7 |
| 26 Leaming(S-FS)C6 XNDBS 21 (R-T)C9 | Cross | 65.1 | 66.8 | 68.0 | 65.1 | 69.2 | 58.3 | 62.4 | 68.6 | 61.6 | 63.8 |
| 27 NDBSK(HIM)C3 XEARLYGEM 21 a | Cross | 66.0 | 66.9 | 68.9 | 64.7 | 69.7 | 61.1 | 63.9 | 67.9 | 63.9 | 67.5 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 62.2 | 63.1 | 65.9 | 60.1 | 66.6 | 58.9 | 63.6 | 67.4 | 65.4 | 63.0 |
| 29 EARLYGEM 2 1a XEARLYGEM 21 c | Cross | 68.7 | 71.9 | 71.9 | 71.0 | 64.4 | 67.3 | 65.8 | 69.9 |  | 62.7 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 68.0 | 69.8 | 71.2 | 67.7 | 75.6 | 65.5 | 71.0 | 70.6 | 62.5 | 69.4 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 60.6 | 63.8 | 66.3 | 59.6 | 68.3 | 56.6 | 63.7 | 63.5 | 53.8 | 59.7 |
| 32 NDBSK(HIM)C3 XEARLYGEM 21 c | Cross | 66.6 | 67.4 | 68.5 | 67.1 | 70.0 | 64.0 | 65.4 | 70.4 | 68.1 | 66.6 |
| 33 NDBS 1011 X EARLYGEM 2 lb | Cross | 64.5 | 67.8 | 69.9 | 68.1 | 70.5 | 62.1 | 67.0 | 69.8 | 69.6 | 68.5 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 1a | Cross | 65.7 | 66.2 | 70.3 | 68.1 | 71.0 | 61.3 | 61.7 | 67.9 | 68.2 | 65.8 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 65.3 | 67.6 | 68.2 | 65.2 | 70.4 | 62.0 | 64.7 | 64.4 | 61.8 | 67.4 |
| 36 NDSAB(MER-FS)C 15 X NDSHLC(M-FS)C5 | Cross | 65.7 | 67.8 | 68.8 | 65.3 | 65.8 | 60.4 | 62.4 | 66.9 | 66.3 | 60.4 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 63.6 | 62.9 | 66.6 | 61.5 | 67.1 | 61.4 | 64.6 | 67.5 | 68.6 | 67.5 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 67.2 | 68.9 | 69.7 | 68.9 | 74.3 | 63.0 | 70.7 | 70.3 | 69.6 | 70.0 |
| 39 EARLYGEM 2 lb X EARLYGEM 21 c | Cross | 69.9 | 72.1 | 69.3 | 68.3 | 72.9 | 63.7 | 70.8 |  |  |  |
| 40 NDBSK(HI-M)C3 X NDSAB(MER-FS)C 15 | Cross | 63.1 | 66.9 | 70.4 | 66.8 | 66.6 | 57.9 | 66.4 | 71.0 | 65.9 | 67.9 |

Table B4 (continued). Test weight ( $\mathrm{kg} \mathrm{hL}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 10 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 65.1 | 67.9 | 70.7 | 64.3 | 66.3 | 61.6 | 63.3 | 65.2 | 66.5 | 63.2 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 69.2 | 68.5 | 71.9 | 69.1 | 72.4 | 63.5 | 71.5 | 71.9 | 69.6 | 70.3 |
| $43 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{X}$ NDBS 22 (R-T 1)C9 | Cross | 64.3 | 66.3 | 67.6 | 64.0 | 69.2 | 58.3 | 61.9 | 59.1 | 64.2 | 63.5 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 64.2 | 63.4 | 66.3 | 62.6 | 66.6 | 58.6 | 60.7 | 66.2 | 64.1 | 63.7 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 62.6 | 64.4 | 69.4 | 60.4 | 65.3 | 56.8 | 62.2 | 69.3 | 64.0 | 59.4 |
| 46 NDL XNDBS22(R-Tl)C9 | Cross | 61.6 | 61.6 | 69.4 | 64.3 | 69.7 | 58.4 | 65.5 | 68.3 | 61.1 | 67.7 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 63.2 | 64.3 | 68.3 | 62.3 | 66.6 | 58.8 | 60.3 | 63.1 | 53.8 | 61.6 |
| 48 NDBS 11(FR-M)C3 X NDSAB(MER-FS)C 15 | Cross | 63.4 | 70.1 | 67.0 | 65.9 | 66.6 | 59.3 | 61.7 | 65.0 | 65.1 | 65.2 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 64.0 | 65.8 | 69.8 | 69.3 | 65.6 | 60.1 | 67.2 | 53.0 | 67.8 | 64.1 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 65.1 | 68.8 | 71.2 | 65.8 | 69.7 | 59.6 | 67.5 | 60.4 | 69.9 | 66.7 |
| 51 NDBS 22(R-T1)C9 | Parent | 63.8 | 63.1 | 67.2 | 62.1 | 65.9 | 61.7 | 64.5 | 71.0 | 64.5 | 59.5 |
| 52 NDSS XNDBS 1011 | Cross | 63.9 | 61.8 | 68.3 | 61.3 | 64.8 | 62.1 | 63.0 | 55.6 | 67.4 | 64.0 |
| 53 NDL | P arent | 63.4 | 62.3 | 67.8 | 58.8 | 66.1 | 60.6 | 62.6 | 68.6 | 58.9 | 62.3 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 63.9 | 60.6 | 69.2 | 63.6 | 64.3 | 58.1 | 63.6 | 68.1 | 67.4 | 63.2 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 63.7 | 62.9 | 66.9 | 61.7 | 64.1 | 59.1 | 61.5 | 62.2 | 64.8 | 62.6 |
| 56 NDSAB(MER-FS)C 15 XNDBS 21 (R-T)C9 | Cross | 66.2 | 69.6 | 70.3 | 66.9 | 71.1 | 59.3 | 65.6 | 68.6 | 69.1 | 66.9 |
| 57 NDBS 11(FR-M)C3 X NDBS 22 (R-Tl)C9 | Cross | 64.5 | 65.9 | 68.0 | 63.6 | 65.8 | 59.8 | 62.3 | 69.1 | 67.1 | 64.3 |
| 58 EARLYGEM 2 lb | Parent | 69.1 | 68.7 | 74.0 | 71.4 | 73.8 | 50.2 | 67.7 | 50.4 |  | 55.6 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 68.8 | 72.1 | 68.9 | 67.4 | 69.0 | 58.4 | 68.0 | 67.4 | 56.8 | 66.3 |
| 60 Check 2 DKC 36-34 VT3 | Check | 66.8 | 68.7 | 69.0 | 67.7 | 71.1 | 60.6 | 66.0 | 67.2 | 69.9 | 68.0 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 62.0 | 64.9 | 66.9 | 60.9 | 67.6 | 57.8 | 63.6 | 65.6 | 65.2 | 60.5 |
| 62 NDBS 22(R-T1)C9 XEARLYGEM 21 c | Cross | 64.3 | 69.3 | 70.6 | 66.3 | 72.1 | 61.8 | 69.6 | 70.4 | 62.4 | 69.3 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 62.1 | 66.8 | 67.3 | 64.6 | 65.3 | 60.3 | 61.8 | 66.4 | 64.7 | 64.3 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 64.3 | 66.4 | 66.2 | 58.8 | 62.9 | 57.4 | 61.3 | 69.3 | 65.0 | 60.7 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T) C 9 | Cross | 64.9 | 63.9 | 67.1 | 64.3 | 65.8 | 59.8 | 62.5 | 59.9 | 68.1 | 61.2 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 63.5 | 67.0 | 66.0 | 66.2 | 68.3 | 58.7 | 64.0 | 64.9 | 68.6 | 59.5 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 63.4 | 63.4 | 66.8 | 66.1 | 63.3 | 60.7 | 61.5 | 68.9 | 64.1 | 64.3 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 65.8 | 65.1 | 70.2 | 65.2 | 69.9 | 59.5 | 66.3 | 70.6 | 66.4 | 68.2 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 63.7 | 62.9 | 67.4 | 62.2 | 64.6 | 62.1 | 61.0 | 59.8 | 67.6 | 60.9 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 63.9 | 64.6 | 68.9 | 60.6 | 67.3 | 58.4 | 61.9 | 66.5 | 65.0 | 64.4 |
| 71 NDBSK(HIM)C3 | Parent | 65.6 | 68.9 | 67.8 | 62.9 | 65.3 | 49.9 | 62.3 | 65.4 |  | 63.2 |
| 72 NDSS XNDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 66.4 | 66.4 | 70.1 | 65.4 | 67.3 | 57.3 | 62.7 | 61.8 | 61.4 | 64.7 |
| 73 NDSS XEARLYGEM 21 c | Cross | 67.3 | 66.9 | 72.7 | 66.7 | 72.8 | 61.1 | 66.6 | 69.3 | 66.4 | 62.7 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 63.6 | 63.6 | 67.4 | 61.7 | 63.6 | 59.4 | 60.1 | 57.1 | 56.3 | 63.6 |
| 75 NDCG(FS)C1 | Parent | 66.4 | 67.8 | 70.5 | 64.9 | 72.4 | 62.1 | 65.2 | 68.4 | 64.3 | 59.1 |
| 76 NDSAB(MER-FS)C 15 | P arent | 63.7 | 69.0 | 71.1 | 64.4 | 66.6 | 59.4 | 65.6 | 66.9 |  | 65.3 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 62.0 | 66.3 | 64.1 | 60.4 | 65.4 | 58.3 | 62.4 | 67.6 | 60.8 | 62.7 |
| 78 NDBS 1011 X NDBS 21 (R-T)C9 | Cross | 63.4 | 65.3 | 67.1 | 65.7 | 65.6 | 60.3 | 62.0 | 62.5 | 63.6 | 65.3 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 67.7 | 68.2 | 70.4 | 68.8 | 72.6 | 61.4 | 64.7 | 66.1 | 69.6 | 69.6 |
| 80 NDBS21(R-T)C9 XEARLYGEM 21 a | Cross | 69.6 | 71.1 | 71.5 | 68.1 | 70.2 | 62.7 | 64.8 | 68.7 | 68.7 | 70.4 |

Table B4 (continued). Test weight ( $\mathrm{kg} \mathrm{hL}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 10 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 65.1 | 66.8 | 68.6 | 64.6 | 69.3 | 62.7 | 62.8 | 69.3 | 64.9 | 66.5 |
| $82 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3$ X Leaming(S-FS)C6 | Cross | 63.0 | 62.8 | 66.1 | 61.1 | 64.9 | 60.6 | 61.5 | 68.8 | 66.0 | 67.2 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 65.3 | 66.2 | 67.2 | 63.5 | 65.4 | 62.3 | 61.3 | 68.6 | 67.9 | 65.7 |
| 84 NDSM(M-FS)C9 | P arent | 71.3 | 71.2 | 73.9 | 68.9 | 69.4 | 60.9 | 67.1 | 57.8 | 56.8 | 63.7 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 64.1 | 64.2 | 68.4 | 65.6 | 68.5 | 60.1 | 62.4 | 67.1 | 65.5 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 65.2 | 66.0 | 66.9 | 63.4 | 67.8 | 63.0 | 65.7 | 67.5 | 52.0 | 66.9 |
| 87 NDCG(FS)C1 ${ }^{\text {N }}$ NDBS 11(FR-M)C3 | Cross | 64.8 | 65.8 | 67.8 | 59.8 | 72.4 | 60.1 | 65.1 | 69.4 | 69.1 | 69.5 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 64.3 | 68.0 | 69.6 | 62.9 | 68.5 | 60.6 | 65.5 | 69.9 | 67.5 | 66.3 |
| 89 NDBS 1011 | P arent | 66.0 | 63.6 | 65.4 | 61.0 | 65.6 | 57.1 | 60.8 | 70.8 | 54.0 | 69.3 |
| 90 NDBS 1011 XNDSAB(MER-FS)C 15 | Cross | 63.7 | 63.2 | 70.3 | 64.8 | 68.3 | 59.3 | 65.6 | 69.6 | 65.5 | 66.0 |
| 91 Check 3 P IONEER 39N99 | Check | 63.4 | 66.1 | 66.9 | 67.8 | 70.9 | 57.3 | 66.4 | 70.6 | 67.7 | 69.4 |
| 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 65.2 | 66.8 | 67.8 | 62.2 | 64.4 | 59.4 | 64.4 | 66.4 | 65.9 | 62.6 |
| 93 B 22 LEAM (R-FR)C 1 XLEAMING22 (S-FR)C1 | Check | 63.0 | 63.5 | 66.5 | 59.3 | 61.1 | 56.9 | 60.4 | 64.3 | 68.3 | 61.6 |
| 94 NDL XNDBS 1011 | Cross | 64.2 | 65.3 | 67.4 | 64.9 | 66.6 | 62.4 | 62.5 | 68.4 | 64.9 | 65.6 |
| 95 NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 65.8 | 67.6 | 71.1 | 60.3 | 67.8 | 58.1 | 67.0 | 68.1 | 54.6 | 66.3 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 64.2 | 60.5 | 68.8 | 68.7 | 67.6 | 58.9 | 65.3 | 68.8 | 67.9 | 65.6 |
| 97 NDSS | P arent | 63.4 | 65.1 | 68.7 | 63.8 | 67.2 | 60.2 | 61.4 |  | 64.3 | 61.7 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 64.2 | 61.7 | 66.3 | 64.5 | 68.4 | 58.3 | 62.7 | 68.3 | 57.8 | 61.8 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 65.4 | 69.1 | 67.2 | 64.9 | 65.9 | 61.6 | 68.1 | 64.2 | 66.4 | 61.6 |
| 100 NDL X NDBSK(HFM)C3 | Cross | 63.0 | 64.9 | 65.8 | 62.8 | 67.7 | 59.1 | 63.2 | 63.6 | 64.9 | 61.3 |
| 101 NDBS 22(R-T1)C9 XEARLYGEM 2 lb | Cross | 67.7 | 68.9 | 68.9 | 63.3 | 71.8 | 60.8 | 66.0 | 68.8 | 70.1 | 67.8 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 63.7 | 64.0 | 64.3 | 59.3 | 64.9 | 63.1 | 63.2 | 65.2 | 66.6 | 61.8 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 66.5 | 68.6 | 67.1 | 65.4 | 69.7 | 54.2 | 66.8 | 69.9 | 67.2 | 66.3 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 67.5 | 70.0 | 69.4 | 70.0 | 72.9 | 64.0 | 69.4 | 70.6 | 71.8 | 70.1 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 66.0 | 66.5 | 70.6 | 65.6 | 63.4 | 60.8 | 62.4 | 66.9 | 62.1 | 65.1 |
| 106 NDSAB(MER-FS)C 15 XEARLYGEM 21 c | Cross | 65.4 | 69.3 | 71.3 | 67.1 | 72.2 | 63.9 | 67.8 | 70.4 | 65.2 | 67.5 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 21 l | Cross | 65.8 | 65.7 | 68.3 | 64.1 | 72.2 | 62.5 | 66.0 | 70.3 | 69.3 | 66.2 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 64.0 | 67.6 | 70.3 | 68.0 | 70.6 | 60.1 | 66.4 | 66.9 | 68.9 | 65.8 |
| 109 NDSM(M-FS)C9 X EARLYGEM 21 l | Cross | 65.7 | 65.7 | 71.4 | 64.1 | 72.9 | 61.9 | 70.4 | 69.1 | 66.5 | 61.9 |
| 110 NDBS 21 (R-T)C9 X EAR LYGEM 21 b | Cross | 67.0 | 68.8 | 71.3 | 70.8 | 71.1 | 65.4 | 69.7 | 70.8 | 69.1 | 68.3 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 65.3 | 70.1 | 70.3 | 58.2 | 69.1 | 63.0 | 67.0 | 61.3 | 68.3 | 64.9 |
| 112 NDSS XEARLYGEM 21 a | Cross | 66.0 | 66.5 | 71.2 | 63.3 | 71.4 | 60.8 | 66.0 | 64.1 | 67.2 | 64.3 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 65.8 | 71.3 | 71.9 | 68.9 | 73.9 | 64.0 | 69.6 | 70.1 | - 69.8 | 68.0 |
| 114 NDCG(FS)C1XNDL | Cross | 63.4 | 66.8 | 69.0 | 62.8 | 69.3 | 64.7 | 69.1 | 68.1 | 65.4 | 68.4 |
| 115 NDLXEARLYGEM 21 a | Cross | 65.1 | 67.3 | 70.2 | 63.8 | 69.4 | 63.8 | 68.9 | 68.9 | 69.1 | 67.0 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 65.9 | 69.4 | 73.7 | 68.8 | 72.8 | 64.7 | 66.9 | 58.4 | 69.3 | 66.1 |
| 117 NDBS 11(FR-M)C3 X NDBS 21 (R-T)C9 | Cross | 62.1 | 63.1 | 67.8 | 63.0 | 65.3 | 56.9 | 60.8 | 62.8 | 63.3 | 64.6 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 66.6 | 66.9 | 69.8 | 66.1 | 73.4 | 60.9 | 64.7 | 70.4 | 69.3 | 69.1 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 21 b | Cross | 63.5 | 66.8 | 69.4 | 64.2 | 67.7 | 62.3 | 65.7 | 67.9 | 68.6 | 68.4 |
| 120 NDBS 11(FR-M)C3 X Leaming(S-FS)C6 | Cross | 64.2 | 66.3 | 67.1 | 60.4 | 66.1 | 58.6 | 62.8 | 66.2 | 64.8 | 66.0 |

Table B4 (continued). Test weight ( $\mathrm{kg} \mathrm{hL}^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 10 environments.


Table B5. Stand (plants ha ${ }^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.


Table B5 (continued). Stand (plants ha ${ }^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 49513 | 44132 | 41734 | 40047 | 62989 | 88570 | 72140 | 78576 | 61780 | 70375 | 77499 | 81186 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 15069 | 34444 | 32594 | 36228 | 64072 | 78517 | 72095 | 78576 | 60348 | 65185 | 82881 | 73563 |
| 43 NDBSK(HIM)C3 X NDBS 22 (R-T 1)C9 | Cross | 33368 | 39826 | 32633 | 35176 | 68950 | 85814 | 88421 | 66736 | 81864 | 74014 | 77499 | 73268 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 40902 | 48437 | 38402 | 40067 | 63333 | 88451 | 86923 | 76423 | 78363 | 90608 | 76423 | 87261 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 35521 | 36597 | 36694 | 25877 | 62185 | 90327 | 84665 | 83958 | 68920 | 70844 | 79652 | 65925 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 27986 | 43055 | 46916 | 31947 | 61146 | 86506 | 84744 | 81805 | 77369 | 71963 | 61354 | 79107 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 27986 | 38750 | 30803 | 30699 | 66132 | 83089 | 68049 | 86110 | 32599 | 81943 | 85034 | 78723 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS)C 15 | Cross | 37673 | 36597 | 38698 | 33589 | 58254 | 85241 | 86950 | 82881 | 68000 | 81272 | 79652 | 82158 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 47361 | 52743 | 40103 | 49612 | 67139 | 86713 | 81181 | 80729 | 61176 | 69709 | 67812 | 65243 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 25833 | 50590 | 42456 | 21847 | 59228 | 83513 | 80812 | 75347 | 77428 | 83270 | 88263 | 86156 |
| 51 NDBS 22(R-T1)C9 | P arent | 22604 | 20451 | 26697 | 37039 | 44741 | 81361 | 78105 | 83958 | 65221 | 75954 | 74270 | 75582 |
| 52 NDSS XNDBS 1011 | Cross | 48437 | 41979 | 52588 | 49268 | 52184 | 85666 | 80390 | 81805 | 73443 | 85087 | 77499 | 81215 |
| 53 NDL | P arent | 64583 | 54895 | 46968 | 45410 | 56632 | 85340 | 82644 | 85034 | 60822 | 78245 | 61354 | 76320 |
| 54 NDBS 1011 XLeaming(S-FS )C6 | Cross | 33368 | 44132 | 32446 | 52355 | 60945 | 86051 | 82600 | 82881 | 70154 | 70902 | 75347 | 74079 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 33368 | 54895 | 48630 | 48074 | 66899 | 79356 | 83856 | 80729 | 77677 | 75427 | 74270 | 82395 |
| 56 NDSAB(MER-FS)C 15 XNDBS 21 (R-T)C9 | Cross | 44132 | 50590 | 46864 | 40047 | 47289 | 87375 | 82358 | 78576 | 69870 | 83409 | 82881 | 79166 |
| 57 NDBS 11(FR-M)C3 X NDBS 22 (R-Tl)C9 | Cross | 46284 | 35521 | 46233 | 51691 | 64439 | 88174 | 84406 | 85034 | 70115 | 75485 | 78576 | 76128 |
| 58 EARLYGEM 2 lb | P arent | 34444 | 32291 | 33851 | 25470 | 60171 | 88658 | 82332 | 72117 | 51654 | 70146 | 79652 | 68859 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 49513 | 37673 | 50029 | 31756 | 59776 | 86318 | 83935 | 77499 | 58551 | 68286 | 79652 | 78163 |
| 60 Check 2 DKC 36-34 VT3 | Check | 64583 | 63506 | 65459 | 63708 | 58356 | 88470 | 97454 | 79652 | 82111 | 80531 | 82881 | 81597 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 27986 | 38750 | 25317 | 27715 | 54565 | 77322 | 72592 | 66736 | 38667 | 70961 | 72117 | 85149 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 26909 | 38750 | 35205 | 29013 | 57417 | 85962 | 89445 | 77499 | 62454 | 74835 | 69965 | 75923 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 37673 | 45208 | 53890 | 40976 | 57999 | 87039 | 84586 | 82881 | 69621 | 81512 | 86110 | 83648 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 19375 | 33368 | 38879 | 24142 | 48220 | 82733 | 79336 | 77499 | 54162 | 73423 | 78576 | 79593 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 40902 | 44132 | 63397 | 39659 | 63432 | 88866 | 86972 | 77499 | 71681 | 76269 | 73194 | 72545 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 46284 | 41979 | 44570 | 50909 | 53752 | 82042 | 80469 | 77499 | 72402 | 80766 | 74270 | 77839 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 27986 | 40902 | 33845 | 25101 | 48942 | 88263 | 87108 | 88263 | 60550 | 78832 | 76423 | 82925 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 51666 | 63506 | 50377 | 60130 | 57318 | 82289 | 88839 | 85034 | 54895 | 78203 | 78576 | 72162 |
| $69 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDBS} 11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ | Cross | 40902 | 36597 | 49746 | 40558 | 64781 | 85241 | 73664 | 77499 | 55141 | 74585 | 78576 | 84194 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 49513 | 49513 | 58892 | 40170 | 55131 | 86802 | 86660 | 88263 | 65742 | 74627 | 76423 | 79077 |
| 71 NDBSK(HIM)C3 | P arent | 51666 | 55972 | 50313 | 50762 | 67652 | 85537 | 79652 | 82881 | 53264 | 71691 | 75347 | 79770 |
| 72 NDSS XNDBS21(R-T)C9 | Cross | 48437 | 54895 | 47445 | 40736 | 64080 | 89843 | 73796 | 76423 | 68213 | 81784 | 77499 | 82128 |
| 73 NDSS XEARLYGEM 21 c | Cross | 39826 | 41979 | 44409 | 42686 | 62088 | 83928 | 81914 | 69965 | 63200 | 76402 | 59201 | 77791 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 29062 | 30139 | 27386 | 37526 | 56330 | 85034 | 79393 | 82881 | 75147 | 75970 | 66736 | 72871 |
| 75 NDCG(FS)C1 | P arent | 38750 | 43055 | 40690 | 40878 | 54759 | 86110 | 87450 | 83958 | 72627 | 78341 | 76423 | 79519 |
| 76 NDSAB(MER-FS)C 15 | Parent | 35521 | 16146 | 21373 | 29426 | 53591 | 82881 | 84353 | 73194 | 72237 | 77787 | 72117 | 77617 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 35521 | 39826 | 41586 | 41714 | 47275 | 81479 | 88760 | 86110 | 55311 | 76327 | 66736 | 49042 |
| 78 NDBS 1011 N NDBS 21 (R-T)C9 | Cross | 46284 | 55972 | 49668 | 40047 | 68810 | 84343 | 87639 | 82881 | 72178 | 87283 | 67812 | 75863 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 30139 | 34444 | 44325 | 30384 | 65077 | 86258 | 78132 | 75347 | 68937 | 74585 | 77499 | 75568 |
| 80 NDBS 21 (R-T)C9 XEARLYGEM 21 a | Cross | 36597 | 41979 | 40406 | 37427 | 53001 | 83513 | 72328 | 79652 | 67588 | 77185 | 78576 | 83102 |

Table B5 (continued). Stand (plants ha ${ }^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.


Table B5 (continued). Stand (plants ha ${ }^{-1}$ ) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.


Table B6. Stalk lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.


Table B6 (continued). Stalk lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS 21 (R-T)C9 | P arent | 1.9 | 5.2 | 0.0 | 0.1 | 1.4 | 11.0 | 5.0 | 9.3 | 13.0 | 44.6 | 43.1 | 26.7 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 0.0 | 0.1 | 0.0 | -0.2 | 0.2 | 16.3 | 11.7 | 19.9 | 35.5 | 17.7 | 29.6 | 36.1 |
| 43 NDBSK(HI-M)C3 X NDBS 22 (R-T1)C9 | Cross | 3.5 | 0.3 | 0.0 | 0.1 | -0.1 | 4.4 | 3.2 | 32.3 | 31.5 | 26.7 | 42.9 | 17.2 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | -0.1 | 0.2 | 0.0 | -0.2 | 0.0 | 4.8 | 7.1 | 17.0 | 20.7 | 32.7 | 39.6 | 31.0 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 0.1 | 0.2 | 2.8 | 0.1 | 0.0 | 11.8 | 7.2 | 6.9 | 17.4 | 28.0 | 25.9 | 29.5 |
| 46 NDLXNDBS22(R-Tl)C9 | Cross | -0.2 | 0.0 | 0.0 | 2.8 | 0.0 | 9.8 | 2.9 | 19.7 | 16.6 | 27.2 | 24.8 | 17.6 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 0.1 | 0.2 | 0.0 | 0.2 | 0.0 | 12.7 | 5.1 | 15.0 | 21.8 | 29.7 | 24.0 | 38.6 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS ) 15 | Cross | -0.1 | -0.2 | 0.0 | -0.2 | 0.0 | 0.6 | 6.3 | 16.4 | 6.5 | 16.3 | 28.0 | 16.5 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 0.4 | 0.1 | 3.3 | 0.0 | -0.1 | 15.0 | 4.9 | 15.9 | 21.8 | 58.1 | 40.4 | 26.1 |
| 50 NDBS 22(R-T1)C9 X EARLYGEM 21 la | Cross | -0.2 | -0.3 | 0.0 | 0.1 | -0.1 | 9.5 | 5.2 | 22.0 | 16.8 | 22.8 | 19.5 | 18.2 |
| 51 NDBS 22(R-T1)C9 | Parent | 0.1 | 5.0 | 0.0 | 0.0 | 0.0 | 6.6 | 4.4 | 20.3 | 0.1 | 12.4 | 22.9 | 11.4 |
| 52 NDSS X NDBS 1011 | Cross | 1.9 | -0.3 | 2.3 | 0.3 | -0.1 | 7.5 | 3.5 | 8.7 | 26.9 | 17.1 | 23.1 | 16.1 |
| 53 NDL | P arent | 1.8 | -0.1 | 2.8 | 0.2 | -0.1 | 13.9 | 10.1 | 17.7 | 11.2 | 33.7 | 39.5 | 33.9 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 0.0 | -0.1 | 0.0 | -0.2 | 0.1 | 15.2 | 13.2 | 17.6 | 42.6 | 35.6 | 39.3 | 30.3 |
| 55 NDBSK(HI-M)C3 X NDBS 1011 | Cross | 0.1 | 0.1 | 0.0 | 0.2 | -0.1 | 6.7 | 3.0 | 17.5 | 24.0 | 52.6 | 35.9 | 10.7 |
| 56 NDSAB(MER-FS)C 15 XNDBS 21 (R-T)C9 | Cross | -0.1 | 0.0 | 0.0 | -0.2 | -0.1 | 7.8 | 4.4 | 14.6 | 16.2 | 23.6 | 23.3 | 9.5 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-Tl)C9 | Cross | 0.0 | -0.1 | 0.0 | 0.1 | -0.1 | 10.2 | 7.9 | 10.7 | 17.0 | 16.5 | 15.3 | 15.8 |
| 58 EARLYGEM 2 lb | Parent | -0.3 | -0.2 | 0.0 | 3.7 | 3.1 | 24.5 | 31.2 | 40.1 | 62.0 | 51.7 | 64.3 | 47.7 |
| 59 NDSAB(MER-FS)C15 XNDSM(M-FS)C9 | Cross | 0.1 | 0.0 | 0.0 | 0.2 | 5.4 | 10.4 | 4.9 | 33.2 | 24.4 | 48.9 | 29.0 | 25.1 |
| 60 Check 2 DKC 36-34 VT3 | Check | -0.2 | -0.5 | 0.0 | -0.2 | -0.1 | 1.2 | 2.3 | 15.4 | 3.9 | 10.0 | 17.8 | 5.5 |
| 61 NDBSK(HI-M)C3 XNDSCD(FS-CS ) C 2 | Cross | 0.3 | 0.3 | 0.0 | 0.0 | 3.2 | 27.0 | 12.3 | 36.1 | 27.5 | 60.6 | 25.6 | 23.8 |
| 62 NDBS22(R-T1)C9 X EARLYGEM 21 c | Cross | -0.2 | -0.2 | 0.0 | 0.1 | 1.4 | 14.5 | 9.4 | 28.4 | 17.6 | 22.6 | 36.6 | 20.9 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 2.7 | 0.2 | 0.0 | 0.0 | 0.1 | 5.2 | 1.4 | 13.8 | 25.0 | 25.1 | 21.2 | 15.4 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | -0.1 | -0.2 | 0.0 | 0.3 | 0.0 | 10.5 | 7.2 | 11.9 | 11.4 | 45.3 | 22.1 | 14.4 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 2.4 | 0.1 | 1.6 | 0.2 | 0.0 | 6.4 | 3.4 | 24.7 | 13.9 | 52.0 | 39.4 | 22.8 |
| 66 NDBS22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | -0.1 | 0.1 | 0.0 | 3.9 | 1.5 | 20.5 | 6.3 | 20.2 | 3.7 | 21.9 | 23.1 | 22.8 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 0.1 | 0.2 | 0.0 | 0.2 | -0.1 | 8.9 | 2.6 | 15.9 | 14.3 | 16.7 | 33.0 | 15.4 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | -0.1 | 2.0 | 0.0 | -0.2 | 0.0 | 11.4 | 2.7 | 7.3 | 20.6 | 28.7 | 34.1 | 18.9 |
| 69 NDBSK(HIM)C3 X NDBS 11(FR-M)C3 | Cross | 0.0 | 0.1 | 0.0 | 0.1 | 0.0 | 9.6 | 8.0 | 17.1 | 12.3 | 37.2 | 31.1 | 24.7 |
| 70 NDSS XNDBS $11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ | Cross | 2.0 | 0.0 | 0.0 | 0.2 | 0.0 | 13.4 | 0.8 | 10.6 | 34.4 | 29.0 | 26.5 | 15.1 |
| 71 NDBSK(HIM)C3 | P arent | 3.9 | 0.1 | 0.0 | 0.2 | 1.3 | 9.4 | 8.0 | 28.6 | 35.8 | 46.3 | 44.9 | 21.8 |
| 72 NDSS X NDBS 21 (R-T)C9 | Cross | 1.8 | 1.4 | 0.0 | -0.2 | 0.0 | 13.6 | 5.6 | 21.6 | 34.3 | 26.3 | 35.3 | 22.1 |
| 73 NDSS XEARLYGEM 21 c | Cross | 0.3 | 3.1 | 0.0 | 7.9 | 0.0 | 27.1 | 12.3 | 16.4 | 30.9 | 25.4 | 39.0 | 27.5 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | -0.2 | -0.2 | 0.0 | 0.2 | 1.4 | 7.8 | 3.8 | 3.9 | 18.2 | 41.9 | 45.5 | 21.9 |
| 75 NDCG(FS)C1 | P arent | 0.1 | 0.2 | 4.2 | 2.6 | 0.1 | 12.2 | 6.1 | 8.1 | 14.4 | 35.7 | 24.2 | 11.7 |
| 76 NDSAB(MER-FS)C 15 | P arent | -0.1 | -0.1 | 0.0 | 0.4 | 0.0 | 25.4 | 4.5 | 17.1 | 17.2 | 17.2 | 26.9 | 24.4 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | -0.1 | 2.7 | 3.6 | 0.3 | 7.0 | 28.6 | 8.5 | 24.6 | 25.4 | 54.0 | 37.1 | 38.6 |
| 78 NDBS 1011 X NDBS 21 (R-T)C9 | Cross | 2.1 | 0.1 | 0.0 | 2.7 | 0.2 | 7.6 | 3.3 | 18.2 | 27.2 | 20.8 | 35.9 | 17.2 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 21 a | Cross | 0.1 | 0.2 | 0.0 | 0.3 | 0.0 | 8.4 | 10.4 | 29.1 | 27.0 | 13.9 | 33.7 | 26.2 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 a | Cross | -0.1 | 6.8 | 2.6 | 0.0 | 0.0 | 17.3 | 15.6 | 14.0 | 18.8 | 34.6 | 39.8 | 20.1 |

Table B6 (continued). Stalk lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 2.1 | 0.1 | 0.0 | 0.3 | 0.0 | 12.6 | 9.5 | 12.1 | 31.0 | 29.5 | 23.8 | 11.2 |
| 82 NDBSK(HI-M)C3 X Leaming(S-FS)C6 | Cross | -0.3 | 3.3 | 0.0 | 0.3 | 0.0 | 9.6 | 6.1 | 4.7 | 37.9 | 36.9 | 37.5 | 10.8 |
| 83 NDL X NDBS21(R-T)C9 | Cross | 0.1 | 0.1 | 4.8 | 0.4 | 2.7 | 8.3 | 4.8 | 9.8 | 18.1 | 16.8 | 38.3 | 18.6 |
| 84 NDSM(M-FS)C9 | P arent | -0.2 | -0.3 | 2.5 | -0.1 | 0.0 | 15.0 | 0.7 | 27.7 | 42.2 | 37.1 | 32.7 | 19.6 |
| 85 NDSS XNDSAB (MER-FS)C 15 | Cross | 0.5 | 0.4 | 0.0 | -0.3 | 0.0 | 4.1 | 5.5 | 20.4 | 18.9 | 33.9 | 20.3 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 0.0 | 5.8 | 0.0 | -0.2 | -0.1 | 22.9 | 11.4 | 15.6 | 22.1 | 28.3 | 48.4 | 26.1 |
| 87 NDCG(FS)C1 ${ }^{\text {N }}$ NDBS 11(FR-M)C3 | Cross | 0.3 | 0.3 | 2.0 | -0.3 | 0.1 | 7.9 | 1.8 | 19.2 | 22.9 | 21.5 | 37.6 | 7.5 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 3.6 | 3.1 | 0.0 | 4.1 | 0.0 | 21.4 | 6.2 | 33.5 | 21.8 | 36.5 | 37.2 | 39.0 |
| 89 NDBS 1011 | P arent | 0.1 | 0.2 | 0.0 | -0.1 | 0.0 | 12.4 | 8.7 | 13.8 | 27.6 | 16.3 | 24.2 | 19.3 |
| 90 NDBS 1011 X NDS AB (MER-FS)C 15 | Cross | 0.1 | 0.2 | 0.0 | -0.4 | 0.2 | 12.3 | 10.3 | 15.5 | 19.9 | 22.1 | 17.6 | 12.5 |
| 91 Check 3 P IONEER 39N99 | Check | 0.3 | 0.3 | 0.0 | -0.1 | 0.0 | 1.3 | 0.6 | 13.0 | 1.2 | 3.6 | 7.2 | 14.5 |
| 92 NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 0.1 | 0.2 | 0.0 | -0.5 | 1.6 | 13.4 | 5.5 | 18.9 | 35.7 | 35.4 | 25.7 | 21.4 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 0.2 | 0.2 | 0.0 | 4.8 | 0.0 | 22.0 | 5.4 | 12.9 | 26.4 | 31.9 | 19.8 | 19.7 |
| 94 NDL X NDBS 1011 | Cross | -0.1 | 0.1 | 0.0 | -0.1 | 0.0 | 4.2 | 6.6 | 26.7 | 30.5 | 20.8 | 39.0 | 13.8 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 0.3 | 0.2 | 0.0 | -0.1 | 1.5 | 17.7 | 0.1 | 34.6 | 23.2 | 38.3 | 33.9 | 18.2 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 0.0 | -0.2 | 0.0 | -0.5 | 0.0 | 8.8 | 6.2 | 11.5 | 29.2 | 25.0 | 24.0 | 33.8 |
| 97 NDSS | P arent | 11.7 | 5.4 | 0.0 | 2.2 | -0.1 | 17.7 | 10.2 | 22.7 | 22.8 | 40.7 | 32.6 | 24.9 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 7.7 | 2.8 | 4.5 | 0.1 | -0.2 | 24.5 | 2.3 | 23.3 | 5.4 | 43.6 | 20.3 | 31.6 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 0.0 | 9.2 | 0.0 | 0.0 | 0.0 | 18.0 | 10.3 | 22.6 | 10.9 | 28.2 | 33.1 | 25.0 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | -0.3 | 7.9 | 2.0 | 0.3 | -0.1 | 11.7 | 5.8 | 11.5 | 18.8 | 46.3 | 27.0 | 14.2 |
| 101 NDBS 22(R-T1)C9 X EARLYGEM 21 b | Cross | -0.3 | 0.2 | 0.0 | 0.2 | -0.1 | 16.6 | 15.8 | 16.1 | 30.0 | 10.3 | 30.1 | 25.6 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | -0.2 | 0.1 | 0.0 | 3.2 | 6.4 | 10.6 | 6.7 | 13.8 | 23.1 | 28.4 | 14.7 | 32.3 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 21 b | Cross | 0.0 | 4.3 | 0.0 | 2.9 | -0.2 | 11.0 | 13.1 | 22.6 | 18.7 | 39.3 | 36.0 | 37.6 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | -0.3 | 0.2 | 0.0 | 2.6 | 6.1 | 8.3 | 8.7 | 13.0 | 26.9 | 37.2 | 37.8 | 43.6 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | -0.1 | 0.2 | 0.0 | 0.2 | 1.3 | 5.8 | 9.1 | 11.3 | 36.8 | 42.1 | 23.7 | 20.8 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | -0.4 | 2.0 | 0.0 | 0.2 | -0.1 | 16.4 | 12.7 | 27.5 | 49.6 | 26.9 | 25.6 | 36.3 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | -0.1 | 0.2 | 0.0 | 0.3 | 2.6 | 10.4 | 36.2 | 25.2 | 23.7 | 31.2 | 44.3 | 28.4 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | -0.4 | 3.5 | 2.2 | 3.0 | -0.1 | 11.2 | 7.0 | 17.8 | 9.2 | 16.0 | 26.2 | 22.6 |
| 109 NDSM(M-FS)C9 X EARLYGEM 21 a | Cross | 5.2 | 11.6 | 0.0 | -0.1 | 0.1 | 19.6 | 12.3 | 27.2 | 15.6 | 56.3 | 57.3 | 22.8 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 l | Cross | 2.0 | 2.3 | 0.0 | -0.1 | 0.0 | 10.6 | 9.6 | 20.5 | 19.8 | 22.5 | 53.8 | 41.9 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 3.6 | 4.8 | 11.0 | -0.1 | 6.0 | 20.0 | 14.8 | 14.5 | 23.6 | 63.2 | 42.6 | 39.6 |
| 112 NDSS XEARLYGEM 21 a | Cross | -0.2 | 0.1 | 0.0 | 0.1 | 0.1 | 30.3 | 8.0 | 32.2 | 10.5 | 41.7 | 32.2 | 31.8 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 1.8 | 0.3 | 0.0 | 0.0 | 0.0 | 25.0 | 4.5 | 23.4 | 10.3 | 24.6 | 39.1 | 39.8 |
| 114 NDCG(FS)C1XNDL | Cross | -0.2 | 0.3 | 0.0 | -0.3 | 0.3 | 25.5 | 8.6 | 17.8 | 21.0 | 33.6 | 27.9 | 20.7 |
| 115 NDLXEARLYGEM 21 a | Cross | 4.1 | 0.5 | 0.0 | 0.0 | 1.3 | 14.3 | 9.1 | 30.2 | 29.0 | 35.4 | 34.1 | 30.2 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 2.5 | 0.4 | 0.0 | -0.3 | 2.6 | 25.6 | 13.0 | 29.9 | 43.1 | 56.8 | 82.9 | 33.8 |
| 117 NDBS 11(FR-M)C3 X NDBS 21 (R-T)C9 | Cross | -0.1 | 0.3 | 0.0 | 0.0 | 0.1 | 6.7 | 5.0 | 17.8 | 21.6 | 41.2 | 18.5 | 24.5 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | -0.4 | 2.1 | 0.0 | 0.0 | 0.1 | 14.9 | 11.2 | 29.2 | 20.6 | 22.2 | 42.8 | 32.8 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 21 b | Cross | -0.1 | 0.4 | 1.9 | 0.1 | 0.0 | 12.2 | 4.3 | 19.2 | 21.4 | 41.2 | 45.2 | 17.3 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | -0.3 | 1.5 | 0.0 | 2.1 | 0.1 | 9.4 | 4.3 | 17.0 | 20.8 | 34.6 | 26.1 | 36.0 |

