QUANTITATIVE GENETICS OF DROUGHT RESISTANCE IN EARLY MATURING

MAIZE (*ZEA MAYS* L.)

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Title

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The Supervisory Committee certifies that this ***disquisition*** complies with North Dakota State

University's regulations and meets the accepted standards for the degree of

DOCTOR OF PHILOSOPHY

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ABSTRACT

Drought stress is paramount in limiting worldwide maize (*Zea mays* L.) production and productivity. In addition, drought has limited expansion of maize production to marginal conditions in areas including western North Dakota (ND) and eastern Montana (MT) where short-season drought tolerance is essential. The development of new cultivars in these dryer areas has been slow in part due to unavailability of reliable field phenotyping methods for breeding purposes and existing insufficient information on the genetic control of agronomic and grain quality attributes under drought stress. Our objectives were (1) to investigate root and stalk quantitative traits as novel field phenotyping methods for drought resistance, (2) to examine the variability and genetic control of agronomic and grain compositional attributes across soil moisture regimes, and (3) to discuss implications of findings for developing new maize cultivars under drought stress environments. Ninety-four partial diallel crosses including 47 diverse maize inbred parents and checks were tested in 12 water stress (WS), well-watered (WW) and random drought (RDT) environments in 2013 and 2014. A new high throughput non-destructive maize phenotyping method for drought tolerance is proposed, including the quantitative traits visible brace root number count and its spread width. Additive gene action was predominant in most of the agronomic and grain quality attributes, while non-additive gene action was important for grain yield, root lodging, stalk diameter, and grain oil content. Root and stalk lodging were negatively associated ($P < 0.01$) with brace root count and spread width. The estimates of narrow sense heritability were higher for brace root spread width (0.23) and number of brace root count (0.24) as compared to grain yield (0.06) and root lodging (0.1) in WS environments. High relative narrow sense heritability (> 0.40) was estimated for grain compositional attributes except for grain protein and amino acids. Stress environments were largely associated for grain oil and

total and extractable starch contents (> 0.60). A reciprocal recurrent selection program can be vital to develop cultivars with high grain yield and quality in drought stress.

ACKNOWLEDGMENTS

DEDICATION

To my parents Bhubaneswor and Parbata,

my wife Durga and our son Shrey

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DISSERTATION ORGANIZATION

The dissertation has been divided into four chapters. Chapters 2 and 3 each comprise of a manuscript to be submitted for publications. Chapter 1 includes general introduction of research followed by review of literature. The literature reviews include importation of maize and its tolerance to drought, importance of stress resistance in genetic improvement of yield, characterization of drought stress in maize production, physiological mechanisms of drought resistance, management of drought stress for precision phenotyping, importance of secondary traits for drought resistance, phenotyping for drought resistance, concept of estimation of quantitative genetic parameters, quantitative genetics of agronomic traits in drought environments, importance of breeding for maize grain quality, general review on quantitative genetics of grain compositional attributes in drought environments and future of drought resistance in maize. Chapter 2 investigates the new field phenotyping method for short season drought resistance. Chapter 3 examines the variability and genetic architecture of maize grain compositional attributes in three soil moisture regimes and discusses the implications of breeding these traits in drought environment. Chapter 4 discusses the implications of findings for cultivar development in drought stress environment as general conclusion. Appendix with individual means for each trait from each experiment follows the general conclusion.

CHAPTER 1. INTRODUCTION

Maize (*Zea mays* L.) is one of the largest crops on earth in terms of total production. In 2014 US total maize production was 361 million metric tons (USDA, 2014). The U.S. is also largest exporter of maize accounting for a total of 39 % of the 2013 – 2014 world export market (US Grain Council, 2013). The large production of maize is because of its various end uses. In year 2013 29.6 % of maize production was processed for fuel ethanol, 40.3 % for feed, 8.4 % for distillers dried grains with solubles (DDGS), 11 % for export, and the remaining 10.7 % for industrial uses including sweeteners, starch, seeds and high fructose corn syrup, cereal and beverages (USDA, ERS, FEED outlook, Jan 2014).

There is a potential to increase world maize grain production by moving maize to more marginal areas with drought stress (Carena et al, 2009). In order for this to happen, new constitutive traits and their interactions should be discovered and a diverse and large sample of genotypes should be screened for adaptation to environments with drought stresses.

Stress tolerance has shown to be physiologically related to grain yield. The yield improvement achieved in temperate maize hybrids was attributed to their greater stress tolerance mechanisms rather than improvement in yield per se (Tollenaar and Lee, 2004; Duvick, 2005). Historically, drought stress has detrimental effects on maize production. Worldwide loss of yield of maize due to drought was estimated to be 15 % of well-watered yield potential every year (Edmeades, 2013). Drought in 2012 itself decreased 21 % of national maize yield or 38 % national maize production compared to the 2009-11 mean yield level in US (USDA, 2013).

Drought resistance is governed by hundreds of small effect genetic loci controlling many morphological and physiological differences, making this trait a genetically complex (Hu and Xiong, 2014). Drought is also one of the major limiting factors in order to increase maize yield

of short-season hybrids in western North Dakota (ND) and eastern Montana (MT) (Carena et al, 2009). This region has a characteristic cyclical drought scenario (USGS, 2012). The western half of the ND is affected by semi-arid conditions and low annual rainfall whereas eastern ND experiences more precipitation in normal years (Karetinkov et al., 2008). In maize, drought during grain filling has been the usual pattern throughout western ND and eastern MT with less than 50 mm of rain during July and August (NDAWN, 2015).

The most critical drought stress periods for maize production are the flowering and grain filling growth stages (Blum, 2011). However, the genetic gains from tolerance to drought stress, in grain filling, have been low due to the lack of genetic variation in elite temperate germplasm. This was speculated to be related to the considerable selection pressure applied for improving tolerance through extensive multi-environment testing in genetically narrow-based hybrid development (Campos et al., 2004). Trait-based selection (Richards et al., 2002) in genetically diverse germplasm, including stem diameter and brace root spread, may ensure the genetic variation in breeding populations for selection in drought stress environments. The use of genetically broad-based germplasm is essential for achieving significant genetic gains for drought tolerance (Carena, 2013).

Maize is a major source of energy for livestock and human world consumption. Improvement of yield along with excellent grain quality traits like grain oil, protein, starch, extractable starch, and essential amino acids (e.g., methionine, cysteine and lysine) can boost rural economies by adding value to the crops for farmers (Pollak and Scott, 2005; Sanchez and Cardona, 2008; Carena, 2013b). This becomes more important for farmers in marginal crop areas to improve their living because they have few choices (Carena, 2013). Historically, grain quality genetic improvement, has been conducted through quantitative genetic approaches and the

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utilization of mutants (Dudley and Lambert, 2004; Pollak and Scott, 2005; Sharma and Carena, 2011; Laude and Carena, 2014). But, there has been very few researches on quantitative genetic variation and control of grain quality traits in different soil water regimes to help breeders managing resources in breeding programs targeted for drought environments. The increase in ethanol processing in western ND is also demanding new methods of breeding early maturing maize for drought resistance with excellent grain quality traits for processing (Carena, 2013).