Table B6 (continued). Stalk lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 12 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 NDL XNDSHLC(M-FS)C5 | Cross | 0.6 | 0.2 | 8.5 | -0.1 | 0.1 | 17.1 | 3.8 | 11.0 | 16.1 | 22.5 | 24.3 | 17.2 |
| 122 NDL X NDSAB(MER-FS)C 15 | Cross | 3.7 | -0.3 | 0.0 | 0.0 | 0.0 | 8.0 | 3.4 | 25.1 | 13.0 | 29.8 | 20.3 | 29.6 |
| 123 NDCG(FS)C1XNDBS22(R-T1)C9 | Cross | 0.4 | 0.1 | 0.0 | -0.1 | 0.2 | 6.9 | 1.5 | 12.3 | 17.1 | 17.3 | 18.0 | 12.1 |
| 124 NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 2.1 | 6.8 | 2.3 | 0.2 | 0.1 | 18.8 | 5.6 | 18.3 | 20.4 | 60.4 | 40.8 | 23.8 |
| 125 CGSS $21(\mathrm{~S}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGSS}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 0.2 | 3.9 | 0.0 | 0.1 | 0.1 | 16.6 | -0.5 | 25.9 | 19.5 | 28.6 | 25.5 | 35.4 |
| 126 NDCG(FS)C1XNDBS21(R-T)C9 | Cross | 0.2 | 3.2 | 0.0 | -0.2 | 0.3 | 13.7 | 0.8 | 2.9 | 27.3 | 10.2 | 31.2 | 18.7 |
| 127 NDBS22(R-T1)C9 X NDBS 21 (R-T)C9 | Cross | 0.4 | 0.1 | 5.3 | 5.1 | 0.1 | 3.5 | 0.0 | 9.0 | 31.2 | 9.6 | 13.5 | 16.8 |
| 128 Leaming(S-FS)C6 XEARLYGEM 21 b | Cross | 0.2 | 2.8 | 2.0 | 2.4 | 1.8 | 14.1 | 4.8 | 18.0 | 29.7 | 30.7 | 31.2 | 36.7 |
| 129 NDBS 1011 XNDSM(M-FS)C9 | Cross | 0.3 | 0.0 | 0.0 | 0.1 | 1.5 | 8.4 | 3.8 | 6.5 | 21.2 | 41.0 | 21.6 | 18.6 |
| 130 NDLXEARLYGEM 21 c | Cross | 0.0 | 7.3 | 0.0 | 3.1 | 0.1 | 11.9 | 7.5 | 43.9 | 26.4 | 21.3 | 24.6 | 35.4 |
| 131 NDL XNDSCD(FS-CS)C2 | Cross | 0.4 | 0.0 | 2.1 | 3.8 | 3.0 | 17.0 | 9.8 | 29.3 | 41.2 | 48.8 | 32.5 | 29.5 |
| 132 EARLYGEM 21 a | P arent | 2.4 | 2.9 | 0.0 | -0.2 | 0.1 | 13.3 | 14.2 | 50.2 | 49.3 | 40.4 | 61.6 | 17.6 |
| 133 NDCG(FS)C1XNDBSK(HI-M)C3 | Cross | 0.2 | 0.1 | 0.0 | -0.2 | 0.1 | 10.6 | 4.0 | 13.0 | 29.5 | 31.7 | 36.4 | 16.7 |
| 134 NDSCD(FS-CS)C2 XEARLYGEM 21 c | Cross | 2.5 | -0.3 | 0.0 | -0.1 | 1.5 | 28.8 | 25.0 | 31.9 | 42.4 | 66.7 | 57.3 | 31.9 |
| 135 NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 0.0 | 0.0 | 0.0 | -0.2 | 0.2 | 17.2 | 5.1 | 32.7 | 25.2 | 30.7 | 41.4 | 21.9 |
| 136 NDSAB(MER-FS)C 15 XNDSCD(FS-CS)C2 | Cross | 3.1 | 4.0 | 0.0 | 0.1 | 0.1 | 28.9 | 8.6 | 21.8 | 18.8 | 43.1 | 33.9 | 15.0 |
| 137 NDSM(M-FS)C9 X EARLYGEM 21 c | Cross | -0.2 | 4.3 | 0.0 | 4.0 | 2.7 | 20.5 | 24.1 | 16.3 | 38.4 | 44.2 | 53.0 | 37.1 |
| 138 Leaming(S-FS)C6 X EARLYGEM 2 a | Cross | -0.2 | 11.2 | 1.9 | -0.3 | 0.3 | 22.1 | 7.6 | 32.5 | 24.3 | 20.3 | 20.8 | 35.3 |
| 139 NDSS XNDCG(FS)C1 | Cross | 4.6 | 0.1 | 5.6 | 0.0 | 0.0 | 22.0 | 6.8 | 14.9 | 15.6 | 26.5 | 20.8 | 9.9 |
| 140 NDSM(M-FS)C9 X NDSCD(FS-CS)C2 | Cross | -0.2 | 0.0 | 0.0 | -0.3 | 0.1 | 18.9 | 8.2 | 12.1 | 44.6 | 61.8 | 51.7 | 23.9 |
| 141 NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | -0.1 | 2.0 | 2.0 | 0.0 | 0.1 | 20.6 | 18.7 | 23.1 | 26.4 | 37.9 | 23.8 | 23.4 |
| 142 NDCG(FS)C1XNDBS 1011 | Cross | -0.4 | 2.3 | 0.0 | 0.0 | 0.1 | 14.3 | 6.4 | 14.7 | 22.5 | 27.2 | 20.6 | 10.8 |
| 143 NDBS 1011 X EARLYGEM 21 a | Cross | 3.8 | 0.0 | 0.0 | 0.1 | 0.0 | 8.1 | 4.6 | 21.6 | 32.7 | 35.1 | 27.7 | 39.3 |
| 144 NDSHLC(M-FS)C5 | P arent | -0.3 | 2.5 | 0.0 | -0.3 | 0.1 | 8.6 | 3.5 | 9.3 | 31.6 | 25.5 | 22.8 | 10.6 |
| Experiment mean |  | 0.8 | 1.5 | 1.0 | 0.8 | 0.8 | 14.6 | 7.7 | 20.0 | 24.4 | 32.5 | 34.1 | 23.5 |
| Mean of parental populations |  | 1.3 | 2.8 | 1.4 | 0.7 | 0.7 | 17.6 | 10.3 | 21.6 | 28.8 | 34.6 | 38.2 | 21.8 |
| Mean of population crosses |  | 0.8 | 1.4 | 1.0 | 0.7 | 0.8 | 14.6 | 7.7 | 20.2 | 24.4 | 32.9 | 34.0 | 24.1 |
| Mean of checks |  | 0.0 | 0.6 | 0.3 | 1.3 | 0.2 | 8.2 | 2.5 | 13.4 | 16.3 | 22.7 | 26.8 | 19.2 |
| LSD (0.05) |  | 4.9 | 6.7 | 5.1 | 4.7 | 4.1 | 14.7 | 11.1 | 20.1 | 26.4 | 20.1 | 22.4 | 20.6 |
| CV |  | 301.3 | 220.7 | 261.5 | 309.1 | 272.1 | 50.7 | 72.5 | 50.9 | 54.6 | 31.2 | 33.2 | 44.2 |
| MSE |  | 6.0 | 11.3 | 6.6 | 5.5 | 4.4 | 54.8 | 31.3 | 103.4 | 177.4 | 102.9 | 128.1 | 108.4 |

Table B7. Root lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

|  | Entry | Pedigree | Type |  | 2010 |  |  | 20 |  |  |  | 201 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
|  |  | Leaming(S-FS)C6 X EARLYGEM 21 c | Cross | 10.0 | 0.0 | -0.1 | 0.6 | 22.8 | -0.3 | 31.9 | 1.2 | 0.0 | 1.5 | 49.3 |
|  | 2 | Leaming(S-FS)C6 X NDSAB (MER-FS)C 15 | Cross | 3.8 | 0.0 | 0.0 | 0.4 | 13.6 | 0.0 | 31.7 | -0.2 | 0.0 | 2.2 | 51.5 |
|  | 3 | NDBSK(HIM) C3 X NDSM(M-FS)C9 | Cross | 0.0 | 0.0 | 0.0 | 0.6 | 11.0 | 0.1 | 42.3 | 2.4 | 0.0 | 1.0 | 66.2 |
|  | 4 | B S 21 AB (R-FR) C 1 X NDS AB $21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 4.5 | 2.0 | -0.1 | 5.6 | 2.4 | 0.0 | 52.5 | 3.5 | 2.6 | 7.3 | 59.7 |
|  | 5 | EARLYGEM 2 la XEARLYGEM 21 lb | Cross | 7.7 | 0.0 | 0.0 | 0.5 | 30.5 | 1.2 | 81.3 | 3.5 | 0.0 | 12.1 | 72.6 |
|  | 6 | NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 0.0 | 0.0 | 0.0 | 0.4 | 19.6 | 0.1 | 37.6 | 8.2 | 2.6 | 7.2 | 49.7 |
|  | 7 | NDSS XNDL | Cross | 0.0 | 0.0 | 0.0 | 2.0 | 7.8 | 0.0 | 31.6 | 1.5 | 0.0 | 1.5 | 33.9 |
|  | 8 | NDBS K(HI-M)C3 X EARLYGEM 2 lb | Cross | 0.0 | 0.0 | -0.1 | 0.7 | 5.6 | 0.1 | 40.4 | 2.2 | 0.0 | 5.6 | 65.2 |
|  | 9 | NDL XEARLYGEM 2 lb | Cross | 2.5 | 0.0 | 0.0 | 0.5 | 1.6 | 0.0 | 25.8 | 3.8 | 1.5 | 7.5 | 74.0 |
|  | 10 | NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 7.4 | 0.0 | -0.2 | 0.8 | 10.1 | 0.1 | 45.6 | 6.6 | 3.7 | 4.2 | 49.6 |
|  | 11 | NDBS 11(FR-M)C3 | P arent | 2.2 | 0.0 | 0.0 | 0.4 | 13.7 | 0.0 | 32.0 | -0.5 | 4.7 | 0.5 | 48.3 |
|  | 12 | NDBSK(HI-M)C3 X NDSHLC(M-FS)C5 | Cross | 10.8 | 0.0 | 0.0 | 17.7 | 11.2 | 0.0 | 29.4 | 2.7 | 0.0 | 0.2 | 65.1 |
|  | 13 | NDSCD(FS-CS)C2 | P arent | 24.3 | 0.0 | 8.2 | 3.5 | 53.0 | -0.2 | 62.3 | 6.5 | 17.4 | 11.7 | 65.8 |
|  | 14 | NDSHLC(M-FS)C5 XEARLYGEM 21c | Cross | 2.9 | 0.0 | 0.0 | 0.1 | 16.0 | 0.1 | 61.7 | -0.4 | 0.0 | 6.8 | 64.4 |
|  | 15 | NDSS XNDBS22(R-T1)C9 | Cross | 5.9 | 0.0 | 3.9 | 0.3 | 4.3 | 0.1 | 31.6 | -0.8 | 0.0 | 1.3 | 43.6 |
|  | 16 | Check 4 DKC 43-27 VT3 | Check | 3.1 | 0.0 | -0.1 | 6.1 | 1.9 | 0.1 | 1.4 | 0.6 | 0.0 | 1.8 | 4.8 |
|  | 17 | NDSS X NDSHLC(M-FS)C5 | Cross | 6.7 | 0.0 | 0.1 | 0.2 | 34.6 | 0.0 | 60.4 | 4.0 | 5.4 | 3.9 | 58.1 |
|  | 18 | EARLYGEM 21 c | P arent | 12.9 | 0.0 | 8.1 | 0.0 | 28.8 | 0.1 | 52.7 | 4.1 | 0.0 | 7.6 | 81.7 |
|  | 19 | Leaming(S-FS)C6 | P arent | 0.0 | 0.0 | 0.0 | 1.5 | 13.5 | 0.0 | 50.5 | -0.4 | 5.5 | 3.1 | 38.7 |
|  | 20 | NDBS 1011 X NDBS22(R-T1)C9 | Cross | 3.6 | 6.3 | 0.0 | 0.3 | 17.5 | 0.1 | 59.7 | 1.3 | 0.0 | 0.1 | 28.0 |
| N | 21 | Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 4.3 | 0.0 | 0.0 | 0.2 | 19.3 | 0.1 | 63.5 | 1.7 | 0.0 | 3.6 | 58.8 |
| N | 22 | NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 2.4 | 1.8 | -0.2 | 0.5 | 9.9 | 0.1 | 35.0 | 4.9 | 0.0 | 5.1 | 28.6 |
|  | 23 | Check 1P IONEER 39V07 | Check | 0.0 | 3.4 | 0.0 | 0.0 | 2.7 | 3.6 | 11.3 | 0.3 | 0.0 | -0.3 | 33.5 |
|  | 24 | NDCG(FS)C 1 X NDSAB (MER-FS)C 15 | Cross | 7.4 | 0.0 | 0.0 | 0.4 | 13.0 | 0.1 | 52.7 | 5.4 | 0.0 | 13.3 | 32.4 |
|  | 25 | Leaming(S-FS)C6 X NDBS 22(R-T ) C9 | Cross | 2.8 | 4.0 | 2.4 | -0.3 | 43.1 | -0.3 | 54.9 | 2.1 | 0.0 | 0.5 | 40.0 |
|  | 26 | Leaming(S-FS)C6 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 5.6 | 0.0 | 0.1 | -0.4 | 11.2 | 0.0 | 37.8 | 1.0 | 0.0 | 2.9 | 7.4 |
|  | 27 | NDBS K(HI-M)C3 X EARLYGEM 2 la | Cross | 0.0 | 0.0 | 0.2 | 1.9 | 11.3 | 0.1 | 29.8 | 8.7 | 0.0 | 0.2 | 55.1 |
|  | 28 | NDL XLeaming(S-FS)C6 | Cross | 0.0 | 0.0 | 0.0 | -1.5 | 18.0 | 0.0 | 55.0 | 3.0 | 0.0 | 3.6 | 21.9 |
|  | 29 | EARLYGEM 2 a X XARLYGEM 21 c | Cross | 10.8 | 0.0 | 0.2 | 4.0 | 21.2 | -0.1 | 42.9 | -0.6 | 6.4 | 6.1 | 80.3 |
|  | 30 | NDCG(FS)C1X EARLYGEM 21 b | Cross | 6.1 | 0.0 | 0.2 | 2.3 | 24.3 | 0.1 | 46.4 | -0.6 | 0.0 | 11.0 | 41.7 |
|  |  | Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 27.2 | 0.0 | 0.1 | 2.8 | 22.4 | 1.3 | 61.1 | 1.0 | 4.5 | 8.4 | 36.5 |
|  | 32 | NDBSK(HI-M)C3 X EARLYGEM 21 c | Cross | 4.0 | 0.0 | 0.1 | -0.2 | 5.5 | 0.1 | 28.4 | 6.9 | 1.4 | 2.8 | 16.3 |
|  | 33 | NDBS 1011 X EARLYGEM 2 lb | Cross | 25.6 | 4.9 | 0.1 | -0.4 | 13.0 | 0.0 | 27.2 | 16.9 | 0.0 | 8.2 | 37.5 |
|  | 34 | NDSCD(FS-CS)C2 XEARLYGEM 21 a | Cross | 37.8 | 0.0 | 8.8 | 8.2 | 51.5 | 0.1 | 60.6 | 8.4 | 11.8 | 0.7 | 42.5 |
|  | 35 | NDSS XEARLYGEM 21 b | Cross | 4.2 | 0.0 | 0.1 | 4.5 | 19.8 | 0.0 | 22.3 | 3.4 | 9.1 | 2.6 | 36.4 |
|  | 36 | NDSAB(MER-FS)C 15 X NDSHLC(M-FS)C5 | Cross | 13.0 | 0.0 | 0.2 | 1.1 | 17.8 | 0.0 | 37.1 | 11.8 | 0.0 | 3.7 | 49.8 |
|  | 37 | NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 2.9 | 0.0 | -0.1 | 0.3 | 26.9 | -0.3 | 42.1 | 2.4 | 0.0 | 3.7 | 45.7 |
|  | 38 | NDCG(FS)C1XEARLYGEM 21 l | Cross | 0.0 | 0.0 | 2.8 | 4.1 | 16.3 | 0.0 | 51.0 | 8.1 | 1.3 | 0.4 | 40.3 |
|  | 39 | EARLYGEM 2 lb XEARLYGEM 2 lc | Cross | 6.7 | 0.0 | 0.1 | 0.3 | 25.2 | 0.1 | 52.2 | -2.1 | 6.1 | 0.3 | 49.9 |
|  | 40 | NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 6.5 | 0.0 | -0.1 | -1.0 | 15.2 | 0.0 | 36.6 | 2.7 | 0.0 | 5.3 | 43.0 |

Table B7 (continued). Root lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 2.5 | 12.4 | 0.1 | 0.2 | 5.1 | -0.1 | 37.2 | 0.5 | 0.0 | 1.5 | 31.1 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 8.3 | 0.0 | 0.1 | 2.4 | 33.8 | 1.5 | 45.4 | 4.2 | 3.4 | 2.0 | 59.8 |
| $43 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{Tl}) \mathrm{C} 9$ | Cross | 0.0 | 0.0 | 0.0 | 0.2 | 20.3 | 0.0 | 38.3 | 0.9 | 0.0 | 0.7 | 24.5 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 0.0 | 4.6 | 0.0 | 0.4 | 5.2 | 0.0 | 69.0 | 4.0 | 0.0 | 1.5 | 43.9 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 3.1 | 0.0 | 0.0 | 1.7 | 10.8 | 1.3 | 59.9 | 5.0 | 3.1 | 10.0 | 48.4 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 3.1 | 0.0 | -0.2 | 0.5 | 26.0 | 0.0 | 29.6 | -0.2 | 1.4 | 2.1 | 16.0 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 3.3 | 0.0 | 0.0 | 4.2 | 21.7 | 0.0 | 61.7 | 20.4 | 0.0 | 8.7 | 33.2 |
| 48 NDBS 11(FR-M)C3 XNDSAB (MER-FS)C 15 | Cross | 0.0 | 0.0 | 0.1 | 0.6 | 7.1 | 1.2 | 34.2 | -1.0 | 1.4 | -0.5 | 43.1 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 0.0 | 0.0 | -0.1 | 0.1 | 18.0 | 1.3 | 54.8 | 0.4 | 0.0 | 2.1 | 47.1 |
| 50 NDBS 22(R-T1)C9 X EARLYGEM 21 la | Cross | 0.0 | 0.0 | 0.0 | -0.1 | 7.7 | -0.1 | 27.8 | 4.8 | 0.0 | 11.0 | 32.2 |
| 51 NDBS 22 (R-T1)C9 | P arent | 4.2 | 0.0 | 0.1 | 0.1 | 7.9 | 0.0 | 26.2 | 18.4 | 0.0 | 3.0 | 55.0 |
| 52 NDSS XNDBS 1011 | Cross | 2.0 | 0.0 | -0.1 | -1.2 | 18.4 | 0.0 | 31.6 | 15.4 | 0.0 | 11.9 | 53.0 |
| 53 NDL | P arent | 3.0 | 0.0 | 0.1 | 0.0 | 5.9 | 1.1 | 28.6 | 1.5 | 0.0 | -0.1 | 52.1 |
| 54 NDBS 1011 XLeaming (S-FS) C6 | Cross | 9.4 | 0.0 | 0.1 | -0.2 | 19.0 | 1.4 | 47.3 | 3.4 | 0.0 | 0.7 | 42.8 |
| 55 NDBSK(H)M C C 3 X NDBS 1011 | Cross | 0.0 | 0.0 | 0.0 | 0.0 | 18.6 | -0.1 | 47.0 | -0.7 | 2.6 | 3.4 | 43.8 |
| 56 NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 2.2 | 0.0 | 0.0 | 0.1 | 3.5 | 0.0 | 27.2 | 8.1 | 0.0 | 2.4 | 23.2 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-T1)C9 | Cross | 0.0 | 0.0 | 0.0 | 1.4 | 0.9 | 0.0 | 39.5 | 7.6 | 2.8 | 1.7 | 33.9 |
| 58 EARLYGEM 2 lb | P arent | 21.9 | 0.0 | 3.4 | 0.2 | 34.6 | 1.3 | 52.1 | -0.5 | 0.0 | 4.5 | 83.6 |
| 59 NDSAB(MER-FS)C15 X NDSM(M-FS)C9 | Cross | 0.0 | 0.0 | 0.0 | -0.2 | 21.5 | -0.1 | 54.1 | 5.5 | 0.0 | 5.0 | 55.9 |
| 60 Check 2 DKC 36-34 VT3 | Check | 0.0 | 0.0 | 0.1 | -1.1 | 0.3 | 0.0 | 16.6 | 0.0 | 0.0 | -0.7 | 16.9 |
| 61 NDBSK(HI-M)C3 XNDSCD(FS-CS)C2 | Cross | 4.2 | 0.0 | -0.1 | 0.2 | 26.6 | 8.7 | 29.3 | 0.9 | 3.3 | 8.5 | 51.1 |
| 62 NDBS22(R-T1)C9 X EARLYGEM 21 c | Cross | 0.0 | 0.0 | 0.0 | 0.0 | 14.5 | 0.1 | 29.5 | 7.6 | 4.3 | 3.4 | 35.1 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 23.7 | 0.0 | 0.1 | 0.2 | 21.0 | 0.2 | 20.8 | 0.7 | 5.4 | 1.5 | 33.9 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 10.0 | 0.0 | -0.1 | -1.1 | 11.6 | 0.1 | 42.7 | 17.9 | 1.7 | 7.9 | 46.9 |
| $65 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 0.0 | 0.0 | 0.1 | 1.6 | 7.3 | 0.0 | 21.9 | 3.4 | 0.0 | 0.2 | 53.2 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 2.3 | 0.0 | 0.1 | 0.0 | 13.9 | 2.9 | 44.0 | 0.3 | 0.0 | 3.9 | 29.8 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 7.7 | 0.0 | 0.0 | 0.2 | 12.5 | 0.1 | 46.6 | 1.7 | 0.0 | 9.0 | 26.3 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 2.3 | 0.0 | 0.0 | 0.3 | 1.6 | 0.1 | 27.0 | 2.2 | 0.0 | 0.3 | 12.0 |
| $69 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDBS} 11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ | Cross | 2.2 | 0.0 | 0.0 | 1.5 | 5.0 | 0.1 | 53.1 | 3.7 | 0.0 | 2.1 | 66.7 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 2.3 | 0.0 | 3.2 | 0.4 | 7.5 | 0.2 | 33.8 | 6.7 | 2.8 | 0.9 | 38.3 |
| 71 NDBSK(HIM) C3 | P arent | 0.0 | 0.0 | 0.0 | 0.0 | 8.4 | 0.1 | 34.0 | 0.5 | 2.9 | -0.1 | 35.8 |
| 72 NDSS X NDBS 21 (R-T) C9 | Cross | 6.0 | 0.0 | 0.1 | 3.3 | 24.0 | 0.1 | 30.2 | 0.5 | 0.0 | 3.7 | 48.9 |
| 73 NDSS XEARLYGEM 21 c | Cross | 5.3 | 4.8 | -0.2 | 1.5 | 10.6 | -0.3 | 51.1 | 0.5 | 0.0 | 3.9 | 66.5 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 5.9 | 0.0 | 3.1 | 1.3 | 6.9 | 0.0 | 32.6 | 7.9 | 0.0 | -0.5 | 45.3 |
| 75 NDCG(FS)C1 | P arent | 13.9 | 0.0 | 0.0 | 0.0 | 9.7 | 0.0 | 37.9 | 4.3 | 12.4 | 4.9 | 54.8 |
| 76 NDSAB(MER-FS)C 15 | P arent | 2.9 | 0.0 | -0.1 | -1.2 | 31.4 | 1.3 | 59.0 | 3.5 | 2.8 | 8.8 | 70.0 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 6.8 | 0.0 | 0.0 | 5.5 | 17.6 | -0.1 | 47.4 | 15.7 | 3.9 | 11.9 | 69.8 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 4.7 | 0.0 | 0.0 | 2.1 | 9.0 | 0.0 | 5.1 | 3.0 | 1.1 | 3.0 | 25.4 |
| 79 NDSAB (MER-FS)C 15 X EARLYGEM 21 a | Cross | 0.0 | 0.0 | 0.0 | 1.5 | 17.3 | -0.1 | 56.6 | 2.7 | 1.5 | 14.0 | 72.4 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 a | Cross | 2.5 | 0.0 | 2.8 | 2.4 | 3.6 | 0.0 | 29.6 | 4.6 | 0.0 | 2.2 | 26.8 |

Table B7 (continued). Root lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

|  | Entry Pedigree | Type |  | 2010 |  |  | 201 | 11 |  |  | 20 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
|  | 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 6.3 | 0.0 | 0.0 | 1.5 | 4.6 | 0.0 | 38.3 | 4.4 | 0.0 | -0.4 | 47.4 |
|  | 82 NDBSK(HI-M)C3 X Leaming(S-FS)C6 | Cross | 6.5 | 3.3 | -0.2 | 3.0 | 11.4 | 0.0 | 41.7 | 5.3 | 4.5 | 1.3 | 39.6 |
|  | 83 NDL X NDBS 21 (R-T)C9 | Cross | 0.0 | 0.0 | 0.0 | -0.2 | 10.8 | 1.3 | 26.7 | 0.2 | 0.0 | -1.1 | 19.9 |
|  | 84 NDSM(M-FS)C9 | Parent | 3.8 | 0.0 | 2.1 | -1.1 | 24.1 | 0.0 | 45.5 | 0.5 | 2.7 | 7.3 | 57.8 |
|  | 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 2.6 | 0.0 | -0.2 | 0.2 | 2.7 | -0.3 | 48.1 | 4.7 | 1.6 | 6.3 |  |
|  | 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 3.6 | 0.0 | 0.0 | 0.0 | 11.4 | 0.0 | 47.9 | 8.5 | 1.6 | 0.1 | 75.3 |
|  | 87 NDCG(FS)C1 ${ }^{\text {N }}$ NDBS 11(FR-M)C3 | Cross | 2.9 | 0.0 | 0.0 | 0.2 | 11.2 | 0.1 | 29.1 | -1.1 | 0.0 | 3.0 | 30.2 |
|  | 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 0.0 | 0.0 | -0.2 | -1.1 | 20.2 | 0.0 | 41.3 | 5.0 | 4.1 | 6.1 | 47.8 |
|  | 89 NDBS 1011 | P arent | 3.1 | 0.0 | 2.8 | 0.1 | 16.8 | 1.1 | 40.0 | 1.4 | 3.6 | -0.1 | 20.8 |
|  | 90 NDBS 1011 XNDS AB(MER-FS)C 15 | Cross | 0.0 | 0.0 | 0.0 | 3.1 | 26.2 | 3.3 | 39.3 | 4.0 | 0.0 | 0.6 | 40.8 |
|  | 91 Check 3 P IONEER 39N99 | Check | 0.0 | 0.0 | 0.0 | 0.2 | 4.3 | 0.0 | 27.6 | -0.7 | 0.0 | 1.8 | 39.1 |
|  | 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 2.5 | 0.0 | -0.1 | 0.3 | 5.9 | 2.4 | 25.6 | 4.3 | 2.9 | 0.0 | 71.0 |
|  | 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 3.3 | 0.0 | 0.0 | 0.1 | 6.9 | 0.0 | 50.2 | 9.1 | 0.0 | 9.0 | 30.6 |
|  | 94 NDL XNDBS 1011 | Cross | 1.4 | 0.0 | -0.2 | 0.4 | 16.9 | 0.1 | 34.4 | -0.5 | 0.0 | 8.1 | 45.4 |
|  | 95 NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 0.0 | 0.0 | 0.0 | 0.0 | 33.3 | 0.0 | 28.1 | 5.2 | 20.5 | -0.4 | 38.0 |
|  | 96 NDL XNDSM(M-FS)C9 | Cross | 3.6 | 0.0 | 0.0 | 0.2 | 15.8 | 0.0 | 41.3 | 0.0 | 0.0 | 8.7 | 57.5 |
|  | 97 NDSS | Parent | 11.5 | 0.0 | -0.1 | 5.7 | 29.9 | -0.3 | 40.4 | 5.0 | 12.2 | -1.2 | 72.1 |
|  | 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 4.2 | 0.0 | 0.0 | 0.2 | 17.6 | 0.0 | 37.6 | 20.4 | 1.5 | -0.1 | 25.5 |
|  | 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 7.7 | 0.0 | 0.0 | 3.3 | 24.4 | 0.1 | 32.9 | 3.7 | 4.1 | 3.9 | 53.0 |
|  | 100 NDL X NDBSK(HI-M)C3 | Cross | 4.2 | 0.0 | -0.1 | -0.9 | 8.6 | 0.0 | 14.5 | 6.8 | 0.0 | 3.3 | 18.7 |
| N | 101 NDBS22(R-T 1)C9 X EARLYGEM 2 lb | Cross | 2.9 | 0.0 | 0.0 | 0.3 | 23.2 | -0.1 | 51.4 | 7.3 | 1.6 | 9.9 | 44.1 |
| ค | 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 0.0 | 0.0 | 0.0 | 0.2 | 8.2 | 0.1 | 46.4 | 1.1 | 0.0 | 6.3 | 35.6 |
|  | 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 10.6 | 0.0 | 0.0 | 0.3 | 26.9 | 0.0 | 46.8 | 8.7 | 6.8 | 3.1 | 29.4 |
|  | 104 NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ X EARLYGEM 21 c | Cross | 8.3 | 0.0 | -0.1 | 0.5 | 10.3 | 0.0 | 29.5 | 0.7 | 0.0 | 3.7 | 28.9 |
|  | $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 10.2 | 0.0 | 0.0 | 0.3 | 9.8 | 0.0 | 25.5 | 6.6 | 0.0 | 1.9 | 33.8 |
|  | 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 7.7 | 0.0 | -0.2 | 0.6 | 28.2 | 0.0 | 57.9 | 0.8 | 0.0 | 5.9 | 41.9 |
|  | 107 NDBS 11(FR-M)C3 X EARLYGEM 21 l | Cross | 0.0 | 0.0 | 0.0 | 0.1 | 2.8 | 0.0 | 27.4 | 1.3 | 0.0 | -0.7 | 35.0 |
|  | 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 2.4 | 0.0 | 0.0 | 19.3 | 19.6 | 0.0 | 29.6 | 3.8 | 0.0 | -0.9 | 25.3 |
|  | 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 5.0 | 0.0 | -0.1 | 0.2 | 21.5 | 12.4 | 31.7 | 1.9 | 5.8 | 6.1 | 67.4 |
|  | 110 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 11.7 | 0.0 | 0.0 | 1.8 | 17.8 | 0.2 | 33.9 | 3.5 | 0.0 | 2.9 | 36.4 |
|  | 111 NDSCD(FS-CS)C2 XEARLYGEM 21 b | Cross | 0.0 | 0.0 | 0.1 | 0.2 | 53.0 | 0.3 | 51.3 | 9.9 | 6.5 | 3.3 | 66.3 |
|  | 112 NDSS XEARLYGEM 2 la | Cross | 0.0 | 0.0 | -0.1 | 6.3 | 12.9 | 0.2 | 18.4 | 6.7 | 6.8 | 3.9 | 41.8 |
|  | 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 10.3 | 0.0 | 0.1 | 0.1 | 24.3 | 1.4 | 72.4 | 1.4 | 0.0 | 2.9 | 55.3 |
|  | 114 NDCG(FS)C1XNDL | Cross | 0.0 | 0.0 | 0.1 | 0.0 | 10.8 | 0.3 | 30.2 | 1.3 | 2.9 | 0.9 | 29.6 |
|  | 115 NDLXEARLYGEM 21a | Cross | 4.2 | 0.0 | 0.0 | 0.2 | 10.1 | 0.2 | 31.0 | 5.2 | 0.0 | 0.7 | 40.9 |
|  | 116 NDSM(M-FS)C9 X EARLYGEM 2 lb | Cross | 7.8 | 0.0 | 2.6 | 1.8 | 36.3 | 0.2 | 56.5 | 6.3 | 7.4 | 0.3 | 69.5 |
|  | 117 NDBS 11(FR-M)C3 X NDBS21(R-T)C9 | Cross | 6.8 | 0.0 | 0.0 | 0.1 | 6.7 | 0.2 | 3.2 | 2.9 | 0.0 | 0.6 | 41.8 |
|  | 118 NDBS 1011 XEARLYGEM 21 c | Cross | 0.0 | 0.0 | -0.2 | 0.4 | 17.6 | 0.2 | 33.2 | 1.1 | 0.0 | 3.2 | 35.4 |
|  | 119 NDBS 11(FR-M)C3 XEARLYGEM 21 b | Cross | 3.1 | 1.5 | 0.0 | 0.0 | 20.8 | 0.2 | 28.2 | 3.6 | 1.4 | 3.7 | 48.8 |
|  | 120 NDBS 11(FR-M)C3 X Leaming(S-FS)C6 | Cross | 3.8 | 1.6 | 0.1 | -0.9 | 7.3 | 0.2 | 43.9 | 6.4 | 9.0 | 4.5 | 30.3 |

Table B7 (continued). Root lodging (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B8. Dropped ears (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.


Table B8 (continued). Dropped ears (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.


Table B8 (continued). Dropped ears (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry Pedigree |  | Type | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 | NDBS 11(FR-M)C3 X NDSM(M-FS)C9 |  | Cross | -0.1 | 2.6 | 0.1 | 4.6 | 0.0 | 0.0 | 9.0 | 2.4 |
| 82 | NDBSK(HIM)C3 X Leaming(S-FS)C6 | Cross | 0.0 | 2.7 | 3.7 | 10.5 | 1.9 | 1.5 | 3.7 | 3.0 |
| 83 | NDL X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | -0.5 | 2.4 | 1.2 | 6.3 | 0.0 | 0.0 | 5.4 | 0.7 |
| 84 | NDSM(M-FS)C9 | Parent | 0.0 | 6.5 | 0.0 | 4.3 | 0.0 | 0.0 | 5.6 | 0.4 |
| 85 | NDSS XNDSAB(MER-FS)C 15 | Cross | 0.2 | 0.0 | 1.2 | 4.7 | 2.7 | 1.4 | 11.2 |  |
| 86 | Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 0.0 | 4.1 | 0.1 | 6.5 | 0.0 | 0.0 | 5.0 | -0.2 |
| 87 | NDCG(FS)C1XNDBS 11(FR-M)C3 | Cross | 0.1 | 0.0 | 0.0 | 11.8 | 2.9 | 2.6 | 2.6 | -0.1 |
| 88 | NDSHLC(M-FS)C5 XEARLYGEM 2 la | Cross | 0.2 | 0.0 | 1.3 | 8.9 | 0.0 | 1.6 | 2.1 | 1.6 |
| 89 | NDBS 1011 | Parent | 0.0 | 1.3 | -0.1 | -1.2 | 0.0 | 0.0 | 2.6 | 4.1 |
| 90 | NDBS 1011 X NDSAB(MER-FS)C 15 | Cross | 0.2 | 11.8 | -0.1 | -0.1 | 9.5 | 2.9 | 6.9 | 2.8 |
| 91 | Check 3 P IONEER 39N99 | Check | 0.2 | 1.3 | -0.1 | 13.2 | 0.0 | 0.0 | 2.8 | 1.2 |
| 92 | NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 0.1 | 2.6 | -0.2 | 6.9 | 0.0 | 0.0 | 5.0 | 0.2 |
| 93 | B S22LEAM (R-FR)C 1 X LEAM ${ }^{\text {a }}$ ( 22 (S-FR)C1 | Check | 1.6 | 1.3 | 4.8 | 13.9 | 1.7 | 2.9 | 0.5 | -0.6 |
| 94 | NDL X NDBS 1011 | Cross | 0.2 | 2.4 | -0.2 | 9.8 | 0.0 | 1.4 | 4.5 | -0.2 |
| 95 | NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 5.1 | 4.0 | 1.4 | 22.9 | 0.0 | 0.0 | 6.4 | 0.4 |
| 96 | NDL XNDSM(M-FS)C9 | Cross | 0.1 | 0.0 | 0.0 | -0.7 | 0.0 | 0.0 | 3.2 | 0.0 |
| 97 | NDSS | Parent | 0.2 | 0.0 | 2.5 | 4.4 | 0.0 | 1.4 | 4.5 | 0.2 |
| 98 | NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 0.1 | 3.4 | 1.7 | 7.7 | 1.7 | 0.0 | 2.3 | 2.9 |
| 99 | NDCG(FS)C 1 X NDSHLC(M-FS)C5 | Cross | 0.2 | 5.1 | 0.2 | 2.9 | 0.0 | 2.8 | 2.1 | 0.2 |
| 100 | NDL X NDBSK(HI-M)C3 | Cross | 0.2 | 2.5 | 0.2 | 0.9 | 1.6 | 0.0 | 6.3 | 1.6 |
| 101 | NDBS22(R-T1)C9 XEARLYGEM 2 lb | Cross | 1.6 | 1.2 | 0.1 | 5.4 | 0.0 | 0.0 | 4.0 | 2.0 |
| 102 | NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 0.2 | 0.0 | 0.1 | 15.6 | 0.0 | 1.4 | 3.5 | 3.5 |
| 103 | NDSHLC(M-FS)C5 XEARLYGEM 2 lb | Cross | 0.2 | 2.6 | 0.1 | 1.1 | 1.5 | 1.2 | 2.3 | 1.6 |
| 104 | NDBS 21 (R-T)C9 XEARLYGEM 21 c | Cross | 0.1 | 3.8 | 1.2 | 0.3 | 0.0 | 1.4 | 1.4 | 1.7 |
| 105 | CGL(S-FR2)C1XBS $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 0.1 | 0.0 | 1.4 | 5.9 | 0.0 | 0.0 | 3.2 | 2.4 |
| 106 | NDSAB(MER-FS)C 15 XEARLYGEM 21 c | Cross | 0.2 | 1.3 | 0.0 | 0.9 | 0.0 | 0.0 | 2.9 | 3.9 |
| 107 | NDBS 11(FR-M)C3 X EAR LYGEM 2 la | Cross | 1.1 | 6.8 | 0.2 | 0.8 | 0.0 | 0.0 | 3.1 | 1.9 |
| 108 | NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 0.2 | 5.4 | 1.4 | 6.6 | 1.3 | 2.7 | 6.6 | 3.0 |
| 109 | NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 0.2 | 5.3 | -0.2 | 0.0 | 0.0 | 0.0 | 0.6 | -0.4 |
| 110 | NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 0.1 | 0.0 | 2.6 | 0.4 | 0.0 | 0.0 | 4.6 | 0.9 |
| 111 | NDSCD(FS-CS)C2 XEARLYGEM 21 b | Cross | 1.7 | 0.0 | 2.4 | 2.6 | 4.6 | 4.4 | 1.3 | 1.1 |
| 112 | NDSS XEARLYGEM 2 a | Cross | 0.2 | 2.4 | 2.4 | 8.1 | 0.0 | 2.3 | 2.6 | 1.0 |
| 113 | NDCG(FS)C1X EARLYGEM 21 c | Cross | 0.0 | 0.0 | 4.9 | 1.5 | 0.0 | 0.0 | -0.2 | -0.1 |
| 114 | NDCG(FS)C1XNDL | Cross | 0.2 | 4.1 | 1.6 | 11.3 | 0.0 | 1.6 | 8.7 | -0.3 |
| 115 | NDLXEARLYGEM 21 a | Cross | 0.2 | 0.0 | 2.7 | 7.7 | 0.0 | 2.4 | 2.9 | 2.8 |
| 116 | NDSM(M-FS)C9 X EARLYGEM 2 lb | Cross | 0.1 | 0.0 | -0.3 | 2.7 | 0.0 | 0.0 | 2.5 | 1.1 |
| 117 | NDBS $11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ XNDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 1.6 | 0.0 | 0.0 | 5.6 | 2.4 | 1.6 | 0.3 | -0.9 |
| 118 | NDBS 1011 XEARLYGEM 21 c | Cross | 0.2 | 2.5 | -0.2 | 7.2 | 0.0 | 0.0 | 0.7 | 2.4 |
| 119 | NDBS 11(FR-M)C3 XEARLYGEM 2 lb | Cross | 1.3 | 5.0 | -0.1 | 3.0 | 1.3 | 1.4 | 3.0 | 5.0 |
| 120 | NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 0.1 | 3.8 | -0.1 | 14.9 | 0.0 | 4.5 | 5.6 | -0.7 |

Table B8 (continued). Dropped ears (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

|  | Entry Pedigree |  | Type | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
|  |  | NDL X NDSHLC(M-FS)C5 |  | Cross | 0.1 | 3.6 | -0.1 | -0.5 | 0.0 | 2.7 | 3.8 | 4.4 |
|  | 122 N | NDL XNDSAB(MER-FS)C 15 | Cross | 0.0 | 0.0 | 3.8 | 8.0 | 4.5 | 0.0 | 6.8 | 2.5 |
|  | 123 N | NDCG(FS)C1XNDBS22(R-Tl)C9 | Cross | 1.4 | 1.2 | -0.1 | 3.3 | 8.0 | 0.0 | 3.1 | -0.1 |
|  | 124 N | NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 1.8 | 0.0 | -0.1 | 15.9 | 2.6 | 0.0 | 5.2 | 3.5 |
|  | 125 | CGSS21(S-FR)C1XBS21CGSS (R-FR)C1 | Check | -0.1 | 5.3 | 1.0 | 5.0 | 0.0 | 0.0 | 4.1 | 0.2 |
|  | 126 N | NDCG(FS)C1XNDBS21(R-T)C9 | Cross | 0.1 | 8.9 | -0.1 | 16.0 | 0.0 | 1.3 | 2.5 | 2.6 |
|  | 127 N | NDBS 22(R-T1)C9 X NDBS 21 (R-T)C9 | Cross | 1.8 | 0.0 | -0.2 | 1.6 | 1.6 | 0.0 | 3.4 | 1.4 |
|  | 128 L | Leaming(S-FS)C6 XEARLYGEM 21 b | Cross | 0.0 | 6.3 | -0.2 | 7.0 | 0.0 | 0.0 | 2.7 | 1.6 |
|  | 129 N | NDBS $1011 \mathrm{XNDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ | Cross | 0.0 | 0.0 | 3.7 | -0.1 | 0.0 | 1.4 | 2.3 | -0.6 |
|  | 130 N | NDL XEARLYGEM 21 c | Cross | 0.1 | 3.8 | 1.0 | 5.2 | 5.3 | 0.0 | 3.8 | 3.8 |
|  | 131 N | NDL XNDSCD(FS-CS)C2 | Cross | 2.6 | 4.2 | 0.0 | 9.4 | 8.3 | 0.0 | 4.5 | 3.1 |
|  | 132 E | EARLYGEM 21 l | P arent | 0.1 | 0.0 | -0.1 | 5.1 | 0.0 | 0.0 | 2.9 | 0.1 |
|  | 133 N | NDCG(FS)C1X NDBSK(HI-M)C3 | Cross | 0.1 | 2.5 | -0.1 | 4.2 | 1.6 | 0.0 | 7.2 | 1.2 |
|  | 134 N | NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 2.9 | 2.8 | 3.8 | 3.3 | 0.0 | 0.0 | 0.7 | -0.2 |
|  | 135 N | NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 0.1 | 10.5 | 0.0 | 10.6 | 0.0 | 1.4 | 3.2 | -0.2 |
|  | 136 N | NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 0.1 | 7.2 | 1.3 | 8.0 | 3.4 | 2.7 | 4.5 | 1.5 |
|  | 137 N | NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | -0.1 | 1.4 | 0.0 | 4.6 | 3.1 | 0.0 | 1.9 | 2.6 |
|  | 138 L | Leaming(S-FS)C6 XEARLYGEM 2 1a | Cross | 0.1 | 0.0 | 0.0 | 9.0 | 1.4 | 0.0 | 0.8 | 2.6 |
|  | 139 N | NDSS XNDCG(FS)C1 | Cross | 0.1 | 4.1 | -0.1 | 6.4 | 7.1 | 1.2 | 0.6 | 1.2 |
| N | 140 N | NDSM(M-FS)C9 XNDSCD(FS-CS)C2 | Cross | 0.0 | 6.8 | -0.1 | 3.0 | 1.9 | 3.1 | 1.4 | 1.5 |
|  |  | NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | 0.0 | 0.0 | 3.0 | 9.6 | 4.5 | 1.6 | 1.3 | -0.7 |
|  | 142 N | NDCG(FS)C1XNDBS 1011 | Cross | 0.1 | 5.3 | -0.1 | 4.7 | 2.3 | 1.5 | 22.0 | 6.2 |
|  | 143 N | NDBS 1011 XEARLYGEM 21 a | Cross | -0.3 | 2.5 | 2.4 | 3.3 | 0.0 | 0.0 | -0.6 | 0.4 |
|  | 144 N | NDSHLC(M-FS)C5 | P arent | 3.4 | 5.9 | 0.0 | 5.6 | 0.0 | 1.3 | 2.0 | 2.8 |
|  |  | Experiment mean |  | 0.5 | 2.5 | 1.0 | 6.2 | 1.4 | 0.9 | 3.6 | 1.4 |
|  |  | Mean of parental populations |  | 0.4 | 2.2 | 0.8 | 4.6 | 1.0 | 1.0 | 4.2 | 1.2 |
|  |  | Mean of population crosses |  | 0.6 | 2.6 | 1.1 | 6.3 | 1.6 | 0.9 | 3.6 | 1.4 |
|  |  | Mean of checks |  | 0.2 | 1.6 | 0.9 | 7.7 | 0.2 | 0.5 | 2.3 | 1.6 |
|  |  | LSD (0.05) |  | 2.9 | 6.5 | 3.8 | 13.4 | 6.8 | 3.6 | 8.9 | 4.2 |
|  |  | CV |  | 275.3 | 133.6 | 189.0 | 109.6 | 237.0 | 199.5 | 124.6 | 148.9 |
|  |  | MSE |  | 2.2 | 10.8 | 3.6 | 45.6 | 11.7 | 3.3 | 20.0 | 4.4 |

Table B9. Ear height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21c | Cross | 80.5 | 80.8 | 81.9 | 55.4 | 113.8 | 83.6 | 108.8 | 82.3 | 91.1 | 105.0 | 94.5 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C 15 | Cross | 83.8 | 74.9 | 83.6 | 44.4 | 129.5 | 91.5 | 107.2 | 85.4 | 95.3 | 101.3 | 96.5 |
| $3 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ | Cross | 79.8 | 71.9 | 78.9 | 45.2 | 123.5 | 91.2 | 104.7 | 81.5 | 84.2 | 96.8 | 101.8 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 86.8 | 88.1 | 87.7 | 59.8 | 136.8 | 99.6 | 125.0 | 99.8 | 98.6 | 128.5 | 108.8 |
| 5 EARLYGEM 2 la XEARLYGEM 2 lb | Cross | 84.9 | 78.1 | 76.9 | 41.5 | 120.5 | 77.4 | 101.6 | 68.5 | 85.9 | 109.3 | 91.1 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 103.9 | 88.8 | 102.7 | 63.7 | 129.8 | 105.6 | 129.2 | 98.6 | 96.4 | 126.5 | 122.9 |
| 7 NDSS XNDL | Cross | 85.1 | 81.4 | 88.1 | 51.8 | 118.3 | 89.0 | 108.8 | 81.2 | 93.7 | 109.6 | 103.3 |
| 8 NDBSK(HI-M)C3 XEARLYGEM 21 b | Cross | 91.5 | 70.7 | 81.5 | 54.6 | 123.5 | 95.7 | 102.6 | 91.5 | 95.8 | 114.7 | 100.4 |
| 9 NDL XEARLYGEM 2 lb | Cross | 83.3 | 73.8 | 78.0 | 48.9 | 125.3 | 94.5 | 117.0 | 87.5 | 89.9 | 114.6 | 105.3 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 79.0 | 72.4 | 75.5 | 56.7 | 127.8 | 90.8 | 106.3 | 86.3 | 90.2 | 109.0 | 97.8 |
| 11 NDBS 11(FR-M)C3 | Parent | 73.6 | 70.6 | 75.2 | 49.3 | 120.3 | 86.6 | 115.9 | 82.6 | 82.3 | 106.9 | 95.5 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 94.3 | 72.0 | 79.1 | 48.3 | 106.3 | 88.3 | 110.4 | 89.7 | 91.9 | 104.8 | 99.1 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Parent | 91.3 | 102.0 | 99.1 | 65.0 | 145.0 | 100.4 | 122.1 | 101.2 | 103.8 | 138.6 | 126.8 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 86.5 | 71.6 | 71.5 | 51.0 | 122.8 | 88.1 | 104.5 | 85.8 | 88.1 | 113.7 | 97.3 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 83.4 | 82.7 | 81.1 | 52.8 | 123.5 | 91.5 | 112.4 | 88.6 | 88.2 | 110.9 | 100.0 |
| 16 Check 4 DKC 43-27 VT3 | Check | 84.8 | 82.2 | 83.0 | 49.2 | 125.0 | 82.2 | 111.2 | 75.2 | 87.4 | 105.2 | 104.5 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 89.3 | 72.3 | 72.8 | 58.1 | 133.8 | 92.2 | 119.3 | 99.1 | 94.4 | 119.9 | 108.3 |
| 18 EARLYGEM 2 lc | P arent | 71.5 | 65.1 | 70.7 | 44.2 | 115.8 | 79.6 | 99.1 | 75.2 | 83.1 | 105.2 | 92.4 |
| 19 Leaming(S-FS)C6 | P arent | 73.4 | 66.2 | 70.0 | 45.9 | 114.5 | 75.8 | 105.3 | 77.8 | 92.4 | 114.2 | 89.8 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{T} 1) \mathrm{C} 9$ | Cross | 85.3 | 87.8 | 88.4 | 52.1 | 126.8 | 90.9 | 102.3 | 85.1 | 93.3 | 119.6 | 108.5 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 87.6 | 78.4 | 72.8 | 46.7 | 115.8 | 84.8 | 109.0 | 87.9 | 93.4 | 102.0 | 94.5 |
| 22 NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 85.0 | 76.7 | 73.4 | 56.0 | 126.0 | 90.4 | 117.3 | 86.9 | 92.7 | 114.9 | 108.8 |
| 23 Check 1P IONEER 39V07 | Check | 81.2 | 96.9 | 99.9 | 50.6 | 140.8 | 88.1 | 123.6 | 93.8 | 103.5 | 124.3 | 117.8 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 81.0 | 73.8 | 80.2 | 51.4 | 127.5 | 82.8 | 108.6 | 89.0 | 102.2 | 105.4 | 98.8 |
| 25 Leaming(S-FS)C6 X NDBS 22(R-T ) C9 | Cross | 81.1 | 75.8 | 82.2 | 52.3 | 129.0 | 84.5 | 112.3 | 91.1 | 98.9 | 108.0 | 101.0 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T)C9 | Cross | 76.1 | 77.8 | 79.3 | 49.7 | 13.8 | 89.4 | 115.4 | 80.7 | 91.7 | 105.2 | 106.3 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 la | Cross | 74.5 | 72.9 | 84.5 | 53.6 | 120.3 | 86.7 | 112.6 | 92.6 | 92.9 | 115.0 | 102.3 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 78.2 | 73.9 | 83.4 | 52.6 | 131.5 | 87.7 | 114.2 | 89.1 | 92.3 | 112.5 | 98.0 |
| 29 EARLYGEM 21 la XEARLYGEM 21 c | Cross | 75.5 | 65.4 | 73.3 | 44.7 | 114.0 | 80.0 | 97.5 | 67.6 | 82.8 | 108.0 | 96.7 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 82.9 | 75.1 | 84.3 | 51.3 | 115.3 | 89.2 | 108.1 | 85.6 | 87.0 | 110.8 | 98.5 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 104.2 | 92.1 | 106.7 | 57.0 | 128.8 | 93.6 | 122.8 | 99.0 | 99.1 | 118.1 | 102.2 |
| 32 NDBS K(HI-M)C3 X EARLYGEM 21 c | Cross | 79.3 | 71.9 | 75.6 | 48.9 | 123.8 | 84.0 | 98.3 | 83.0 | 90.2 | 103.0 | 99.3 |
| 33 NDBS 1011 X EARLYGEM 2 lb | Cross | 85.4 | 84.7 | 82.5 | 57.3 | 127.5 | 87.3 | 109.2 | 98.1 | 95.1 | 111.3 | 103.0 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 1a | Cross | 113.0 | 89.2 | 104.6 | 60.3 | 128.8 | 100.2 | 111.2 | 106.9 | 94.9 | 121.2 | 118.0 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 86.4 | 84.5 | 96.7 | 49.4 | 128.5 | 84.9 | 113.6 | 82.9 | 90.2 | 110.1 | 104.3 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 89.9 | 67.8 | 82.0 | 59.7 | 116.3 | 91.6 | 110.6 | 98.5 | 91.1 | 120.8 | 111.0 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 96.4 | 82.7 | 101.9 | 64.8 | 133.0 | 96.2 | 132.1 | 94.5 | 100.1 | 124.0 | 116.3 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 81.6 | 79.2 | 87.5 | 50.5 | 130.0 | 82.4 | 112.3 | 83.3 | 89.6 | 102.8 | 94.0 |
| 39 EARLYGEM 2 lb X EARLYGEM 2 lc | Cross | 80.1 | 69.8 | 69.0 | 46.4 | 111.5 | 78.0 | 96.7 | 67.4 | 77.1 | 107.3 | 85.9 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 83.8 | 76.0 | 88.9 | 53.8 | 129.8 | 84.2 | 115.0 | 91.4 | 92.7 | 121.8 | 106.5 |

Table B9 (continued). Ear height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 76.0 | 74.9 | 78.5 | 42.4 | 117.5 | 81.5 | 104.1 | 73.9 | 84.8 | 103.3 | 96.5 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 76.9 | 71.6 | 80.6 | 50.3 | 129.5 | 86.5 | 102.7 | 81.5 | 86.9 | 105.6 | 101.0 |
| 43 NDBSK(HIM)C3 X NDBS 22 (R-T 1)C9 | Cross | 78.9 | 73.2 | 76.9 | 49.5 | 124.5 | 79.9 | 101.1 | 87.3 | 90.8 | 109.3 | 87.3 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 86.9 | 80.6 | 85.0 | 55.0 | 120.5 | 91.0 | 111.1 | 89.9 | 95.6 | 124.0 | 100.0 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 86.3 | 71.0 | 83.5 | 69.3 | 139.3 | 96.1 | 120.3 | 87.2 | 100.3 | 116.6 | 105.5 |
| 46 NDLXNDBS22(R-Tl)C9 | Cross | 82.6 | 65.6 | 79.2 | 56.8 | 132.3 | 86.2 | 115.8 | 85.7 | 93.1 | 111.2 | 112.5 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 89.5 | 81.0 | 91.6 | 63.9 | 130.3 | 110.4 | 125.4 | 98.0 | 102.4 | 120.9 | 114.0 |
| 48 NDBS 11(FR-M)C3 X NDSAB (MER-FS)C 15 | Cross | 80.5 | 70.9 | 80.6 | 46.7 | 122.3 | 88.4 | 107.6 | 79.3 | 88.5 | 116.0 | 97.5 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 85.3 | 78.0 | 88.5 | 51.8 | 133.5 | 86.8 | 112.2 | 80.2 | 88.5 | 116.6 | 96.3 |
| 50 NDBS22(R-T1)C9 X EARLYGEM 21 a | Cross | 77.3 | 68.3 | 75.1 | 51.5 | 127.3 | 82.2 | 108.1 | 84.3 | 87.8 | 107.7 | 98.5 |
| 51 NDBS 22(R-T1)C9 | P arent | 70.1 | 61.3 | 73.7 | 42.6 | 115.8 | 78.1 | 98.8 | 89.9 | 78.7 | 108.7 | 88.3 |
| 52 NDSS XNDBS 1011 | Cross | 88.9 | 85.6 | 93.1 | 61.4 | 119.8 | 95.3 | 117.4 | 94.4 | 92.9 | 116.4 | 101.8 |
| 53 NDL | P arent | 86.3 | 73.6 | 82.3 | 51.9 | 128.5 | 91.6 | 110.7 | 84.9 | 88.9 | 116.2 | 100.5 |
| 54 NDBS 1011 XLeaming (S-FS) C6 | Cross | 83.6 | 75.6 | 96.0 | 51.5 | 134.0 | 87.7 | 109.0 | 88.4 | 95.6 | 113.0 | 100.3 |
| 55 NDBSK(HI-M)C3 X NDBS 1011 | Cross | 80.4 | 71.2 | 90.8 | 55.4 | 127.5 | 89.2 | 114.9 | 92.6 | 99.9 | 115.0 | 102.3 |
| 56 NDSAB(MER-FS)C 15 XNDBS21(R-T)C9 | Cross | 82.1 | 76.9 | 81.7 | 49.4 | 129.5 | 97.1 | 112.4 | 87.6 | 100.0 | 112.2 | 103.3 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-T1)C9 | Cross | 93.8 | 74.7 | 85.1 | 46.8 | 123.0 | 89.2 | 109.9 | 86.6 | 85.4 | 111.0 | 95.3 |
| 58 EARLYGEM 2 lb | P arent | 77.2 | 63.9 | 70.0 | 45.0 | 116.8 | 84.2 | 92.2 | 76.4 | 84.7 | 110.4 | 94.9 |
| 59 NDSAB(MER-FS)C15 X NDSM(M-FS)C9 | Cross | 90.1 | 74.1 | 85.6 | 51.4 | 131.3 | 88.5 | 116.2 | 87.2 | 91.0 | 118.1 | 102.5 |
| 60 Check 2 DKC 36-34 VT3 | Check | 79.3 | 76.3 | 82.9 | 42.4 | 124.5 | 73.9 | 108.0 | 88.5 | 93.2 | 111.9 | 95.3 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 91.0 | 81.5 | 82.0 | 62.6 | 134.0 | 96.0 | 117.3 | 101.5 | 104.0 | 119.6 | 110.5 |
| 62 NDBS22(R-T1)C9 X EARLYGEM 21 c | Cross | 81.0 | 68.4 | 71.7 | 51.8 | 123.8 | 86.4 | 111.2 | 84.4 | 86.0 | 100.6 | 94.5 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 81.7 | 77.9 | 79.3 | 47.2 | 131.8 | 90.5 | 106.9 | 85.0 | 86.2 | 113.7 | 95.8 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 87.1 | 74.9 | 83.8 | 58.3 | 125.0 | 91.7 | 112.8 | 94.8 | 90.4 | 115.7 | 104.0 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T) C 9 | Cross | 84.7 | 66.6 | 78.9 | 50.0 | 122.8 | 91.7 | 117.4 | 96.2 | 93.9 | 95.4 | 100.0 |
| 66 NDBS22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 78.5 | 70.5 | 90.7 | 46.4 | 118.5 | 86.9 | 106.1 | 91.8 | 92.8 | 109.4 | 106.5 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 68.9 | 62.4 | 72.4 | 52.3 | 117.5 | 91.6 | 113.3 | 87.9 | 93.2 | 112.0 | 101.0 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 86.4 | 81.1 | 93.3 | 50.0 | 121.3 | 90.7 | 110.3 | 80.9 | 86.3 | 96.9 | 95.3 |
| $69 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDBS} 11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ | Cross | 89.4 | 73.6 | 75.3 | 53.8 | 126.3 | 85.8 | 110.8 | 94.0 | 78.1 | 108.7 | 93.0 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 87.3 | 77.3 | 78.4 | 57.9 | 134.3 | 92.2 | 119.7 | 89.5 | 88.0 | 109.8 | 109.5 |
| 71 NDBSK(HIM)C3 | P arent | 78.8 | 79.4 | 73.7 | 42.2 | 123.5 | 77.2 | 109.6 | 81.6 | 93.8 | 98.5 | 94.3 |
| 72 NDSS XNDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 68.2 | 77.9 | 81.6 | 53.0 | 122.5 | 85.9 | 125.6 | 93.1 | 94.7 | 118.9 | 98.3 |
| 73 NDSS XEARLYGEM 21 c | Cross | 77.3 | 75.0 | 86.3 | 54.0 | 124.5 | 83.5 | 104.8 | 84.1 | 87.0 | 111.5 | 93.0 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 89.1 | 77.4 | 100.0 | 54.5 | 129.8 | 88.6 | 112.2 | 85.4 | 89.6 | 119.0 | 104.5 |
| 75 NDCG(FS)C1 | P arent | 73.5 | 83.1 | 72.9 | 53.1 | 120.5 | 86.5 | 105.9 | 79.8 | 88.7 | 108.3 | 91.4 |
| 76 NDSAB(MER-FS)C 15 | P arent | 79.4 | 81.9 | 86.1 | 58.2 | 117.3 | 88.7 | 107.8 | 93.1 | 94.1 | 122.5 | 109.2 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 99.7 | 82.2 | 101.7 | 63.8 | 143.5 | 97.5 | 124.4 | 100.5 | 106.7 | 126.5 | 114.3 |
| 78 NDBS 1011 N NDBS 21 (R-T)C9 | Cross | 79.0 | 77.2 | 90.6 | 55.8 | 130.0 | 91.7 | 122.9 | 85.6 | 83.8 | 107.8 | 115.5 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 2 la | Cross | 85.3 | 87.0 | 89.3 | 53.5 | 127.0 | 92.3 | 109.8 | 87.0 | 92.7 | 119.1 | 11.0 |
| 80 NDBS21(R-T)C9 X EARLYGEM 21 a | Cross | 85.3 | 76.8 | 92.2 | 56.2 | 131.0 | 91.0 | 117.3 | 91.8 | 93.5 | 114.2 | 104.8 |

Table B9 (continued). Ear height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 82.8 | 84.6 | 76.3 | 54.0 | 130.5 | 91.8 | 122.5 | 93.8 | 96.4 | 114.8 | 101.8 |
| 82 NDBSK(HI-M)C3 X Leaming(S-FS)C6 | Cross | 80.1 | 75.8 | 79.5 | 53.1 | 125.5 | 91.2 | 99.3 | 82.1 | 98.5 | 105.2 | 98.5 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 78.2 | 76.9 | 82.8 | 56.1 | 124.5 | 89.2 | 117.6 | 86.6 | 97.5 | 104.1 | 97.3 |
| 84 NDSM(M-FS)C9 | P arent | 74.8 | 69.4 | 78.4 | 42.4 | 126.5 | 84.9 | 105.6 | 86.9 | 83.9 | 96.3 | 84.5 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 83.2 | 79.7 | 78.3 | 61.6 | 129.0 | 90.8 | 113.8 | 90.5 | 91.7 | 114.9 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 80.4 | 74.7 | 80.4 | 53.6 | 110.5 | 86.7 | 109.5 | 81.1 | 90.8 | 103.2 | 99.0 |
| 87 NDCG(FS)C1 ${ }^{\text {d }}$ NDBS 11(FR-M)C3 | Cross | 94.5 | 82.8 | 88.8 | 48.4 | 121.5 | 91.3 | 113.9 | 86.4 | 87.5 | 111.4 | 101.5 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 85.1 | 70.4 | 88.5 | 60.8 | 119.0 | 88.8 | 112.2 | 80.5 | 98.9 | 109.9 | 105.0 |
| 89 NDBS 1011 | P arent | 90.8 | 84.1 | 94.1 | 47.5 | 130.8 | 94.6 | 118.3 | 94.9 | 91.9 | 119.4 | 99.3 |
| 90 NDBS 1011 X NDS AB(MER-FS ) C 15 | Cross | 95.1 | 72.8 | 101.3 | 54.3 | 131.5 | 98.0 | 119.4 | 86.5 | 93.6 | 114.7 | 111.8 |
| 91 Check 3 P IONEER 39N99 | Check | 89.4 | 86.5 | 98.0 | 46.5 | 131.5 | 83.7 | 110.0 | 86.4 | 94.7 | 119.2 | 108.3 |
| 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 88.5 | 73.8 | 83.4 | 52.5 | 120.8 | 89.6 | 111.1 | 91.9 | 94.0 | 106.1 | 97.0 |
| 93 BS22LEAM(R-FR)C1XLEAMING22 (S-FR)C1 | Check | 84.7 | 76.6 | 86.2 | 51.1 | 138.3 | 90.9 | 112.8 | 92.2 | 92.4 | 110.0 | 103.8 |
| 94 NDL X NDBS 1011 | Cross | 81.5 | 80.7 | 84.0 | 57.9 | 129.3 | 92.8 | 114.5 | 86.2 | 100.5 | 110.6 | 97.0 |
| 95 NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 84.8 | 70.5 | 74.0 | 52.0 | 126.8 | 86.8 | 115.6 | 83.3 | 97.5 | 102.3 | 100.0 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 79.4 | 79.9 | 87.5 | 47.8 | 127.8 | 90.4 | 102.6 | 84.6 | 91.4 | 105.7 | 100.0 |
| 97 NDSS | P arent | 85.5 | 77.4 | 88.3 | 57.5 | 136.3 | 86.6 | 116.2 | 89.1 | 94.1 | 117.3 | 97.8 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 93.2 | 87.3 | 88.6 | 60.5 | 137.8 | 97.3 | 12.8 | 89.7 | 101.4 | 120.4 | 116.5 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 78.0 | 73.9 | 82.6 | 58.6 | 116.5 | 92.6 | 107.0 | 76.8 | 91.0 | 93.6 | 102.3 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 84.2 | 78.0 | 79.6 | 57.7 | 133.5 | 94.6 | 107.8 | 81.4 | 98.2 | 117.2 | 101.0 |
| 101 NDBS 22(R-T 1)C9 X EARLYGEM 21 b | Cross | 77.9 | 71.2 | 66.9 | 50.6 | 12.0 | 84.4 | 114.9 | 89.6 | 86.5 | 111.4 | 100.3 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 83.5 | 74.0 | 85.8 | 54.6 | 132.5 | 97.8 | 111.3 | 95.1 | 100.6 | 111.9 | 113.5 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 79.5 | 67.8 | 80.3 | 56.6 | 126.5 | 86.0 | 110.9 | 91.8 | 96.7 | 110.4 | 99.8 |
| 104 NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ X EARLYGEM 2 lc | Cross | 80.3 | 79.4 | 87.8 | 49.0 | 124.5 | 94.6 | 114.4 | 86.3 | 99.6 | 113.4 | 102.3 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XB}$ - $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 77.5 | 83.8 | 94.0 | 56.8 | 125.8 | 92.2 | 115.4 | 87.8 | 105.2 | 113.0 | 111.3 |
| 106 NDSAB(MER-FS)C 15 XEARLYGEM 21 c | Cross | 81.3 | 83.4 | 87.8 | 57.3 | 122.8 | 81.3 | 108.9 | 89.4 | 89.8 | 111.3 | 103.0 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | 85.9 | 72.2 | 81.9 | 55.1 | 126.0 | 91.6 | 116.9 | 87.9 | 88.8 | 112.0 | 99.8 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 83.9 | 81.7 | 86.2 | 49.7 | 123.5 | 85.3 | 112.5 | 86.7 | 91.7 | 102.4 | 96.3 |
| 109 NDSM(M-FS)C9 X EARLYGEM 21 a | Cross | 74.8 | 70.3 | 77.6 | 55.3 | 123.0 | 79.7 | 108.1 | 81.1 | 95.3 | 110.9 | 102.8 |
| 110 NDBS 21 (R-T)C9 X EARLYGEM 2 lb | Cross | 81.4 | 75.9 | 88.9 | 53.0 | 126.5 | 87.3 | 110.5 | 85.4 | 83.9 | 110.0 | 103.5 |
| 111 NDSCD(FS-CS)C2 XEARLYGEM 21 b | Cross | 97.0 | 90.7 | 98.8 | 60.1 | 128.8 | 91.2 | 120.9 | 100.5 | 87.8 | 117.7 | 118.0 |
| 112 NDSS XEARLYGEM 2 la | Cross | 88.5 | 83.6 | 88.3 | 61.0 | 127.5 | 90.4 | 112.5 | 88.8 | 86.4 | 112.0 | 98.8 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 87.7 | 77.8 | 85.5 | 52.4 | 116.5 | 93.7 | 113.4 | 63.7 | 94.2 | 108.5 | 98.3 |
| 114 NDCG(FS)C1XNDL | Cross | 91.5 | 81.5 | 89.6 | 49.5 | 132.8 | 91.6 | 107.4 | 84.6 | 94.7 | 110.2 | 99.5 |
| 115 NDLXEARLYGEM 21a | Cross | 76.9 | 76.6 | 76.8 | 52.2 | 127.8 | 83.3 | 115.6 | 88.7 | 97.0 | 117.5 | 99.8 |
| 116 NDSM(M-FS)C9 X EARLYGEM 2 lb | Cross | 91.4 | 78.4 | 85.9 | 41.4 | 125.8 | 82.5 | 107.6 | 79.7 | 89.4 | 103.2 | 98.5 |
| 117 NDBS 11(FR-M)C3 XNDBS 21 (R-T)C9 | Cross | 85.6 | 80.8 | 92.2 | 54.8 | 130.3 | 89.5 | 115.0 | 83.8 | 107.5 | 110.8 | 103.0 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 97.6 | 82.8 | 89.8 | 57.1 | 129.5 | 93.1 | 112.8 | 91.0 | 101.1 | 112.2 | 104.8 |
| 119 NDBS 11(FR-M)C3 XEAR LYGEM 2 lb | Cross | 91.5 | 71.7 | 81.0 | 55.9 | 124.3 | 89.4 | 113.1 | 80.6 | 90.6 | 113.9 | 104.3 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 79.8 | 73.6 | 83.9 | 48.4 | 126.8 | 87.1 | 111.4 | 90.2 | 96.3 | 115.0 | 100.5 |

Table B9 (continued). Ear height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

|  | Entry Pedigree | Type |  | 2010 |  |  | 20 |  |  |  | 201 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
|  | 121 NDL XNDSHLC(M-FS)C5 | Cross | 88.5 | 80.7 | 83.5 | 55.2 | 121.8 | 80.5 | 105.5 | 96.8 | 91.6 | 109.8 | 104.0 |
|  | 122 NDL XNDSAB(MER-FS)C 15 | Cross | 84.1 | 72.5 | 78.0 | 50.1 | 130.8 | 88.9 | 115.4 | 88.3 | 89.7 | 116.1 | 106.3 |
|  | 123 NDCG(FS) C 1 X NDB S 22(R-T1)C9 | Cross | 73.8 | 69.3 | 78.4 | 52.0 | 123.8 | 83.3 | 110.8 | 97.4 | 92.8 | 112.3 | 96.0 |
|  | $124 \mathrm{NDCG}(\mathrm{FS}) \mathrm{C} 1 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 86.5 | 84.4 | 98.6 | 58.6 | 136.3 | 100.3 | 125.6 | 90.7 | 95.2 | 111.8 | 105.3 |
|  | $125 \mathrm{CGSS} 21(\mathrm{~S}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGSS}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 84.4 | 83.7 | 83.1 | 56.0 | 125.8 | 93.8 | 118.5 | 91.9 | 96.0 | 122.3 | 112.5 |
|  | $126 \mathrm{NDCG}(\mathrm{FS}) \mathrm{C} 1 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 76.3 | 78.1 | 85.3 | 47.9 | 123.0 | 88.2 | 112.0 | 83.8 | 91.4 | 98.6 | 104.3 |
|  | 127 NDBS 22(R-T 1)C9 X NDBS 21 (R-T)C9 | Cross | 69.3 | 67.3 | 76.2 | 52.6 | 119.3 | 85.9 | 113.4 | 86.1 | 90.3 | 110.4 | 106.3 |
|  | 128 Leaming(S-FS)C6 X EARLYGEM 2 lb | Cross | 85.5 | 75.9 | 78.4 | 48.3 | 119.5 | 83.0 | 103.2 | 89.7 | 99.4 | 109.8 | 97.5 |
|  | 129 NDBS 1011 XNDSM(M-FS)C9 | Cross | 78.3 | 80.0 | 84.9 | 52.9 | 126.8 | 89.1 | 113.7 | 91.4 | 97.5 | 119.1 | 109.5 |
|  | 130 NDLXEARLYGEM 21 c | Cross | 86.4 | 76.9 | 80.9 | 50.2 | 129.5 | 88.2 | 110.4 | 82.5 | 91.8 | 108.5 | 100.8 |
|  | 131 NDL X NDSCD(FS-CS)C2 | Cross | 85.4 | 98.2 | 88.8 | 57.5 | 131.8 | 95.2 | 128.0 | 94.6 | 99.6 | 125.9 | 124.3 |
|  | 132 EARLYGEM 21 a | P arent | 76.7 | 73.9 | 75.6 | 42.3 | 117.5 | 78.4 | 105.7 | 75.6 | 86.8 | 115.6 | 80.4 |
|  | 133 NDCG(FS)C1 ${ }^{\text {P NDBSK}}$ (HI-M)C3 | Cross | 79.2 | 73.5 | 87.6 | 53.6 | 115.8 | 84.7 | 106.4 | 86.4 | 90.1 | 106.9 | 95.5 |
|  | 134 NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 94.3 | 85.5 | 94.4 | 56.6 | 134.0 | 96.4 | 110.6 | 89.9 | 93.1 | 121.0 | 113.3 |
|  | 135 NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 81.0 | 71.2 | 74.4 | 50.7 | 130.3 | 85.2 | 114.0 | 82.0 | 95.5 | 106.0 | 97.3 |
|  | 136 NDSAB(MER-FS)C 15 XNDSCD(FS-CS)C2 | Cross | 91.7 | 92.3 | 106.8 | 60.5 | 140.5 | 103.7 | 127.8 | 102.1 | 107.4 | 128.7 | 121.8 |
|  | 137 NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | 70.9 | 82.5 | 75.7 | 47.7 | 121.0 | 86.5 | 105.2 | 80.0 | 87.2 | 112.5 | 99.7 |
|  | 138 Leaming(S-FS)C6 X EARLYGEM 2 a | Cross | 84.4 | 73.8 | 70.5 | 48.4 | 118.3 | 95.7 | 114.2 | 85.6 | 92.2 | 110.5 | 103.5 |
|  | 139 NDSS XNDCG(FS)C1 | Cross | 75.9 | 69.9 | 79.6 | 53.0 | 122.3 | 90.8 | 117.4 | 81.3 | 92.7 | 117.5 | 101.0 |
|  | 140 NDSM(M-FS)C9 X NDSCD(FS-CS)C2 | Cross | 80.9 | 89.9 | 100.9 | 62.5 | 134.5 | 97.2 | 108.4 | 102.0 | 101.6 | 114.1 | 108.1 |
| w | 141 NDBS 21 (R-T)C9 X NDSCD(FS-CS)C2 | Cross | 90.2 | 76.2 | 88.6 | 58.9 | 144.8 | 100.6 | 126.1 | 96.0 | 98.7 | 12.5 | 120.3 |
| $\omega$ | 142 NDCG(FS)C1XNDBS 1011 | Cross | 89.2 | 82.2 | 84.4 | 54.9 | 132.8 | 97.4 | 118.9 | 87.3 | 98.8 | 111.1 | 113.5 |
|  | 143 NDBS 1011 X EARLYGEM 21 a | Cross | 83.3 | 83.8 | 89.4 | 55.2 | 127.5 | 92.9 | 115.2 | 87.9 | 98.4 | 112.1 | 111.8 |
|  | 144 NDSHLC(M-FS)C5 | P arent | 84.5 | 68.0 | 69.7 | 45.8 | 116.0 | 82.3 | 94.5 | 81.9 | 86.8 | 98.0 | 82.0 |
|  | Experiment mean |  | 83.8 | 77.2 | 84.0 | 52.9 | 126.1 | 89.2 | 112.1 | 87.5 | 92.8 | 112.1 | 102.4 |
|  | Mean of parental populations |  | 78.9 | 74.7 | 78.6 | 48.5 | 122.6 | 84.8 | 107.0 | 84.1 | 88.7 | 111.2 | 95.2 |
|  | Mean of population crosses |  | 84.4 | 77.1 | 84.4 | 53.6 | 126.2 | 89.8 | 112.6 | 87.8 | 93.2 | 111.9 | 103.0 |
|  | Mean of checks |  | 83.5 | 84.3 | 89.3 | 51.6 | 131.0 | 88.1 | 115.6 | 89.4 | 96.4 | 116.8 | 107.8 |
|  | LSD (0.05) |  | 15.7 | 10.3 | 11.5 | 8.4 | 10.9 | 11.0 | 11.0 | 11.2 | 10.0 | 12.2 | 13.2 |
|  | CV |  | 9.4 | 6.8 | 6.9 | 8.0 | 4.4 | 6.2 | 4.9 | 6.5 | 5.4 | 5.5 | 6.5 |
|  | MSE |  | 62.7 | 27.3 | 33.9 | 17.8 | 30.2 | 30.8 | 30.7 | 32.0 | 25.4 | 38.0 | 44.2 |

Table B10. Plant height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21 c | Cross | 186.7 | 187.0 | 181.3 | 14.6 | 226.3 | 200.1 | 219.9 | 173.3 | 181.2 | 230.4 | 201.5 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C 15 | Cross | 207.3 | 188.8 | 205.0 | 142.5 | 244.5 | 204.8 | 222.5 | 187.0 | 185.3 | 223.5 | 215.6 |
| 3 NDBSK(HIM)C3 X NDSM(M-FS)C9 | Cross | 187.5 | 165.7 | 18.9 | 132.4 | 226.0 | 201.3 | 209.7 | 175.8 | 168.5 | 215.8 | 207.1 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 202.2 | 192.1 | 200.9 | 149.7 | 253.3 | 221.3 | 238.0 | 199.6 | 187.4 | 250.0 | 216.4 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 182.1 | 169.9 | 174.8 | 134.0 | 217.0 | 183.3 | 198.3 | 147.6 | 167.3 | 208.7 | 182.7 |
| 6 NDBS 1011 XNDSCD(FS-CS)C2 | Cross | 216.1 | 206.8 | 222.2 | 156.0 | 243.5 | 215.9 | 239.9 | 190.2 | 182.2 | 243.6 | 224.4 |
| 7 NDSS XNDL | Cross | 195.7 | 189.9 | 202.0 | 137.2 | 224.8 | 202.4 | 222.6 | 179.1 | 193.6 | 228.2 | 209.2 |
| 8 NDBSK(HI-M)C3 X EARLYGEM 2 lb | Cross | 197.2 | 174.4 | 188.7 | 139.4 | 229.8 | 200.5 | 207.6 | 183.4 | 187.8 | 228.5 | 200.4 |
| 9 NDLXEARLYGEM 2 lb | Cross | 195.9 | 169.7 | 184.1 | 14.1 | 234.0 | 201.7 | 224.4 | 176.0 | 177.9 | 230.4 | 212.5 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 185.0 | 175.4 | 177.4 | 140.9 | 236.5 | 195.1 | 210.0 | 180.3 | 172.9 | 225.9 | 203.6 |
| 11 NDBS 11(FR-M)C3 | P arent | 179.7 | 169.0 | 180.2 | 138.3 | 224.8 | 194.3 | 226.4 | 175.7 | 174.2 | 214.9 | 201.8 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 202.1 | 174.4 | 188.0 | 128.8 | 208.0 | 196.2 | 212.5 | 173.7 | 178.6 | 217.6 | 202.0 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Parent | 198.6 | 190.5 | 204.2 | 145.0 | 242.8 | 218.6 | 233.0 | 183.6 | 202.2 | 239.0 | 22.4 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 191.4 | 172.6 | 178.4 | 136.4 | 227.3 | 192.1 | 203.7 | 168.6 | 176.2 | 22.1 | 198.8 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 201.0 | 192.8 | 203.7 | 145.1 | 244.8 | 206.4 | 225.9 | 191.9 | 175.0 | 236.5 | 215.5 |
| 16 Check 4 DKC 43-27 VT3 | Check | 194.3 | 187.1 | 198.9 | 127.6 | 237.5 | 192.1 | 216.7 | 169.2 | 176.0 | 229.7 | 212.1 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 194.6 | 167.9 | 189.4 | 144.7 | 240.0 | 207.8 | 223.7 | 182.2 | 180.5 | 234.6 | 209.7 |
| 18 EARLYGEM 2 lc | Parent | 165.0 | 155.2 | 163.4 | 123.2 | 214.0 | 176.2 | 196.8 | 148.5 | 162.6 | 203.5 | 183.0 |
| 19 Leaming(S-FS)C6 | Parent | 195.7 | 175.3 | 192.0 | 132.9 | 234.5 | 200.9 | 217.3 | 170.8 | 199.5 | 234.1 | 208.3 |
| 20 NDBS 1011 X NDBS22(R-T 1)C9 | Cross | 187.5 | 193.6 | 201.2 | 142.8 | 242.5 | 198.8 | 217.3 | 186.8 | 188.0 | 239.7 | 220.5 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 204.4 | 182.1 | 182.4 | 139.5 | 226.5 | 203.2 | 219.0 | 178.4 | 175.8 | 228.1 | 209.7 |
| 22 NDBS 21 (R-T)C9 X NDSHLC(M-FS)C5 | Cross | 198.1 | 176.8 | 186.7 | 142.6 | 241.3 | 205.4 | 229.4 | 179.4 | 179.0 | 230.5 | 219.7 |
| 23 Check 1P IONEER 39V07 | Check | 179.9 | 189.4 | 197.6 | 134.9 | 239.3 | 189.9 | 223.3 | 175.8 | 187.3 | 230.8 | 216.2 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 189.0 | 179.5 | 184.8 | 137.4 | 239.3 | 190.8 | 216.1 | 171.3 | 192.5 | 226.3 | 201.7 |
| 25 Leaming(S-FS)C6 X NDBS 22(R-T ) C9 | Cross | 205.0 | 182.3 | 196.3 | 147.7 | 245.3 | 207.6 | 222.7 | 191.1 | 189.6 | 241.7 | 216.1 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T)C9 | Cross | 203.9 | 185.4 | 201.3 | 136.2 | 244.3 | 206.6 | 224.8 | 182.8 | 195.4 | 233.0 | 217.4 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 la | Cross | 183.1 | 173.3 | 186.6 | 139.4 | 223.8 | 199.4 | 216.5 | 176.9 | 182.2 | 233.9 | 206.4 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 203.0 | 187.1 | 206.3 | 138.1 | 242.0 | 200.5 | 225.1 | 182.5 | 190.5 | 240.1 | 207.5 |
| 29 EARLYGEM 2 la XEARLYGEM 21 c | Cross | 170.8 | 163.4 | 166.6 | 123.2 | 217.5 | 185.3 | 192.6 | 135.4 | 165.2 | 211.3 | 189.3 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 194.0 | 174.0 | 190.0 | 137.2 | 225.0 | 193.5 | 210.8 | 174.8 | 182.3 | 220.2 | 205.1 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 229.4 | 199.0 | 227.8 | 145.4 | 241.5 | 210.4 | 230.9 | 189.0 | 188.7 | 234.0 | 211.9 |
| 32 NDBSK(HIM)C3 XEARLYGEM 21 c | Cross | 185.4 | 165.4 | 173.2 | 133.5 | 227.8 | 188.8 | 199.7 | 171.7 | 172.7 | 220.6 | 199.9 |
| 33 NDBS 1011 XEARLYGEM 21 l | Cross | 182.6 | 188.1 | 190.5 | 14.0 | 232.5 | 193.7 | 212.7 | 189.6 | 181.3 | 229.7 | 211.4 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 1a | Cross | 228.0 | 185.0 | 209.6 | 143.0 | 233.8 | 213.6 | 220.1 | 187.4 | 181.3 | 232.9 | 220.4 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 191.0 | 183.0 | 202.4 | 130.9 | 228.5 | 194.6 | 215.0 | 170.3 | 182.8 | 224.9 | 205.8 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 196.6 | 177.3 | 192.7 | 140.7 | 218.5 | 197.3 | 216.0 | 185.3 | 182.7 | 229.9 | 201.8 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 215.5 | 195.8 | 215.1 | 147.2 | 239.8 | 206.8 | 233.9 | 183.9 | 194.3 | 235.0 | 216.0 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 186.9 | 178.4 | 194.5 | 132.9 | 237.5 | 197.8 | 221.5 | 175.6 | 174.8 | 217.9 | 194.9 |
| 39 EARLYGEM 2 lb XEARLYGEM 2 lc | Cross | 176.0 | 156.4 | 166.6 | 133.4 | 210.0 | 175.0 | 189.2 | 142.7 | 153.0 | 203.2 | 188.0 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 189.0 | 182.1 | 193.0 | 143.7 | 230.0 | 202.5 | 218.5 | 189.0 | 181.6 | 231.7 | 208.7 |