This research represents some of the NDSU maize breeding program efforts to assess the quantitative genetics of drought resistance and grain quality traits in short-season maize with the goal of moving maize west in ND and MT drier environments. This particular research will test the genetic variation and control of constitutive agronomic and grain quality traits in three water regimes of drought, well-watered and random abiotic stress. These traits include stem and brace root traits to understand the quantitative genetics of drought resistance in early maturing maize.

Literature Review

Importance of maize and its tolerance to drought

Maize is one of the largest crops globally in terms of production and the most produced commodity in 2013 in the U.S. The total U.S. maize production was 353.6 million metric tons followed by 218.4 metric tons of China (FAO STAT, 2013). The market coverage for U.S. maize export in 2013/2014 was 39 % of world maize export making the U.S. the largest maize world exporter. The world export and production of maize is in part due its various end uses. In the year 2013 29.6 % of the total maize produced in the US was processed to produce ethanol, 40 % for animal and poultry feed, 8.4 % for distillers dried grains and soluble (DDGS), 11 % for export, and the remaining10 % for various industrial uses ranging from production of high

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fructose corn syrup, cereal beverage/alcohol, seeds, sweeteners and starch (USDA, ERS, Feed outlook, Jan 2014).

Drought stress has significantly impacted world maize yield. The 2012 historic U.S. drought had a record decrease of national maize yield by about 21 %. National maize production also decreased by about 38 % compared with the 2009-2011 mean levels (USDA, 2013). Worldwide, the average total loss of maize yield due to drought equals to 15 % of the total yield from well-watered yield potential every year (Edmeades, 2013). Availability of water is the most important yield-reducing factor in western North Dakota (ND) and eastern Montana (MT) (Carena et al, 2009). The western half of ND and eastern MT has semi-arid conditions and low annual rainfall while the eastern half of ND experiences more precipitation in normal years (Fig. 1) (Karetinkov et al., 2008). In maize, terminal drought has been the usual pattern throughout western ND and eastern MT with less than two inches of rain during July and August (NDAWN, 2012).

In 2014 maize was planted in 1,133,120 ND hectares with a total production of 7,968,909 tons and an average grain yield of 7.78 tons per hectare. In the same year the national average yield was 10.73 tons per hectare (USDA, National Agriculture Statistics Service, 2015). Low yield in ND has been attributed to early frost, cool temperature throughout the growing season in northern ND and drought and salinity stresses in western ND and eastern Montana (Carena et al., 2009). There is a high potential to increase maize yield in rural marginal drought environments ultimately increasing the economy of farmers who do not have many choices to improve their farm economy (Carena, 2013).

The availability of soil water is the most important abiotic stress factor limiting crop growth worldwide and efficient water use in plants is a major breeding objective to increase

productivity (Blum, 2011, Araus et al., 2012). The current and future genetic gains are limited by

gradual changes in the world climate. Change of climate includes changes in temperature,

precipitation, and frequency of extremes such as storms and drought (Franks and Hoffmann,

2012).
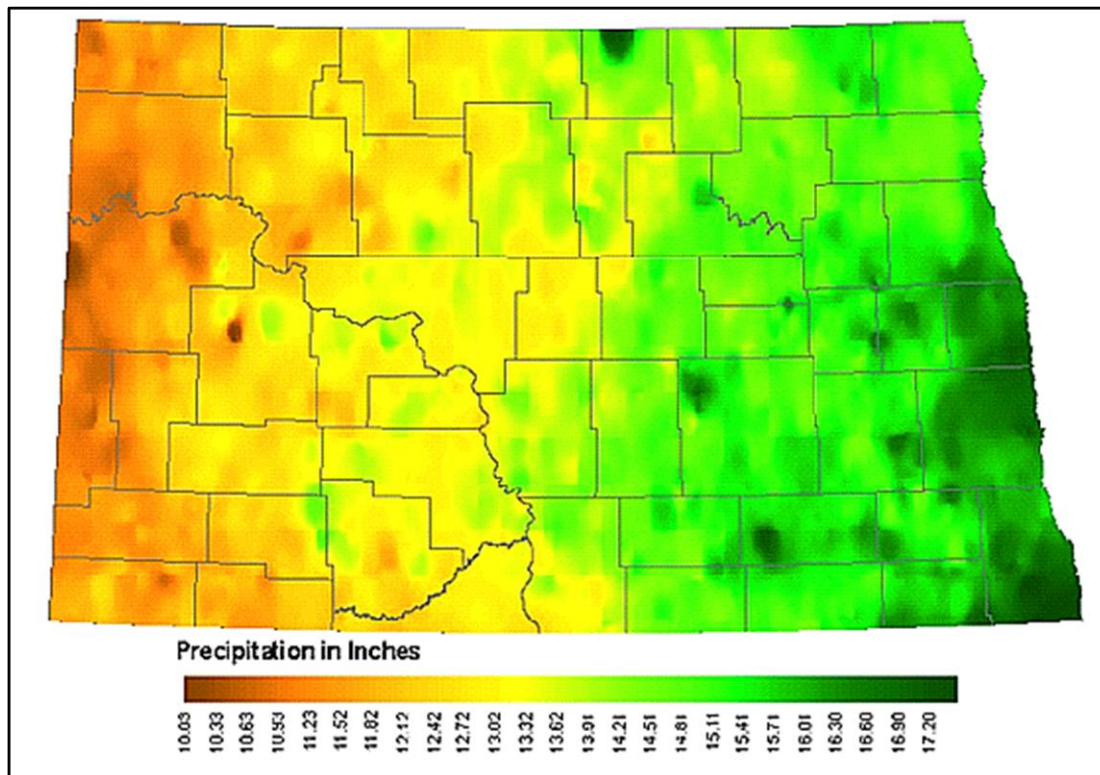
Figure 1. Maize growing areas in North Dakota showing 30-year (1977-2006) average
precipitation during the critical period for maize growth and development from April to
September. Adapted from NDARB cooerative observer network (ARBCON) North Dakota State
water comissiion (http://www.swc.state.nd.us/ accessed July 15, 2015).