Table B10 (continued). Plant height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree |  | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Pros per | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 | NDBS21(R-T)C9 |  | P arent | 182.7 | 164.6 | 186.8 | 128.2 | 22.5 | 193.7 | 209.8 | 170.7 | 17.1 | 217.1 | 204.8 |
| 42 | NDSAB(MER-FS)C 15 XEARLYGEM 21 b | Cross | 188.0 | 179.2 | 191.0 | 135.2 | 230.5 | 194.4 | 208.4 | 174.5 | 176.7 | 220.3 | 201.8 |
| 43 | NDBSK(HI-M)C3 X NDBS22(R-T1)C9 | Cross | 186.4 | 172.0 | 185.5 | 138.1 | 236.8 | 193.1 | 214.1 | 186.5 | 182.1 | 227.9 | 202.2 |
| 44 | NDSS XNDBSK(HI-M)C3 | Cross | 202.5 | 186.6 | 190.8 | 144.7 | 231.3 | 203.0 | 213.9 | 186.0 | 179.8 | 230.9 | 205.6 |
| 45 | NDSS XLeaming(S-FS)C6 | Cross | 208.7 | 186.0 | 199.9 | 160.5 | 249.3 | 215.2 | 230.9 | 188.9 | 193.7 | 250.6 | 222.3 |
| 46 | NDL XNDBS22(R-T1)C9 | Cross | 194.9 | 175.4 | 192.0 | 146.1 | 250.8 | 197.3 | 226.5 | 186.4 | 182.9 | 232.5 | 220.3 |
| 47 | NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 197.5 | 180.9 | 206.7 | 159.9 | 235.8 | 214.8 | 235.9 | 180.1 | 19.9 | 231.8 | 218.5 |
| 48 | NDBS 11(FR-M)C3 X NDS AB (MER-FS ) C 15 | Cross | 190.7 | 177.5 | 194.4 | 133.0 | 233.5 | 197.4 | 217.0 | 173.5 | 178.6 | 229.3 | 202.2 |
| 49 | NDSS XNDSM(M-FS)C9 | Cross | 200.0 | 177.4 | 196.1 | 140.2 | 242.3 | 203.2 | 219.7 | 176.8 | 174.2 | 231.0 | 203.9 |
| 50 | NDBS 22(R-T1)C9 X EARLYGEM 21 l | Cross | 183.9 | 172.9 | 182.3 | 134.6 | 238.5 | 194.2 | 209.8 | 179.5 | 172.5 | 229.4 | 199.2 |
|  | NDBS 22(R-T1)C9 | P arent | 172.4 | 164.5 | 186.2 | 133.6 | 227.0 | 191.5 | 207.0 | 182.3 | 169.7 | 231.2 | 197.1 |
| 52 | NDSS XNDBS 1011 | Cross | 198.7 | 185.7 | 210.1 | 156.2 | 242.3 | 209.6 | 232.3 | 191.3 | 182.3 | 237.7 | 209.5 |
| 53 | NDL | Parent | 197.3 | 179.9 | 195.0 | 135.6 | 245.0 | 206.9 | 218.8 | 171.8 | 185.0 | 230.6 | 203.8 |
| 54 | NDBS $1011 \mathrm{XLeaming}(\mathrm{S}-\mathrm{FS}) \mathrm{C} 6$ | Cross | 205.7 | 191.6 | 216.1 | 142.9 | 247.0 | 211.3 | 222.0 | 191.9 | 186.9 | 240.5 | 212.1 |
| 55 | NDB S K(HI-M)C3 X NDB S 1011 | Cross | 182.1 | 168.2 | 204.4 | 141.3 | 231.8 | 199.8 | 221.2 | 183.6 | 181.8 | 233.6 | 203.5 |
| 56 | NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 190.6 | 176.6 | 195.5 | 144.2 | 245.3 | 209.9 | 221.4 | 181.4 | 192.5 | 234.2 | 210.9 |
| 57 | NDBS 11(FR-M)C3 X NDBS22(R-Tl)C9 | Cross | 203.0 | 183.0 | 195.9 | 136.5 | 241.5 | 199.1 | 221.2 | 180.8 | 178.6 | 236.1 | 203.1 |
| 58 | EARLYGEM 2 lb | P arent | 179.0 | 162.1 | 177.9 | 126.8 | 220.8 | 186.9 | 186.6 | 152.3 | 165.1 | 215.1 | 191.8 |
| 59 | NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 190.0 | 170.0 | 196.4 | 140.4 | 237.8 | 202.0 | 222.2 | 175.9 | 172.9 | 234.5 | 204.8 |
| 60 | Check 2 DKC 36-34 VT3 | Check | 196.3 | 191.4 | 204.7 | 132.2 | 243.5 | 189.4 | 229.0 | 195.2 | 188.8 | 243.0 | 209.0 |
| 61 | NDBSK(HI-M)C3 X NDSCD(FS-CS $) \mathrm{C} 2$ | Cross | 197.9 | 176.3 | 194.6 | 155.3 | 239.8 | 209.5 | 223.7 | 193.2 | 198.6 | 235.1 | 217.4 |
| 62 | NDBS22(R-T1)C9 X EARLYGEM 21 c | Cross | 187.0 | 167.0 | 177.8 | 137.5 | 233.8 | 189.8 | 216.8 | 172.4 | 169.2 | 219.4 | 199.0 |
| 63 | NDL X NDBS 11(FR-M ) C3 | Cross | 199.1 | 186.4 | 191.6 | 134.7 | 239.8 | 200.5 | 222.3 | 178.2 | 178.9 | 233.8 | 199.3 |
| 64 | NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 195.2 | 179.4 | 193.2 | 153.6 | 230.5 | 206.0 | 222.3 | 180.2 | 180.7 | 225.2 | 205.1 |
| 65 | NDBSK(HI-M)C3 X NDB S 21 (R-T)C9 | Cross | 199.0 | 178.3 | 192.0 | 138.3 | 226.0 | 204.2 | 222.6 | 191.2 | 178.4 | 220.2 | 205.2 |
| 66 | NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 204.2 | 186.7 | 203.7 | 136.2 | 231.3 | 206.4 | 220.0 | 192.3 | 183.5 | 230.6 | 213.0 |
| 67 | NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 172.0 | 159.2 | 180.9 | 137.5 | 217.3 | 195.8 | 221.4 | 181.5 | 187.2 | 220.2 | 205.2 |
| 68 | NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 203.4 | 184.9 | 206.3 | 145.6 | 227.3 | 196.0 | 216.2 | 169.5 | 179.7 | 220.7 | 201.8 |
| 69 | NDBSK(HL-M)C3 X NDBS 11(FR-M)C3 | Cross | 197.6 | 186.6 | 182.5 | 141.3 | 227.8 | 195.9 | 217.2 | 188.4 | 161.5 | 224.1 | 199.0 |
| 70 | NDSS XNDBS 11(FR-M)C3 | Cross | 198.7 | 186.2 | 187.3 | 144.2 | 255.5 | 208.8 | 230.4 | 188.4 | 186.0 | 232.4 | 215.2 |
|  | NDBS K(HI-M)C3 | P arent | 196.0 | 168.5 | 180.1 | 124.3 | 228.5 | 176.1 | 203.5 | 165.9 | 182.3 | 205.8 | 200.5 |
| 72 | NDSS XNDBS21(R-T)C9 | Cross | 189.0 | 183.6 | 195.2 | 139.6 | 231.3 | 200.2 | 234.3 | 190.1 | 183.4 | 235.6 | 208.9 |
| 73 | NDSS XEARLYGEM 21 c | Cross | 180.7 | 165.8 | 184.6 | 138.7 | 223.0 | 191.5 | 206.2 | 172.1 | 173.6 | 223.1 | 200.2 |
| 74 | NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 195.5 | 184.2 | 218.7 | 137.6 | 243.8 | 200.2 | 217.9 | 183.6 | 182.9 | 240.8 | 208.1 |
| 75 | NDCG(FS)C1 | P arent | 181.1 | 189.7 | 189.0 | 134.3 | 229.5 | 196.5 | 213.8 | 170.9 | 170.4 | 225.4 | 200.1 |
| 76 | NDSAB(MER-FS)C 15 | Parent | 190.0 | 174.8 | 200.6 | 145.0 | 230.3 | 201.1 | 225.1 | 181.5 | 187.7 | 241.3 | 218.3 |
| 77 | NDSS XNDSCD(FS-CS)C2 | Cross | 217.2 | 186.9 | 223.3 | 155.3 | 256.0 | 213.2 | 236.4 | 192.4 | 199.4 | 245.3 | 216.8 |
| 78 | NDBS 1011 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 190.5 | 183.9 | 206.7 | 145.4 | 244.8 | 204.3 | 228.8 | 181.5 | 17.0 | 235.9 | 218.0 |
| 79 | NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 194.0 | 186.0 | 192.0 | 139.3 | 234.8 | 199.8 | 212.5 | 174.5 | 176.0 | 231.3 | 206.2 |
| 80 | NDBS21(R-T)C9 X EARLYGEM 2 la | Cross | 194.3 | 179.5 | 197.6 | 143.2 | 235.5 | 196.2 | 218.5 | 180.5 | 178.0 | 234.1 | 211.6 |

Table B10 (continued). Plant height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  | 2011 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Thompson | Casselton | Larimore | Pros per | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 196.0 | 187.3 | 190.0 | 144.2 | 240.8 | 199.1 | 230.7 | 182.9 | 187.5 | 237.2 | 208.3 |
| 82 NDBSK(HIM)C3 X Leaming(S-FS)C6 | Cross | 193.4 | 184.6 | 195.4 | 138.0 | 240.8 | 201.7 | 211.4 | 179.4 | 187.5 | 231.7 | 212.0 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 186.4 | 186.5 | 200.5 | 143.6 | 244.8 | 199.5 | 240.3 | 187.3 | 190.0 | 229.9 | 209.5 |
| 84 NDSM(M-FS)C9 | P arent | 181.7 | 162.6 | 182.1 | 125.5 | 228.3 | 192.1 | 211.1 | 172.4 | 168.7 | 217.7 | 186.7 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 197.3 | 177.5 | 197.1 | 142.8 | 238.5 | 205.1 | 227.2 | 189.8 | 180.9 | 232.1 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 201.6 | 184.3 | 198.9 | 143.5 | 233.3 | 201.9 | 220.1 | 178.0 | 192.5 | 225.0 | 214.0 |
| 87 NDCG(FS)C1 ${ }^{\text {N }}$ NDBS 11(FR-M)C3 | Cross | 209.0 | 190.0 | 198.9 | 135.7 | 236.0 | 193.4 | 218.3 | 176.3 | 175.4 | 229.3 | 214.3 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 185.0 | 167.2 | 189.4 | 142.5 | 226.3 | 195.6 | 212.6 | 17.1 | 182.5 | 216.0 | 201.9 |
| 89 NDBS 1011 | P arent | 203.8 | 183.6 | 207.0 | 126.5 | 240.5 | 192.6 | 221.3 | 186.8 | 182.7 | 236.3 | 200.0 |
| 90 NDBS 1011 X NDS AB (MER-FS)C 15 | Cross | 199.1 | 176.7 | 210.0 | 14.0 | 241.8 | 213.5 | 226.0 | 195.4 | 185.1 | 232.1 | 215.0 |
| 91 Check 3 P IONEER 39N99 | Check | 199.4 | 194.8 | 211.3 | 134.4 | 246.3 | 187.7 | 225.5 | 188.4 | 185.7 | 242.5 | 220.2 |
| 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 196.1 | 174.2 | 193.3 | 132.3 | 225.3 | 197.9 | 217.2 | 177.4 | 184.0 | 226.0 | 198.5 |
| 93 B 22 LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 202.0 | 178.5 | 202.7 | 148.0 | 253.8 | 199.0 | 224.7 | 186.0 | 186.0 | 235.4 | 218.3 |
| 94 NDL X NDBS 1011 | Cross | 201.9 | 186.3 | 192.6 | 150.1 | 248.0 | 205.6 | 222.6 | 180.0 | 193.0 | 230.1 | 206.5 |
| 95 NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 203.5 | 173.8 | 184.3 | 139.0 | 240.5 | 195.4 | 233.5 | 172.2 | 184.6 | 222.4 | 206.0 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 186.2 | 179.2 | 190.9 | 140.4 | 239.3 | 195.0 | 205.8 | 179.4 | 182.0 | 229.1 | 206.9 |
| 97 NDSS | P arent | 189.3 | 182.5 | 198.1 | 137.6 | 236.3 | 199.2 | 224.8 | 175.9 | 178.7 | 232.8 | 202.3 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 215.6 | 192.3 | 197.6 | 152.0 | 254.3 | 212.9 | 239.2 | 178.9 | 200.8 | 248.9 | 220.7 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 188.0 | 173.1 | 190.9 | 14.9 | 225.5 | 202.7 | 212.1 | 164.9 | 172.3 | 222.5 | 212.5 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 189.2 | 181.4 | 190.0 | 135.6 | 238.5 | 202.3 | 219.2 | 172.7 | 187.1 | 230.7 | 204.5 |
| 101 NDBS 22(R-T 1)C9 X EARLYGEM 21 b | Cross | 190.0 | 175.4 | 179.1 | 136.2 | 233.8 | 205.4 | 220.2 | 178.7 | 175.0 | 231.4 | 212.9 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 191.8 | 179.7 | 192.4 | 143.1 | 241.8 | 204.3 | 225.4 | 181.3 | 182.6 | 231.3 | 214.6 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 190.0 | 168.4 | 187.8 | 138.5 | 228.0 | 197.5 | 218.5 | 177.2 | 182.1 | 225.1 | 204.5 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 190.6 | 175.0 | 191.8 | 136.3 | 227.5 | 205.6 | 216.0 | 174.7 | 176.1 | 228.9 | 204.9 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 192.9 | 192.2 | 215.3 | 140.4 | 241.5 | 211.8 | 233.3 | 187.4 | 202.6 | 234.1 | 219.9 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 185.3 | 180.2 | 197.2 | 14.6 | 229.3 | 19.7 | 210.4 | 180.4 | 175.4 | 223.1 | 206.1 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 1a | Cross | 195.8 | 172.8 | 189.8 | 135.8 | 232.8 | 200.4 | 220.3 | 171.8 | 178.7 | 221.3 | 203.8 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 195.0 | 193.6 | 209.0 | 142.2 | 245.3 | 203.8 | 229.4 | 181.3 | 182.6 | 234.0 | 209.5 |
| 109 NDSM(M-FS)C9 X EARLYGEM 21 l | Cross | 186.0 | 170.2 | 177.2 | 144.4 | 228.5 | 195.3 | 212.1 | 175.2 | 185.0 | 227.7 | 209.2 |
| 110 NDBS 21 (R-T) C9 X EARLYGEM 21 b | Cross | 197.1 | 172.1 | 200.8 | 139.9 | 234.8 | 200.0 | 215.0 | 179.1 | 168.0 | 220.3 | 216.0 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 209.8 | 199.7 | 215.3 | 147.8 | 238.5 | 201.1 | 223.2 | 193.4 | 176.0 | 239.9 | 219.1 |
| 112 NDSS XEARLYGEM 2 la | Cross | 189.7 | 181.3 | 196.1 | 144.2 | 231.8 | 196.2 | 215.5 | 176.5 | 169.3 | 224.6 | 193.6 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 197.3 | 177.5 | 191.9 | 139.4 | 226.3 | 200.3 | 214.0 | 147.2 | 177.0 | 225.3 | 197.3 |
| 114 NDCG(FS)C1XNDL | Cross | 208.3 | 193.0 | 204.5 | 135.1 | 244.5 | 20.7 | 217.0 | 174.8 | 188.1 | 235.5 | 210.7 |
| 115 NDLXEARLYGEM 2 la | Cross | 196.9 | 180.3 | 176.4 | 137.1 | 232.8 | 195.8 | 219.1 | 178.8 | 178.0 | 231.8 | 201.6 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 195.9 | 177.8 | 187.3 | 134.5 | 237.3 | 195.0 | 209.1 | 168.8 | 172.3 | 224.9 | 204.0 |
| 117 NDBS 11(FR-M)C3 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 197.7 | 184.7 | 209.0 | 146.0 | 239.8 | 205.9 | 230.1 | 183.2 | 207.1 | 237.8 | 213.0 |
| 118 NDBS 1011 X EARLYGEM 21 c | Cross | 205.2 | 188.7 | 199.0 | 142.3 | 237.3 | 200.0 | 219.8 | 183.4 | 192.1 | 228.5 | 203.2 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 2 lb | Cross | 194.6 | 177.7 | 185.6 | 138.6 | 226.5 | 191.8 | 216.7 | 175.6 | 191.1 | 231.2 | 204.2 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 196.6 | 184.8 | 198.7 | 137.8 | 242.5 | 201.5 | 224.2 | 189.6 | 185.0 | 235.7 | 213.0 |

Table B10 (continued). Plant height (cm) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B11. Silking and anthesis dates (days) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 5 environments.


Table B11 (continued). Silking and anthesis dates (days) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 5 environments.


Table B11 (continued). Silking and anthesis dates (days) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 5 environments.

| Pedigree | Type | Days to silking |  |  |  |  | Days to anthes is |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 2010 |  | 2011 |  | 2012 | 2010 |  | 2011 |  | 2012 |
|  |  | Casselton | Prosper | Casselton | Prosper | Prosper | Casselton | Prosper | Casselton | Prosper | Prosper |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 61.6 | 64.6 | 74.2 | 66.6 | 58.5 | 60.6 | 63.5 | 70.4 | 64.2 | 55.5 |
| 82 NDBSK(HI-M)C3 XLeaming(S-FS)C6 | Cross | 59.8 | 61.6 | 73.0 | 63.8 | 56.4 | 60.3 | 60.5 | 69.4 | 62.3 | 53.4 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 60.6 | 61.5 | 74.6 | 65.4 | 57.2 | 58.7 | 62.0 | 68.7 | 64.4 | 54.1 |
| 84 NDSM(M-FS)C9 | P arent | 58.7 | 61.1 | 72.3 | 67.7 | 58.7 | 57.3 | 60.0 | 69.1 | 63.4 | 54.6 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 61.7 | 63.9 | 71.4 | 64.7 | 58.7 | 60.9 | 63.9 | 69.7 | 64.2 | 55.6 |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 59.0 | 61.4 | 73.3 | 65.0 | 56.7 | 58.5 | 61.5 | 68.3 | 62.4 | 53.6 |
| 87 NDCG(FS)C1XNDBS 11(FR-M)C3 | Cross | 62.0 | 62.6 | 72.6 | 64.2 | 55.1 | 62.1 | 62.0 | 70.1 | 63.6 | 54.5 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 58.4 | 60.4 | 72.5 | 64.2 | 56.6 | 59.1 | 60.0 | 68.6 | 63.2 | 54.5 |
| 89 NDBS 1011 | Parent | 62.3 | 66.0 | 75.4 | 68.3 | 59.4 | 62.3 | 65.0 | 71.7 | 65.9 | 55.9 |
| 90 NDBS 1011 X NDS AB (MER-FS ) C 15 | Cross | 62.3 | 64.5 | 75.4 | 66.3 | 59.1 | 62.0 | 64.5 | 70.6 | 64.4 | 57.1 |
| 91 Check 3 P IONEER 39N99 | Check | 62.8 | 64.0 | 69.9 | 63.8 | 58.2 | 61.4 | 62.5 | 67.8 | 62.9 | 55.9 |
| 92 NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 59.8 | 60.4 | 74.0 | 66.2 | 58.2 | 59.1 | 60.0 | 69.7 | 63.3 | 54.0 |
| 93 BS22LEAM (R-FR)C1XLEAMNG22 (S-FR)C1 | Check | 61.1 | 63.1 | 74.5 | 66.1 | 57.6 | 61.0 | 62.5 | 70.9 | 64.7 | 55.0 |
| 94 NDL X NDBS 1011 | Cross | 63.2 | 65.0 | 73.3 | 65.8 | 58.7 | 61.8 | 63.5 | 70.8 | 65.3 | 55.8 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 60.1 | 62.5 | 73.9 | 66.9 | 57.3 | 59.6 | 61.5 | 68.2 | 64.4 | 54.6 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 60.2 | 63.5 | 76.4 | 67.7 | 58.3 | 60.3 | 62.5 | 71.9 | 64.3 | 55.1 |
| 97 NDSS | P arent | 66.6 | 63.8 | 76.3 | 65.7 | 58.9 | 65.3 | 63.4 | 72.0 | 64.6 | 56.6 |
| 98 NDBS22(R-T1)C9 XNDSCD(FS-CS)C2 | Cross | 62.9 | 63.9 | 73.3 | 67.5 | 58.9 | 61.8 | 63.4 | 70.2 | 65.3 | 55.6 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 58.4 | 63.0 | 69.5 | 63.7 | 55.3 | 57.5 | 61.0 | 66.5 | 62.5 | 53.4 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 62.8 | 64.3 | 70.4 | 67.7 | 58.3 | 61.9 | 62.4 | 70.4 | 64.6 | 54.9 |
| 101 NDBS22(R-T1)C9 X EARLYGEM 2 lb | Cross | 59.7 | 59.9 | 72.4 | 63.3 | 55.1 | 59.6 | 60.5 | 67.6 | 62.7 | 54.3 |
| 102 NDBS 1011 XNDSHLC(M-FS)C5 | Cross | 63.2 | 63.4 | 75.4 | 67.8 | 57.3 | 63.4 | 64.0 | 72.5 | 63.8 | 54.5 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 21 b | Cross | 61.1 | 60.4 | 73.3 | 66.3 | 54.9 | 61.8 | 59.4 | 68.1 | 64.8 | 53.4 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 59.6 | 60.9 | 71.0 | 62.7 | 53.4 | 58.0 | 60.4 | 68.5 | 60.7 | 52.0 |
| 105 CGL(S-FR2)C1X B S $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 60.5 | 60.5 | 74.0 | 65.1 | 56.8 | 59.4 | 60.5 | 71.8 | 63.6 | 54.0 |
| 106 NDSAB(MER-FS)C 15 XEARLYGEM 21 c | Cross | 61.6 | 64.4 | 73.3 | 63.8 | 55.8 | 60.1 | 62.4 | 68.2 | 62.2 | 53.9 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | 61.4 | 62.9 | 72.9 | 63.9 | 56.0 | 61.0 | 62.5 | 69.1 | 62.8 | 55.0 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 61.5 | 61.4 | 71.0 | 63.7 | 54.5 | 60.7 | 61.5 | 67.5 | 61.7 | 53.1 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 60.2 | 61.9 | 72.4 | 65.0 | 56.1 | 59.9 | 61.4 | 68.1 | 63.6 | 54.2 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 58.5 | 60.9 | 69.8 | 64.3 | 54.6 | 58.9 | 60.9 | 68.3 | 62.3 | 53.1 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 2 lb | Cross | 60.5 | 63.1 | 71.6 | 65.5 | 56.0 | 60.0 | 62.5 | 68.1 | 63.0 | 55.0 |
| 112 NDSS XEARLYGEM 2 la | Cross | 60.9 | 62.4 | 71.5 | 65.1 | 55.5 | 60.5 | 62.4 | 68.5 | 63.1 | 54.0 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 60.8 | 60.5 | 71.0 | 63.7 | 54.4 | 60.2 | 59.5 | 67.2 | 61.7 | 52.9 |
| 114 NDCG(FS)C1XNDL | Cross | 63.3 | 65.0 | 72.9 | 64.2 | 56.0 | 63.0 | 63.5 | 71.1 | 63.3 | 54.6 |
| 115 NDLXEARLYGEM 21 a | Cross | 61.8 | 62.5 | 71.4 | 63.7 | 55.6 | 61.9 | 61.9 | 70.2 | 63.3 | 54.5 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 59.8 | 62.4 | 72.0 | 65.1 | 54.6 | 59.1 | 61.9 | 68.1 | 63.2 | 52.1 |
| 117 NDBS 11(FR-M)C3 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 62.1 | 63.6 | 72.0 | 65.9 | 59.1 | 61.0 | 62.0 | 69.9 | 65.1 | 56.1 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 59.7 | 64.0 | 71.3 | 65.1 | 55.0 | 60.7 | 63.4 | 67.8 | 63.7 | 54.5 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 21 b | Cross | 60.1 | 61.5 | 72.0 | 63.2 | 56.2 | 60.1 | 62.5 | 68.2 | 62.8 | 55.1 |
| 120 NDBS 11(FR-M)C3 X Leaming(S-FS)C6 | Cross | 61.2 | 63.0 | 75.1 | 67.1 | 56.8 | 61.2 | 62.0 | 71.0 | 64.2 | 55.2 |

Table B11 (continued). Silking and anthesis dates (days) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 5 environments.

| Entry P | Pedigree | Type | Days to silking |  |  |  |  | Days to anthes is |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | 2010 |  | 2011 |  | 2012 | 2010 |  | 2011 |  | 2012 |
|  |  |  | Casselton | Prosper | Casselton | Prosper | Prosper | Casselton | Prosper | Casselton | Prosper | Prosper |
|  | NDL X NDSHLC(M-FS)C5 | Cross | 65.0 | 66.0 | 73.0 | 66.7 | 57.2 | 64.2 | 63.5 | 69.2 | 64.3 | 54.6 |
| 122 N | NDL X NDSAB (MER-FS)C 15 | Cross | 63.8 | 66.5 | 73.9 | 66.5 | 58.7 | 62.8 | 64.0 | 69.3 | 64.0 | 55.6 |
| 123 N | NDCG(FS)C1XNDBS22(R-T1)C9 | Cross | 62.3 | 64.6 | 72.2 | 64.7 | 56.6 | 62.4 | 62.1 | 67.6 | 63.7 | 55.0 |
| 124 N | NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 61.7 | 62.5 | 71.1 | 67.2 | 55.6 | 61.4 | 60.5 | 68.6 | 64.3 | 54.5 |
| 125 | CGSS21(S-FR)C1XBS21CGSS(R-FR)C1 | Check | 61.1 | 62.1 | 73.0 | 66.8 | 56.4 | 60.1 | 61.1 | 69.2 | 63.9 | 54.9 |
| 126 N | NDCG(FS)C1XNDBS 21 (R-T)C9 | Cross | 59.6 | 63.0 | 70.5 | 65.4 | 54.6 | 59.8 | 61.1 | 68.6 | 62.5 | 52.1 |
| 127 N | NDBS 22(R-T1)C9 X NDBS 21 (R-T) C 9 | Cross | 62.1 | 62.5 | 71.5 | 66.9 | 56.2 | 60.7 | 62.0 | 68.3 | 65.0 | 54.0 |
| 128 L | Leaming(S-FS)C6 XEARLYGEM 2 lb | Cross | 61.6 | 62.5 | 73.1 | 63.8 | 55.2 | 61.5 | 63.0 | 69.7 | 62.9 | 53.1 |
| 129 N | NDBS 1011 XNDSM(M-FS)C9 | Cross | 60.9 | 64.1 | 75.1 | 66.1 | 58.6 | 60.8 | 62.1 | 70.9 | 64.7 | 55.5 |
| 130 N | NDLXEARLYGEM 21 c | Cross | 62.0 | 62.0 | 70.4 | 63.8 | 55.1 | 61.6 | 62.5 | 67.8 | 63.9 | 53.9 |
|  | NDL X NDSCD(FS-CS)C2 | Cross | 62.9 | 65.0 | 74.0 | 66.4 | 59.8 | 63.0 | 64.1 | 69.7 | 65.5 | 56.1 |
| 132 E | EARLYGEM 21 l | P arent | 62.5 | 64.0 | 73.6 | 65.7 | 56.3 | 62.6 | 63.1 | 69.1 | 64.4 | 55.1 |
| 133 N | NDCG(FS)C1X NDBSK(HI-M)C3 | Cross | 59.8 | 63.5 | 71.3 | 64.6 | 54.6 | 59.3 | 62.5 | 68.6 | 63.3 | 53.5 |
| 134 N | NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 59.6 | 61.6 | 70.7 | 62.9 | 56.1 | 57.9 | 62.5 | 68.7 | 62.5 | 55.0 |
| 135 N | NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 59.6 | 63.2 | 72.5 | 64.6 | 55.5 | 59.0 | 62.0 | 68.0 | 63.1 | 53.4 |
| 136 N | NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 64.0 | 63.5 | 75.9 | 67.2 | 59.0 | 60.5 | 62.5 | 71.0 | 65.2 | 55.9 |
| 137 N | NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | 59.9 | 61.1 | 71.3 | 64.8 | 55.3 | 59.7 | 60.6 | 68.6 | 62.4 | 53.3 |
| 138 L | Leaming(S-FS)C6 XEARLYGEM 2 1a | Cross | 60.4 | 61.1 | 75.8 | 63.8 | 55.0 | 60.4 | 61.1 | 71.5 | 61.9 | 53.5 |
| 139 N | NDSS XNDCG(FS)C1 | Cross | 59.9 | 61.1 | 72.8 | 65.3 | 57.1 | 59.8 | 61.0 | 69.7 | 63.9 | 54.8 |
| 140 N | NDSM(M-FS)C9 XNDSCD(FS-CS)C2 | Cross | 60.9 | 64.6 | 71.9 | 67.7 | 59.0 | 59.0 | 63.5 | 69.6 | 63.3 | 55.0 |
| 141 N | NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | 59.7 | 59.7 | 72.4 | 65.0 | 57.0 | 59.4 | 59.6 | 69.8 | 63.7 | 54.4 |
| 142 N | NDCG(FS)C1XNDBS 1011 | Cross | 59.8 | 63.1 | 73.2 | 65.2 | 57.5 | 59.7 | 63.0 | 69.3 | 64.3 | 54.3 |
| 143 N | NDBS 1011 XEARLYGEM 21 a | Cross | 62.2 | 65.6 | 72.8 | 64.3 | 55.7 | 61.0 | 64.0 | 69.6 | 63.4 | 55.0 |
| 144 N | NDSHLC(M-FS)C5 | P arent | 59.8 | 63.1 | 76.9 | 65.7 | 57.2 | 60.2 | 60.5 | 71.5 | 63.3 | 54.0 |
|  | Experiment mean |  | 61.3 | 62.8 | 72.7 | 65.4 | 56.8 | 60.7 | 62.2 | 69.4 | 63.7 | 54.6 |
|  | Mean of parental populations |  | 62.1 | 63.2 | 73.5 | 66.3 | 57.7 | 61.5 | 62.6 | 69.9 | 64.4 | 55.1 |
|  | Mean of population crosses |  | 61.2 | 62.8 | 72.7 | 65.3 | 56.6 | 60.7 | 62.2 | 69.3 | 63.6 | 54.5 |
|  | Mean of checks |  | 61.0 | 62.3 | 72.5 | 64.6 | 56.9 | 60.6 | 61.9 | 69.9 | 63.7 | 55.2 |
|  | LSD (0.05) |  | 2.3 | 2.8 | 2.8 | 2.4 | 1.4 | 2.5 | 2.5 | 2.2 | 1.5 | 1.1 |
|  | CV |  | 1.9 | 2.3 | 1.9 | 1.9 | 1.3 | 2.1 | 2.0 | 1.6 | 1.2 | 1.1 |
|  | MSE |  | 1.4 | 2.0 | 1.9 | 1.5 | 0.5 | 1.6 | 1.6 | 1.3 | 0.6 | 0.3 |

Table B12. Protein (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B12 (continued). Protein (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 10.1 | 13.4 | 12.1 | 11.2 | 11.3 | 10.6 | 11.2 | 12.2 | 13.0 | 12.2 | 11.1 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 10.0 | 13.1 | 12.6 | 10.2 | 10.8 | 9.4 | 10.7 | 10.2 | 12.6 | 11.2 | 11.3 |
| 43 NDBSK(HI-M)C3 X NDBS 22(R-T 1)C9 | Cross | 10.3 | 12.7 | 11.6 | 11.0 | 10.9 | 10.3 | 10.4 | 11.0 | 12.6 | 10.8 | 10.7 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 10.6 | 12.6 | 11.7 | 10.9 | 12.6 | 10.6 | 11.5 | 11.7 | 13.7 | 11.9 | 11.9 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 9.7 | 13.2 | 12.7 | 10.0 | 11.0 | 10.7 | 11.0 | 11.5 | 13.9 | 11.0 | 11.8 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 9.7 | 12.2 | 11.3 | 10.7 | 11.1 | 9.3 | 10.2 | 10.6 | 13.1 | 11.0 | 11.1 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 10.9 | 13.1 | 11.2 | 10.7 | 11.3 | 11.4 | 12.1 | 11.2 | 13.6 | 12.6 | 11.4 |
| 48 NDBS 11(FR-M)C3 XNDSAB(MER-FS)C 15 | Cross | 11.3 | 12.9 | 11.8 | 10.0 | 10.7 | 10.2 | 10.4 | 10.9 | 13.0 | 11.4 | 10.9 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 11.4 | 14.6 | 12.0 | 10.1 | 11.5 | 11.1 | 11.7 | 11.8 | 13.7 | 12.3 | 12.8 |
| 50 NDBS22(R-T1)C9 X EARLYGEM 21 la | Cross | 10.7 | 13.6 | 12.3 | 9.9 | 11.7 | 10.5 | 10.4 | 10.5 | 13.2 | 10.8 | 11.0 |
| 51 NDBS 22(R-T1)C9 | P arent | 11.7 | 13.4 | 12.0 | 10.9 | 12.0 | 10.9 | 11.6 | 11.9 | 13.7 | 12.3 | 12.1 |
| 52 NDSS XNDBS 1011 | Cross | 10.1 | 12.9 | 12.0 | 10.7 | 11.3 |  | 11.2 | 11.6 | 13.5 | 11.8 | 11.9 |
| 53 NDL | P arent | 9.3 | 12.2 | 10.9 | 9.7 | 10.5 | 9.6 | 10.1 | 9.8 | 12.7 | 11.0 | 11.0 |
| 54 NDBS 1011 XLeaming (S-FS ) C6 | Cross | 10.3 | 12.8 | 10.9 | 9.7 | 10.4 | 10.5 | 10.4 | 9.6 | 12.9 | 10.5 | 11.0 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 10.9 | 13.0 | 11.4 | 10.8 | 10.4 | 9.9 | 10.4 | 9.9 | 12.4 | 11.0 | 10.8 |
| 56 NDSAB(MER-FS)C 15 XNDBS21(R-T)C9 | Cross | 9.1 | 13.1 | 11.5 | 10.5 | 10.9 | 10.2 | 10.7 | 10.6 | 12.8 | 11.0 | 11.3 |
| 57 NDBS 11(FR-M)C3 X NDBS 22(R-T 1)C9 | Cross | 10.2 | 13.3 | 11.6 | 10.3 | 11.6 | 11.0 | 11.7 | 10.8 | 13.6 | 10.8 | 11.6 |
| 58 EARLYGEM 2 lb | P arent | 10.8 | 13.0 | 12.0 | 9.9 | 11.3 | 10.1 | 10.8 | 10.6 | 12.7 | 10.9 | 11.7 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 10.7 | 12.8 | 11.5 | 10.4 | 11.6 | 10.8 | 10.9 | 11.7 | 13.6 | 11.6 | 11.8 |
| 60 Check 2 DKC 36-34 VT3 | Check | 8.9 | 12.5 | 9.4 | 9.2 | 9.7 | 10.3 | 9.8 | 8.8 | 11.5 | 9.4 | 10.1 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 10.4 | 12.6 | 11.6 | 9.8 | 11.7 | 10.9 | 11.0 | 11.3 | 12.6 | 11.9 | 11.9 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 10.1 | 13.2 | 12.1 | 10.5 | 10.9 | 10.1 | 10.8 | 10.4 | 12.8 | 10.8 | 10.9 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 10.5 | 12.6 | 11.6 | 10.3 | 10.5 | 10.5 | 10.6 | 10.4 | 13.1 | 11.0 | 10.9 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 11.8 | 13.1 | 12.7 | 10.8 | 11.1 | 10.7 | 11.6 | 10.8 | 13.5 | 11.2 | 11.1 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 10.4 | 12.2 | 11.5 | 10.4 | 10.7 | 10.2 | 10.5 | 11.5 | 12.7 | 11.9 | 11.2 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 10.2 | 13.3 | 11.9 | 10.1 | 11.5 | 11.1 | 11.2 | 11.0 | 12.8 | 11.4 | 11.1 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 10.8 | 13.0 | 12.2 | 10.1 | 11.8 | 10.2 | 11.4 | 11.5 | 13.0 | 11.7 | 10.8 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 11.2 | 13.1 | 12.7 | 10.9 | 11.2 | 10.8 | 11.4 | 11.6 | 12.5 | 11.5 | 10.8 |
| 69 NDBSK(HIM)C3 X NDBS 11(FR-M)C3 | Cross | 10.1 | 12.1 | 11.7 | 9.9 | 10.9 | 10.1 | 10.8 | 10.9 | 13.0 | 10.9 | 11.2 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 11.1 | 13.0 | 12.5 | 11.4 | 11.7 | 10.2 | 11.7 | 11.4 | 13.6 | 12.0 | 11.5 |
| 71 NDBSK(HI-M)C3 | P arent | 10.5 | 13.2 | 11.0 | 10.0 | 10.9 | 9.8 | 10.9 | 10.6 | 13.0 | 11.4 | 11.0 |
| 72 NDSS X NDBS 21 (R-T) C 9 | Cross | 11.3 | 13.4 | 12.2 | 10.6 | 11.6 | 10.5 | 10.8 | 11.8 | 13.5 | 11.4 | 11.1 |
| 73 NDSS XEARLYGEM 21 c | Cross | 10.0 | 13.4 | 11.8 | 9.9 | 11.7 | 10.7 | 10.9 | 11.1 | 14.1 | 11.6 | 11.8 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 10.8 | 12.9 | 11.5 | 10.3 | 11.6 | 10.1 | 11.3 | 10.9 | 14.0 | 11.4 | 11.9 |
| 75 NDCG(FS)C1 | P arent | 10.2 | 12.7 | 11.7 | 10.0 | 10.9 | 10.2 | 10.7 | 11.8 | 14.1 | 11.4 | 11.9 |
| 76 NDSAB(MER-FS)C 15 | P arent | 10.8 | 13.2 | 12.1 | 10.7 | 10.8 | 11.0 | 11.7 | 11.9 | 14.1 | 10.7 | 12.0 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 10.4 | 13.4 | 12.9 | 10.5 | 11.6 | 10.0 | 11.5 | 11.9 | 13.5 | 12.3 | 12.3 |
| 78 NDBS 1011 X NDBS 21 (R-T)C9 | Cross | 11.4 | 13.0 | 12.0 | 10.3 | 11.2 | 10.5 | 11.2 | 11.6 | 13.3 | 10.9 | 11.6 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 2 1a | Cross | 10.4 | 12.7 | 12.0 | 9.7 | 10.9 | 9.8 | 10.2 | 10.8 | 12.7 | 10.7 | 11.4 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 11.0 | 12.5 | 12.5 | 10.6 | 10.4 | 9.9 | 10.6 | 10.4 | 12.4 | 10.4 | 10.9 |