Importance of stress resistance in genetic improvement of yield

Yield potential in agricultural crops refers to the yield of a cultivar when resource capture

and utilization are not limiting (Evans and Fischer, 1999; Tollenaar and Lee, 2002). Nutrients,

water, and light are important resources of plants. The factor that reduces the capture of one or

more of these resources is defined as 'stress'. The stress tolerance, hence, is the ability of plants

to mitigate the impact of stress on physiological processes in resource capture (e.g., nutrient

uptake, absorption of incident solar radiation) and utilization (e.g. rate of leaf photosynthesis, rate of dry matter accumulation).

Mitigation of stresses can be a way to reach genetic potential in maize grain yield. The improvement in maize yield from 1 Mg ha^{-1} in 1930s to about 7 Mg ha^{-1} in 1990s was attributed largely to yield heterosis after hybrids were extensively introduced (Frey, 1971). However, similar rates of yield improvement were found both in maize inbreds and hybrids in the U.S. Corn Belt (Duvick, 1984), suggesting heterosis may not be efficient enough for genetic gain after the first exploitation of the maize hybrid technique in North America. The yield improvement in temperate maize was instead found to be due to greater environmental stress tolerance mechanisms (Troyer and Rosembrook, 1983; Russell, 1991; Tollenaar et al., 2004; Duvick, 2005; Hyrkas and Carena, 2005). This stress tolerance was shown to be from increased capture and use of resources by plants. Increased interception of seasonal incident radiation and greater uptake of nutrients and water ultimately improving the efficiency of maize (Tollenaar and Wu, 1999). Increased longevity of leaf and active root system, as well as a high ratio between assimilate supply by the leaf canopy, and demand of assimilate by maize grain during main period of grain filling, were found to be associated with improved resource capture by plants. More partitioning to kernel during sensitive kernel number determination period was found to be an important factor to increase kernel number in both heterosis and historical genetic gain in maize (Tollenaar and Lee, 2006).

Heterosis has been associated with greater drought resistance in maize. Heterosis for grain yield was found to be closely related to water use in tropical maize. Maize hybrids were found to have better water use efficiency than inbred lines regardless of the water conditions (Araus et al., 2010). In each growing condition (drought, irrigated, and random drought) most

variations in grain yield between hybrids and inbred lines were explained by differences in plant

water-use traits (Araus et al., 2010). Heterosis was found to be larger for grain yield under

drought stress (Betran et al., 2003c, Araus et al., 2010).

<u>Drought stress characterization in maize production</u>

People interpret drought differently, however, for a plant-breeding program drought is

defined as insufficient moisture supply causing a reduction in plant production (Blum, 2011).

Drought usually is also associated with limited availability of nutrient supply from the soil

(Rouphael et al., 2012). Suffering starts when plant water deficit is initiated and the crop demand

for water exceeds the supply (Blum 2011).

During crop growth various drought stress scenarios are created by different field

conditions (Blum, 2011). Even if it is dry on top, soil moisture may be available at depths with or

without fluctuating water table. Under this condition, deep root systems can be the plant

mechanisms to capture moisture from different depths. In addition, water can be available but

soil is hard enough creating resistance to root penetration. In this case plants, which penetrate the

hard soil, are beneficial to capture the moisture needed. Another case is when moisture is stored

in soil with limited or no seasonal rainfall. This scenario is often found in dry land farming. In

this condition, plants with reduced needs for soil moisture use during first half of the season are

able to conserve sufficient moisture for the reproductive growth stage and perform best. Another

scenario could be that deep water is not available. In this condition it is not predictable when

drought will occur and its intensity. The greater soil moisture extraction by roots to lower soil

water potential can be important in this condition (Blum, 2011).

Drought stress in the reproductive growth stages of crops including flowering and grain

development is more frequent than at seedling and early vegetative stages (Mahalakshmi and

Blum, 2006). Previous research has shown that, the availability of each mm water during grain filling can increase grain yield by 50-60 kg ha^{-1} in wheat (Kirkegaard et al., 2007) and 30 kg ha^{-1} more in sorghum (Hammer, 2006). In a subset of maize hybrids released from 1953 to 2001, it was found that compared to well-watered control, the reduction in grain yield was 55 % when drought was imposed on flowering, 66 % when it was on early-fill, 71 % when it was on mid-fill, 69 % when it was on late-fill, and 36 % when it was imposed on terminal growth stage. This clearly shows the highest yield reduction occurred when the drought stress was present during 25 days after flowering in maize (Edmeades, 2003; Campos et al., 2004). However this may vary with corn maturity. The irregular rainfall distribution that creates a drought is also a factor to decrease the maize yield increasing its unpredictability (Fischer et al., 1983; Edmeades, 2013).

Physiological mechanisms of drought resistance

Drought resistance, from the agriculture perspective, can be described as the ability of a crop plant to produce its economic product in limited available water, which is different from the ability of plant or species to survive under limited soil moisture from an evolutionary perspective (Fischer et al., 1983). Levitt (1972) classified major mechanisms for drought resistance as drought escape, drought tolerance, and drought avoidance. The easiest form of resistance is drought escape, which happens with a variation in genotype maturity and planting dates. However, drought is not predictable in most cases so the selection for avoidance/or tolerance mechanisms is considered more important to develop resistance.

Stem reserve is one of the important desiccation tolerance mechanisms in plants (Blum, 2011). Within a total of 2-4 weeks of major accumulation period of carbohydrates in the maize stem, the quantity of sugar accumulated is believed to be equivalent to 12-25 % of final grain dry matter yield (Setter and Meller, 1984). The carbohydrate content of the maize stem has been

reported to decline during the grain filling period when sugar is remobilized from stems to kernels. Since in the late grain filling stage during moisture stress many of the lower leaves dry out, the net export from stems can support kernel growth, minimizing the effects of terminal drought stress. However, this shows the stem is also a strong sink, which may compete with other sinks during kernel development. This indicate the stem reserve may have detrimental effect on kernel set and yield due to being a strong stem sink. The lack of stem reserves has been found to limit kernel development, however, not effecting kernel loss which is contributed by current assimilate from photosynthesis in leaves (Schussler and Wastgate, 1994). Fairey and Dynard (1978) showed an increase in the concentration of sugars in stem dry matter at early kernel growth and then a decline during later kernel development. In maize, higher concentrations of soluble solids were found on the lower two to three stem nodes in comparison to the rest of the stalk. This could be a consequence of selection for stalk lodging resistance that has ultimately increased yield of maize (Windstrom et al., 1988). The larger stem reserves under moisture stress conditions can be mobilized for increasing grain yield when many of the leaves start senescing during grain filling. This makes stem diameter a potential trait for stress avoidance. Since the moisture stress depresses the photosynthetic sources in sorghum, large stem reserve storage at the onset of grain filling was found to be associated with stable filling under moisture stress (Blum et al., 1997). However, in maize, scientists have not found associations between stem traits and grain yield under drought stress. In a defoliation study which was carried out during grain filling of tropical maize, taller genotypes with larger stem volumes did not have larger kernel weight than the shorter genotypes under stress (Edmeades and Lafitte, 1993).

Rapid silk extrusion has been associated with fast growth of spikelet, making it an important trait to mitigate drought stress (Araus et al., 2012). Maize grain yield was found highly

dependent upon water availability during the period between tasseling and silking and for approximately two weeks after silking (Otegui et al., 1995). During this period, the number of kernels was not increased when fresh pollen was applied to late appearing silks. It indicated that ovaries that failed to expose their silks with pollen shedding were deleteriously affected by water stress. Under stress, the egg sac normally gets fertilized, but the endosperm, embryo, and seed coat did not develop beyond two or three days (Westgate and Boyer, 1985). Kernel number was found to be an important drought tolerance trait (Andrade et al., 1999). The kernel number (ear length) is highly influenced by the environment. A curvilinear relationship between maize growth rates and number of kernels fixed during the period bracketing silking was reported when plant growth ranges vary through plant density, plant to plant variability, incident radiation, night temperatures, or year showing effect of environment (Andrade et al., 1999). Hence, at flowering the anthesis-silking interval (ASI) becomes a sensitive measure of genotypic tolerance to, reduced photo assimilation per plant from many causes (Boyle et al., 1991). As a consequence, selection for decreased ASI shown to increase yield under drought stress in four cycles of selection in Tuxpeno Sequia (Edmeades et al., 1993). Edmeades et al. (1993) found with the increase of ASI from -0.5 to 5 a substantial decrease of kernel per plant was about 75 % under drought. The yield increase in drought stress due to decreased ASI was largely due to an increased rate of biomass accumulation per spikelet, and development of flower spikelets per ear (Bolaños and Edmeades, 1993).

Senescence is another form of resistance to drought. The senescence progress is normally caused by loss of chlorophyll. Stay green is a variant in which senescence is delayed compared with the standard reference genotype (Thomas and Howarth, 2000). Stay green in grain sorghum has been found to be associated with higher yield under water deficit conditions. This has been

attributed basically to maintenance of photosynthetic capability during the grain filling period (Rosenow et al. 1983; Borrell et al., 2000) and also due to lodging resistance (Rosenow, 1984). In maize stay green is associated with delayed senescence, higher water and chlorophyll contents, higher level of sucrose and protein content in husk and cobs, higher grain protein content, and larger kernel weight (Gentinetta et al., 1986). However, in some cases, stay green was not found to be associated with high grain yield in drought stress environments (Chapman and Edmeades, 1999; Badu-Apraku et al., 2013).

Roots are very important plant parts utilized for adaptation to several stresses. To exploit heterogeneous soil resources the spatial configuration of root systems, called root architecture, was described to be an important trait to increase plant productivity (Lynch, 1995). The potential importance of longer deep and vigorous maize root systems of maize was recognized (Tuberosa et al., 2003; Landi et al., 2010; Hund et al., 2011). A change in root system architecture and how water is captured in maize were found to have a direct effect on biomass accumulation and historic yield trends in maize (Hammer et al., 2009). Root length density was also found to help in increasing yield under low resource availability (Herrera and Govaerts, 2012). The benefit of the trait was found to decrease if there is no resource scarcity (Herrera and Govaerts, 2012). The importance of root systems could also be detrimental because of the metabolic cost associated with maintenance or development of vigorous root systems under drought stress (Tuberosa, 2012). Bolaños and Edmeades (1993) found a decrease in root mass on the upper 30 cm of soil surface when a tropical maize population was under recurrent selection for increased grain yield in drought stressed environments. However, the lack of accurate root phenotyping methods and the recent bottleneck in field phenotyping techniques have been described as principle factor for inaccurate root studies and uses (Richards, 2008; Tuberosa, 2012).

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The post-embryonic shoot borne root system in maize is the major backbone of rootstocks (Hochholdinger et al., 2004). These roots that are initiated from consecutive underground and aboveground nodes of the stem are called crown and brace roots, respectively. The formation of the crown root is believed to start after 10 days of germination, whereas brace roots appear around six weeks after germination. During the entire lifetime of maize approximately 70 shoot borne roots are developed, which are organized, on average, in six whorls of underground crown roots and two to three whorls of above ground brace roots (Hoppe et al., 1986). The crowns roots are responsible for the majority of the water uptake by the plant via branch roots. The brace roots form lateral roots only after penetrating the soil. These lateral roots provide additional lodging resistance and water and nutrient uptake. The development of brace roots was found to decrease under low moisture and high heat stress environments (Thomison, 1995) making plants more vulnerable to root lodging. Hence roots play an important role in lodging resistance. Increasing bending strength and angle of spread of the adventitious root in soil were described as potential mechanisms to improve lodging resistance (Ennos et al., 1993). This makes the brace roots a potential plant constitutive trait for selection of drought resistance, in addition to lodging resistance.

The ideotype for best utilization of water and N by maize root systems was described as maize having (1) a large diameter of primary roots with few but long lateral root branches, (2) seminal root systems with shallow angles, having thin diameter, many laterals and long root hairs, (3) crown root with steep growth angles and few but long lateral branches (4) one whorl of brace roots and the above ground nodes with highly occupied brace roots having less steep root angle than crown roots to avoid competition, intermediate growth angles for mechanical support and (5) having abundant cortical parenchyma with large cortical cell size, abundant number of

cortical cell files and high senescence of the cells (Lynch, 2013). There are many criteria, like root distribution and pattern, to be considered an ideal root system for stress environments. Length is not the only criteria. In an unspecified maize genotype grown in a fine sandy loam soil, about 50 % of the total root length density was found in top 10 cm and 30 % more on 20 cm depth, and the remaining 20 % below 30 cm of soil depth. This shows almost 80 % of the length density is found in the top 30 cm of soil (Yu et al., 2007). When the soil was wet, maize roots extracted water from all depths (0-70 cm) directly or indirectly after transport. When soil was dry the significant water uptake was only found in the region with high root length density. The results found that the water uptake from deeper roots reaching to wetter layers cannot compensate the water deficit in upper layer of soil (Grahan and Nobel, 1999; Yu et al., 2007).