Table B12 (continued). Protein (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B12 (continued). Protein (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 NDLXNDSHLC(M-FS)C5 | Cross | 11.3 | 12.7 | 11.8 | 9.7 | 10.9 | 9.8 | 10.6 | 10.8 | 12.8 | 10.6 | 11.3 |
| 122 NDL X NDSAB(MER-FS)C 15 | Cross | 9.8 | 12.6 | 10.9 | 9.6 | 10.3 | 9.7 | 10.1 | 10.9 | 13.0 | 11.3 | 10.9 |
| 123 NDCG(FS)C 1 X NDBS $22(\mathrm{R}-\mathrm{T}$ 1)C9 | Cross | 9.3 | 13.3 | 12.1 | 10.8 | 11.5 | 10.4 | 11.2 | 11.2 | 13.4 | 10.8 | 11.1 |
| 124 NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 10.1 | 13.6 | 11.8 | 9.9 | 10.9 | 10.8 | 11.5 | 12.4 | 13.8 | 11.6 | 11.8 |
| $125 \mathrm{CGSS} 21(\mathrm{~S}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGSS}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 9.3 | 13.6 | 10.8 | 10.1 | 11.3 | 10.6 | 11.1 | 11.3 | 12.7 | 10.8 | 11.1 |
| 126 NDCG(FS)C1 ${ }^{\text {d }}$ NDBS21(R-T)C9 | Cross | 10.1 | 13.5 | 11.7 | 10.4 | 10.7 | 10.5 | 10.9 | 11.7 | 13.4 | 11.7 | 11.2 |
| 127 NDBS 22(R-T1)C9 X NDBS21(R-T)C9 | Cross | 10.2 | 12.9 | 11.4 | 11.2 | 11.0 | 10.7 | 11.2 | 11.5 | 12.9 | 10.3 | 11.3 |
| 128 Leaming(S-FS)C6 XEARLYGEM 2 lb | Cross | 9.4 | 12.5 | 11.6 | 9.7 | 10.7 | 10.4 | 10.1 | 10.0 | 12.9 | 10.8 | 10.7 |
| 129 NDBS 1011 XNDSM(M-FS)C9 | Cross | 10.7 | 13.1 | 11.4 | 10.1 | 11.5 | 10.7 | 10.9 | 10.6 | 13.8 | 11.2 | 11.3 |
| 130 NDLXEARLYGEM 21 c | Cross | 9.3 | 12.7 | 11.1 | 9.4 | 11.1 | 10.0 | 10.4 | 10.3 | 12.7 | 9.9 | 10.6 |
| 131 NDL X NDSCD(FS-CS)C2 | Cross | 11.0 | 12.9 | 12.1 | 11.1 | 11.3 | 10.2 | 10.4 | 11.1 | 12.9 | 11.4 | 11.4 |
| 132 EARLYGEM 21 l | P arent | 9.6 | 13.5 | 12.0 | 9.7 | 11.4 | 9.4 | 11.3 | 11.2 | 13.1 | 10.3 | 11.5 |
| 133 NDCG(FS)C1 ${ }^{\text {P NDBSK}}$ (HI-M)C3 | Cross | 10.6 | 13.7 | 11.1 | 10.2 | 11.2 | 10.3 | 10.8 | 10.5 | 13.8 | 10.5 | 11.5 |
| 134 NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 9.6 | 12.6 | 11.4 | 10.5 | 10.8 | 11.1 | 11.0 | 9.9 | 12.6 | 11.1 | 11.2 |
| 135 NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 10.9 | 13.1 | 12.9 | 11.2 | 12.0 | 11.0 | 11.6 | 11.9 | 14.3 | 13.0 | 11.8 |
| 136 NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 10.3 | 13.5 | 12.4 | 11.1 | 11.6 | 10.6 | 11.5 | 11.4 | 13.0 | 12.4 | 11.6 |
| 137 NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | 10.8 | 13.0 | 11.9 | 10.7 | 11.2 | 10.2 | 11.2 | 10.9 | 13.0 | 10.9 | 11.7 |
| 138 Leaming(S-FS)C6 XEARLYGEM 21 a | Cross | 9.8 | 12.7 | 11.1 | 10.2 | 10.9 | 10.1 | 10.0 | 10.5 | 12.6 | 10.9 | 11.3 |
| 139 NDSS X NDCG(FS)C1 | Cross | 11.2 | 13.3 | 12.1 | 11.2 | 12.6 | 10.8 | 12.0 | 11.8 | 13.6 | 11.7 | 11.8 |
| 140 NDSM(M-FS)C9 X NDSCD(FS-CS)C2 | Cross | 10.9 | 13.4 | 13.3 | 11.1 | 11.8 | 10.3 | 11.1 | 12.1 | 13.8 | 11.9 | 11.2 |
| 141 NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | 10.7 | 13.5 | 11.3 | 10.2 | 12.0 | 10.8 | 11.6 | 12.0 | 13.6 | 11.4 | 11.7 |
| 142 NDCG(FS)C1XNDBS 1011 | Cross | 10.0 | 13.8 | 11.0 | 9.4 | 11.1 | 10.2 | 11.0 | 11.2 | 12.9 | 11.4 | 11.2 |
| 143 NDBS 1011 X EARLYGEM 21 a | Cross | 10.7 | 12.8 | 11.8 | 10.1 | 11.0 | 10.1 | 10.7 | 10.4 | 13.5 | 9.7 | 10.7 |
| 144 NDSHLC(M-FS)C5 | P arent | 10.4 | 13.8 | 11.5 | 9.7 | 12.1 | 10.7 | 11.2 | 11.5 | 13.2 | 12.2 | 11.6 |
| Experiment mean |  | 10.3 | 13.0 | 11.6 | 10.2 | 11.1 | 10.4 | 10.9 | 10.9 | 13.2 | 11.1 | 11.2 |
| Mean of parental populations |  | 10.5 | 13.2 | 11.9 | 10.4 | 11.3 | 10.5 | 11.1 | 11.3 | 13.3 | 11.6 | 11.6 |
| Mean of population crosses |  | 10.4 | 13.0 | 11.7 | 10.3 | 11.2 | 10.4 | 10.9 | 10.8 | 13.2 | 11.1 | 11.2 |
| Mean of checks |  | 8.9 | 12.3 | 10.4 | 9.5 | 10.2 | 9.7 | 10.0 | 10.2 | 12.4 | 10.1 | 10.4 |
| LSD (0.05) |  | 1.1 | 1.1 | 1.0 | 0.8 | 0.9 | 0.8 | 0.7 | 1.3 | 0.8 | 0.9 | 0.7 |
| CV |  | 5.3 | 4.2 | 4.3 | 3.7 | 4.0 | 4.0 | 3.3 | 6.2 | 3.0 | 4.2 | 3.1 |
| MSE |  | 0.3 | 0.3 | 0.3 | 0.1 | 0.2 | 0.2 | 0.1 | 0.4 | 0.2 | 0.2 | 0.1 |

Table B13. Oil (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21 c | Cross | 4.9 | 4.6 | 5.1 | 4.7 | 4.8 | 4.6 | 4.8 | 5.2 | 4.8 | 4.9 | 4.6 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 4.8 | 4.4 | 4.7 | 4.7 | 4.6 | 4.2 | 4.6 | 5.1 | 4.3 | 4.9 | 4.7 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 4.5 | 4.3 | 4.4 | 4.4 | 4.3 | 4.3 | 4.4 | 5.0 | 4.2 | 4.6 | 4.5 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 5.1 | 4.5 | 4.6 | 4.7 | 4.3 | 4.2 | 4.7 | 5.5 | 4.6 | 4.8 | 4.6 |
| 5 EARLYGEM 2 la XEARLYGEM 2 lb | Cross | 4.4 | 4.4 | 4.7 | 4.6 | 4.4 | 4.2 | 4.5 | 5.3 | 4.3 | 4.4 | 4.5 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 4.8 | 4.5 | 4.9 | 4.8 | 4.6 | 4.4 | 5.0 | 5.3 | 4.7 | 4.8 | 4.7 |
| 7 NDSS XNDL | Cross | 4.6 | 3.9 | 4.5 | 4.6 | 4.3 | 4.2 | 4.4 | 4.9 | 4.3 | 4.4 | 4.6 |
| 8 NDBSK(HI-M)C3 XEARLYGEM 21 b | Cross | 4.6 | 4.4 | 4.9 | 4.5 | 4.2 | 4.0 | 4.3 | 5.0 | 4.2 | 4.5 | 4.4 |
| 9 NDL XEARLYGEM 2 lb | Cross | 4.6 | 4.3 | 4.7 | 4.6 | 4.3 | 4.3 | 4.3 | 4.9 | 4.0 | 4.6 | 4.4 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 4.9 | 4.5 | 4.7 | 4.8 | 4.5 | 4.2 | 4.7 | 5.5 | 4.5 | 4.9 | 4.7 |
| 11 NDBS 11(FR-M)C3 | P arent | 4.8 | 4.7 | 5.0 | 4.7 | 4.6 | 4.3 | 4.7 | 5.6 | 4.5 | 5.0 | 4.7 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 4.8 | 4.3 | 4.7 | 4.6 | 4.3 | 4.3 | 4.5 | 5.0 | 4.4 | 4.8 | 4.1 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 5.1 | 4.6 | 5.0 | 4.8 | 4.7 | 4.5 | 4.8 | 5.0 | 4.8 | 4.9 | 4.9 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 5.2 | 4.4 | 5.0 | 4.6 | 4.5 | 4.3 | 4.8 | 5.3 | 4.7 | 4.7 | 4.7 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 4.8 | 4.2 | 4.7 | 4.3 | 4.1 | 4.1 | 4.3 | 5.0 | 4.2 | 4.6 | 4.4 |
| 16 Check 4 DKC 43-27 VT3 | Check | 4.5 | 3.7 | 4.3 | 4.1 | 3.9 | 3.9 | 3.8 | 4.8 | 3.8 | 4.2 | 4.4 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 5.4 | 4.5 | 5.1 | 4.6 | 4.4 | 4.2 | 4.7 | 5.2 | 4.6 | 4.9 | 4.5 |
| 18 EARLYGEM 21 c | Parent | 4.6 | 4.1 | 4.6 | 4.5 | 4.4 | 4.3 | 4.5 | 5.0 | 4.4 | 4.6 | 4.4 |
| 19 Leaming(S-FS)C6 | Parent | 5.0 | 4.4 | 4.9 | 4.7 | 4.8 | 4.5 | 4.6 | 5.0 | 4.4 | 4.6 | 4.4 |
| 20 NDBS 1011 XNDBS22(R-T1)C9 | Cross | 4.5 | 4.2 | 4.6 | 4.5 | 4.2 | 4.0 | 4.4 | 5.0 | 4.3 | 4.9 | 4.8 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 5.0 | 4.5 | 5.1 | 4.7 | 4.6 | 4.4 | 4.9 | 5.1 | 4.8 | 4.9 | 4.6 |
| 22 NDBS21(R-T)C9 XNDSHLC(M-FS)C5 | Cross | 5.0 | 4.5 | 4.9 | 4.7 | 4.4 | 4.3 | 4.7 | 5.0 | 4.4 | 4.8 | 4.6 |
| 23 Check 1P IONEER 39V07 | Check | 4.2 | 4.0 | 4.3 | 4.4 | 4.3 | 4.1 | 4.1 | 4.7 | 4.3 | 4.5 | 4.5 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 4.6 | 4.5 | 4.8 | 4.6 | 4.8 | 4.4 | 4.3 | 5.2 | 4.5 | 4.8 | 4.6 |
| 25 Leaming(S-FS)C6 XNDBS22(R-T1)C9 | Cross | 4.5 | 4.2 | 4.8 | 4.6 | 4.4 | 3.9 | 4.5 | 5.0 | 4.5 | 4.7 | 4.5 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T) C 9 | Cross | 5.2 | 4.2 | 5.1 | 4.7 | 4.6 | 4.5 | 4.7 | 5.3 | 4.4 | 4.7 | 4.6 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 21 a | Cross | 4.5 | 4.4 | 4.6 | 4.2 | 4.4 | 4.2 | 4.4 | 5.3 | 4.1 | 4.7 | 4.4 |
| 28 NDLXLeaming(S-FS)C6 | Cross | 4.5 | 4.4 | 4.8 | 4.6 | 4.4 | 4.3 | 4.5 | 5.1 | 4.5 | 4.7 | 4.4 |
| 29 EARLYGEM 2 a X X EARLYGEM 21 c | Cross | 4.9 | 4.4 | 4.6 | 4.1 | 4.3 | 4.4 | 4.5 | 5.0 | 4.4 | 4.4 | 4.5 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 4.8 | 4.4 | 5.1 | 4.5 | 4.7 | 4.8 | 4.6 | 5.3 | 4.3 | 4.8 | 4.6 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 5.0 | 4.5 | 5.4 | 4.7 | 4.9 | 4.3 | 4.7 | 5.5 | 4.6 | 4.9 | 4.5 |
| 32 NDBSK(HIM)C3 XEARLYGEM 21 c | Cross | 4.5 | 4.2 | 4.7 | 4.6 | 4.3 | 4.2 | 4.3 | 5.3 | 4.4 | 4.7 | 4.8 |
| 33 NDBS 1011 XEARLYGEM 21 b | Cross | 4.8 | 4.2 | 4.9 | 4.9 | 4.2 | 4.3 | 4.6 | 5.0 | 4.5 | 4.8 | 4.7 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 5.1 | 4.5 | 5.1 | 4.9 | 4.9 | 4.5 | 4.8 | 5.6 | 4.7 | 4.9 | 4.6 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 4.8 | 4.5 | 4.9 | 4.6 | 4.6 | 4.4 | 4.6 | 5.1 | 4.4 | 4.8 | 4.6 |
| 36 NDSAB(MER-FS)C15 X NDSHLC(M-FS)C5 | Cross | 4.7 | 4.6 | 5.0 | 4.8 | 4.5 | 4.3 | 4.8 | 5.2 | 4.6 | 4.9 | 4.8 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 4.9 | 4.8 | 4.9 | 4.9 | 4.5 | 4.4 | 4.8 | 5.4 | 4.7 | 5.1 | 4.7 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 4.6 | 4.4 | 4.9 | 4.4 | 4.6 | 4.5 | 4.8 | 5.2 | 4.6 | 4.8 | 4.8 |
| 39 EARLYGEM 2 lb XEARLYGEM 21 c | Cross | 4.6 | 4.5 | 4.8 | 4.5 | 4.4 | 4.4 | 4.3 | 5.3 | 4.3 | 4.6 | 4.3 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 4.5 | 4.2 | 4.5 | 4.4 | 4.2 | 4.2 | 4.4 | 4.9 | 4.3 | 4.5 | 4.4 |

Table B13 (continued). Oil (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 4.6 | 4.4 | 4.7 | 4.6 | 4.3 | 4.2 | 4.6 | 5.1 | 4.4 | 4.5 | 4.5 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 4.7 | 4.6 | 4.8 | 4.8 | 4.6 | 4.2 | 4.5 | 5.3 | 4.4 | 4.7 | 4.7 |
| 43 NDBSK(HIM)C3 X NDBS 22 (R-T 1)C9 | Cross | 4.2 | 4.1 | 4.5 | 4.4 | 3.9 | 4.0 | 4.1 | 5.0 | 4.1 | 4.4 | 4.0 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 4.5 | 4.2 | 4.7 | 4.5 | 4.2 | 4.1 | 4.1 | 4.9 | 4.2 | 4.5 | 4.2 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 5.0 | 4.6 | 5.1 | 4.7 | 4.6 | 4.6 | 4.5 | 5.4 | 4.5 | 5.1 | 4.6 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 4.4 | 4.2 | 4.2 | 4.3 | 4.0 | 3.9 | 4.1 | 5.2 | 4.3 | 4.5 | 4.4 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 5.1 | 4.5 | 5.1 | 4.9 | 4.7 | 4.3 | 5.0 | 5.8 | 4.9 | 4.9 | 4.6 |
| 48 NDBS 11(FR-M)C3 X NDSAB(MER-FS)C 15 | Cross | 4.6 | 4.5 | 4.8 | 4.7 | 4.6 | 4.2 | 4.5 | 5.4 | 4.7 | 4.9 | 4.7 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 4.5 | 4.3 | 4.9 | 4.4 | 4.2 | 4.2 | 4.2 | 5.2 | 4.5 | 4.6 | 4.3 |
| 50 NDBS22(R-T1)C9 X EARLYGEM 21 la | Cross | 4.6 | 4.2 | 4.7 | 4.5 | 4.4 | 4.4 | 4.5 | 5.1 | 4.2 | 4.8 | 4.5 |
| 51 NDBS 22(R-T1)C9 | P arent | 4.3 | 4.1 | 4.3 | 4.3 | 3.9 | 3.9 | 4.1 | 4.9 | 4.3 | 4.5 | 4.2 |
| 52 NDSS XNDBS 1011 | Cross | 5.0 | 4.2 | 4.8 | 4.7 | 4.6 | 4.2 | 4.5 | 5.2 | 4.5 | 4.7 | 4.7 |
| 53 NDL | P arent | 4.1 | 3.7 | 4.2 | 3.9 | 3.8 | 4.0 | 4.0 | 4.7 | 4.1 | 4.2 | 4.3 |
| 54 NDBS 1011 XLeaming (S-FS ) C6 | Cross | 4.9 | 4.5 | 4.6 | 4.8 | 4.7 | 4.4 | 4.6 | 5.5 | 4.6 | 4.7 | 4.6 |
| 55 NDBSK(HL-M)C3 X NDBS 1011 | Cross | 4.4 | 4.0 | 4.5 | 4.1 | 4.4 | 3.8 | 4.4 | 5.1 | 4.5 | 4.7 | 4.4 |
| 56 NDSAB(MER-FS)C 15 XNDBS21(R-T)C9 | Cross | 4.8 | 4.4 | 4.6 | 4.6 | 4.5 | 4.1 | 4.4 | 5.1 | 4.5 | 4.8 | 4.6 |
| 57 NDBS 11(FR-M)C3 X NDBS 22(R-T1)C9 | Cross | 5.2 | 4.4 | 4.5 | 4.7 | 4.2 | 4.0 | 4.5 | 5.2 | 4.5 | 4.8 | 4.6 |
| 58 EARLYGEM 2 lb | P arent | 4.7 | 4.4 | 4.6 | 4.5 | 4.5 | 4.3 | 4.4 | 5.3 | 4.3 | 4.5 | 4.4 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 4.5 | 4.4 | 4.9 | 4.6 | 4.5 | 4.1 | 4.5 | 5.2 | 4.3 | 4.7 | 4.4 |
| 60 Check 2 DKC 36-34 VT3 | Check | 4.6 | 4.0 | 4.4 | 4.4 | 4.3 | 4.4 | 4.1 | 4.5 | 4.1 | 4.3 | 4.3 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 4.8 | 4.3 | 4.8 | 5.0 | 4.3 | 4.2 | 4.4 | 5.4 | 4.4 | 4.6 | 4.4 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 4.6 | 4.1 | 4.5 | 4.4 | 4.3 | 4.1 | 4.5 | 5.0 | 4.3 | 4.6 | 4.5 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 4.3 | 4.1 | 4.8 | 4.7 | 4.3 | 4.3 | 4.4 | 5.0 | 4.3 | 4.6 | 4.4 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 5.3 | 4.4 | 5.1 | 4.8 | 4.4 | 4.7 | 4.7 | 5.4 | 4.6 | 4.8 | 4.7 |
| 65 NDBSK(HI-M)C3 X NDB S 21 (R-T)C 9 | Cross | 5.0 | 4.3 | 4.7 | 4.7 | 4.5 | 4.2 | 4.5 | 5.1 | 4.4 | 4.7 | 4.5 |
| 66 NDBS22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 5.0 | 4.4 | 4.9 | 4.6 | 4.1 | 3.9 | 4.3 | 4.9 | 4.3 | 4.7 | 4.3 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 4.7 | 4.0 | 5.1 | 4.7 | 4.4 | 4.0 | 4.7 | 5.3 | 4.8 | 4.8 | 4.4 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 4.6 | 4.5 | 4.9 | 4.6 | 4.5 | 4.3 | 4.6 | 5.4 | 4.7 | 4.8 | 4.5 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 4.6 | 4.3 | 4.7 | 4.6 | 4.0 | 4.2 | 4.4 | 5.2 | 4.2 | 4.5 | 4.5 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 4.7 | 4.7 | 5.0 | 4.7 | 4.6 | 4.3 | 4.7 | 5.4 | 4.4 | 4.7 | 4.9 |
| 71 NDBSK(HIM)C3 | P arent | 4.3 | 4.1 | 4.5 | 4.3 | 4.2 | 3.9 | 4.1 | 4.8 | 4.3 | 4.4 | 4.3 |
| 72 NDSS X NDBS 21 (R-T)C9 | Cross | 4.7 | 4.5 | 4.9 | 4.8 | 4.5 | 4.1 | 4.6 | 5.2 | 4.5 | 4.8 | 4.6 |
| 73 NDSS XEARLYGEM 21 c | Cross | 4.8 | 4.1 | 4.8 | 4.4 | 4.4 | 4.2 | 4.5 | 5.1 | 4.4 | 4.7 | 4.5 |
| 74 NDBS 11(FR-M)C3 XNDBS 1011 | Cross | 4.7 | 4.6 | 5.1 | 4.6 | 4.3 | 4.2 | 4.7 | 5.5 | 4.6 | 5.0 | 4.6 |
| 75 NDCG(FS)C1 | P arent | 4.5 | 4.5 | 4.9 | 4.6 | 4.8 | 4.4 | 4.5 | 5.6 | 4.5 | 4.9 | 4.8 |
| 76 NDSAB(MER-FS)C 15 | Parent | 4.7 | 4.4 | 5.0 | 4.6 | 4.4 | 4.0 | 4.4 | 5.4 | 4.2 | 4.9 | 4.6 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 4.7 | 4.6 | 4.7 | 4.6 | 4.7 | 4.3 | 4.6 | 5.5 | 4.7 | 5.0 | 4.7 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 4.8 | 4.3 | 4.6 | 4.4 | 4.3 | 4.2 | 4.6 | 5.2 | 4.5 | 4.8 | 4.6 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 2 la | Cross | 4.8 | 4.5 | 4.8 | 4.5 | 4.6 | 4.2 | 4.5 | 5.2 | 4.5 | 4.9 | 4.7 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 4.8 | 4.7 | 4.7 | 4.8 | 4.5 | 4.6 | 4.7 | 5.4 | 4.5 | 4.7 | 4.7 |

Table B13 (continued). Oil (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 4.9 | 4.5 | 4.9 | 4.6 | 4.7 | 4.2 | 4.6 | 5.5 | 4.6 | 4.8 | 4.5 |
| $82 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3$ X Leaming(S-FS)C6 | Cross | 4.7 | 4.3 | 4.7 | 4.6 | 4.5 | 4.3 | 4.4 | 5.5 | 4.4 | 4.7 | 4.8 |
| 83 NDL X NDBS21(R-T)C9 | Cross | 4.8 | 4.3 | 4.6 | 4.4 | 4.1 | 4.2 | 4.5 | 5.0 | 4.3 | 4.4 | 4.2 |
| 84 NDSM(M-FS)C9 | Parent | 4.5 | 4.5 | 4.7 | 4.2 | 4.4 | 4.1 | 4.4 | 5.4 | 4.6 | 4.8 | 4.6 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 4.6 | 4.2 | 4.8 | 4.6 | 4.4 | 4.2 | 4.1 | 4.9 | 4.1 | 4.5 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 4.8 | 4.4 | 4.9 | 4.7 | 4.5 | 4.4 | 4.6 | 5.2 | 4.5 | 4.8 | 4.8 |
| 87 NDCG(FS)C 1 X NDBS 11(FR-M)C3 | Cross | 4.9 | 4.6 | 4.9 | 4.6 | 4.7 | 4.4 | 4.8 | 5.5 | 4.7 | 5.0 | 4.8 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 4.8 | 4.3 | 5.2 | 4.9 | 4.5 | 4.2 | 4.9 | 5.5 | 4.7 | 4.8 | 4.7 |
| 89 NDBS 1011 | P arent | 4.5 | 4.2 | 4.8 | 4.6 | 4.2 | 4.4 | 4.7 | 5.7 | 4.6 | 4.8 | 4.6 |
| 90 NDBS 1011 XNDS AB(MER-FS)C 15 | Cross | 4.7 | 4.5 | 4.7 | 4.6 | 4.3 | 4.1 | 4.4 | 5.2 | 4.4 | 4.7 | 4.6 |
| 91 Check 3 P IONEER 39N99 | Check | 5.1 | 4.3 | 5.0 | 4.8 | 4.5 | 4.3 | 4.4 | 5.2 | 4.4 | 4.7 | 4.8 |
| 92 NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 5.0 | 4.4 | 5.2 | 4.9 | 4.6 | 4.0 | 4.9 | 5.6 | 4.8 | 4.8 | 4.4 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 4.5 | 4.5 | 4.8 | 4.6 | 4.4 | 4.2 | 4.3 | 5.1 | 4.5 | 4.5 | 4.5 |
| 94 NDL X NDBS 1011 | Cross | 4.6 | 4.3 | 4.6 | 4.5 | 4.1 | 4.0 | 4.2 | 5.3 | 4.3 | 4.5 | 4.5 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 4.5 | 4.5 | 4.7 | 4.5 | 4.2 | 4.1 | 4.3 | 4.9 | 4.3 | 4.6 | 4.4 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 4.5 | 4.4 | 4.5 | 4.5 | 4.3 | 4.0 | 4.4 | 5.2 | 4.1 | 4.8 | 4.5 |
| 97 NDSS | Parent | 5.0 | 4.5 | 4.8 | 4.7 | 4.4 | 4.2 | 4.5 | 5.3 | 4.4 | 4.7 | 4.6 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 4.5 | 4.5 | 4.8 | 4.8 | 4.3 | 4.0 | 4.6 | 5.1 | 4.4 | 4.6 | 4.6 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 5.1 | 4.1 | 4.8 | 4.8 | 4.8 | 4.5 | 5.0 | 5.1 | 4.6 | 4.8 | 4.5 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 4.6 | 4.1 | 4.5 | 4.7 | 4.1 | 4.0 | 4.2 | 4.8 | 4.1 | 4.5 | 4.2 |
| 101 NDBS22(R-T1)C9 XEARLYGEM 21 b | Cross | 4.7 | 4.4 | 5.0 | 4.6 | 4.4 | 4.0 | 4.4 | 5.3 | 4.5 | 4.5 | 4.6 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 4.7 | 4.2 | 4.7 | 4.9 | 4.4 | 4.2 | 4.9 | 5.6 | 4.6 | 4.9 | 4.5 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 4.6 | 4.5 | 5.0 | 4.8 | 4.7 | 4.4 | 4.8 | 5.5 | 4.6 | 4.9 | 4.8 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 4.7 | 4.6 | 4.7 | 4.8 | 4.5 | 4.4 | 4.7 | 5.4 | 4.5 | 4.7 | 4.7 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 5.0 | 4.7 | 5.1 | 4.7 | 4.6 | 4.5 | 4.9 | 5.3 | 4.7 | 5.0 | 4.7 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 4.8 | 4.4 | 4.8 | 4.7 | 4.4 | 4.4 | 4.6 | 5.1 | 4.4 | 4.5 | 4.6 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | 4.9 | 4.4 | 5.0 | 4.7 | 4.6 | 4.3 | 4.7 | 5.4 | 4.6 | 4.5 | 4.6 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 4.8 | 4.3 | 5.0 | 4.7 | 4.6 | 4.6 | 4.8 | 5.2 | 4.6 | 4.9 | 4.6 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 4.9 | 4.4 | 4.9 | 4.6 | 4.6 | 4.2 | 4.5 | 5.2 | 4.4 | 4.7 | 4.7 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 4.7 | 4.6 | 4.8 | 4.6 | 4.5 | 4.3 | 4.6 | 5.3 | 4.5 | 4.7 | 4.7 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 5.1 | 4.4 | 5.2 | 4.9 | 4.8 | 4.8 | 4.9 | 5.5 | 4.5 | 5.0 | 4.7 |
| 112 NDSS XEARLYGEM 21 a | Cross | 4.6 | 4.5 | 4.7 | 4.5 | 4.5 | 4.2 | 4.4 | 5.3 | 4.5 | 4.6 | 4.6 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 4.9 | 4.5 | 5.1 | 4.6 | 4.6 | 4.4 | 4.8 | 5.1 | 4.4 | 4.7 | 4.5 |
| 114 NDCG(FS)C1XNDL | Cross | 4.7 | 4.1 | 4.9 | 4.6 | 4.5 | 4.4 | 4.8 | 4.9 | 4.3 | 4.7 | 4.5 |
| 115 NDLXEARLYGEM 2 la | Cross | 4.6 | 4.4 | 4.9 | 4.6 | 4.2 | 4.1 | 4.3 | 5.0 | 4.3 | 4.5 | 4.4 |
| 116 NDSM(M-FS)C9 XEARLYGEM 21 b | Cross | 4.7 | 4.2 | 4.6 | 4.4 | 4.6 | 4.3 | 4.3 | 5.1 | 4.2 | 5.0 | 4.3 |
| 117 NDBS 11(FR-M)C3 X NDBS 21 (R-T)C9 | Cross | 4.8 | 4.3 | 4.8 | 4.5 | 4.5 | 4.2 | 4.6 | 5.1 | 4.4 | 4.8 | 4.5 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 4.9 | 4.3 | 4.8 | 4.5 | 4.6 | 4.3 | 4.5 | 5.2 | 4.3 | 4.9 | 4.7 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 21 b | Cross | 4.6 | 4.1 | 4.9 | 4.6 | 4.6 | 4.3 | 4.7 | 5.0 | 4.7 | 4.9 | 4.8 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 4.9 | 4.6 | 5.1 | 4.7 | 4.6 | 4.5 | 4.7 | 5.6 | 4.6 | 4.8 | 5.0 |

Table B13 (continued). Oil (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B14. Starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21 c | Cross | 70.4 | 67.6 | 68.7 | 70.5 | 69.6 | 70.5 | 69.8 | 69.8 | 68.0 | 69.8 | 70.0 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C 15 | Cross | 69.6 | 67.4 | 69.0 | 69.8 | 69.1 | 69.8 | 69.9 | 68.5 | 68.3 | 69.3 | 69.5 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 69.6 | 68.2 | 68.4 | 70.0 | 69.0 | 70.2 | 69.4 | 68.2 | 67.7 | 68.6 | 69.2 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 69.6 | 68.2 | 67.8 | 70.1 | 69.0 | 70.5 | 68.8 | 67.6 | 66.8 | 69.2 | 69.4 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 70.7 | 68.1 | 68.9 | 70.4 | 69.4 | 71.3 | 69.5 | 68.7 | 68.3 | 70.0 | 69.7 |
| 6 NDBS 1011 XNDSCD(FS-CS)C2 | Cross | 69.4 | 67.7 | 67.4 | 69.2 | 68.6 | 70.2 | 68.9 | 68.2 | 67.1 | 68.1 | 69.0 |
| 7 NDSS XNDL | Cross | 69.7 | 68.6 | 68.7 | 69.4 | 69.4 | 70.8 | 69.4 | 68.0 | 67.3 | 69.2 | 69.3 |
| 8 NDBSK(HIM)C3 X EARLYGEM 2 lb | Cross | 70.4 | 68.8 | 68.2 | 70.5 | 69.9 | 70.8 | 70.3 | 69.7 | 68.5 | 70.5 | 70.2 |
| 9 NDL XEARLYGEM 21 b | Cross | 70.9 | 68.8 | 68.9 | 70.8 | 70.4 | 71.3 | 70.2 | 68.9 | 68.3 | 70.8 | 70.2 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 69.9 | 68.2 | 68.6 | 69.8 | 69.8 | 70.9 | 69.4 | 69.2 | 67.8 | 69.2 | 70.0 |
| 11 NDBS 11(FR-M)C3 | P arent | 69.1 | 67.6 | 67.3 | 69.9 | 68.5 | 69.6 | 68.5 | 67.3 | 66.3 | 67.9 | 69.2 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 69.0 | 67.9 | 68.5 | 70.6 | 69.3 | 70.3 | 69.4 | 69.2 | 68.3 | 68.6 | 70.4 |
| 13 NDSCD(FS-CS)C2 | P arent | 67.9 | 68.0 | 67.4 | 69.2 | 68.5 | 69.1 | 67.6 | 68.5 | 67.9 | 67.4 | 67.7 |
| 14 NDSHLC(M-FS)C5 X EARLYGEM 21c | Cross | 69.3 | 68.5 | 68.2 | 71.1 | 69.1 | 70.8 | 68.8 | 68.5 | 68.5 | 69.1 | 69.9 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 69.4 | 67.9 | 67.5 | 69.9 | 68.7 | 70.1 | 68.6 | 67.9 | 66.6 | 68.6 | 68.5 |
| 16 Check 4 DKC 43-27 VT3 | Check | 72.1 | 70.7 | 71.4 | 72.1 | 72.5 | 72.1 | 72.1 | 70.6 | 70.5 | 71.6 | 71.4 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 68.2 | 67.9 | 66.4 | 69.7 | 68.4 | 70.8 | 68.7 | 67.9 | 66.8 | 68.3 | 69.4 |
| 18 EARLYGEM 21 c | P arent | 70.9 | 68.1 | 67.5 | 70.9 | 70.0 | 71.0 | 70.8 | 69.7 | 69.1 | 69.6 | 70.5 |
| 19 Leaming(S-FS)C6 | P arent | 69.4 | 67.4 | 68.1 | 70.0 | 69.3 | 69.8 | 69.9 | 68.3 | 67.5 | 68.2 | 69.2 |
| 20 NDBS 1011 XNDBS22(R-T1)C9 | Cross | 69.4 | 68.7 | 67.5 | 70.3 | 69.7 | 70.6 | 69.5 | 68.6 | 67.9 | 69.2 | 69.6 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 69.4 | 68.0 | 67.5 | 70.7 | 69.6 | 70.5 | 69.0 | 69.1 | 67.9 | 69.2 | 70.2 |
| 22 NDBS 21 (R-T)C9 X NDSHLC(M-FS)C5 | Cross | 69.6 | 68.6 | 68.4 | 70.1 | 69.5 | 70.2 | 68.7 | 69.0 | 68.0 | 68.7 | 69.6 |
| 23 Check 1P IONEER 39V07 | Check | 72.1 | 68.7 | 70.6 | 70.8 | 70.6 | 71.2 | 71.1 | 69.7 | 69.1 | 69.8 | 70.2 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 69.6 | 67.0 | 68.5 | 70.3 | 68.9 | 70.2 | 69.6 | 68.0 | 68.3 | 68.1 | 69.1 |
| 25 Leaming(S-FS)C6 XNDBS22(R-T1)C9 | Cross | 70.6 | 68.2 | 69.1 | 70.0 | 68.9 | 70.3 | 69.4 | 68.8 | 67.5 | 69.6 | 69.4 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T) C 9 | Cross | 70.0 | 67.7 | 68.5 | 70.4 | 70.5 | 70.8 | 69.8 | 69.3 | 67.2 | 69.1 | 70.1 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 la | Cross | 70.0 | 68.4 | 68.3 | 70.3 | 70.1 | 70.2 | 69.4 | 69.1 | 67.7 | 69.5 | 69.7 |
| 28 NDLXLeaming(S-FS)C6 | Cross | 70.8 | 67.8 | 68.9 | 70.3 | 70.2 | 69.7 | 70.6 | 69.7 | 67.3 | 69.7 | 70.1 |
| 29 EARLYGEM 21 a X EARLYGEM 21 c | Cross | 70.4 | 68.2 | 69.2 | 71.0 | 70.2 | 70.6 | 70.0 | 69.5 | 68.6 | 70.2 | 69.9 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 70.4 | 67.2 | 67.9 | 70.0 | 69.0 | 70.3 | 69.6 | 69.2 | 67.9 | 69.6 | 69.7 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 69.0 | 67.1 | 67.2 | 69.4 | 68.5 | 69.6 | 68.7 | 68.0 | 67.8 | 68.5 | 69.6 |
| 32 NDBSK(HI-M)C3 X EARLYGEM 21 c | Cross | 70.2 | 68.6 | 68.9 | 70.6 | 69.6 | 71.2 | 70.7 | 69.4 | 68.1 | 69.8 | 70.2 |
| 33 NDBS 1011 XEARLYGEM 2 lb | Cross | 71.1 | 68.0 | 68.6 | 70.3 | 69.8 | 70.8 | 69.9 | 70.2 | 68.3 | 69.5 | 69.3 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 69.9 | 68.0 | 67.8 | 69.6 | 67.7 | 70.6 | 69.2 | 69.0 | 66.8 | 68.9 | 69.2 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 70.2 | 67.6 | 67.3 | 69.7 | 68.7 | 70.0 | 69.4 | 69.6 | 67.2 | 68.9 | 69.5 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 69.7 | 68.1 | 68.1 | 70.4 | 69.0 | 70.5 | 68.9 | 69.2 | 68.0 | 69.1 | 69.3 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 69.7 | 68.1 | 67.4 | 69.2 | 68.4 | 69.5 | 68.4 | 68.4 | 67.1 | 68.4 | 68.7 |
| 38 NDCG(FS)C1XEARLYGEM 21 a | Cross | 70.3 | 68.1 | 68.1 | 70.1 | 69.2 | 70.9 | 69.2 | 69.0 | 67.9 | 69.3 | 69.1 |
| 39 EARLYGEM 2 lb XEARLYGEM 2 lc | Cross | 71.5 | 68.6 | 68.5 | 70.2 | 69.3 | 71.0 | 70.3 | 69.7 | 68.4 | 69.8 | 70.1 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 70.3 | 68.0 | 68.8 | 70.4 | 70.0 | 70.3 | 69.1 | 69.1 | 68.1 | 69.8 | 70.0 |

Table B14 (continued). Starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 69.9 | 67.6 | 67.7 | 69.5 | 69.4 | 70.7 | 69.2 | 67.6 | 68.1 | 68.6 | 69.8 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 70.3 | 67.7 | 67.3 | 69.9 | 69.6 | 71.5 | 69.9 | 69.3 | 68.5 | 69.3 | 69.4 |
| 43 NDBSK(HIM)C3 X NDBS 22 (R-T 1)C9 | Cross | 70.1 | 68.4 | 68.5 | 69.5 | 69.9 | 70.8 | 70.0 | 68.7 | 68.5 | 69.6 | 70.6 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 69.5 | 68.7 | 68.0 | 69.6 | 68.0 | 70.5 | 69.1 | 68.3 | 67.4 | 68.6 | 69.1 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 69.8 | 67.4 | 66.5 | 70.1 | 69.0 | 69.2 | 69.1 | 67.8 | 66.8 | 68.7 | 68.6 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 70.6 | 68.7 | 69.0 | 70.0 | 69.9 | 71.9 | 70.4 | 68.8 | 67.8 | 69.4 | 69.7 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 69.0 | 68.0 | 68.3 | 69.5 | 68.9 | 70.1 | 67.6 | 67.8 | 67.0 | 67.8 | 69.4 |
| 48 NDBS 11(FR-M)C3 X NDSAB (MER-FS)C 15 | Cross | 68.8 | 67.9 | 68.1 | 70.2 | 69.4 | 70.6 | 69.8 | 68.3 | 67.5 | 68.6 | 69.4 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 68.9 | 66.6 | 67.6 | 70.5 | 69.1 | 69.8 | 68.8 | 67.8 | 67.2 | 68.2 | 68.3 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 69.8 | 67.9 | 67.8 | 70.6 | 69.0 | 70.4 | 70.1 | 69.4 | 68.1 | 69.5 | 69.8 |
| 51 NDBS 22(R-T1)C9 | P arent | 69.2 | 67.7 | 68.1 | 69.6 | 69.0 | 70.3 | 69.1 | 67.9 | 67.4 | 68.3 | 69.1 |
| 52 NDSS XNDBS 1011 | Cross | 69.8 | 68.4 | 67.8 | 69.6 | 68.8 | 70.2 | 69.0 | 67.9 | 67.4 | 68.5 | 68.6 |
| 53 NDL | P arent | 71.3 | 69.0 | 69.5 | 71.2 | 70.6 | 71.5 | 70.8 | 70.0 | 68.4 | 69.7 | 69.8 |
| 54 NDBS 1011 XLeaming (S-FS ) C6 | Cross | 69.5 | 67.9 | 68.9 | 70.0 | 69.6 | 70.4 | 69.6 | 69.4 | 67.7 | 69.7 | 69.4 |
| 55 NDBSK(HI-M)C3 X NDBS 1011 | Cross | 69.6 | 68.3 | 68.6 | 70.4 | 70.0 | 72.1 | 69.8 | 69.6 | 68.4 | 69.2 | 70.0 |
| 56 NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 70.6 | 68.2 | 68.5 | 69.9 | 69.5 | 71.0 | 69.7 | 69.0 | 68.0 | 69.1 | 69.4 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-T1)C9 | Cross | 69.4 | 67.3 | 68.5 | 69.8 | 69.1 | 70.4 | 68.6 | 68.7 | 67.2 | 69.3 | 69.1 |
| 58 EARLYGEM 2 lb | P arent | 69.6 | 68.3 | 68.2 | 71.0 | 69.4 | 71.0 | 69.9 | 69.1 | 68.5 | 69.8 | 69.6 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 69.8 | 68.3 | 68.0 | 69.8 | 68.8 | 70.1 | 69.4 | 67.9 | 67.6 | 68.7 | 69.1 |
| 60 Check 2 DKC 36-34 VT3 | Check | 70.9 | 68.7 | 70.5 | 71.0 | 70.6 | 70.0 | 70.8 | 71.0 | 69.5 | 70.8 | 70.6 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 69.3 | 68.5 | 68.0 | 69.9 | 68.8 | 69.8 | 69.3 | 68.1 | 68.2 | 68.5 | 69.0 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 70.3 | 68.2 | 68.2 | 70.3 | 70.1 | 70.8 | 69.8 | 69.4 | 68.4 | 69.7 | 70.0 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 70.1 | 68.4 | 68.0 | 69.9 | 70.0 | 70.7 | 69.8 | 69.1 | 67.8 | 69.3 | 70.0 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 67.9 | 68.0 | 66.9 | 69.6 | 69.6 | 69.8 | 68.6 | 68.5 | 67.3 | 69.1 | 69.5 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 69.2 | 69.0 | 68.3 | 69.9 | 69.8 | 71.1 | 69.8 | 68.1 | 68.4 | 68.5 | 69.5 |
| 66 NDBS22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 69.4 | 67.2 | 67.6 | 70.1 | 69.3 | 70.1 | 69.3 | 68.8 | 68.1 | 68.8 | 69.8 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 69.5 | 68.5 | 67.3 | 70.3 | 69.0 | 71.3 | 68.8 | 68.1 | 67.6 | 68.7 | 70.3 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 69.2 | 68.0 | 67.1 | 69.7 | 69.4 | 70.2 | 68.9 | 67.9 | 68.2 | 68.7 | 70.2 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 70.0 | 68.8 | 68.2 | 70.3 | 70.1 | 71.3 | 69.5 | 68.5 | 68.1 | 69.6 | 69.6 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 68.9 | 67.5 | 66.9 | 69.1 | 68.3 | 70.2 | 68.1 | 67.8 | 67.2 | 68.2 | 68.7 |
| 71 NDBSK(HI-M)C3 | P arent | 69.8 | 67.9 | 69.0 | 70.3 | 69.6 | 71.0 | 69.5 | 69.2 | 68.0 | 69.1 | 69.8 |
| 72 NDSS X NDBS 21 (R-T)C9 | Cross | 68.6 | 67.7 | 67.5 | 69.6 | 68.8 | 70.7 | 69.4 | 67.9 | 67.3 | 68.8 | 69.4 |
| 73 NDSS XEARLYGEM 21 c | Cross | 70.0 | 67.9 | 68.0 | 70.8 | 69.0 | 70.4 | 69.5 | 68.7 | 67.1 | 68.9 | 69.0 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 69.5 | 67.8 | 67.8 | 70.1 | 69.1 | 71.2 | 68.7 | 68.3 | 66.9 | 68.5 | 68.8 |
| 75 NDCG(FS)C1 | P arent | 70.1 | 68.1 | 67.9 | 70.3 | 69.1 | 70.4 | 69.5 | 67.3 | 66.8 | 68.6 | 68.6 |
| 76 NDSAB(MER-FS)C 15 | P arent | 69.3 | 67.6 | 67.4 | 69.7 | 69.7 | 69.8 | 68.6 | 67.5 | 67.2 | 69.0 | 68.6 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 69.3 | 66.9 | 67.0 | 69.8 | 68.2 | 70.4 | 68.5 | 67.3 | 67.0 | 67.6 | 68.4 |
| 78 NDBS 1011 X NDBS 21 (R-T)C9 | Cross | 68.9 | 68.1 | 68.0 | 70.5 | 69.6 | 70.9 | 69.2 | 68.2 | 67.6 | 69.2 | 69.4 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 2 la | Cross | 69.6 | 68.2 | 67.8 | 70.9 | 69.3 | 71.5 | 70.1 | 68.9 | 68.2 | 69.4 | 69.3 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 69.2 | 68.5 | 67.5 | 70.0 | 70.2 | 70.7 | 69.8 | 69.1 | 68.6 | 70.0 | 69.9 |