Drought stress management for precision phenotyping

Managed stress environments help reveal higher genetic variation for stress tolerance traits compared to random drought or optimal environmental conditions (Chapman and Edmeades, 1999; Bänziger et al., 2000; Carena et al., 2009; Weber et al., 2012). The main challenges in breeding for drought resistance have been described as lack of useful variation in germplasm for drought, low precision of assessing the drought condition, and the need to apply higher selection intensity (Bänziger et al., 2000). Extensive multienvironment testing of genetically narrow-based hybrids is the main method to select for improving drought tolerance worldwide. This tradition was speculated to be the reason to have low genetic gain in grain filling stage due to lack of useful genetic variation in elite temperate maize germplasm (Campos et al., 2004). The selection of genotypes under stress conditions in early generations was found to be important as the multi-location testing at later stages of breeding only exposes few varieties tolerant to stress conditions (Bänziger et al., 2000; Carena et al., 2009). This has showed the

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importance of managed stress trials to genetically differentiate the drought related trials from others. Bänziger et al. (2000) described the crucial factors considered while stress management in managed stress trials are timing, intensity, and uniformity of stresses. The timing of stress in trials should be such that the targeted growth stage is affected most that modifies the drought resistance related traits. The drought stress intensity should be such that it affects traits that are important for grain yield. The stress should be uniform over space that can reveal genetic differences so that there will be more progress to selection. Under managed stress trials in early maturing maize, heritability was found highest in optimal conditions (0.92), lowest in drought environments (0.44) and low in random abiotic stress conditions (0.55). The selection efficiency was moderate between random drought and managed stress conditions (0.70) while it was high for well-watered condition (1.12) (Weber et al., 2012). The genetic correlation for grain yield between drought and well-watered environments was found to be 0.61 in temperate maize (Zimoyo and Bernardo, 2013).

A cross over interaction was found to occur in most of cereals at one third of the yield potential between cultivars which yield high in well water condition and the cultivar which yield high in water stress condition (Blum, 2011). One reason of cross over may be due to shift in plant constitutive traits favoring moderate water use like early flowering, low leaf transpiration rates, and reduced tillering. Secondly, it may be due to a large sink in higher yielding cultivars constituting a load on the plant in terms of water use and water status, which in drought condition expresses as low water status (Blum, 2011). This also showed the importance of managed stress trials to differentiate the traits in contrasting stresses. Bänziger et al. (2000) showed that the goal for drought stress applied at flowering should be such that the ASI should average 4 to 8 days and yield should range 1 to 2 Mg ha^{-1} or about 15-20 % of well-watered yield

trials. On the other hand, the goal for drought stress applied during grain filling should be such that ASI is not affected much, however, yield is reduced by 50 % of yield potential.

Importance of secondary traits for drought resistance

Direct selection for grain yield under random drought environments has been less successful because of large genotype-by-environment interactions causing low heritability of grain yield (Araus et al., 2008, Lopes et al., 2011). The large genotype-by-environment interaction in drought environments is caused by variation in severity and timing of water deficits in soil, variation in flowering time in the experiment, sample of germplasm under study or the interaction of water deficits with nutrient deficiency and toxicities (Cooper et al., 1999; Bänziger and Cooper, 2001). Hence, indirect selection using secondary traits as complement to phenotypic selection or completely replacing selection based on yield as single most important phenotypic trait could be important (Bänziger and Cooper, 2001). Secondary-trait selection can also prevent the confounding effects of stress time in yield like drought at flowering time (Blum, 2011). Trait based selection also could be more important since large seasonal variation in yield and high genotype-by-environment interaction can slow down the genetic gain when yield is targeted directly, and also it ensures there is enough genetic variation in breeding population for selection (Richards et al., 2002).

In order to be successful the secondary traits should have higher heritability than grain yield, enough genetic variability, and should be correlated positively with grain yield or other important agronomic traits across stresses. Also the trait measurement should be rapid, nondestructive, cost effective and done in single plants or in small plots (Bänziger et al., 2000; Ribaut et al., 2009; Araus et al., 2012; Tuberosa, 2012).

Phenotyping for drought resistance

The recent bottleneck in phenotyping methods could hinder the future advances in breeding because most research recently is focused on more fashionable breeding approaches utilizing molecular marker-assisted selection (MAS), genetic modification and various 'omics' techniques (Araus et al., 2012; Tuberosa, 2012). Grain yield across environment is still the most important trait for phenotyping in drought environments by breeders, however, the heritability of yield decreases severely with increase of drought conditions due to high genotype-by-environment interactions (Bänziger et al., 2000; Araus et al., 2012).

Anthesis silking interval (ASI) has been found to be very useful in selection for drought resistance in tropical maize. In tropical maize, a strong correlation between ASI and grain yield was found (r_p = -0.53, P < 0.01) whereas a stronger correlation was found with kernel number per plant (r_p = 0.90, P < 0.01) (Bolanos and Edmeades, 1996). This makes both kernel number per plant and ASI to be important traits for selection against drought occurring at flowering stage. However, ASI could provide an erroneous reading when delays are small (> 3 days) (Araus et al., 2012). Delayed senescence was found to be associated with higher grain yield in maize hybrids (Gentinetta et al., 1986). Other traits affecting kernel weight like individual kernel weight, stay green, and remobilization of stem reserves have been used in past for selection in drought environments (Araus et al., 2012). Remobilization of stem reserves can be measured by loss of stem dry weight or from reduction in stem diameter. However, the method has not been used extensively to study genotypic differences in drought (Tuberosa, 2012).

Measurement of transpiration has also been used to estimate water status. Infrared thermometers have been used to measure canopy temperature depression. However, the method has been more useful for crops with more homogenous canopies like cotton or small grain

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cereals, which fully cover the soil and it is less useful for maize (Araus et al., 2012). Infrared thermal imaging has been recently used to study maize genotypes in different water regimes. Significant differences were reported between early and late maturing genotypes at blister stage for canopy temperature changes caused by high transpiration loss during water stress (Zia et al., 2013).

Measurement of oxygen isotope composition has been used to study drought adaptation of small grain cereals. In this method the stable $^{13}C/^{12}C$ isotope composition ($\delta^{13}C$) is measured in plant matter (Araus et al., 2012). The trait is related to transpiration or water use efficiency or the amount of dry matter produced per unit of water transpired. The principle is variation in ^{13}C discrimination (δ) in C_3 plants depends on the ratio of intracellular CO_2 concentration and ambient CO_2 concentration (Farquhar et al., 1982). However, in C_4 plants like maize the C_4 mechanism was found to be antagonistic to the use of ($\delta^{13}C$) as a tool for drought screening (Araus et al., 2012; Monneveux et al., 2012). The technique was also criticized for being very expensive (Monneceux et al., 2012).

Portable spectrodiometer has been used to assess biomass in maize using the normalized difference vegetation index (NDVI). At the leaf level, the portable chlorophyll meter like SPAD^{TM} can be used or, at the whole plant level, portable spectodiometer like GreenSeeker^{TM} can be used (Araus et al., 2008; Araus et al., 2012). The principle is based on measurement of chlorophyll content. It is based on the shift of light absorbed in the visible (400-700 nm) wavelength, also utilized by photosynthetic pigment) vs. near infrared bands (700-1000nm) of the spectrum (Areus et al., 2012). The cross validation showed that leaf canopy reflectance at milk grain stage showed maximum of 40% of grain yield variation. However, since the data was collected in a single location, it needs further validation (Weber et al., 2012). In a study of 550

inbred lines from a worldwide collection, the broad sense heritability was found to be high for NDVI in the range of 0.79 in well-watered (WW) and 0.83 in water stressed (WS) environments (Lu et al., 2011).

Root system phenotyping through quantification and analysis is one of the main challenges plant biologists face for many crops (Lynch, 1995; Richards, 2008; Tuberosa, 2012). Roots grow in varying length and breadth within an opaque medium. It is composed of thousands of individual root axes, very different from each other developmentally, physiologically and morphologically. Therefore, nondestructive phenotyping through quantification and analysis of roots is very challenging (Lynch, 1995). Some techniques have been developed for root system phenotyping in the field as well as in laboratory. But these techniques require different levels of damage to root systems and plants. Vertical pulling resistance of root or the force required to pull the maize plant vertically from the soil was found highly correlated with root volume and also have been used for phenotyping and analysis of root systems (Zuber et al., 1968). This is very destructive, however, and considered a high throughput method for field phenotyping (Tuberosa, 2012). Field phenotyping through 'shovelomics' was introduced as another method to study root architecture in maize (Trachsel et al., 2011). The method includes excavation by removing a soil cylinder with shovels, cleaning roots, and visually scoring root related traits. This method is also destructive and could be very labor consuming if we need to study adult maize plants. Excavation and coring methods also have been utilized to investigate root mass and distribution in soybean. However, the technique, according to scientists, is very time consuming and labor intensive (Nissen et al., 2008).

Nondestructive methods obviously produce less damage to the root system. Transparent walls placed against the soil profiles are called rhizotrons (Bohm, 1979). Minirhizotrons have

been used as *In Situ* methods for viewing and investigating fine root systems in plants (Johnson et al., 2001). The method uses clear tubes installed close to root systems that can be used to study root production, turnover or lifespan by image capturing devices. This technique, however, needs continued improvements and updates on image analysis of large research field data for top accuracy within and across plots (Rewald, 2013). Tube installation is very crucial as it causes soil damage, which ultimately can create atrifacts in data (Johnson et al., 2001). Hand held capacitance meters have also been used to measure root capacitance as a nondestructive fast method to estimate root mass. (van Been et al., 1998; McBride, 2008; Dietrich et al., 2013). In field studies, van Been et al. (1998) found that the electrical capacitance of maize inbred and hybrids roots measured between one electrode inserted in rooting substrate and another at base of stem, were highly correlated with fresh root mass ($r^2 = 0.69$, $P < 0.001$) at flowering. However, this method has not been used widely (Tuberosa, 2012).

There are techniques based on hydroponics, pot experiments, and minirhizotrons developed for phenotyping root systems in controlled environmental conditions (Grieder et al., 2014). The controlled environment can give a more rapid and accurate analysis of root structures because of less soil heterogeneity compared to field conditions. However, due to the unnatural environment, very weak correlations are found between these studies and real field situation (Araus et al., 2012; Tuberosa et al., 2012) making it less beneficial for applied plant breeding. Metabolic changes has also been measured in maize for study of drought resistance. Increase in absccisic acid (ABA) and carbohydrates concentration (Sanguineti et al., 1999; Settler, 2006) was found to be associated with drought resistance in maize. Cost effective ABA-specific monoclonal antibodies (Tuberosa, 2012) have been utilized to measure ABA concentration. A significant decrease in capacity to accumulate ABA in seedlings was found in a study of maize

hybrids developed from 1930 to 2000 in response to stress (Sanguineti et al., 2006). However, studies have not found a clear relationship between ABA and grain yield in drought environments (Tuberosa, 2012).

Selection indices have been found to be most effective to increase yield in drought environments combining different drought related traits (Bolaños and Edmeades, 1993; Bänziger et al., 2000; Araus et al, 2012). A selection index including leaf senescence, ASI, yield, and leaf and stem extension in Tuxpeno population led to gains in grain yield in mild (320 kg ha^{-1} cycle^{-1}), medium (420 kg ha^{-1} cycle^{-1}) and severe stress conditions (410 kg ha^{-1} cycle^{-1}) with 33% progeny-selection intensity (Fischer et al., 1989).

Estimation of quantitative genetics parameters

Quantitative traits are governed by many loci with small individual effects which require study of these traits utilizing statistical approaches appropriate for continuous variables like means, variances and covariances (Moll and Stuber, 1974). Historically, many quantitative traits have been studied utilizing different mating designs to understand genetic control and variation in these traits across stresses in maize (Hallauer et al., 2010). Mating designs or the system of mating to develop progenies have been used to estimate additive and dominance genetic variances (Cockerham, 1963). The most used mating designs to study of quantitative traits are diallel design, designs I, II and III, partial diallel, triallel and quadriallele designs, half-sib progenies and polycross progenies (Dudley and Moll, 1969).

The pioneering work of Fisher (1918) on partitioning the total genetic variance into additive genetic variance, dominance genetic variance, and epistatic variances based on analysis of populations utilizing covariance between relatives helped develop the foundation of quantitative genetic analysis. Later, the concepts of general combining ability (GCA) and

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specific combining ability (SCA) have played important role in determining the usefulness of lines in future breeding (Hallauer et al., 2010). Sprague and Tatum (1942) first divided combining ability into specific and general combining ability utilizing the diallel cross. The average performance of lines in hybrid combination was called GCA and the cases where certain combination of hybrids became relatively better or worse than would be generally expected on average was called SCA. Griffing (1956a and 1956b) provided the analysis of full diallel with parents, half diallel with parents, full diallel without parents and half diallel without parents to estimate GCA and SCA variances and their genetic expectations. The genetic expectations are the additive and dominance genetic variances utilizing completely generalized gene models in sets of inbreds representing a random sample from a population.

The low numbers of parents utilized in most common diallel mating designs are less likely to represent a true sample for quantitative genetic studies (Hallauer et al., 2010). The crosses in diallel among n inbred lines with no parents and no reciprocals involve a total of n (n-1)/2 crosses. The number of crosses increase with n. Therefore, with fixed resources available; a diallel with relatively small numbers of inbred lines is only possible (Hallauer et al., 2010). This causes the GCA variance to have large sampling bias and for breeders many potential inbred lines remain untested (Kempthorne and Curnow, 1961). The partial diallel introduced by Kempthorne and Curnow (1961) was developed to include more parents and was found more efficient than other designs on estimation of variances for GCA and SCA. The inclusion of more random parents could represent the possible range of genetic variation in a population (Hallauer et al., 2010).