Table B14 (continued). Starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Pros per | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Pros per | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 69.1 | 67.3 | 67.2 | 70.1 | 68.0 | 70.4 | 68.5 | 68.0 | 66.7 | 68.6 | 69.5 |
| 82 NDBSK(HI-M)C3 XLeaming(S-FS)C6 | Cross | 70.7 | 68.1 | 68.3 | 70.6 | 69.8 | 70.8 | 69.7 | 68.8 | 67.7 | 69.1 | 69.8 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 69.7 | 69.3 | 68.7 | 71.3 | 70.5 | 70.9 | 70.1 | 70.0 | 67.8 | 70.2 | 70.3 |
| 84 NDSM(M-FS)C9 | P arent | 68.2 | 67.9 | 67.0 | 69.5 | 68.5 | 70.1 | 69.1 | 67.8 | 66.4 | 68.4 | 68.4 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 69.3 | 67.5 | 68.4 | 70.3 | 68.2 | 69.8 | 69.6 | 68.7 | 67.6 | 68.6 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 69.8 | 68.2 | 67.9 | 70.3 | 69.3 | 69.8 | 69.5 | 68.8 | 67.2 | 68.4 | 68.7 |
| 87 NDCG(FS)C1 ${ }^{\text {N }}$ NDBS 11(FR-M)C3 | Cross | 69.8 | 69.0 | 68.3 | 69.7 | 69.4 | 69.5 | 69.1 | 68.0 | 66.7 | 69.3 | 68.6 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 69.3 | 68.0 | 68.0 | 70.3 | 69.0 | 71.3 | 69.0 | 69.1 | 68.0 | 69.3 | 69.7 |
| 89 NDBS 1011 | P arent | 70.2 | 68.6 | 68.3 | 70.0 | 69.2 | 70.2 | 69.0 | 68.2 | 68.3 | 69.1 | 69.8 |
| 90 NDBS 1011 X NDS AB (MER-FS)C 15 | Cross | 69.4 | 68.3 | 68.1 | 70.0 | 69.2 | 71.0 | 69.5 | 68.7 | 68.3 | 68.9 | 69.9 |
| 91 Check 3 P IONEER 39N99 | Check | 71.9 | 70.1 | 69.9 | 71.4 | 70.3 | 71.9 | 71.8 | 69.9 | 69.2 | 70.6 | 70.5 |
| 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 69.0 | 67.9 | 67.8 | 70.5 | 68.9 | 70.3 | 68.7 | 68.4 | 67.0 | 68.4 | 70.1 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 71.1 | 68.6 | 69.0 | 70.3 | 70.1 | 71.1 | 69.9 | 69.0 | 67.8 | 70.1 | 70.1 |
| 94 NDL X NDBS 1011 | Cross | 70.3 | 69.0 | 68.8 | 70.7 | 70.3 | 71.3 | 70.2 | 69.4 | 68.1 | 69.9 | 69.5 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 69.3 | 67.9 | 67.5 | 70.0 | 68.5 | 70.6 | 69.1 | 68.7 | 67.7 | 68.1 | 69.4 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 69.5 | 68.6 | 68.9 | 70.8 | 69.2 | 70.3 | 69.6 | 69.2 | 68.4 | 68.8 | 69.3 |
| 97 NDSS | P arent | 69.8 | 66.9 | 67.2 | 69.3 | 68.3 | 68.7 | 67.8 | 67.2 | 66.4 | 67.9 | 68.1 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 69.7 | 67.6 | 67.5 | 69.0 | 69.4 | 70.3 | 68.7 | 68.3 | 67.5 | 68.4 | 69.2 |
| 99 NDCG(FS)C 1 X NDSHLC(M-FS)C5 | Cross | 68.9 | 67.7 | 68.0 | 70.3 | 68.6 | 70.1 | 68.4 | 69.5 | 67.2 | 68.2 | 70.5 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 70.7 | 68.7 | 69.1 | 70.7 | 70.5 | 71.2 | 70.2 | 69.4 | 67.9 | 70.4 | 70.2 |
| 101 NDBS22(R-T1)C9 XEARLYGEM 2 lb | Cross | 69.9 | 68.4 | 68.1 | 70.2 | 69.8 | 71.4 | 69.9 | 68.8 | 68.1 | 70.2 | 69.7 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 69.6 | 68.9 | 68.7 | 70.1 | 69.9 | 70.7 | 68.5 | 67.9 | 67.8 | 69.3 | 70.1 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 70.3 | 68.3 | 68.2 | 70.5 | 68.8 | 71.1 | 69.4 | 68.3 | 67.9 | 69.4 | 70.1 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 70.3 | 68.0 | 68.3 | 70.6 | 70.0 | 71.5 | 69.7 | 68.6 | 68.3 | 70.0 | 70.2 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 69.5 | 67.2 | 67.1 | 69.8 | 69.4 | 70.1 | 69.1 | 68.3 | 67.1 | 68.7 | 69.7 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 70.3 | 67.4 | 68.7 | 70.3 | 69.6 | 70.8 | 69.9 | 69.3 | 68.2 | 69.6 | 69.5 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 1a | Cross | 69.9 | 68.4 | 68.2 | 70.5 | 69.2 | 70.9 | 69.5 | 68.9 | 67.6 | 70.5 | 69.7 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 69.8 | 67.1 | 67.8 | 70.2 | 69.6 | 69.3 | 69.3 | 68.3 | 67.2 | 68.7 | 69.2 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 69.5 | 68.3 | 67.1 | 70.5 | 69.0 | 70.5 | 69.2 | 69.1 | 67.8 | 69.5 | 69.2 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 68.9 | 67.6 | 68.4 | 70.5 | 70.1 | 70.4 | 69.4 | 69.4 | 67.7 | 69.7 | 70.1 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 69.1 | 67.7 | 68.1 | 69.7 | 69.1 | 70.1 | 68.8 | 68.3 | 68.0 | 69.5 | 69.7 |
| 112 NDSS XEARLYGEM 2 la | Cross | 69.1 | 67.9 | 68.4 | 70.2 | 69.0 | 69.8 | 69.1 | 68.3 | 67.1 | 69.1 | 69.1 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 69.3 | 68.4 | 67.4 | 69.9 | 69.8 | 70.3 | 69.8 | 69.2 | 68.3 | 69.9 | 70.2 |
| 114 NDCG(FS)C1XNDL | Cross | 69.0 | 69.0 | 67.8 | 70.3 | 69.6 | 70.4 | 69.6 | 68.9 | 68.3 | 69.6 | 69.8 |
| 115 NDLXEARLYGEM 21 a | Cross | 69.4 | 68.2 | 68.4 | 70.7 | 70.5 | 71.6 | 70.8 | 69.6 | 68.5 | 70.0 | 70.2 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 69.5 | 68.1 | 67.8 | 70.5 | 68.8 | 70.5 | 69.8 | 68.5 | 68.1 | 68.6 | 70.1 |
| 117 NDBS 11(FR-M)C3 X NDBS 21 (R-T)C9 | Cross | 69.5 | 68.4 | 67.2 | 70.2 | 69.4 | 70.5 | 69.1 | 69.6 | 67.4 | 69.6 | 69.5 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 70.1 | 68.4 | 69.0 | 70.8 | 69.6 | 70.9 | 69.7 | 69.9 | 68.8 | 69.9 | 69.9 |
| 119 NDBS 11(FR-M)C3 X EARLYGEM 21 b | Cross | 69.5 | 68.4 | 68.0 | 70.0 | 69.4 | 70.6 | 69.6 | 69.4 | 67.4 | 69.3 | 69.7 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 68.9 | 67.8 | 67.8 | 70.4 | 69.7 | 69.3 | 69.9 | 68.6 | 67.1 | 69.9 | 69.3 |

Table B14 (continued). Starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B15. Lysine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21c | Cross | 0.28 | 0.29 | 0.32 | 0.26 | 0.29 | 0.27 | 0.28 | 0.31 | 0.33 | 0.31 | 0.30 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 0.31 | 0.31 | 0.32 | 0.29 | 0.31 | 0.29 | 0.29 | 0.33 | 0.33 | 0.33 | 0.31 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 0.28 | 0.29 | 0.31 | 0.28 | 0.29 | 0.27 | 0.28 | 0.32 | 0.34 | 0.33 | 0.31 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 0.29 | 0.29 | 0.31 | 0.27 | 0.29 | 0.24 | 0.29 | 0.32 | 0.35 | 0.32 | 0.31 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 0.27 | 0.28 | 0.30 | 0.27 | 0.28 | 0.24 | 0.29 | 0.31 | 0.32 | 0.31 | 0.30 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 0.29 | 0.32 | 0.31 | 0.28 | 0.29 | 0.26 | 0.29 | 0.32 | 0.34 | 0.33 | 0.32 |
| 7 NDSS XNDL | Cross | 0.30 | 0.29 | 0.32 | 0.29 | 0.29 | 0.26 | 0.30 | 0.34 | 0.35 | 0.33 | 0.32 |
| 8 NDBSK(HI-M)C3 X EARLYGEM 21 b | Cross | 0.27 | 0.28 | 0.30 | 0.27 | 0.28 | 0.27 | 0.27 | 0.31 | 0.33 | 0.31 | 0.31 |
| 9 NDL XEARLYGEM 2 lb | Cross | 0.28 | 0.28 | 0.31 | 0.27 | 0.27 | 0.25 | 0.28 | 0.32 | 0.34 | 0.31 | 0.31 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 0.28 | 0.28 | 0.30 | 0.28 | 0.29 | 0.26 | 0.29 | 0.31 | 0.34 | 0.32 | 0.30 |
| 11 NDBS 11(FR-M)C3 | P arent | 0.31 | 0.30 | 0.32 | 0.27 | 0.29 | 0.27 | 0.30 | 0.32 | 0.35 | 0.34 | 0.32 |
| 12 NDBSK(HI-M)C3 X NDSHLC(M-FS)C5 | Cross | 0.30 | 0.30 | 0.31 | 0.27 | 0.29 | 0.27 | 0.29 | 0.31 | 0.34 | 0.34 | 0.32 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 0.33 | 0.30 | 0.32 | 0.28 | 0.30 | 0.30 | 0.31 | 0.32 | 0.35 | 0.35 | 0.35 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 0.29 | 0.29 | 0.30 | 0.25 | 0.28 | 0.24 | 0.29 | 0.32 | 0.32 | 0.31 | 0.29 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 0.29 | 0.29 | 0.32 | 0.27 | 0.29 | 0.27 | 0.30 | 0.33 | 0.36 | 0.33 | 0.33 |
| 16 Check 4 DKC 43-27 VT3 | Check | 0.25 | 0.25 | 0.29 | 0.26 | 0.26 | 0.26 | 0.26 | 0.30 | 0.31 | 0.31 | 0.29 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 0.30 | 0.28 | 0.32 | 0.29 | 0.30 | 0.23 | 0.30 | 0.32 | 0.35 | 0.34 | 0.31 |
| 18 EARLYGEM 21 c | P arent | 0.27 | 0.28 | 0.30 | 0.26 | 0.28 | 0.25 | 0.26 | 0.31 | 0.31 | 0.31 | 0.29 |
| 19 Leaming(S-FS)C6 | P arent | 0.29 | 0.32 | 0.32 | 0.29 | 0.30 | 0.28 | 0.30 | 0.33 | 0.35 | 0.35 | 0.33 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{T} 1) \mathrm{C} 9$ | Cross | 0.30 | 0.29 | 0.31 | 0.26 | 0.29 | 0.25 | 0.29 | 0.32 | 0.33 | 0.32 | 0.31 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 0.28 | 0.28 | 0.31 | 0.26 | 0.28 | 0.25 | 0.30 | 0.32 | 0.33 | 0.33 | 0.30 |
| 22 NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 0.28 | 0.27 | 0.31 | 0.27 | 0.28 | 0.27 | 0.29 | 0.31 | 0.34 | 0.33 | 0.31 |
| 23 Check 1P IONEER 39 V 07 | Check | 0.29 | 0.29 | 0.31 | 0.29 | 0.28 | 0.31 | 0.29 | 0.34 | 0.34 | 0.33 | 0.32 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 0.30 | 0.31 | 0.32 | 0.27 | 0.30 | 0.26 | 0.30 | 0.31 | 0.34 | 0.34 | 0.31 |
| 25 Leaming(S-FS)C6 XNDBS22(R-T ) C9 | Cross | 0.29 | 0.31 | 0.31 | 0.29 | 0.30 | 0.27 | 0.30 | 0.32 | 0.35 | 0.33 | 0.31 |
| 26 Leaming(S-FS)C6 XNDBS 21 (R-T)C9 | Cross | 0.29 | 0.30 | 0.31 | 0.28 | 0.28 | 0.27 | 0.28 | 0.31 | 0.35 | 0.33 | 0.30 |
| 27 NDBSK(HI-M)C3 XEARLYGEM 21 l | Cross | 0.28 | 0.28 | 0.31 | 0.28 | 0.28 | 0.27 | 0.29 | 0.31 | 0.33 | 0.31 | 0.31 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 0.30 | 0.31 | 0.32 | 0.29 | 0.28 | 0.29 | 0.29 | 0.31 | 0.35 | 0.33 | 0.31 |
| 29 EARLYGEM 2 a X EARLYGEM 21 c | Cross | 0.27 | 0.29 | 0.29 | 0.26 | 0.27 | 0.26 | 0.27 | 0.31 | 0.31 | 0.30 | 0.30 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 0.27 | 0.30 | 0.30 | 0.28 | 0.28 | 0.27 | 0.28 | 0.31 | 0.33 | 0.31 | 0.31 |
| 31 Leaming(S-FS)C6 XNDSCD(FS-CS)C2 | Cross | 0.31 | 0.31 | 0.32 | 0.28 | 0.30 | 0.29 | 0.30 | 0.32 | 0.34 | 0.34 | 0.32 |
| 32 NDB SK(HIM)C3 XEARLYGEM 21 c | Cross | 0.28 | 0.29 | 0.30 | 0.27 | 0.27 | 0.25 | 0.27 | 0.31 | 0.34 | 0.32 | 0.29 |
| 33 NDBS 1011 XEARLYGEM 21 b | Cross | 0.27 | 0.29 | 0.30 | 0.27 | 0.28 | 0.28 | 0.28 | 0.30 | 0.32 | 0.32 | 0.31 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 0.29 | 0.29 | 0.31 | 0.29 | 0.30 | 0.25 | 0.29 | 0.30 | 0.34 | 0.33 | 0.31 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 0.28 | 0.30 | 0.31 | 0.29 | 0.29 | 0.26 | 0.29 | 0.31 | 0.34 | 0.32 | 0.30 |
| 36 NDSAB(MER-FS)C 15 X NDSHLC(M-FS)C5 | Cross | 0.28 | 0.29 | 0.31 | 0.27 | 0.28 | 0.28 | 0.29 | 0.31 | 0.33 | 0.32 | 0.31 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 0.29 | 0.29 | 0.32 | 0.29 | 0.29 | 0.29 | 0.30 | 0.32 | 0.34 | 0.33 | 0.31 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 0.28 | 0.29 | 0.30 | 0.27 | 0.28 | 0.24 | 0.28 | 0.32 | 0.33 | 0.32 | 0.30 |
| 39 EARLYGEM 2 lb X EARLYGEM 2 lc | Cross | 0.26 | 0.27 | 0.30 | 0.27 | 0.28 | 0.24 | 0.26 | 0.29 | 0.32 | 0.31 | 0.30 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 0.28 | 0.29 | 0.31 | 0.27 | 0.29 | 0.28 | 0.29 | 0.32 | 0.33 | 0.33 | 0.30 |

Table B15 (continued). Lysine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 0.28 | 0.30 | 0.32 | 0.28 | 0.29 | 0.25 | 0.28 | 0.32 | 0.32 | 0.33 | 0.30 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 0.28 | 0.29 | 0.31 | 0.27 | 0.28 | 0.25 | 0.27 | 0.31 | 0.33 | 0.31 | 0.30 |
| 43 NDBSK(HI-M)C3 X NDBS 22 (R-T 1)C9 | Cross | 0.28 | 0.29 | 0.31 | 0.29 | 0.29 | 0.27 | 0.28 | 0.32 | 0.33 | 0.33 | 0.31 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 0.31 | 0.28 | 0.32 | 0.29 | 0.30 | 0.27 | 0.29 | 0.33 | 0.35 | 0.34 | 0.32 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 0.30 | 0.31 | 0.33 | 0.28 | 0.31 | 0.31 | 0.29 | 0.33 | 0.35 | 0.33 | 0.33 |
| 46 NDLXNDBS22(R-T1)C9 | Cross | 0.29 | 0.30 | 0.31 | 0.29 | 0.29 | 0.25 | 0.28 | 0.31 | 0.35 | 0.32 | 0.31 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 0.30 | 0.29 | 0.31 | 0.28 | 0.28 | 0.31 | 0.30 | 0.31 | 0.34 | 0.34 | 0.32 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS)C 15 | Cross | 0.31 | 0.29 | 0.32 | 0.28 | 0.29 | 0.28 | 0.29 | 0.33 | 0.34 | 0.32 | 0.31 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 0.30 | 0.32 | 0.32 | 0.27 | 0.29 | 0.28 | 0.29 | 0.33 | 0.34 | 0.34 | 0.34 |
| 50 NDBS22(R-T1)C9 XEARLYGEM 21 l | Cross | 0.28 | 0.29 | 0.30 | 0.27 | 0.29 | 0.26 | 0.27 | 0.31 | 0.33 | 0.31 | 0.30 |
| 51 NDBS 22(R-T1)C9 | P arent | 0.28 | 0.30 | 0.31 | 0.29 | 0.29 | 0.28 | 0.28 | 0.32 | 0.33 | 0.32 | 0.31 |
| 52 NDSS XNDBS 1011 | Cross | 0.28 | 0.28 | 0.31 | 0.28 | 0.29 | 0.26 | 0.30 | 0.32 | 0.34 | 0.34 | 0.32 |
| 53 NDL | P arent | 0.28 | 0.28 | 0.30 | 0.28 | 0.27 | 0.27 | 0.29 | 0.31 | 0.34 | 0.33 | 0.32 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 0.29 | 0.29 | 0.31 | 0.28 | 0.28 | 0.27 | 0.29 | 0.32 | 0.34 | 0.32 | 0.31 |
| 55 NDBSK(HIM) C3 X NDBS 1011 | Cross | 0.29 | 0.30 | 0.30 | 0.26 | 0.28 | 0.27 | 0.28 | 0.31 | 0.33 | 0.32 | 0.30 |
| 56 NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 0.28 | 0.29 | 0.30 | 0.28 | 0.28 | 0.24 | 0.28 | 0.32 | 0.33 | 0.31 | 0.31 |
| 57 NDBS 11(FR-M)C3 X NDBS 22 (R-Tl)C9 | Cross | 0.30 | 0.31 | 0.31 | 0.27 | 0.29 | 0.26 | 0.29 | 0.31 | 0.34 | 0.32 | 0.31 |
| 58 EARLYGEM 2 lb | P arent | 0.28 | 0.29 | 0.30 | 0.25 | 0.27 | 0.24 | 0.28 | 0.30 | 0.33 | 0.31 | 0.31 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 0.29 | 0.29 | 0.31 | 0.28 | 0.29 | 0.28 | 0.29 | 0.32 | 0.34 | 0.31 | 0.32 |
| 60 Check 2 DKC 36-34 VT3 | Check | 0.30 | 0.28 | 0.29 | 0.26 | 0.27 | 0.27 | 0.27 | 0.30 | 0.32 | 0.31 | 0.30 |
| 61 NDBSK(HIM) C3 X NDSCD(FS-CS ) C 2 | Cross | 0.30 | 0.29 | 0.31 | 0.28 | 0.30 | 0.27 | 0.29 | 0.32 | 0.33 | 0.34 | 0.32 |
| 62 NDBS 22(R-T 1)C9 XEARLYGEM 21 c | Cross | 0.28 | 0.29 | 0.30 | 0.26 | 0.28 | 0.27 | 0.28 | 0.31 | 0.33 | 0.31 | 0.30 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 0.29 | 0.30 | 0.33 | 0.28 | 0.29 | 0.27 | 0.29 | 0.33 | 0.34 | 0.32 | 0.30 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 0.30 | 0.28 | 0.31 | 0.27 | 0.28 | 0.27 | 0.30 | 0.32 | 0.34 | 0.32 | 0.29 |
| 65 NDBS K(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 0.29 | 0.28 | 0.30 | 0.28 | 0.28 | 0.26 | 0.28 | 0.32 | 0.34 | 0.33 | 0.31 |
| 66 NDBS 22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 0.28 | 0.33 | 0.31 | 0.28 | 0.30 | 0.28 | 0.29 | 0.32 | 0.35 | 0.33 | 0.31 |
| 67 NDBS22(R-T1)C9 XNDSHLC(M-FS)C5 | Cross | 0.28 | 0.28 | 0.31 | 0.26 | 0.28 | 0.27 | 0.29 | 0.31 | 0.33 | 0.32 | 0.30 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 0.29 | 0.28 | 0.32 | 0.28 | 0.29 | 0.26 | 0.28 | 0.32 | 0.33 | 0.33 | 0.30 |
| 69 NDBSK(HIM) C 3 X NDBS 11(FR-M)C3 | Cross | 0.29 | 0.29 | 0.32 | 0.28 | 0.28 | 0.25 | 0.30 | 0.32 | 0.35 | 0.33 | 0.31 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 0.31 | 0.29 | 0.32 | 0.28 | 0.31 | 0.26 | 0.32 | 0.33 | 0.34 | 0.34 | 0.32 |
| 71 NDB S K (HI-M)C3 | P arent | 0.29 | 0.31 | 0.30 | 0.28 | 0.29 | 0.26 | 0.28 | 0.31 | 0.33 | 0.32 | 0.30 |
| 72 NDSS XNDBS21(R-T)C9 | Cross | 0.31 | 0.30 | 0.33 | 0.28 | 0.30 | 0.26 | 0.28 | 0.33 | 0.35 | 0.33 | 0.32 |
| 73 NDSS XEARLYGEM 21 c | Cross | 0.28 | 0.30 | 0.30 | 0.26 | 0.29 | 0.27 | 0.28 | 0.32 | 0.34 | 0.32 | 0.32 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 0.28 | 0.29 | 0.31 | 0.28 | 0.29 | 0.25 | 0.29 | 0.33 | 0.34 | 0.33 | 0.32 |
| 75 NDCG(FS)C1 | P arent | 0.29 | 0.29 | 0.31 | 0.27 | 0.30 | 0.26 | 0.29 | 0.33 | 0.34 | 0.33 | 0.32 |
| 76 NDSAB(MER-FS)C 15 | P arent | 0.29 | 0.30 | 0.32 | 0.29 | 0.29 | 0.30 | 0.30 | 0.34 | 0.35 | 0.33 | 0.33 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 0.29 | 0.32 | 0.32 | 0.28 | 0.30 | 0.26 | 0.31 | 0.33 | 0.34 | 0.35 | 0.33 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 0.28 | 0.28 | 0.31 | 0.26 | 0.28 | 0.25 | 0.28 | 0.32 | 0.34 | 0.32 | 0.31 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 0.29 | 0.29 | 0.31 | 0.27 | 0.29 | 0.24 | 0.28 | 0.31 | 0.33 | 0.31 | 0.31 |
| 80 NDBS 21 (R-T)C9 XEARLYGEM 21 a | Cross | 0.29 | 0.28 | 0.31 | 0.27 | 0.27 | 0.25 | 0.27 | 0.31 | 0.32 | 0.31 | 0.30 |

Table B15 (continued). Lysine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B15 (continued). Lysine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B16. Methionine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21c | Cross | 0.22 | 0.26 | 0.25 | 0.20 | 0.23 | 0.21 | 0.22 | 0.23 | 0.26 | 0.22 | 0.23 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 0.24 | 0.29 | 0.26 | 0.23 | 0.23 | 0.23 | 0.22 | 0.26 | 0.26 | 0.23 | 0.24 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 0.25 | 0.27 | 0.27 | 0.24 | 0.26 | 0.23 | 0.24 | 0.27 | 0.28 | 0.26 | 0.25 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 0.24 | 0.26 | 0.28 | 0.22 | 0.25 |  | 0.23 | 0.27 | 0.28 | 0.24 | 0.23 |
| 5 EARLYGEM 2 la X EARLYGEM 2 lb | Cross | 0.22 | 0.27 | 0.25 | 0.22 | 0.24 | 0.22 | 0.23 | 0.26 | 0.27 | 0.23 | 0.24 |
| 6 NDBS 1011 XNDSCD(FS-CS)C2 | Cross | 0.25 | 0.28 | 0.28 | 0.24 | 0.25 | 0.21 | 0.23 | 0.26 | 0.28 | 0.26 | 0.25 |
| 7 NDSS XNDL | Cross | 0.24 | 0.27 | 0.26 | 0.24 | 0.24 | 0.23 | 0.23 | 0.27 | 0.29 | 0.25 | 0.24 |
| 8 NDBSK(HI-M)C3 X EARLYGEM 21 lb | Cross | 0.23 | 0.26 | 0.27 | 0.21 | 0.23 | 0.22 | 0.22 | 0.24 | 0.26 | 0.21 | 0.23 |
| 9 NDL XEARLYGEM 2 lb | Cross | 0.22 | 0.26 | 0.25 | 0.20 | 0.22 | 0.21 | 0.22 | 0.26 | 0.28 | 0.21 | 0.22 |
| 10 NDBS 11(FR-M)C3 X EARLYGEM 21 c | Cross | 0.23 | 0.26 | 0.26 | 0.23 | 0.24 | 0.23 | 0.23 | 0.24 | 0.27 | 0.24 | 0.24 |
| 11 NDBS 11(FR-M)C3 | P arent | 0.26 | 0.28 | 0.28 | 0.23 | 0.26 | 0.24 | 0.25 | 0.28 | 0.31 | 0.27 | 0.25 |
| $12 \mathrm{NDBSK}(\mathrm{HI}-\mathrm{M}) \mathrm{C} 3 \mathrm{XNDSHLC}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 5$ | Cross | 0.23 | 0.29 | 0.27 | 0.23 | 0.25 | 0.23 | 0.22 | 0.25 | 0.27 | 0.25 | 0.24 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 0.26 | 0.26 | 0.28 | 0.23 | 0.23 | 0.25 | 0.26 | 0.27 | 0.26 | 0.27 | 0.26 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 0.24 | 0.26 | 0.26 | 0.21 | 0.25 | 0.23 | 0.24 | 0.26 | 0.25 | 0.25 | 0.23 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 0.25 | 0.28 | 0.29 | 0.23 | 0.25 | 0.22 | 0.25 | 0.27 | 0.29 | 0.25 | 0.26 |
| 16 Check 4 DKC 43-27 VT3 | Check | 0.19 | 0.22 | 0.22 | 0.19 | 0.18 | 0.20 | 0.19 | 0.20 | 0.22 | 0.19 | 0.19 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 0.25 | 0.27 | 0.29 | 0.23 | 0.27 |  | 0.24 | 0.27 | 0.29 | 0.25 | 0.24 |
| 18 EARLYGEM 21 c | P arent | 0.21 | 0.26 | 0.28 | 0.21 | 0.23 | 0.21 | 0.21 | 0.24 | 0.25 | 0.24 | 0.22 |
| 19 Leaming(S-FS)C6 | P arent | 0.23 | 0.27 | 0.27 | 0.22 | 0.24 | 0.24 | 0.22 | 0.27 | 0.28 | 0.26 | 0.24 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{T} 1) \mathrm{C} 9$ | Cross | 0.24 | 0.28 | 0.29 | 0.22 | 0.23 | 0.24 | 0.23 | 0.26 | 0.27 | 0.23 | 0.23 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 0.26 | 0.26 | 0.28 | 0.21 | 0.23 | 0.23 | 0.24 | 0.25 | 0.27 | 0.24 | 0.23 |
| 22 NDBS21(R-T)C9 X NDSHLC(M-FS)C5 | Cross | 0.25 | 0.25 | 0.27 | 0.24 | 0.24 | 0.24 | 0.25 | 0.25 | 0.27 | 0.25 | 0.25 |
| 23 Check 1P IONEER 39V07 | Check | 0.21 | 0.25 | 0.24 | 0.21 | 0.22 | 0.21 | 0.21 | 0.24 | 0.25 | 0.24 | 0.22 |
| 24 NDCG(FS)C 1 X NDSAB (MER-FS)C 15 | Cross | 0.24 | 0.27 | 0.26 | 0.21 | 0.23 | 0.22 | 0.24 | 0.27 | 0.26 | 0.27 | 0.25 |
| 25 Leaming(S-FS)C6 X NDBS 22(R-T 1)C9 | Cross | 0.22 | 0.27 | 0.25 | 0.22 | 0.25 | 0.24 | 0.22 | 0.25 | 0.27 | 0.24 | 0.24 |
| 26 Leaming(S-FS)C6 XNDBS 21 (R-T) C 9 | Cross | 0.23 | 0.28 | 0.26 | 0.20 | 0.21 | 0.21 | 0.21 | 0.24 | 0.29 | 0.25 | 0.22 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 la | Cross | 0.24 | 0.25 | 0.27 | 0.23 | 0.23 | 0.22 | 0.24 | 0.24 | 0.28 | 0.24 | 0.24 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 0.22 | 0.27 | 0.26 | 0.22 | 0.23 | 0.23 | 0.20 | 0.23 | 0.28 | 0.23 | 0.24 |
| 29 EARLYGEM 21 a X EARLYGEM 21 c | Cross | 0.22 | 0.26 | 0.26 | 0.21 | 0.23 | 0.22 | 0.23 | 0.24 | 0.26 | 0.24 | 0.24 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 0.22 | 0.28 | 0.26 | 0.23 | 0.24 | 0.21 | 0.23 | 0.24 | 0.28 | 0.22 | 0.23 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 0.24 | 0.27 | 0.27 | 0.23 | 0.25 | 0.26 | 0.23 | 0.26 | 0.27 | 0.25 | 0.24 |
| 32 NDBSK(HI-M)C 3 X EARLYGEM 21 c | Cross | 0.23 | 0.25 | 0.26 | 0.21 | 0.24 | 0.21 | 0.21 | 0.24 | 0.26 | 0.23 | 0.22 |
| 33 NDBS 1011 XEARLYGEM 2 lb | Cross | 0.23 | 0.26 | 0.26 | 0.22 | 0.23 | 0.22 | 0.21 | 0.23 | 0.26 | 0.23 | 0.24 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 0.22 | 0.26 | 0.26 | 0.23 | 0.25 | 0.21 | 0.23 | 0.24 | 0.28 | 0.24 | 0.26 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 0.23 | 0.27 | 0.29 | 0.22 | 0.24 | 0.22 | 0.22 | 0.23 | 0.29 | 0.25 | 0.24 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 0.23 | 0.26 | 0.27 | 0.22 | 0.25 | 0.23 | 0.24 | 0.24 | 0.28 | 0.24 | 0.23 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 0.24 | 0.27 | 0.28 | 0.24 | 0.26 | 0.24 | 0.25 | 0.25 | 0.29 | 0.25 | 0.25 |
| 38 NDCG(FS)C1XEARLYGEM 21 a | Cross | 0.23 | 0.28 | 0.26 | 0.23 | 0.23 | 0.21 | 0.22 | 0.24 | 0.28 | 0.24 | 0.24 |
| 39 EARLYGEM 2 lb XEARLYGEM 2 lc | Cross | 0.19 | 0.24 | 0.25 | 0.22 | 0.24 | 0.21 | 0.22 | 0.23 | 0.26 | 0.22 | 0.24 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 0.25 | 0.27 | 0.26 | 0.22 | 0.24 | 0.23 | 0.23 | 0.25 | 0.28 | 0.23 | 0.23 |

Table B16 (continued). Methionine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 0.26 | 0.27 | 0.27 | 0.23 | 0.25 | 0.23 | 0.24 | 0.27 | 0.27 | 0.26 | 0.23 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 0.22 | 0.27 | 0.28 | 0.21 | 0.24 | 0.20 | 0.22 | 0.24 | 0.26 | 0.24 | 0.23 |
| 43 NDBSK(HIM)C3 X NDBS 22 (R-T 1)C9 | Cross | 0.24 | 0.27 | 0.26 | 0.24 | 0.25 | 0.22 | 0.22 | 0.25 | 0.26 | 0.24 | 0.24 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 0.25 | 0.27 | 0.28 | 0.23 | 0.26 |  | 0.24 | 0.27 | 0.29 | 0.25 | 0.25 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 0.22 | 0.28 | 0.29 | 0.21 | 0.23 | 0.24 | 0.23 | 0.27 | 0.29 | 0.24 | 0.25 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 0.23 | 0.26 | 0.27 | 0.24 | 0.24 | 0.20 | 0.22 | 0.25 | 0.27 | 0.25 | 0.24 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS $) \mathrm{C} 5$ | Cross | 0.26 | 0.27 | 0.26 | 0.23 | 0.23 |  | 0.26 | 0.26 | 0.28 | 0.27 | 0.23 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS)C 15 | Cross | 0.26 | 0.26 | 0.28 | 0.22 | 0.23 | 0.22 | 0.22 | 0.26 | 0.28 | 0.25 | 0.23 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 0.26 | 0.29 | 0.27 | 0.21 | 0.24 | 0.24 | 0.26 | 0.28 | 0.28 | 0.26 | 0.27 |
| 50 NDBS22(R-T1)C9 X EARLYGEM 21 la | Cross | 0.24 | 0.27 | 0.27 | 0.21 | 0.25 | 0.23 | 0.21 | 0.24 | 0.27 | 0.23 | 0.22 |
| 51 NDBS 22(R-T1)C9 | P arent | 0.26 | 0.27 | 0.28 | 0.24 | 0.25 | 0.21 | 0.23 | 0.26 | 0.29 | 0.26 | 0.26 |
| 52 NDSS XNDBS 1011 | Cross | 0.23 | 0.27 | 0.28 | 0.23 | 0.23 |  | 0.24 | 0.26 | 0.28 | 0.26 | 0.25 |
| 53 NDL | P arent | 0.23 | 0.26 | 0.27 | 0.23 | 0.23 | 0.21 | 0.23 | 0.24 | 0.27 | 0.24 | 0.24 |
| 54 NDBS 1011 XLeaming (S-FS) C6 | Cross | 0.25 | 0.27 | 0.26 | 0.22 | 0.22 | 0.22 | 0.22 | 0.23 | 0.27 | 0.24 | 0.24 |
| 55 NDBSK(HL-M)C3 X NDBS 1011 | Cross | 0.26 | 0.28 | 0.26 | 0.25 | 0.23 |  | 0.22 | 0.24 | 0.26 | 0.24 | 0.24 |
| 56 NDSAB(MER-FS)C 15 XNDBS21(R-T)C9 | Cross | 0.23 | 0.27 | 0.27 | 0.23 | 0.24 | 0.21 | 0.24 | 0.25 | 0.27 | 0.25 | 0.24 |
| 57 NDBS 11(FR-M)C3 X NDBS 22 (R-Tl)C9 | Cross | 0.25 | 0.28 | 0.26 | 0.22 | 0.24 |  | 0.25 | 0.26 | 0.29 | 0.24 | 0.25 |
| 58 EARLYGEM 2 lb | P arent | 0.24 | 0.26 | 0.27 | 0.20 | 0.23 | 0.21 | 0.23 | 0.23 | 0.25 | 0.23 | 0.26 |
| 59 NDSAB(MER-FS)C15 X NDSM(M-FS)C9 | Cross | 0.25 | 0.26 | 0.27 | 0.23 | 0.24 | 0.22 | 0.23 | 0.27 | 0.29 | 0.25 | 0.25 |
| 60 Check 2 DKC 36-34 VT3 | Check | 0.22 | 0.24 | 0.22 | 0.20 | 0.22 | 0.22 | 0.21 | 0.21 | 0.24 | 0.21 | 0.22 |
| 61 NDBSK(HI-M)C3 X NDSCD(FS-CS)C2 | Cross | 0.25 | 0.26 | 0.27 | 0.22 | 0.26 | 0.24 | 0.24 | 0.26 | 0.27 | 0.26 | 0.26 |
| 62 NDBS22(R-T1)C9 XEARLYGEM 21 c | Cross | 0.22 | 0.26 | 0.28 | 0.22 | 0.23 | 0.22 | 0.22 | 0.24 | 0.26 | 0.23 | 0.23 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 0.25 | 0.26 | 0.28 | 0.23 | 0.24 |  | 0.23 | 0.25 | 0.27 | 0.25 | 0.24 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 0.27 | 0.29 | 0.29 | 0.24 | 0.24 | 0.23 | 0.25 | 0.25 | 0.28 | 0.25 | 0.24 |
| 65 NDBSK(HI-M)C3 X NDB S 21 (R-T)C 9 | Cross | 0.25 | 0.26 | 0.27 | 0.23 | 0.24 |  | 0.22 | 0.26 | 0.27 | 0.26 | 0.24 |
| 66 NDBS 22(R-T1)C9 XNDSAB (MER-FS)C 15 | Cross | 0.24 | 0.27 | 0.28 | 0.22 | 0.25 |  | 0.23 | 0.26 | 0.26 | 0.24 | 0.23 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 0.26 | 0.28 | 0.28 | 0.22 | 0.26 | 0.22 | 0.24 | 0.26 | 0.27 | 0.25 | 0.23 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 0.26 | 0.27 | 0.29 | 0.24 | 0.25 | 0.23 | 0.24 | 0.26 | 0.27 | 0.25 | 0.24 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 0.24 | 0.25 | 0.28 | 0.22 | 0.24 |  | 0.24 | 0.26 | 0.28 | 0.24 | 0.23 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 0.26 | 0.27 | 0.28 | 0.25 | 0.25 | 0.23 | 0.24 | 0.26 | 0.28 | 0.26 | 0.25 |
| 71 NDBSK(HIM)C3 | P arent | 0.25 | 0.27 | 0.26 | 0.23 | 0.24 | 0.21 | 0.23 | 0.25 | 0.27 | 0.25 | 0.23 |
| 72 NDSS X NDBS 21 (R-T)C9 | Cross | 0.25 | 0.27 | 0.28 | 0.23 | 0.24 | 0.22 | 0.22 | 0.27 | 0.28 | 0.24 | 0.23 |
| 73 NDSS XEARLYGEM 21 c | Cross | 0.22 | 0.28 | 0.27 | 0.22 | 0.24 | 0.22 | 0.22 | 0.25 | 0.29 | 0.24 | 0.24 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 0.25 | 0.27 | 0.28 | 0.23 | 0.25 | 0.22 | 0.25 | 0.25 | 0.30 | 0.26 | 0.25 |
| 75 NDCG(FS)C1 | P arent | 0.24 | 0.26 | 0.27 | 0.22 | 0.24 | 0.22 | 0.23 | 0.27 | 0.29 | 0.25 | 0.26 |
| 76 NDSAB(MER-FS)C 15 | Parent | 0.24 | 0.27 | 0.27 | 0.24 | 0.23 | 0.24 | 0.25 | 0.28 | 0.29 | 0.24 | 0.25 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 0.24 | 0.27 | 0.28 | 0.23 | 0.25 | 0.22 | 0.24 | 0.28 | 0.28 | 0.27 | 0.26 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 0.25 | 0.28 | 0.29 | 0.23 | 0.25 | 0.23 | 0.24 | 0.27 | 0.27 | 0.23 | 0.25 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 0.24 | 0.26 | 0.27 | 0.21 | 0.24 | 0.20 | 0.22 | 0.25 | 0.26 | 0.23 | 0.24 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 l | Cross | 0.25 | 0.25 | 0.28 | 0.23 | 0.23 | 0.21 | 0.22 | 0.24 | 0.26 | 0.22 | 0.22 |

Table B16 (continued). Methionine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 0.25 | 0.29 | 0.29 | 0.23 | 0.26 | 0.22 | 0.25 | 0.26 | 0.30 | 0.26 | 0.24 |
| 82 NDBSK(HI-M)C3 XLeaming(S-FS)C6 | Cross | 0.22 | 0.26 | 0.27 | 0.22 | 0.23 | 0.21 | 0.22 | 0.24 | 0.28 | 0.24 | 0.23 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 0.25 | 0.25 | 0.27 | 0.21 | 0.23 | 0.21 | 0.22 | 0.23 | 0.28 | 0.23 | 0.24 |
| 84 NDSM(M-FS)C9 | Parent | 0.27 | 0.27 | 0.29 | 0.25 | 0.26 | 0.24 | 0.24 | 0.27 | 0.30 | 0.26 | 0.27 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 0.25 | 0.28 | 0.26 | 0.23 | 0.26 | 0.24 | 0.23 | 0.26 | 0.28 | 0.25 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 0.24 | 0.27 | 0.27 | 0.21 | 0.24 | 0.23 | 0.23 | 0.25 | 0.29 | 0.26 | 0.24 |
| 87 NDCG(FS)C 1 X NDBS 11(FR-M)C3 | Cross | 0.24 | 0.24 | 0.27 | 0.24 | 0.23 | 0.24 | 0.23 | 0.26 | 0.30 | 0.23 | 0.26 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 2 la | Cross | 0.25 | 0.27 | 0.26 | 0.21 | 0.25 | 0.23 | 0.24 | 0.24 | 0.27 | 0.23 | 0.23 |
| 89 NDBS 1011 | Parent | 0.24 | 0.27 | 0.26 | 0.24 | 0.25 | 0.23 | 0.24 | 0.25 | 0.26 | 0.25 | 0.24 |
| 90 NDBS 1011 X NDS AB (MER-FS)C 15 | Cross | 0.25 | 0.27 | 0.27 | 0.23 | 0.25 |  | 0.24 | 0.25 | 0.27 | 0.25 | 0.24 |
| 91 Check 3 P IONEER 39N99 | Check | 0.20 | 0.23 | 0.24 | 0.19 | 0.22 | 0.19 | 0.18 | 0.23 | 0.25 | 0.22 | 0.21 |
| 92 NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 0.26 | 0.27 | 0.27 | 0.21 | 0.25 | 0.24 | 0.24 | 0.25 | 0.29 | 0.26 | 0.24 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 0.22 | 0.25 | 0.25 | 0.22 | 0.21 | 0.20 | 0.23 | 0.24 | 0.26 | 0.22 | 0.22 |
| 94 NDL XNDBS 1011 | Cross | 0.23 | 0.26 | 0.27 | 0.22 | 0.23 | 0.23 | 0.23 | 0.24 | 0.27 | 0.24 | 0.24 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 0.26 | 0.27 | 0.27 | 0.22 | 0.25 | 0.23 | 0.24 | 0.26 | 0.28 | 0.26 | 0.25 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 0.25 | 0.27 | 0.26 | 0.21 | 0.24 | 0.24 | 0.24 | 0.24 | 0.26 | 0.25 | 0.25 |
| 97 NDSS | Parent | 0.22 | 0.28 | 0.28 | 0.23 | 0.25 | 0.25 | 0.26 | 0.28 | 0.29 | 0.27 | 0.26 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 0.24 | 0.27 | 0.28 | 0.24 | 0.24 |  | 0.23 | 0.26 | 0.28 | 0.26 | 0.23 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 0.25 | 0.28 | 0.28 | 0.23 | 0.25 | 0.23 | 0.24 | 0.24 | 0.28 | 0.26 | 0.23 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 0.23 | 0.27 | 0.26 | 0.21 | 0.23 | 0.22 | 0.23 | 0.25 | 0.27 | 0.21 | 0.23 |
| 101 NDBS 22(R-T1)C9 XEARLYGEM 2 lb | Cross | 0.24 | 0.25 | 0.26 | 0.22 | 0.23 | 0.22 | 0.22 | 0.23 | 0.26 | 0.22 | 0.22 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 0.25 | 0.27 | 0.26 | 0.23 | 0.25 | 0.22 | 0.24 | 0.26 | 0.26 | 0.24 | 0.24 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 0.25 | 0.27 | 0.27 | 0.21 | 0.25 | 0.22 | 0.23 | 0.26 | 0.27 | 0.23 | 0.22 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 0.23 | 0.26 | 0.27 | 0.21 | 0.23 | 0.23 | 0.22 | 0.26 | 0.27 | 0.23 | 0.23 |
| 105 CGL(S-FR 2)C1X B S $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 0.25 | 0.27 | 0.28 | 0.22 | 0.23 | 0.22 | 0.23 | 0.26 | 0.28 | 0.23 | 0.24 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 0.22 | 0.27 | 0.24 | 0.21 | 0.23 | 0.21 | 0.22 | 0.24 | 0.26 | 0.24 | 0.23 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | 0.23 | 0.27 | 0.27 | 0.21 | 0.24 | 0.23 | 0.23 | 0.25 | 0.27 | 0.22 | 0.23 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 0.24 | 0.28 | 0.27 | 0.21 | 0.24 | 0.23 | 0.23 | 0.26 | 0.27 | 0.24 | 0.24 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 0.24 | 0.26 | 0.28 | 0.21 | 0.24 | 0.22 | 0.23 | 0.24 | 0.27 | 0.23 | 0.25 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 0.25 | 0.27 | 0.27 | 0.21 | 0.23 | 0.22 | 0.23 | 0.23 | 0.28 | 0.24 | 0.22 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 2 lb | Cross | 0.24 | 0.27 | 0.25 | 0.23 | 0.23 | 0.22 | 0.22 | 0.26 | 0.26 | 0.22 | 0.23 |
| 112 NDSS XEARLYGEM 21 a | Cross | 0.25 | 0.27 | 0.26 | 0.23 | 0.23 | 0.24 | 0.25 | 0.24 | 0.29 | 0.25 | 0.24 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 0.25 | 0.25 | 0.27 | 0.23 | 0.23 | 0.22 | 0.21 | 0.23 | 0.27 | 0.22 | 0.23 |
| 114 NDCG(FS)C1XNDL | Cross | 0.26 | 0.26 | 0.28 | 0.22 | 0.24 | 0.22 | 0.22 | 0.25 | 0.27 | 0.24 | 0.24 |
| 115 NDLXEARLYGEM 2 1a | Cross | 0.26 | 0.27 | 0.26 | 0.21 | 0.23 | 0.22 | 0.20 | 0.24 | 0.26 | 0.23 | 0.22 |
| 116 NDSM(M-FS)C9 XEARLYGEM 21 b | Cross | 0.24 | 0.27 | 0.28 | 0.22 | 0.24 | 0.22 | 0.23 | 0.26 | 0.28 | 0.24 | 0.24 |
| 117 NDBS 11(FR-M)C3 X NDBS 21 (R-T)C9 | Cross | 0.24 | 0.27 | 0.29 | 0.23 | 0.24 | 0.23 | 0.24 | 0.24 | 0.28 | 0.23 | 0.25 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 0.22 | 0.25 | 0.24 | 0.21 | 0.23 | 0.22 | 0.23 | 0.22 | 0.26 | 0.23 | 0.23 |
| 119 NDBS 11(FR-M)C3 X EARLYGEM 21 b | Cross | 0.26 | 0.27 | 0.26 | 0.22 | 0.24 | 0.23 | 0.22 | 0.24 | 0.27 | 0.23 | 0.23 |
| 120 NDBS 11(FR-M)C3 X Leaming(S-FS)C6 | Cross | 0.26 | 0.28 | 0.28 | 0.22 | 0.23 | 0.25 | 0.22 | 0.25 | 0.28 | 0.23 | 0.23 |

Table B16 (continued). Methionine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.


Table B17. Cysteine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 X EARLYGEM 21 c | Cross | 0.21 | 0.24 | 0.24 | 0.20 | 0.22 | 0.19 | 0.22 | 0.26 | 0.24 | 0.21 | 0.21 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 0.24 | 0.25 | 0.24 | 0.22 | 0.22 | 0.21 | 0.22 | 0.27 | 0.24 | 0.22 | 0.21 |
| 3 NDBSK(HI-M)C3 X NDSM(M-FS)C9 | Cross | 0.12 | 0.25 | 0.25 | 0.22 | 0.24 | 0.21 | 0.24 | 0.28 | 0.26 | 0.24 | 0.23 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 |  | 0.23 | 0.28 | 0.26 | 0.23 | 0.22 |
| 5 EARLYGEM 2 la XEARLYGEM 2 lb | Cross | 0.23 | 0.24 | 0.24 | 0.22 | 0.22 | 0.23 | 0.23 | 0.28 | 0.25 | 0.22 | 0.23 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 0.24 | 0.25 | 0.26 | 0.23 | 0.24 | 0.20 | 0.23 | 0.28 | 0.26 | 0.25 | 0.23 |
| 7 NDSS XNDL | Cross | 0.21 | 0.12 | 0.24 | 0.22 | 0.22 | 0.20 | 0.23 | 0.28 | 0.25 | 0.23 | 0.22 |
| 8 NDBSK(HI-M)C3 XEARLYGEM 21 b | Cross | 0.23 | 0.23 | 0.25 | 0.20 | 0.23 | 0.21 | 0.23 | 0.26 | 0.24 | 0.21 | 0.21 |
| 9 NDLXEARLYGEM 2 lb | Cross | 0.22 | 0.24 | 0.24 | 0.20 | 0.21 | 0.19 | 0.23 | 0.27 | 0.25 | 0.20 | 0.20 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross | 0.23 | 0.24 | 0.24 | 0.23 | 0.22 | 0.22 | 0.23 | 0.26 | 0.25 | 0.22 | 0.23 |
| 11 NDBS 11(FR-M)C3 | P arent | 0.24 | 0.25 | 0.25 | 0.22 | 0.23 | 0.22 | 0.25 | 0.29 | 0.27 | 0.24 | 0.22 |
| 12 NDBSK(HIM)C3 X NDSHLC(M-FS)C5 | Cross | 0.12 | 0.26 | 0.25 | 0.22 | 0.24 | 0.22 | 0.23 | 0.27 | 0.25 | 0.25 | 0.23 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 0.25 | 0.24 | 0.26 | 0.23 | 0.23 | 0.22 | 0.25 | 0.28 | 0.24 | 0.25 | 0.23 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 0.22 | 0.24 | 0.25 | 0.21 | 0.24 | 0.22 | 0.24 | 0.27 | 0.24 | 0.24 | 0.21 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 0.22 | 0.24 | 0.25 | 0.23 | 0.24 | 0.22 | 0.25 | 0.28 | 0.26 | 0.24 | 0.23 |
| 16 Check 4 DKC 43-27 VT3 | Check | 0.17 | 0.20 | 0.20 | 0.17 | 0.18 | 0.18 | 0.20 | 0.24 | 0.22 | 0.19 | 0.19 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross | 0.24 | 0.24 | 0.27 | 0.23 | 0.24 | 0.22 | 0.24 | 0.28 | 0.26 | 0.23 | 0.23 |
| 18 EARLYGEM 21 c | P arent | 0.20 | 0.23 | 0.26 | 0.22 | 0.22 | 0.21 | 0.22 | 0.26 | 0.23 | 0.23 | 0.21 |
| 19 Leaming(S-FS)C6 | P arent | 0.22 | 0.24 | 0.25 | 0.21 | 0.21 | 0.22 | 0.23 | 0.27 | 0.25 | 0.24 | 0.22 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{Tl}) \mathrm{C} 9$ | Cross | 0.23 | 0.25 | 0.26 | 0.22 | 0.23 | 0.23 | 0.24 | 0.27 | 0.25 | 0.23 | 0.21 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 0.23 | 0.24 | 0.26 | 0.21 | 0.22 | 0.22 | 0.24 | 0.26 | 0.25 | 0.23 | 0.22 |
| 22 NDBS 21 (R-T)C9 X NDSHLC(M-FS)C5 | Cross | 0.24 | 0.23 | 0.25 | 0.22 | 0.23 | 0.23 | 0.25 | 0.28 | 0.26 | 0.23 | 0.23 |
| 23 Check 1P IONEER 39V07 | Check | 0.19 | 0.23 | 0.21 | 0.20 | 0.21 | 0.19 | 0.21 | 0.25 | 0.22 | 0.21 | 0.19 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 0.22 | 0.24 | 0.23 | 0.21 | 0.22 | 0.21 | 0.23 | 0.28 | 0.24 | 0.24 | 0.22 |
| 25 Leaming(S-FS)C6 XNDBS22(R-Tl)C9 | Cross | 0.21 | 0.25 | 0.23 | 0.22 | 0.23 | 0.22 | 0.23 | 0.27 | 0.25 | 0.22 | 0.22 |
| 26 Leaming(S-FS)C6 X NDBS 21 (R-T) C 9 | Cross | 0.21 | 0.25 | 0.23 | 0.20 | 0.22 | 0.19 | 0.22 | 0.27 | 0.26 | 0.23 | 0.22 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 21 a | Cross | 0.22 | 0.23 | 0.25 | 0.23 | 0.21 | 0.20 | 0.25 | 0.27 | 0.26 | 0.22 | 0.22 |
| 28 NDL XLeaming(S-FS)C6 | Cross | 0.21 | 0.23 | 0.23 | 0.21 | 0.21 | 0.20 | 0.22 | 0.26 | 0.26 | 0.22 | 0.23 |
| 29 EARLYGEM 2 la XEARLYGEM 21 c | Cross | 0.22 | 0.24 | 0.25 | 0.22 | 0.22 | 0.21 | 0.22 | 0.27 | 0.24 | 0.23 | 0.22 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 0.21 | 0.24 | 0.25 | 0.23 | 0.23 | 0.20 | 0.23 | 0.26 | 0.26 | 0.22 | 0.21 |
| 31 Leaming(S-FS)C6 X NDSCD(FS-CS)C2 | Cross | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.23 | 0.22 | 0.27 | 0.25 | 0.23 | 0.23 |
| 32 NDBSK(HIM)C3 X EARLYGEM 21 c | Cross | 0.22 | 0.23 | 0.25 | 0.20 | 0.23 | 0.20 | 0.22 | 0.26 | 0.25 | 0.22 | 0.21 |
| 33 NDBS 1011 XEARLYGEM 2 lb | Cross | 0.21 | 0.24 | 0.25 | 0.21 | 0.22 | 0.22 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 0.22 | 0.24 | 0.26 | 0.22 | 0.24 | 0.21 | 0.23 | 0.27 | 0.26 | 0.22 | 0.24 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 0.21 | 0.24 | 0.25 | 0.22 | 0.24 | 0.21 | 0.23 | 0.26 | 0.26 | 0.23 | 0.23 |
| 36 NDSAB(MER-FS)C 15 XNDSHLC(M-FS)C5 | Cross | 0.24 | 0.23 | 0.25 | 0.22 | 0.24 | 0.21 | 0.24 | 0.27 | 0.25 | 0.23 | 0.22 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 0.22 | 0.24 | 0.26 | 0.22 | 0.24 | 0.22 | 0.24 | 0.28 | 0.25 | 0.24 | 0.22 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 0.22 | 0.24 | 0.24 | 0.23 | 0.23 | 0.21 | 0.24 | 0.27 | 0.25 | 0.23 | 0.22 |
| 39 EARLYGEM 2 lb X EARLYGEM 21 c | Cross | 0.20 | 0.23 | 0.23 | 0.22 | 0.23 | 0.21 | 0.22 | 0.26 | 0.25 | 0.22 | 0.22 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS ) 15 | Cross | 0.23 | 0.24 | 0.24 | 0.21 | 0.22 | 0.21 | 0.24 | 0.27 | 0.25 | 0.21 | 0.22 |

Table B17 (continued). Cysteine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 0.12 | 0.25 | 0.26 | 0.22 | 0.23 | 0.22 | 0.24 | 0.29 | 0.25 | 0.24 | 0.22 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 2 lb | Cross | 0.22 | 0.24 | 0.26 | 0.21 | 0.22 | 0.18 | 0.23 | 0.26 | 0.24 | 0.23 | 0.21 |
| 43 NDBSK(HI-M)C3 X NDBS 22 (R-T 1)C9 | Cross | 0.23 | 0.24 | 0.25 | 0.23 | 0.23 | 0.21 | 0.23 | 0.27 | 0.24 | 0.23 | 0.23 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 0.23 | 0.24 | 0.25 | 0.23 | 0.25 | 0.22 | 0.24 | 0.28 | 0.25 | 0.24 | 0.23 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 0.23 | 0.24 | 0.26 | 0.21 | 0.22 | 0.20 | 0.23 | 0.28 | 0.26 | 0.23 | 0.22 |
| 46 NDL XNDBS22(R-T1)C9 | Cross | 0.22 | 0.23 | 0.24 | 0.22 | 0.23 | 0.18 | 0.23 | 0.27 | 0.24 | 0.23 | 0.22 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 0.24 | 0.25 | 0.24 | 0.22 | 0.23 |  | 0.24 | 0.28 | 0.25 | 0.24 | 0.22 |
| 48 NDBS 11(FR-M)C3 X NDSAB (MER-FS)C 15 | Cross | 0.24 | 0.23 | 0.25 | 0.22 | 0.22 | 0.20 | 0.23 | 0.27 | 0.25 | 0.24 | 0.21 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 0.23 | 0.27 | 0.25 | 0.22 | 0.23 | 0.22 | 0.25 | 0.28 | 0.26 | 0.24 | 0.25 |
| 50 NDBS22(R-T1)C9 X EARLYGEM 21 la | Cross | 0.23 | 0.25 | 0.25 | 0.22 | 0.24 | 0.22 | 0.23 | 0.26 | 0.25 | 0.22 | 0.22 |
| 51 NDBS 22(R-T1)C9 | P arent | 0.24 | 0.25 | 0.26 | 0.24 | 0.25 | 0.21 | 0.25 | 0.29 | 0.26 | 0.24 | 0.24 |
| 52 NDSS XNDBS 1011 | Cross | 0.21 | 0.25 | 0.25 | 0.23 | 0.22 |  | 0.24 | 0.28 | 0.25 | 0.23 | 0.22 |
| 53 NDL | P arent | 0.22 | 0.24 | 0.24 | 0.21 | 0.22 | 0.20 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 0.23 | 0.24 | 0.24 | 0.22 | 0.22 | 0.22 | 0.22 | 0.25 | 0.25 | 0.22 | 0.22 |
| 55 NDBSK(HIM)C3 X NDBS 1011 | Cross | 0.23 | 0.25 | 0.23 | 0.24 | 0.21 |  | 0.23 | 0.26 | 0.24 | 0.23 | 0.22 |
| 56 NDSAB(MER-FS)C 15 XNDBS21(R-T)C9 | Cross | 0.21 | 0.24 | 0.24 | 0.22 | 0.22 | 0.21 | 0.24 | 0.25 | 0.25 | 0.23 | 0.22 |
| 57 NDBS 11(FR-M)C3 X NDBS 22(R-T l)C9 | Cross | 0.23 | 0.25 | 0.24 | 0.21 | 0.24 | 0.22 | 0.24 | 0.27 | 0.26 | 0.23 | 0.23 |
| 58 EARLYGEM 2 lb | Parent | 0.23 | 0.24 | 0.25 | 0.20 | 0.23 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.24 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 0.24 | 0.24 | 0.25 | 0.23 | 0.23 | 0.22 | 0.24 | 0.27 | 0.26 | 0.23 | 0.23 |
| 60 Check 2 DKC 36-34 VT3 | Check | 0.19 | 0.22 | 0.21 | 0.19 | 0.20 | 0.19 | 0.22 | 0.23 | 0.22 | 0.19 | 0.19 |
| 61 NDBSK(HIM) C 3 X NDSCD(FS-CS)C2 | Cross | 0.22 | 0.24 | 0.25 | 0.21 | 0.24 | 0.22 | 0.24 | 0.28 | 0.25 | 0.24 | 0.23 |
| 62 NDBS 22(R-T 1)C9 XEARLYGEM 21 c | Cross | 0.23 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 63 NDL XNDBS 11(FR-M)C3 | Cross | 0.24 | 0.12 | 0.24 | 0.22 | 0.22 |  | 0.23 | 0.27 | 0.25 | 0.23 | 0.22 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 0.25 | 0.25 | 0.26 | 0.23 | 0.23 | 0.22 | 0.24 | 0.27 | 0.26 | 0.23 | 0.22 |
| 65 NDBSK(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 0.23 | 0.24 | 0.25 | 0.23 | 0.22 |  | 0.23 | 0.28 | 0.24 | 0.24 | 0.22 |
| 66 NDBS22(R-T1)C9 X NDSAB (MER-FS)C 15 | Cross | 0.23 | 0.24 | 0.26 | 0.21 | 0.24 |  | 0.24 | 0.27 | 0.24 | 0.23 | 0.22 |
| 67 NDBS22(R-T1)C9 XNDSHLC(M-FS)C5 | Cross | 0.24 | 0.25 | 0.26 | 0.21 | 0.24 | 0.21 | 0.24 | 0.27 | 0.25 | 0.24 | 0.23 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 0.25 | 0.24 | 0.27 | 0.22 | 0.23 | 0.22 | 0.24 | 0.28 | 0.25 | 0.23 | 0.22 |
| 69 NDBSK(HIM)C3 X NDBS 11(FR-M)C3 | Cross | 0.24 | 0.24 | 0.25 | 0.22 | 0.23 |  | 0.23 | 0.28 | 0.25 | 0.23 | 0.22 |
| 70 NDSS XNDBS 11(FR-M)C3 | Cross | 0.25 | 0.24 | 0.27 | 0.23 | 0.23 | 0.21 | 0.24 | 0.28 | 0.26 | 0.24 | 0.22 |
| 71 NDB S K(HIM) C3 | P arent | 0.24 | 0.24 | 0.25 | 0.22 | 0.23 | 0.20 | 0.24 | 0.28 | 0.26 | 0.24 | 0.22 |
| 72 NDSS XNDBS21(R-T)C9 | Cross | 0.24 | 0.24 | 0.24 | 0.22 | 0.23 | 0.21 | 0.22 | 0.27 | 0.25 | 0.23 | 0.21 |
| 73 NDSS XEARLYGEM 21 c | Cross | 0.21 | 0.25 | 0.25 | 0.22 | 0.23 | 0.21 | 0.23 | 0.27 | 0.26 | 0.23 | 0.22 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 0.25 | 0.24 | 0.25 | 0.22 | 0.24 | 0.21 | 0.24 | 0.28 | 0.26 | 0.24 | 0.23 |
| 75 NDCG(FS)C1 | Parent | 0.22 | 0.24 | 0.25 | 0.22 | 0.22 | 0.20 | 0.23 | 0.28 | 0.27 | 0.23 | 0.23 |
| 76 NDSAB(MER-FS)C 15 | Parent | 0.23 | 0.24 | 0.25 | 0.22 | 0.21 | 0.21 | 0.24 | 0.28 | 0.26 | 0.22 | 0.23 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 0.23 | 0.23 | 0.26 | 0.22 | 0.23 | 0.20 | 0.24 | 0.28 | 0.25 | 0.24 | 0.23 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 0.24 | 0.25 | 0.26 | 0.22 | 0.24 | 0.23 | 0.24 | 0.28 | 0.25 | 0.23 | 0.23 |
| 79 NDSAB(MER-FS)C 15 X EARLYGEM 2 la | Cross | 0.22 | 0.23 | 0.24 | 0.20 | 0.22 | 0.19 | 0.23 | 0.27 | 0.24 | 0.22 | 0.22 |
| 80 NDBS 21 (R-T)C9 XEARLYGEM 21 a | Cross | 0.23 | 0.23 | 0.26 | 0.21 | 0.22 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.21 |

Table B17 (continued). Cysteine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 0.24 | 0.25 | 0.27 | 0.22 | 0.24 | 0.21 | 0.25 | 0.27 | 0.26 | 0.23 | 0.22 |
| 82 NDBSK(HI-M)C3 X Leaming(S-FS)C6 | Cross | 0.22 | 0.23 | 0.24 | 0.22 | 0.22 | 0.21 | 0.23 | 0.27 | 0.25 | 0.23 | 0.22 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 0.25 | 0.23 | 0.24 | 0.21 | 0.22 | 0.20 | 0.23 | 0.26 | 0.26 | 0.21 | 0.23 |
| 84 NDSM(M-FS)C9 | P arent | 0.26 | 0.24 | 0.27 | 0.25 | 0.24 | 0.22 | 0.24 | 0.29 | 0.27 | 0.24 | 0.24 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 0.22 | 0.25 | 0.24 | 0.21 | 0.24 | 0.23 | 0.23 | 0.28 | 0.26 | 0.23 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 0.23 | 0.24 | 0.24 | 0.21 | 0.23 | 0.21 | 0.23 | 0.27 | 0.25 | 0.24 | 0.23 |
| 87 NDCG(FS)C1 ${ }^{\text {N NDBS 11(FR-M)C3 }}$ | Cross | 0.23 | 0.22 | 0.25 | 0.22 | 0.23 | 0.22 | 0.23 | 0.27 | 0.26 | 0.21 | 0.23 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 0.23 | 0.24 | 0.25 | 0.21 | 0.23 | 0.22 | 0.23 | 0.26 | 0.24 | 0.23 | 0.22 |
| 89 NDBS 1011 | Parent | 0.24 | 0.25 | 0.25 | 0.23 | 0.24 | 0.22 | 0.24 | 0.27 | 0.24 | 0.23 | 0.22 |
| 90 NDBS 1011 X NDSAB(MER-FS)C 15 | Cross | 0.23 | 0.24 | 0.26 | 0.22 | 0.23 |  | 0.23 | 0.27 | 0.24 | 0.23 | 0.22 |
| 91 Check 3 P IONEER 39N99 | Check | 0.18 | 0.21 | 0.22 | 0.19 | 0.21 | 0.18 | 0.20 | 0.25 | 0.23 | 0.20 | 0.20 |
| 92 NDSM(M-FS)C9 XNDSHLC(M-FS)C5 | Cross | 0.24 | 0.25 | 0.25 | 0.20 | 0.24 | 0.23 | 0.23 | 0.27 | 0.26 | 0.24 | 0.23 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 0.21 | 0.23 | 0.24 | 0.21 | 0.22 | 0.19 | 0.22 | 0.27 | 0.24 | 0.22 | 0.21 |
| 94 NDL X NDBS 1011 | Cross | 0.23 | 0.23 | 0.25 | 0.21 | 0.22 | 0.21 | 0.23 | 0.26 | 0.25 | 0.23 | 0.23 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 0.26 | 0.24 | 0.26 | 0.21 | 0.24 | 0.22 | 0.23 | 0.28 | 0.25 | 0.25 | 0.23 |
| 96 NDL XNDSM(M-FS)C9 | Cross | 0.24 | 0.24 | 0.25 | 0.21 | 0.23 | 0.21 | 0.24 | 0.26 | 0.24 | 0.23 | 0.23 |
| 97 NDSS | Parent | 0.20 | 0.25 | 0.26 | 0.23 | 0.24 | 0.22 | 0.24 | 0.28 | 0.27 | 0.24 | 0.23 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 0.23 | 0.24 | 0.26 | 0.24 | 0.23 |  | 0.24 | 0.27 | 0.25 | 0.24 | 0.22 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 0.23 | 0.25 | 0.25 | 0.22 | 0.23 | 0.22 | 0.24 | 0.26 | 0.26 | 0.24 | 0.22 |
| 100 NDL X NDBSK(HI-M)C3 | Cross | 0.20 | 0.24 | 0.24 | 0.21 | 0.22 | 0.21 | 0.23 | 0.27 | 0.25 | 0.21 | 0.22 |
| 101 NDBS 22(R-T1)C9 XEARLYGEM 2 lb | Cross | 0.23 | 0.22 | 0.25 | 0.22 | 0.22 | 0.21 | 0.23 | 0.27 | 0.25 | 0.22 | 0.21 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 0.24 | 0.24 | 0.24 | 0.22 | 0.23 | 0.21 | 0.24 | 0.28 | 0.25 | 0.23 | 0.23 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 0.22 | 0.24 | 0.24 | 0.21 | 0.23 | 0.22 | 0.24 | 0.26 | 0.25 | 0.23 | 0.21 |
| 104 NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 0.22 | 0.24 | 0.25 | 0.21 | 0.23 | 0.23 | 0.23 | 0.27 | 0.25 | 0.22 | 0.21 |
| $105 \mathrm{CGL}(\mathrm{S}-\mathrm{FR} 2) \mathrm{C} 1 \mathrm{XB}$ S $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 0.24 | 0.24 | 0.27 | 0.21 | 0.23 | 0.21 | 0.23 | 0.27 | 0.25 | 0.22 | 0.23 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 2 lc | Cross | 0.22 | 0.25 | 0.23 | 0.21 | 0.22 | 0.21 | 0.23 | 0.27 | 0.24 | 0.23 | 0.22 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 21 a | Cross | 0.22 | 0.24 | 0.24 | 0.21 | 0.23 | 0.21 | 0.24 | 0.27 | 0.25 | 0.21 | 0.22 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 0.21 | 0.25 | 0.24 | 0.21 | 0.23 | 0.20 | 0.23 | 0.27 | 0.25 | 0.23 | 0.22 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 0.22 | 0.24 | 0.25 | 0.21 | 0.23 | 0.10 | 0.24 | 0.27 | 0.25 | 0.23 | 0.23 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 0.23 | 0.25 | 0.24 | 0.22 | 0.22 | 0.21 | 0.24 | 0.26 | 0.26 | 0.23 | 0.22 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 0.22 | 0.24 | 0.25 | 0.22 | 0.21 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 112 NDSS XEARLYGEM 21 a | Cross | 0.23 | 0.24 | 0.25 | 0.22 | 0.23 | 0.22 | 0.24 | 0.28 | 0.27 | 0.23 | 0.22 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 0.23 | 0.23 | 0.25 | 0.23 | 0.21 | 0.21 | 0.23 | 0.27 | 0.24 | 0.22 | 0.21 |
| 114 NDCG(FS)C1XNDL | Cross | 0.23 | 0.24 | 0.25 | 0.21 | 0.22 | 0.20 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 115 NDLXEARLYGEM 2 1a | Cross | 0.23 | 0.23 | 0.25 | 0.22 | 0.21 | 0.22 | 0.22 | 0.26 | 0.24 | 0.22 | 0.21 |
| 116 NDSM(M-FS)C9 X EARLYGEM 21 b | Cross | 0.23 | 0.25 | 0.25 | 0.21 | 0.24 | 0.21 | 0.23 | 0.27 | 0.25 | 0.23 | 0.23 |
| 117 NDBS $11(\mathrm{FR}-\mathrm{M}) \mathrm{C} 3$ X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 0.24 | 0.25 | 0.26 | 0.22 | 0.23 | 0.21 | 0.24 | 0.26 | 0.26 | 0.22 | 0.23 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 0.22 | 0.23 | 0.24 | 0.21 | 0.22 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.21 |
| 119 NDBS 11(FR-M)C3 X EARLYGEM 21 b | Cross | 0.24 | 0.25 | 0.25 | 0.22 | 0.23 | 0.22 | 0.23 | 0.27 | 0.25 | 0.22 | 0.22 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 0.24 | 0.25 | 0.25 | 0.21 | 0.22 | 0.23 | 0.21 | 0.27 | 0.26 | 0.22 | 0.21 |

Table B17 (continued). Cysteine (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 11 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2011 |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 NDLXNDSHLC(M-FS)C5 | Cross | 0.24 | 0.12 | 0.25 | 0.21 | 0.23 | 0.20 | 0.23 | 0.27 | 0.24 | 0.22 | 0.23 |
| 122 NDL XNDSAB(MER-FS)C 15 | Cross | 0.11 | 0.24 | 0.23 | 0.22 | 0.22 | 0.20 | 0.22 | 0.27 | 0.24 | 0.22 | 0.21 |
| 123 NDCG(FS)C1XNDBS22(R-T1)C9 | Cross | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.24 | 0.28 | 0.25 | 0.22 | 0.22 |
| 124 NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 0.22 | 0.24 | 0.25 | 0.21 | 0.22 | 0.21 | 0.24 | 0.29 | 0.25 | 0.24 | 0.22 |
| $125 \mathrm{CGSS} 21(\mathrm{~S}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XBS} 21 \mathrm{CGSS}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.24 | 0.27 | 0.24 | 0.21 | 0.23 |
| 126 NDCG(FS)C1 ${ }^{\text {d }}$ NDBS21(R-T)C9 | Cross | 0.22 | 0.25 | 0.25 | 0.22 | 0.22 | 0.21 | 0.23 | 0.28 | 0.25 | 0.23 | 0.22 |
| 127 NDBS 22(R-T1)C9 X NDBS21(R-T)C9 | Cross | 0.23 | 0.24 | 0.25 | 0.23 | 0.22 | 0.22 | 0.23 | 0.27 | 0.24 | 0.22 | 0.21 |
| 128 Leaming(S-FS)C6 X EARLYGEM 2 lb | Cross | 0.21 | 0.24 | 0.25 | 0.22 | 0.22 | 0.22 | 0.23 | 0.26 | 0.24 | 0.22 | 0.21 |
| 129 NDBS 1011 XNDSM(M-FS)C9 | Cross | 0.24 | 0.24 | 0.25 | 0.21 | 0.23 | 0.22 | 0.23 | 0.27 | 0.26 | 0.23 | 0.21 |
| 130 NDLXEARLYGEM 21 c | Cross | 0.22 | 0.23 | 0.24 | 0.20 | 0.23 | 0.20 | 0.23 | 0.26 | 0.24 | 0.21 | 0.21 |
| 131 NDLXNDSCD(FS-CS)C2 | Cross | 0.24 | 0.23 | 0.25 | 0.23 | 0.23 | 0.21 | 0.22 | 0.27 | 0.25 | 0.23 | 0.23 |
| 132 EARLYGEM 21 l | P arent | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.19 | 0.23 | 0.28 | 0.25 | 0.22 | 0.22 |
| 133 NDCG(FS)C1XNDBSK(HI-M)C3 | Cross | 0.23 | 0.25 | 0.24 | 0.22 | 0.24 |  | 0.23 | 0.27 | 0.26 | 0.23 | 0.22 |
| 134 NDSCD(FS-CS)C2 X EARLYGEM 21 c | Cross | 0.22 | 0.23 | 0.25 | 0.22 | 0.22 | 0.21 | 0.23 | 0.26 | 0.24 | 0.22 | 0.22 |
| 135 NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 0.24 | 0.23 | 0.27 | 0.23 | 0.24 | 0.23 | 0.25 | 0.29 | 0.27 | 0.24 | 0.22 |
| 136 NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 0.23 | 0.25 | 0.26 | 0.23 | 0.23 | 0.21 | 0.24 | 0.29 | 0.25 | 0.25 | 0.22 |
| 137 NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | 0.25 | 0.24 | 0.25 | 0.22 | 0.23 | 0.20 | 0.23 | 0.27 | 0.25 | 0.22 | 0.22 |
| 138 Leaming(S-FS)C6 XEARLYGEM 2 la | Cross | 0.23 | 0.23 | 0.24 | 0.22 | 0.22 | 0.20 | 0.22 | 0.27 | 0.25 | 0.22 | 0.21 |
| 139 NDSS XNDCG(FS)C1 | Cross | 0.23 | 0.24 | 0.25 | 0.24 | 0.24 | 0.22 | 0.25 | 0.28 | 0.25 | 0.23 | 0.22 |
| 140 NDSM(M-FS)C9 X NDSCD(FS-CS)C2 | Cross | 0.12 | 0.24 | 0.27 | 0.23 | 0.23 | 0.21 | 0.22 | 0.29 | 0.26 | 0.24 | 0.22 |
| 141 NDBS21(R-T)C9 X NDSCD(FS-CS)C2 | Cross | 0.24 | 0.25 | 0.24 | 0.22 | 0.23 | 0.22 | 0.24 | 0.29 | 0.25 | 0.23 | 0.23 |
| 142 NDCG(FS)C1XNDBS 1011 | Cross | 0.23 | 0.24 | 0.24 | 0.22 | 0.23 | 0.21 | 0.23 | 0.27 | 0.25 | 0.23 | 0.21 |
| 143 NDBS 1011 X EARLYGEM 2 la | Cross | 0.24 | 0.25 | 0.25 | 0.21 | 0.23 | 0.19 | 0.23 | 0.26 | 0.25 | 0.21 | 0.21 |
| 144 NDSHLC(M-FS)C5 | P arent | 0.24 | 0.25 | 0.25 | 0.22 | 0.25 | 0.23 | 0.24 | 0.27 | 0.25 | 0.25 | 0.24 |
| Experiment mean |  | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.23 | 0.27 | 0.25 | 0.23 | 0.22 |
| Mean of parental populations |  | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.24 | 0.28 | 0.25 | 0.23 | 0.23 |
| Mean of population crosses |  | 0.22 | 0.24 | 0.25 | 0.22 | 0.23 | 0.21 | 0.23 | 0.27 | 0.25 | 0.23 | 0.22 |
| Mean of checks |  | 0.20 | 0.23 | 0.23 | 0.20 | 0.21 | 0.19 | 0.22 | 0.26 | 0.23 | 0.21 | 0.21 |
| LSD (0.05) |  | 0.07 | 0.05 | 0.02 | 0.02 | 0.01 | 0.04 | 0.01 | 0.02 | 0.01 | 0.01 | 0.02 |
| CV |  | 14.97 | 10.83 | 4.08 | 4.76 | 3.18 | 8.73 | 2.82 | 3.23 | 2.89 | 2.95 | 3.75 |
| MSE |  | 1.1E-03 | $6.6 \mathrm{E}-04$ | $1.0 \mathrm{E}-04$ | 1.1E-04 | $5.2 \mathrm{E}-05$ | $3.4 \mathrm{E}-04$ | 4.3E-05 | 7.6E-05 | 5.2E-05 | $4.5 \mathrm{E}-05$ | $6.9 \mathrm{E}-05$ |

Table B18. High fermentable corn starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.