Quantitative genetics of agronomic traits in drought environments

Numerous small effect genetic loci and hundreds of genes controlling many morphological and physiological differences have been found for drought resistance, making it a genetically complex trait (Hu and Xiong, 2014). Mating designs through the analysis and genetic parameter estimates have been used in past to study genetic variation and control of drought resistance traits across different environments.

Both GCA and SCA variances have been found to be important for many drought resistance traits. In a study including a diallel cross of 17 white-grained lowland tropical maize inbred lines, significant ($P < 0.05$) GCA and SCA variances were found for ASI, root lodging, plant height, tassel size, and erect leaves (Betran et al., 2003a). However, only GCA was found significant ($P < 0.05$) for grain moisture, senescence, and root capacitance across drought stress and irrigated environments. Both GCA and SCA variances were found non-significant for stalk lodging. The dominance was on partial dominance range for ASI and ear per plant. GCA-by-environment interaction variances were found significant while SCA-by-environment was found non-significant for grain yield across stress environments (Betran et al., 2003b), showing the importance of environment for GCA more than SCA in grain yield across environments. In their study the GCA and SCA variance components were smaller in drought stress environments compared to well-watered environments. In addition, the relative importance of GCA vs. SCA was found higher in drought stress environments. The additive genetic variance explained 61 % of the total genetic variation. Also, a higher expression of heterosis was showed in drought environments compared to non-stress environments (Betran et al., 2003c). In a different diallel study, including this time early maturing maize lines, both GCA and SCA variances were found significant ($P < 0.01$) for grain yield while the GCA accounted for 64.5 % and 62.3 % variation

in drought and irrigated conditions (Oyekunle and Badu-Apraku, 2011, Badu-Apraku et al., 2013). Overall, these studies showed predominance of additive gene action for grain yield, grain moisture, senescence, and root capacitance in drought stress environments. However, more complex gene action was shown for ASI, plant height, tassel size, root and stalk lodging traits, in the same stress environments.

High genetic variation was found for stalk diameter in populations derived from selection for stalk diameter (Bosch et al., 2001). In their study, grain yield was increased in first generation and decreased in the advanced generations and also increased the maturity range. Significant additive genetic variance and non-significant dominance variance was found in maize for stem diameter in F_2 and F_2Syn_3 of the semiexotic maize population Mo17 x La Posta (Casanas et al., 2001). The narrow-sense heritability was found to be low, equal to 0.29 in both F_2 and F_2Syn_3 populations. The correlated response to selection for stem diameter was significant to increase yield in F_2Syn_3 population. However, in a study of F_2s of Illinois Stiff stalk synthetic composite (RSSSC) x South African photoperiod insensitive composite II (PIC2), the selection for higher grain yield resulted in a deterioration of stalk quality (Albrecht and Dudley, 1987). The results showed the stem diameter has more additive genetic variance compared to dominance, however, the correlated response with grain yield varies with the genetic makeup of populations.

The osmotic potential measured with vapor pressure osmometer in the field for full sib families from two tropical maize populations (Laposta Sequia and Pool 26 Sequia) showed that the genetic variation for osmotic adjustment was similar and low for both populations (Guei and Wassom, 1993). Dominance genetic effects were more important than additive genetic effects. But, the association of traits with yield was found weak and not significant. Low genetic variation and high dominance variance of this trait could show less importance for selection in

drought environments. However, this could be only specific to those two populations and needs further validation across populations.

There have been few research studies done on adult plant root characteristics. Mostly the studies are focused on seminal and primary root characters. Significant genetic variation was normally found for root architectural traits including length, number, and diameter and branching of seminal, primary and nodal roots, dry weight of embryonic and nodal roots, and diameter of nodal root system, in seedlings of maize grown in greenhouse (Burton et al., 2013; Burton et al., 2015). Large additive effects and smaller epstatic effects were found for total brace root tier number in maize (Ku et al., 2011).

Significant genetic variation for root pull resistance at milk stage of corn was found (Penny, 1981). The correlation between inbred lines and their testcrosses was significant ($r_p =$ 0.5, $P < 0.01$) and reading between the four testing environments also had positive significant correlations in inbreds ($r_p = 0.85$) and in testcrosses ($r_p = 0.69$). Significantly high additive and non-additive gene action with GCA-by-environment interactions were found for root-pulling resistance ($P < 0.01$) in Griffing's diallel analysis (Peters et al., 1982). The presence of non-additive gene action shows the complex gene action in this trait. In the same study, the correlation between yield and root pulling resistance was not found significant. In another study, however, high positive correlations between root pulling resistance and N-uptake ($r_p = 0.68$) and grain yield ($r_p = 0.71$) were found in maize (Kamara et al., 2002). In the same study there was no correlation with N-use efficiency in breeding lines. The root pulling resistance, which mostly involves the root density in the upper soil layer, could be the reason showing more correlation with N-uptake and grain yield. Vertical root pulling resistance trait was significantly correlated

with root volume and the number of brace roots in maize (Beck et al., 1988) making it an important trait for resistance to root lodging in drought stress.

Root capacitance was found to have low heritability across water regimes. It was reported to be 0.5 in maize under different water regimes (Messmer et al., 2011). In inbred lines, the heritability was found to be 0.25 in well-watered environments while 0.44 for water stressed environments reported (Lu et al., 2011). The correlation of root capacitance was found to be low with grain yield, senescence, and ASI (Monneveux et al., 2008; Messmer et al., 2011). In other cereals like barley, root system size selection based on root capacitance was found to increase yield 8.1 % for every increase of 3.9 % of root system. The mean correlation between different barley varieties was found to be 0.5 for root capacitance (Svacina et al, 2013). The correlation between yield and larger root system was reported to be ($r_p = 0.225$ns) and ($r_p = 0.396$, P < 0.05).

In maize, a high correlation was found between grain yield and ears per plant ($r_p = +0.86$) and a low correlation was observed with ASI ($r_p = -0.33$), both under drought stress environments. The correlation between grain yield and ASI or ears plant^{-1} was found to increase with drought intensity (Bolanos and Edmeades, 1996; Ziyomo and Bernardo, 2013). The correlation of root capacitance and root lodging was found non-significant across environments (Betran et al., 2003). With the increasing severity of drought grain yield, kernel ear^{-1}, kernel plant^{-1} and weight kernel^{-1} decreased while correlation was increased for ASI and ear plant^{-1} (Bolanos and Edmeades, 1996). Therefore, with the adaptation of maize for high yield, ASI has been reported to decrease.