Table B18 (continued). High fermentable corn starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Pros per | Thompson | Casselton | Larimore | Prosper | Thompson |
| 41 NDBS21(R-T)C9 | P arent | 46.4 | 50.3 | 45.4 | 46.6 | 43.4 | 50.6 | 48.9 | 53.6 |
| 42 NDSAB(MER-FS)C 15 XEARLYGEM 21 b | Cross | 46.3 | 50.4 | 44.6 | 46.3 | 43.4 | 52.4 | 50.8 | 53.8 |
| 43 NDBSK(HI-M)C3 X NDBS 22(R-T1)C9 | Cross | 46.3 | 49.1 | 44.5 | 44.9 | 42.3 | 50.6 | 47.4 | 50.7 |
| 44 NDSS XNDBSK(HI-M)C3 | Cross | 45.5 | 48.8 | 43.3 | 47.0 | 43.2 | 50.5 | 48.9 | 53.0 |
| 45 NDSS XLeaming(S-FS)C6 | Cross | 45.9 | 49.5 | 44.4 | 46.8 | 43.3 | 51.9 | 48.3 | 52.8 |
| 46 NDLXNDBS22(R-T 1)C9 | Cross | 46.6 | 49.6 | 44.9 | 46.2 | 41.9 | 51.1 | 48.7 | 51.8 |
| 47 NDSCD(FS-CS)C2 X NDSHLC(M-FS)C5 | Cross | 47.1 | 50.5 | 44.8 | 47.1 | 43.5 | 51.9 | 49.6 | 53.0 |
| 48 NDBS 11(FR-M)C3 X NDS AB (MER-FS)C 15 | Cross | 47.0 | 50.0 | 44.9 | 45.0 | 42.9 | 51.1 | 49.8 | 52.2 |
| 49 NDSS XNDSM(M-FS)C9 | Cross | 46.0 | 50.4 | 44.6 | 45.7 | 43.0 | 51.1 | 50.0 | 52.4 |
| 50 NDBS 22(R-T1)C9 XEARLYGEM 21 l | Cross | 46.3 | 50.5 | 45.6 | 45.5 | 44.3 | 51.3 | 48.9 | 53.8 |
| 51 NDBS 22(R-T1)C9 | Parent | 46.8 | 49.8 | 43.0 | 44.7 | 42.1 | 50.2 | 47.9 | 53.2 |
| 52 NDSS X NDBS 1011 | Cross | 46.2 | 50.2 | 45.0 | 45.9 | 42.1 | 50.9 | 50.1 | 53.1 |
| 53 NDL | Parent | 46.0 | 49.1 | 44.5 | 46.1 | 44.2 | 51.8 | 50.7 | 52.0 |
| 54 NDBS 1011 XLeaming(S-FS)C6 | Cross | 45.2 | 50.5 | 44.4 | 44.5 | 42.3 | 51.6 | 49.5 | 52.0 |
| 55 NDBSK(HI-M)C3 X NDBS 1011 | Cross | 45.7 | 48.8 | 45.5 | 45.0 | 42.3 | 51.9 | 48.5 | 52.2 |
| 56 NDSAB(MER-FS)C 15 X NDBS 21 (R-T)C9 | Cross | 46.3 | 51.2 | 44.5 | 47.1 | 43.7 | 51.1 | 49.4 | 52.1 |
| 57 NDBS 11(FR-M)C3 X NDBS22(R-T 1)C9 | Cross | 45.7 | 49.5 | 45.4 | 45.9 | 43.7 | 51.4 | 50.3 | 52.4 |
| 58 EARLYGEM 2 lb | P arent | 46.3 | 50.8 | 45.0 | 47.4 | 44.2 | 52.7 | 50.4 | 53.1 |
| 59 NDSAB(MER-FS)C 15 X NDSM(M-FS)C9 | Cross | 45.4 | 49.9 | 43.7 | 44.2 | 42.4 | 50.8 | 49.7 | 53.2 |
| 60 Check 2 DKC 36-34 VT3 | Check | 45.6 | 50.2 | 45.0 | 47.0 | 42.3 | 51.8 | 49.6 | 52.9 |
| 61 NDBSK(HIM)C3 X NDSCD(FS-CS ) C 2 | Cross | 45.1 | 49.5 | 43.6 | 45.4 | 42.9 | 50.4 | 47.0 | 53.6 |
| 62 NDBS22(R-T 1)C9 X EARLYGEM 21 c | Cross | 46.3 | 50.3 | 45.3 | 46.1 | 42.0 | 51.3 | 50.2 | 52.6 |
| 63 NDL X NDBS 11(FR-M)C3 | Cross | 46.4 | 49.7 | 44.8 | 45.7 | 43.3 | 51.6 | 48.6 | 53.8 |
| 64 NDBS 11(FR-M)C3 X NDSHLC(M-FS)C5 | Cross | 47.1 | 50.0 | 45.3 | 47.2 | 44.0 | 51.3 | 49.8 | 53.4 |
| 65 NDBS K(HI-M)C3 X NDBS 21 (R-T)C9 | Cross | 45.1 | 50.4 | 44.1 | 45.7 | 43.1 | 51.1 | 48.4 | 53.1 |
| 66 NDBS 22(R-T1)C9 X NDSAB(MER-FS)C 15 | Cross | 45.0 | 50.5 | 44.1 | 45.5 | 42.3 | 51.2 | 48.8 | 52.5 |
| 67 NDBS22(R-T1)C9 X NDSHLC(M-FS)C5 | Cross | 46.1 | 50.5 | 44.1 | 47.4 | 42.6 | 51.3 | 48.5 | 52.4 |
| 68 NDSM(M-FS)C9 X NDBS 21 (R-T)C9 | Cross | 46.4 | 50.0 | 45.0 | 46.6 | 43.2 | 50.9 | 50.0 | 52.3 |
| 69 NDBSK(HI-M)C3 X NDBS 11(FR-M)C3 | Cross | 46.4 | 49.4 | 44.7 | 46.2 | 41.9 | 51.1 | 50.5 | 51.5 |
| 70 NDSS X NDBS 11(FR-M)C3 | Cross | 46.6 | 51.2 | 44.0 | 46.7 | 43.9 | 51.8 | 48.2 | 53.2 |
| 71 NDBSK(HIM)C3 | Parent | 44.5 | 49.8 | 43.6 | 44.6 | 42.8 | 50.4 | 48.7 | 52.4 |
| 72 NDSS XNDBS 21 (R-T)C9 | Cross | 46.0 | 49.8 | 46.0 | 42.9 | 44.7 | 52.4 | 49.4 | 53.1 |
| 73 NDSS XEARLYGEM 21 c | Cross | 46.3 | 50.5 | 44.7 | 47.3 | 43.1 | 51.0 | 50.1 | 52.9 |
| 74 NDBS 11(FR-M)C3 X NDBS 1011 | Cross | 48.8 | 50.1 | 43.7 | 46.1 | 43.3 | 51.3 | 48.2 | 52.6 |
| 75 NDCG(FS)C1 | P arent | 45.2 | 50.3 | 44.1 | 45.0 | 43.8 | 51.0 | 47.6 | 52.9 |
| 76 NDSAB(MER-FS)C 15 | P arent | 45.2 | 49.5 | 45.3 | 44.9 | 42.3 | 51.4 | 48.7 | 52.8 |
| 77 NDSS XNDSCD(FS-CS)C2 | Cross | 45.7 | 50.1 | 46.3 | 46.6 | 42.9 | 52.2 | 49.7 | 53.2 |
| 78 NDBS $1011 \mathrm{XNDBS} 21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross |  | 49.6 | 45.2 | 47.2 | 43.0 | 50.7 | 49.2 | 53.0 |
| 79 NDSAB(MER-FS)C 15 XEARLYGEM 21 a | Cross | 45.6 | 50.4 | 45.4 | 47.0 | 43.0 | 51.6 | 48.8 | 53.5 |
| 80 NDBS 21 (R-T)C9 X EARLYGEM 21 a | Cross | 47.1 | 50.6 | 45.7 | 47.7 | 43.3 | 51.8 | 49.2 | 54.2 |

Table B18 (continued). High fermentable corn starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 NDBS 11(FR-M)C3 X NDSM(M-FS)C9 | Cross | 46.2 | 50.4 | 43.9 | 45.9 | 42.6 | 51.7 | 50.2 | 53.6 |
| 82 NDBSK(HI-M)C3 X Leaming(S-FS)C6 | Cross | 45.5 | 50.4 | 43.8 | 44.1 | 41.9 | 50.7 | 47.7 | 52.0 |
| 83 NDL X NDBS 21 (R-T)C9 | Cross | 46.5 | 51.0 | 44.9 | 45.4 | 42.4 | 52.1 | 49.9 | 52.4 |
| 84 NDSM(M-FS)C9 | P arent | 47.0 | 50.4 | 44.5 | 45.4 | 42.5 | 51.0 | 48.2 | 53.4 |
| 85 NDSS XNDSAB(MER-FS)C 15 | Cross | 45.4 | 50.1 | 44.4 | 46.6 | 42.5 | 50.9 | 50.0 |  |
| 86 Leaming(S-FS)C6 X NDSM(M-FS)C9 | Cross | 45.9 | 50.2 | 44.8 | 45.7 | 42.7 | 50.5 | 49.1 | 52.0 |
| 87 NDCG(FS)C1 ${ }^{\text {N }}$ NBSS 11(FR-M)C3 | Cross | 46.0 | 49.6 | 43.1 | 46.0 | 41.7 | 50.9 | 48.1 | 52.1 |
| 88 NDSHLC(M-FS)C5 XEARLYGEM 21 a | Cross | 47.3 | 50.4 | 44.9 | 45.9 | 43.0 | 52.3 | 49.4 | 52.5 |
| 89 NDBS 1011 | P arent | 45.7 | 49.9 | 44.2 | 45.0 | 42.4 | 51.1 | 49.3 | 52.7 |
| 90 NDBS 1011 X NDS AB (MER-FS)C 15 | Cross | 45.5 | 50.1 | 44.2 | 46.8 | 42.3 | 50.6 | 48.3 | 52.9 |
| 91 Check 3 P IONEER 39N99 | Check | 44.3 | 51.7 | 43.6 | 45.5 | 42.9 | 51.8 | 48.4 | 53.6 |
| 92 NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 46.2 | 50.5 | 45.1 | 46.5 | 42.0 | 51.0 | 50.5 | 52.5 |
| 93 BS22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 45.6 | 49.8 | 44.0 | 45.8 | 42.3 | 51.2 | 49.0 | 52.2 |
| 94 NDL X NDBS 1011 | Cross | 45.6 | 51.2 | 43.2 | 46.2 | 41.7 | 50.9 | 50.0 | 52.7 |
| 95 NDBS22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 45.7 | 50.4 | 44.5 | 46.6 | 42.9 | 52.2 | 48.9 | 53.1 |
| 96 NDLXNDSM(M-FS)C9 | Cross | 46.4 | 49.5 | 44.5 | 45.9 | 43.4 | 51.4 | 48.8 | 52.8 |
| 97 NDSS | P arent | 44.6 | 50.3 | 44.7 | 45.2 | 42.8 | 51.2 | 48.6 | 53.8 |
| 98 NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 45.2 | 49.2 | 44.0 | 45.0 | 42.1 | 51.3 | 49.3 | 53.0 |
| 99 NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 46.0 | 49.6 | 45.3 | 46.5 | 43.0 | 51.4 | 48.9 | 53.0 |
| 100 NDL X NDBSK(HIM)C3 | Cross | 45.6 | 50.6 | 43.9 | 44.8 | 44.0 | 50.8 | 49.6 | 51.8 |
| 101 NDBS22(R-T1)C9 X EARLYGEM 21 b | Cross | 46.2 | 50.9 | 44.9 | 44.6 | 43.0 | 51.4 | 48.8 | 52.2 |
| 102 NDBS 1011 X NDSHLC(M-FS)C5 | Cross | 46.3 | 51.2 | 46.2 | 45.4 | 44.6 | 51.6 | 49.5 | 53.0 |
| 103 NDSHLC(M-FS)C5 X EARLYGEM 2 lb | Cross | 46.7 | 51.2 | 46.2 | 46.4 | 43.8 | 51.6 | 49.3 | 53.7 |
| 104 NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ X EARLYGEM 2 lc | Cross | 45.7 | 50.2 | 46.0 | 46.9 | 43.2 | 51.3 | 48.9 | 52.3 |
| 105 CGL(S-FR2)C1X B S 2 1CGL(R-FR2)C1 | Check | 46.3 | 50.2 | 44.1 | 46.7 | 44.3 | 51.7 | 50.3 | 53.5 |
| 106 NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 46.2 | 50.0 | 45.7 | 47.5 | 42.2 | 51.7 | 50.4 | 51.8 |
| 107 NDBS 11(FR-M)C3 X EARLYGEM 2 la | Cross | 46.0 | 50.9 | 46.2 | 46.3 | 41.5 | 51.3 | 50.1 | 52.5 |
| 108 NDCG(FS)C1XLeaming(S-FS)C6 | Cross | 45.1 | 50.2 | 44.6 | 46.7 | 43.3 | 51.1 | 49.7 | 52.8 |
| 109 NDSM(M-FS)C9 XEARLYGEM 21 a | Cross | 45.9 | 50.8 | 45.5 | 47.6 | 42.7 | 51.7 | 48.6 | 52.5 |
| 110 NDBS 21 (R-T)C9 XEARLYGEM 21 b | Cross | 46.5 | 50.9 | 45.8 | 47.0 | 43.7 | 51.6 | 49.8 | 52.2 |
| 111 NDSCD(FS-CS)C2 X EARLYGEM 21 b | Cross | 46.7 | 50.5 | 44.3 | 46.1 | 45.0 | 51.4 | 50.2 | 53.7 |
| 112 NDSS XEARLYGEM 21 a | Cross | 46.6 | 50.3 | 45.6 | 46.0 | 41.5 | 52.2 | 50.5 | 52.2 |
| 113 NDCG(FS)C1XEARLYGEM 21 c | Cross | 46.4 | 50.8 | 45.1 | 46.2 | 41.9 | 51.4 | 49.5 | 53.2 |
| 114 NDCG(FS)C1XNDL | Cross | 46.4 | 50.0 | 43.9 | 46.1 | 42.1 | 51.3 | 49.8 | 52.5 |
| 115 NDLXEARLYGEM 21a | Cross | 47.0 | 50.9 | 46.2 | 45.6 | 42.9 | 51.8 | 50.1 | 54.1 |
| 116 NDSM(M-FS)C9 X EARLYGEM 2 lb | Cross | 47.1 | 49.9 | 45.8 | 47.5 | 45.0 | 51.3 | 49.4 | 52.8 |
| 117 NDBS 11(FR-M)C3 X NDB S 21 (R-T)C9 | Cross |  | 49.6 | 46.1 | 46.1 | 43.3 | 51.3 | 49.0 | 52.3 |
| 118 NDBS 1011 XEARLYGEM 21 c | Cross | 45.8 | 50.4 | 44.8 | 46.6 | 43.6 | 51.2 | 48.0 | 53.7 |
| 119 NDBS 11(FR-M)C3 XEARLYGEM 2 lb | Cross | 47.5 | 50.3 | 46.2 | 47.3 | 43.5 | 51.4 | 49.8 | 52.6 |
| 120 NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 47.0 | 50.1 | 44.3 | 46.4 | 42.2 | 51.4 | 49.4 | 52.6 |

Table B18 (continued). High fermentable corn starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry | Pedigree | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 | NDLXNDSHLC(M-FS)C5 | Cross | 47.4 | 51.6 | 45.2 | 45.6 | 42.6 | 51.6 | 49.6 | 53.0 |
| 122 | NDL XNDSAB(MER-FS)C 15 | Cross | 45.9 | 50.2 | 46.0 | 45.4 | 43.1 | 51.8 | 49.9 | 54.0 |
| 123 | NDCG(FS)C1XNDBS 22(R-T1)C9 | Cross | 45.0 | 49.7 | 45.0 | 45.6 | 41.5 | 51.3 | 48.5 | 52.6 |
| 124 | NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 45.5 | 49.6 | 44.4 | 44.7 | 42.4 | 50.6 | 48.3 | 52.8 |
| 125 | CGSS21(S-FR)C1XBS21CGSS(R-FR)C1 | Check | 46.1 | 50.1 | 44.1 | 45.5 | 43.1 | 51.0 | 49.0 | 52.8 |
| 126 | NDCG(FS)C1XNDBS21(R-T)C9 | Cross | 45.4 | 50.2 | 44.6 | 46.6 | 43.5 | 51.3 | 49.2 | 51.9 |
| 127 | NDBS22(R-T 1)C9 X NDBS 21 (R-T)C9 | Cross | 46.3 | 50.1 | 44.4 | 46.8 | 42.4 | 51.7 | 48.5 | 53.0 |
| 128 | Leaming(S-FS)C6 XEARLYGEM 21 b | Cross | 45.5 | 50.2 | 44.7 | 45.5 | 43.0 | 51.0 | 48.5 | 52.9 |
| 129 | NDBS $1011 \mathrm{XNDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ | Cross | 47.0 | 50.5 | 44.4 | 46.9 | 42.5 | 51.3 | 49.1 | 52.2 |
| 130 | NDL XEARLYGEM 21 c | Cross | 47.0 | 50.3 | 46.1 | 47.1 | 44.6 | 51.7 | 50.3 | 53.4 |
|  | NDL X NDSCD(FS-CS)C2 | Cross | 45.8 | 50.5 | 44.5 | 46.3 | 42.9 | 50.6 | 49.7 | 52.1 |
| 132 | EARLYGEM 21 l | Parent | 46.5 | 50.7 | 46.1 | 44.9 | 43.0 | 51.4 | 50.3 | 53.3 |
| 133 | NDCG(FS)C1XNDB S K(HI-M)C3 | Cross | 45.1 | 49.7 | 44.4 | 47.0 | 41.8 | 50.7 | 47.1 | 51.3 |
| 134 | NDSCD(FS-CS)C2 XEARLYGEM 21 c | Cross | 46.2 | 51.6 | 44.7 | 46.7 | 43.8 | 51.5 | 49.8 | 53.1 |
| 135 | NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 45.6 | 51.0 | 43.4 | 46.4 | 42.5 | 51.2 | 48.6 | 52.5 |
| 136 | NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 46.3 | 49.8 | 45.6 | 45.3 | 41.8 | 51.9 | 48.2 | 52.7 |
| 137 | NDSM(M-FS)C9 X EARLYGEM 21 c | Cross | 46.1 | 51.0 | 45.1 | 47.7 | 42.3 | 51.7 | 49.7 | 52.9 |
| 138 | Leaming(S-FS)C6 XEARLYGEM 21 l | Cross | 46.1 | 50.9 | 45.2 | 46.2 | 43.0 | 51.8 | 50.3 | 53.8 |
| 139 | NDSS XNDCG(FS)C1 | Cross | 45.6 | 50.2 | 44.0 | 46.0 | 43.0 | 51.4 | 49.2 | 53.4 |
| 140 | NDSM(M-FS)C9 XNDSCD(FS-CS)C2 | Cross | 47.9 | 50.2 | 43.9 | 45.9 | 41.7 | 51.1 | 49.0 | 51.7 |
|  | NDBS 21 (R-T)C9 X NDSCD(FS-CS)C2 | Cross |  | 49.9 | 45.0 | 46.9 | 43.4 | 50.7 | 48.5 | 53.4 |
| 142 | NDCG(FS)C1XNDBS 1011 | Cross | 46.7 | 51.0 | 45.0 | 44.2 | 42.9 | 50.9 | 48.4 | 53.1 |
| 143 | NDBS 1011 X EAR LYGEM 2 la | Cross | 46.5 | 50.4 | 45.3 | 46.8 | 43.6 | 51.2 | 49.7 | 52.2 |
| 144 | NDSHLC(M-FS)C5 | Parent | 47.5 | 51.6 | 45.3 | 47.6 | 44.0 | 51.4 | 50.4 | 52.4 |
|  | Experiment mean |  | 46.1 | 50.3 | 44.8 | 46.1 | 42.9 | 51.3 | 49.2 | 52.8 |
|  | Mean of parental po pulations |  | 46.2 | 50.3 | 44.7 | 45.7 | 43.1 | 51.1 | 49.3 | 53.1 |
|  | Mean of population crosses |  | 46.2 | 50.2 | 44.8 | 46.2 | 42.9 | 51.3 | 49.2 | 52.8 |
|  | Mean of checks |  | 45.5 | 50.5 | 44.7 | 46.1 | 43.2 | 51.7 | 49.5 | 53.2 |
|  | LSD (0.05) |  | 1.2 | 1.4 | 1.5 | 2.0 | 2.0 | 1.2 | 1.9 | 1.5 |
|  | CV |  | 1.3 | 1.5 | 1.7 | 2.2 | 2.4 | 1.2 | 1.9 | 1.4 |
|  | MSE |  | 0.4 | 0.5 | 0.6 | 1.0 | 1.0 | 0.4 | 0.9 | 0.6 |

Table B19. High extractable starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry Pedigree | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 1 Leaming(S-FS)C6 XEARLYGEM 21c | Cross | 63.6 | 59.0 | 62.0 | 64.4 | 62.5 | 59.6 | 61.5 | 60.5 |
| 2 Leaming(S-FS)C6 XNDSAB(MER-FS)C15 | Cross | 59.5 | 57.4 | 59.8 | 61.8 | 59.7 | 57.9 | 59.5 | 59.6 |
| 3 NDBSK(HIM)C3 X NDSM(M-FS)C9 | Cross | 61.4 | 58.4 | 60.2 | 62.4 | 59.5 | 57.4 | 58.2 | 59.2 |
| $4 \mathrm{BS} 21 \mathrm{AB}(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1 \mathrm{XNDSAB} 21(\mathrm{R}-\mathrm{FR}) \mathrm{C} 1$ | Check | 62.6 | 58.2 | 59.5 | 62.8 | 59.9 | 57.2 | 59.8 | 59.1 |
| 5 EARLYGEM 2 la XEARLYGEM 2 lb | Cross | 63.9 | 59.4 | 63.4 | 63.8 | 61.2 | 58.7 | 61.7 | 60.4 |
| 6 NDBS $1011 \mathrm{XNDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | Cross | 60.7 | 58.0 | 60.0 | 60.9 | 59.6 | 57.3 | 58.7 | 58.3 |
| 7 NDSS XNDL | Cross | 61.6 | 58.8 | 60.7 | 61.7 | 57.8 | 56.2 | 59.4 | 59.5 |
| 8 NDBSK(HI-M)C3 XEARLYGEM 21 b | Cross | 61.9 | 59.0 | 60.3 | 63.4 | 62.0 | 58.8 | 62.2 | 61.0 |
| 9 NDL XEARLYGEM 2 lb | Cross | 63.6 | 59.5 | 61.9 | 64.0 | 60.2 | 58.3 | 63.3 | 60.3 |
| 10 NDBS 11(FR-M)C3 XEARLYGEM 21 c | Cross |  | 59.2 | 61.8 | 62.7 | 61.5 | 58.6 | 60.3 | 60.4 |
| 11 NDBS 11(FR-M)C3 | P arent | 61.4 | 57.7 | 60.0 | 61.8 | 58.2 | 55.2 | 57.7 | 58.8 |
| 12 NDBSK(HI-M)C3 X NDSHLC(M-FS)C5 | Cross | 61.4 | 58.1 | 60.0 | 62.4 | 61.0 | 57.5 | 60.0 | 60.2 |
| $13 \mathrm{NDSCD}(\mathrm{FS}-\mathrm{CS}) \mathrm{C} 2$ | P arent | 60.9 | 58.8 | 60.1 | 62.0 | 60.2 | 57.7 | 57.2 | 57.7 |
| 14 NDSHLC(M-FS)C5 XEARLYGEM 21 c | Cross | 62.1 | 58.8 | 61.2 | 64.5 | 60.7 | 59.9 | 60.6 | 61.2 |
| 15 NDSS XNDBS22(R-T1)C9 | Cross | 61.0 | 57.4 | 59.0 | 62.6 | 58.8 | 57.0 | 59.4 | 58.5 |
| 16 Check 4 DKC 43-27 VT3 | Check | 65.2 | 64.4 | 65.4 | 67.2 | 63.7 | 63.5 | 65.0 | 65.6 |
| 17 NDSS XNDSHLC(M-FS)C5 | Cross |  | 58.6 | 59.0 | 62.8 | 60.7 | 56.0 | 59.3 | 59.8 |
| 18 EARLYGEM 21 c | P arent | 64.1 | 60.6 | 61.1 | 65.7 | 62.3 | 60.6 | 60.9 | 61.9 |
| 19 Leaming(S-FS)C6 | P arent | 61.7 | 56.5 | 59.1 | 61.8 | 58.0 | 57.1 | 57.7 | 58.9 |
| 20 NDBS $1011 \mathrm{XNDBS} 22(\mathrm{R}-\mathrm{Tl}) \mathrm{C} 9$ | Cross | 61.7 | 58.2 | 59.1 | 62.6 | 60.7 | 58.6 | 60.6 | 60.0 |
| 21 Leaming(S-FS)C6 X NDSHLC(M-FS)C5 | Cross | 61.2 | 58.5 | 59.4 | 62.9 | 60.5 | 57.4 | 60.4 | 61.4 |
| 22 NDBS 21 (R-T)C9 X NDSHLC(M-FS)C5 | Cross | 62.2 | 59.8 | 61.2 | 63.0 | 62.1 | 58.6 | 59.9 | 59.9 |
| 23 Check 1P IONEER 39 V 07 | Check | 63.9 | 59.6 | 62.1 | 63.7 | 60.0 | 58.2 | 59.4 | 61.4 |
| 24 NDCG(FS)C1XNDSAB(MER-FS)C 15 | Cross | 59.6 | 57.4 | 60.6 | 62.5 | 59.4 | 58.5 | 58.1 | 58.6 |
| 25 Leaming(S-FS)C6 XNDBS22(R-T ) C9 | Cross | 62.2 | 58.3 | 61.2 | 62.2 | 59.9 | 57.6 | 61.1 | 59.2 |
| 26 Leaming(S-FS)C6 XNDBS 21 (R-T) C9 | Cross | 62.1 | 59.3 | 60.3 | 63.3 | 60.1 | 57.6 | 59.2 | 60.9 |
| 27 NDBSK(HI-M)C3 X EARLYGEM 2 la | Cross | 63.8 | 59.9 | 61.0 | 63.6 | 60.8 | 58.8 | 61.2 | 60.5 |
| 28 NDL XLeaming(S-FS)C6 | Cross |  | 56.8 | 59.0 | 61.4 | 61.2 | 56.0 | 59.9 | 60.1 |
| 29 EARLYGEM 2 la XEARLYGEM 21 c | Cross | 63.6 | 60.1 | 62.4 | 65.4 | 62.2 | 58.9 | 61.4 | 61.3 |
| 30 NDCG(FS)C1XEARLYGEM 21 b | Cross | 63.2 | 58.0 | 60.5 | 63.3 | 61.0 | 58.1 | 60.6 | 60.9 |
| 31 Leaming(S-FS)C6 XNDSCD(FS-CS)C2 | Cross | 60.8 | 57.3 | 59.1 | 61.1 | 59.1 | 57.9 | 58.7 | 60.1 |
| 32 NDBS K(HI-M)C3 XEARLYGEM 21 c | Cross | 63.2 | 60.5 | 61.5 | 64.8 | 61.4 | 58.4 | 61.4 | 61.6 |
| 33 NDBS 1011 XEARLYGEM 21 b | Cross | 64.8 | 59.1 | 62.2 | 64.0 | 62.9 | 59.2 | 59.4 | 59.9 |
| 34 NDSCD(FS-CS)C2 XEARLYGEM 2 la | Cross | 62.9 | 59.5 | 61.7 | 63.0 | 61.9 | 57.6 | 60.0 | 60.3 |
| 35 NDSS XEARLYGEM 2 lb | Cross | 63.1 | 58.2 | 59.5 | 62.8 | 61.6 | 57.6 | 60.1 | 59.9 |
| 36 NDSAB(MER-FS)C 15 X NDSHLC(M-FS)C5 | Cross | 61.3 | 57.8 | 60.3 | 63.3 | 60.8 | 58.0 | 60.1 | 59.2 |
| 37 NDBS 11(FR-M)C3 X NDSCD(FS-CS)C2 | Cross | 61.2 | 57.7 | 58.7 | 60.7 | 59.7 | 57.6 | 58.7 | 58.4 |
| 38 NDCG(FS)C1XEARLYGEM 21 l | Cross | 63.6 | 59.0 | 60.9 | 63.5 | 61.5 | 58.7 | 60.7 | 59.7 |
| 39 EARLYGEM 2 lb X EARLYGEM 2 lc | Cross | 64.0 | 60.2 | 60.9 | 64.2 | 62.8 | 59.1 | 61.6 | 60.1 |
| 40 NDBSK(HI-M)C3 X NDSAB (MER-FS)C 15 | Cross | 61.3 | 58.2 | 60.4 | 63.2 | 60.2 | 57.8 | 60.4 | 60.6 |

Table B19 (continued). High extractable starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

|  |  |  |  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Entry Pedigree |  |  |  |  |  |  |  |

Table B19 (continued). High extractable starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry Pedigree |  | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 81 | NDBS 11(FR-M)C3 XNDSM(M-FS)C9 |  | Cross | 60.1 | 57.8 | 58.7 | 61.9 | 60.2 | 55.9 | 58.1 | 59.2 |
| 82 | NDBSK(HIM)C3 XLeaming(S-FS)C6 | Cross | 62.6 | 58.2 | 59.4 | 62.7 | 59.7 | 57.4 | 59.3 | 59.6 |
| 83 | NDL X NDBS21(R-T)C9 | Cross | 60.3 | 60.4 | 60.5 | 63.5 | 61.3 | 58.1 | 60.6 | 60.7 |
| 84 | NDSM(M-FS)C9 | Parent | 59.7 | 57.9 | 58.6 | 61.6 | 59.5 | 55.2 | 58.6 | 56.5 |
| 85 | NDSS XNDSAB(MER-FS)C 15 | Cross | 60.0 | 57.5 | 60.0 | 62.1 | 61.0 | 57.2 | 58.4 |  |
| 86 | Leaming(S-FS)C6 XNDSM(M-FS)C9 | Cross | 60.9 | 58.3 | 59.1 | 63.0 | 59.3 | 56.0 | 58.3 | 58.5 |
| 87 | NDCG(FS)C1X NDBS 11(FR-M)C3 | Cross | 60.8 | 60.1 | 59.8 | 61.2 | 59.2 | 56.1 | 60.2 | 58.6 |
| 88 | NDSHLC(M-FS)C5 X EARLYGEM 2 1a | Cross | 61.8 | 57.2 | 60.6 | 63.5 | 61.6 | 58.5 | 61.4 | 60.9 |
| 89 | NDBS 1011 | Parent | 62.5 | 58.7 | 60.0 | 62.9 | 59.5 | 57.4 | 59.3 | 60.3 |
| 90 | NDBS 1011 X NDS AB(MER-FS ) C 15 | Cross | 62.3 | 58.0 | 59.7 | 62.0 | 60.5 | 58.5 | 59.4 | 60.8 |
|  | Check 3 P IONEER 39N99 | Check | 63.9 | 61.7 | 62.0 | 63.9 | 61.3 | 59.1 | 62.1 | 61.9 |
| 92 | NDSM(M-FS)C9 X NDSHLC(M-FS)C5 | Cross | 60.2 | 57.9 | 60.0 | 63.9 | 60.6 | 57.2 | 59.0 | 60.5 |
| 93 | BS 22LEAM (R-FR)C1XLEAMING22 (S-FR)C1 | Check | 62.5 | 58.5 | 60.4 | 63.4 | 59.5 | 57.7 | 61.3 | 60.7 |
| 94 | NDL X NDBS 1011 | Cross | 61.8 | 58.4 | 60.7 | 63.0 | 60.5 | 58.3 | 59.9 | 59.8 |
| 95 | NDBS 22(R-T1)C9 X NDSM(M-FS)C9 | Cross | 59.8 | 57.7 | 59.5 | 62.7 | 60.1 | 57.6 | 58.1 | 58.8 |
| 96 | NDL X NDSM(M-FS)C9 | Cross | 60.4 | 57.3 | 60.6 | 63.5 | 59.3 | 57.4 | 58.3 | 58.9 |
| 97 | NDSS | Parent | 62.0 | 57.7 | 59.7 | 61.7 | 58.0 | 55.4 | 57.8 | 57.5 |
| 98 | NDBS22(R-T1)C9 X NDSCD(FS-CS)C2 | Cross | 60.0 | 57.9 | 59.5 | 61.3 | 59.5 | 57.1 | 58.9 | 59.0 |
| 99 | NDCG(FS)C1XNDSHLC(M-FS)C5 | Cross | 59.4 | 57.3 | 59.8 | 62.6 | 62.0 | 57.2 | 59.3 | 60.8 |
| 100 | NDL X NDBSK(HI-M)C3 | Cross | 62.1 | 58.8 | 60.9 | 63.3 | 59.4 | 57.2 | 60.9 | 60.5 |
| 101 | NDBS 22(R-T 1)C9 X EARLYGEM 2 lb | Cross | 61.9 | 59.4 | 61.8 | 64.2 | 61.4 | 58.3 | 61.9 | 61.7 |
| 102 | NDBS 1011 XNDSHLC(M-FS)C5 | Cross | 61.5 | 60.1 | 62.1 | 64.4 | 60.0 | 58.3 | 61.1 | 60.5 |
| 103 | NDSHLC(M-FS)C5 XEARLYGEM 21 b | Cross | 63.3 | 59.4 | 60.3 | 64.1 | 59.9 | 58.8 | 61.3 | 61.3 |
| 104 | NDBS 21 (R-T)C9 X EARLYGEM 21 c | Cross | 63.4 | 59.6 | 61.7 | 64.6 | 61.8 | 59.4 | 62.1 | 61.4 |
| 105 | CGL(S-FR2)C1X B S $21 \mathrm{CGL}(\mathrm{R}-\mathrm{FR} 2) \mathrm{C} 1$ | Check | 61.2 | 57.4 | 59.2 | 58.3 | 59.6 | 57.2 | 59.8 | 60.5 |
| 106 | NDSAB(MER-FS)C 15 X EARLYGEM 21 c | Cross | 63.4 | 56.4 | 60.8 | 63.0 | 61.4 | 59.6 | 61.2 | 60.7 |
| 107 | NDBS 11(FR-M)C3 XEARLYGEM 2 1a | Cross | 62.4 | 58.9 | 61.5 | 63.7 | 61.4 | 58.0 | 62.0 | 60.7 |
| 108 | NDCG(FS)C1X Leaming(S-FS)C6 | Cross | 60.0 | 56.2 | 59.3 | 61.7 | 58.7 | 56.4 | 58.3 | 59.6 |
| 109 | NDSM(M-FS)C9 XEARLYGEM 2 1a | Cross | 61.6 | 59.0 | 60.5 | 64.2 | 61.7 | 58.4 | 60.7 | 59.5 |
| 110 | NDBS 21 (R-T)C9 XEARLYGEM 2 lb | Cross | 61.0 | 59.0 | 61.1 | 63.9 | 62.4 | 58.5 | 61.4 | 61.9 |
| 111 | NDSCD(FS-CS)C2 XEARLYGEM 2 lb | Cross | 61.3 | 58.9 | 62.2 | 62.5 | 60.5 | 58.7 | 61.3 | 60.9 |
| 112 | NDSS XEARLYGEM 21 a | Cross | 62.0 | 58.9 | 61.5 | 63.0 | 61.0 | 57.4 | 60.3 | 60.3 |
| 113 | NDCG(FS)C1XEARLYGEM 21 c | Cross | 60.6 | 59.2 | 60.1 | 62.4 | 61.1 | 58.7 | 61.3 | 62.1 |
| 114 | NDCG(FS)C1XNDL | Cross | 57.7 | 58.7 | 59.4 | 62.1 | 60.3 | 57.6 | 59.8 | 58.9 |
| 115 | NDLXEARLYGEM 21 a | Cross | 62.3 | 59.4 | 61.3 | 64.0 | 61.3 | 59.5 | 61.4 | 61.5 |
| 116 | NDSM(M-FS)C9 X EARLYGEM 2 lb | Cross | 61.4 | 59.0 | 60.0 | 63.1 | 60.7 | 58.2 | 59.7 | 60.9 |
| 117 | NDBS 11(FR-M)C3 X NDB S 21 (R-T)C9 | Cross |  | 59.3 | 59.5 | 63.4 | 61.5 | 58.1 | 61.4 | 60.0 |
| 118 | NDBS 1011 X EARLYGEM 21 c | Cross | 63.1 | 60.4 | 63.0 | 64.8 | 62.5 | 59.6 | 61.7 | 60.7 |
| 119 | NDBS 11(FR-M)C3 XEARLYGEM 2 lb | Cross | 61.6 | 58.6 | 60.9 | 62.8 | 61.4 | 58.6 | 60.4 | 60.9 |
| 120 | NDBS 11(FR-M)C3 XLeaming(S-FS)C6 | Cross | 59.7 | 56.5 | 59.2 | 62.3 | 59.5 | 56.2 | 60.6 | 59.7 |

Table B19 (continued). High extractable starch (\%) adjusted means of 16 maize populations, 120 crosses, and 8 checks across 8 environments.

| Entry | Pedigree | Type | 2010 |  |  |  | 2012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Casselton | Larimore | Prosper | Thompson | Casselton | Larimore | Prosper | Thompson |
| 121 | NDL X NDSHLC(M-FS)C5 | Cross | 60.6 | 57.2 | 60.4 | 63.5 | 61.2 | 58.6 | 61.1 | 60.5 |
| 122 | NDL XNDSAB(MER-FS)C 15 | Cross | 60.8 | 58.6 | 60.6 | 62.4 | 58.8 | 57.9 | 58.0 | 59.6 |
| 123 | NDCG(FS)C1 ${ }^{\text {ND }}$ NBS 22(R-T 1)C9 | Cross | 63.0 | 58.3 | 59.1 | 62.4 | 58.9 | 57.0 | 60.2 | 59.7 |
| 124 | NDCG(FS)C1XNDSCD(FS-CS)C2 | Cross | 61.6 | 57.0 | 58.8 | 62.2 | 57.3 | 56.3 | 58.8 | 58.4 |
| 125 | CGSS21(S-FR)C1XBS21CGSS(R-FR)C1 | Check | 62.2 | 58.4 | 60.9 | 62.5 | 60.1 | 58.1 | 60.6 | 59.8 |
| 126 | NDCG(FS)C1XNDBS21(R-T)C9 | Cross | 61.5 | 57.4 | 59.9 | 61.8 | 59.6 | 57.2 | 59.1 | 59.4 |
| 127 | NDBS 22 (R-T1)C9 X NDBS $21(\mathrm{R}-\mathrm{T}) \mathrm{C} 9$ | Cross | 62.8 | 59.1 | 60.8 | 61.4 | 60.5 | 58.2 | 60.8 | 60.1 |
| 128 | Leaming(S-FS)C6 X EARLYGEM 21 lb | Cross | 63.0 | 59.2 | 60.6 | 63.8 | 62.3 | 57.3 | 61.1 | 60.7 |
| 129 | NDBS $1011 \mathrm{XNDSM}(\mathrm{M}-\mathrm{FS}) \mathrm{C} 9$ | Cross | 61.7 | 57.8 | 60.7 | 63.0 | 61.0 | 56.9 | 59.6 | 59.9 |
| 130 | NDL XEARLYGEM 2 lc | Cross | 64.3 | 60.8 | 60.7 | 65.1 | 61.5 | 59.0 | 61.2 | 60.7 |
| 131 | NDL XNDSCD(FS-CS)C2 | Cross | 59.6 | 56.8 | 59.4 | 59.5 | 59.8 | 57.8 | 58.5 | 59.8 |
| 132 | EARLYGEM 21 l | Parent | 64.5 | 59.2 | 62.2 | 65.1 | 61.5 | 59.0 | 61.8 | 59.2 |
| 133 | NDCG(FS)C1X NDB S K(HI-M)C3 | Cross | 60.3 | 57.6 | 61.0 | 62.3 | 60.6 | 57.1 | 60.3 | 60.1 |
| 134 | NDSCD(FS-CS)C2 XEARLYGEM 21 c | Cross | 63.9 | 60.1 | 61.0 | 63.1 | 61.6 | 58.7 | 61.0 | 60.7 |
| 135 | NDCG(FS)C1XNDSM(M-FS)C9 | Cross | 60.8 | 57.9 | 55.9 | 60.4 | 58.8 | 56.5 | 57.6 | 58.5 |
| 136 | NDSAB(MER-FS)C 15 X NDSCD(FS-CS)C2 | Cross | 61.0 | 58.0 | 58.7 | 61.5 | 59.3 | 56.5 | 57.9 | 57.4 |
| 137 | NDSM(M-FS)C9 XEARLYGEM 21 c | Cross | 60.9 | 59.3 | 60.9 | 63.3 | 62.1 | 59.6 | 61.5 | 60.6 |
| 138 | Leaming(S-FS)C6 XEARLYGEM 21 a | Cross | 62.3 | 58.0 | 59.9 | 61.8 | 60.3 | 58.4 | 59.4 | 59.1 |
| 139 | NDSS XNDCG(FS)C1 | Cross | 60.1 | 58.6 | 59.5 | 62.3 | 58.6 | 57.0 | 58.4 | 57.2 |
| 140 | NDSM(M-FS)C9 XNDSCD(FS-CS)C2 | Cross | 60.2 | 58.1 | 57.4 | 61.6 | 59.2 | 55.9 | 57.2 | 58.9 |
| 141 | NDBS 21 (R-T)C9 X NDSCD(FS-CS)C2 | Cross |  | 57.8 | 60.1 | 62.6 | 57.4 | 57.6 | 59.2 | 58.2 |
| 142 | NDCG(FS)C1 ${ }^{\text {P }}$ NDBS 1011 | Cross | 62.1 | 56.7 | 60.9 | 63.1 | 60.0 | 56.9 | 59.1 | 59.3 |
| 143 | NDBS 1011 XEARLYGEM 21 l | Cross | 62.7 | 59.3 | 61.4 | 64.0 | 61.7 | 58.6 | 62.7 | 61.7 |
| 144 | NDSHLC(M-FS)C5 | P arent | 62.0 | 57.8 | 60.3 | 64.0 | 61.0 | 58.1 | 59.0 | 59.9 |
|  | Experiment mean |  | 61.6 | 58.5 | 60.3 | 62.8 | 60.3 | 57.8 | 59.9 | 59.9 |
|  | Mean of parental populations |  | 61.8 | 58.3 | 60.2 | 62.8 | 59.7 | 57.4 | 59.1 | 59.1 |
|  | Mean of population crosses |  | 61.5 | 58.5 | 60.2 | 62.8 | 60.4 | 57.8 | 59.9 | 60.0 |
|  | Mean of checks |  | 63.2 | 59.8 | 61.7 | 63.2 | 60.8 | 58.9 | 61.2 | 61.3 |
|  | LSD (0.05) |  | 1.9 | 1.8 | 1.9 | 1.7 | 2.0 | 1.4 | 1.9 | 1.4 |
|  | CV |  | 1.5 | 1.5 | 1.6 | 1.4 | 1.7 | 1.2 | 1.6 | 1.2 |
|  | MSE |  | 0.9 | 0.8 | 0.9 | 0.8 | 1.1 | 0.5 | 0.9 | 0.5 |


[^0]:    ${ }^{a}$ The values for the percentage of lysine, methionine, and cysteine were multiplied by 10,000 .
    ${ }^{\mathrm{b}}$ Data for cysteine percentage were combined only for 9 environments.