NDVI showed a high genetic correlation with chlorophyll content ($r_A = 0.79$ to 0.83), grain yield ($r_A = 0.38$ to 0.49), and ASI ($r_A = -0.126$ to -0.468). However, the correlation was non-significant with root capacitance (Lu et al., 2011). In subtropical white dent maize lines

CML444 and SC-Malawi and their 236 RILs, leaf senescence ($r_p = 0.33$) and leaf chlorophyll ($r_p = -0.36$) content was found significantly associated with higher grain yield in drought environments and in well-watered environments ($r_p = 0.38$) and ($r_p = -0.50$), respectively (Messmer et al., 2011) making them important drought adaptive traits.

Selection for particular traits can have negative or positive effect with other traits. A study utilizing 18 pioneer hybrids released during year 1953-2001, found that ASI and barrenness have been reduced by selection for yield (Campos et al., 2006). The direct and indirect responses to recurrent selection in two maize populations: drought tolerance population 1 (DTP1) and drought tolerance population 2 (DTP2) selected for yield in drought stress showed that grain yield was associated with higher partitioning of biomass towards developing ear rather change in senescence (Monneveux et al., 2005). The research also showed the significant reduction in tassel size and stem weight with increase of drought resistance. In a study of 90 extra early inbred lines under low N and drought stress environments, the stay green characteristic was not found to be an important trait for selecting drought tolerant genotypes. However, plant aspect and husk cover was found to have importance in selecting for drought tolerance (Badu-Apraku et al., 2013). The correlation found for leaf stem extension ($r_p = +0.39$, P < 0.01), ASI ($r_p = -0.73$, P < 0.01), and leaf senescence rate ($r_p = -0.39$, P < 0.01) for grain yield in drought stress was utilized to create a selection index to select for drought tolerance in Tuxpeno population (Fischer et al., 1989). Similar gains in grain yield were also obtained in other studies. Eight cycles of full-sib recurrent selection for population Tuxpeno Sequia in drought stress conditions either at flowering or grain filling was carried out. The selection was based on an index including yield, morphological, and physiological traits. The yield was increased by an average of 108 kg ha^{-1} cycle^{-1}. The yield increase was found to be mainly due to

gain in harvest index (HI) (Bolanos and Edmeades, 1993). In the same recurrent selection program, plant height, total leaf number, and tassel primary branch numbers was significantly decreased by -0.9%, -0.5% and -2.6% cycle^{-1}, respectively. Root biomass at 50 cm was decreased by 33 % and vertical root pulling resistance was reduced at a rate of -1.2 % cycle^{-1} (Bolanos and Edmeades, 1993). However, the study was done in 2 m deep pots and the profile of root systems may have changed favoring more roots in deeper soil layers causing drought resistance (Yu et al., 2007). In addition, no significant improvement was found for the traits included in the selection index after eight cycles of selection. Indirect selection responses in Fischer et al. (1989) and Bolanos and Edmeades (1993) were different, which could be because of inaccurate measurement of traits (Bolanos and Edmeades, 1993; Blum, 1988; Falconer, 1996).

Excellent root and stalk strength lines have been developed utilizing recurrent selection programs. B104 was developed from B13(S)C5 population after 12 cycles of recurrent selection for improved agronomic traits including grain yield giving equal importance to root strength. In another dryland study, grain yield gain of 5.8 % in population AS-A was found after five cycles of full sib recurrent selection. The gain was 11 % in fully irrigated condition for grain yield (Johnson and Geadelmann, 1989). The higher gain in the irrigated environment could be due to the population genetic structure under selection or due to the lack of a selection index including traits adapted to drought stress environments. A S_1 recurrent selection program was conducted by Chapman and Edmeades, (1999) on populations 'La Posta Sequia' and 'Pool 26 Sequia' for three cycles and a full-sib recurrent selection program for population 'Tuxpeno Sequa' for eight cycles for drought tolerance at flowering and grain filling stages. The gain in selection for grain yield in recurrent selection was associated with higher grain number per plant (grain number per square, ear per plant and grains per ear), shorter ASI, decreased tassel size, and decreased stem size

(Chapman and Edmeades, 1999). The study, however, could not found association with stay green and grain weight. This is in agreement with another research study finding less importance of stay green under stress environments for grain yield (Badu-Apraku et al., 2013). In a study including transgenic maize hybrid (MON87460) with event expressing bacterial cold shock protein B (*CspB*) and non-transgenic control, an average 6 % yield advantage was found over control. The low leaf growth, increase in kernel number, and increased harvest index (HI) was found to be associated with the event (Nemali et al., 2014). In temperate maize, both new and old hybrids showed genetic gains were not associated with change in HI but with grain number at grain filling (Tollenaar and Lee, 2006). The importance of increased partitioning of dry matter to the ear during bracketing silking (two weeks before and after flowering) was also found to increase genetic gains in Argentinian hybrids (Echarte et al, 2004). The study showed that increases in yield in drought environments were mostly associated with increases in HI, more number of grains per ear, decrease tassel size, and decreased stem size. However, inaccurate phenotyping could have effected some associations.

Importance of breeding for maize grain quality

Historically, agronomic trait improvement has been given major importance in maize breeding and very little attention has been given to improve grain quality traits (Scott et al., 2006). Studies of set of maize cultivars grown from the 1920s to 2001 have found a decreasing protein content, increasing starch content, and no significant change in grain oil (Duvick et al., 2004; Scott, 2006) showing the importance of giving independent attention to grain quality traits for improvement of grain yield and quality.

Use of near infrared reflectance (NIR) methods has been found very useful to analyze grain quality traits for genetic improvement in breeding programs. NIR has been utilized to

measure organic constituents in grains like protein, starch, oil, extractable starch, fermentable starch, and amino acids like methionine, cysteine, and lysine in maize as an accurate, high throughput, low cost method (Orman and Schumann, 1991, Paulsen et al., 1999; Paulsen and Singh, 2004, Bastianelli et al., 2007). The screening procedure for NIR based on the principle of proportionate absorption of light by different concentration of chemical bond in the organic materials under screening (Paulsen and Singh, 2004). In the past, cumbersome lab methods were used to estimate the concentration of organic molecules in grains (Echoff et al., 1996; Pollak et al., 2005). Research in maize has showed a strong positive correlation between wet milling starch yield and total grain starch content estimated by NIR machines among inbred and hybrids ($r_p = 0.9$ and $r_p = 0.6$ respectively) (Zehr et al., 1995). Similar strong correlations for NIR starch and wet milling starch as well as NIR protein and gluten was found in F_2S_1 families from Illinois high protein and low protein strain parents (Dijkhuizen et al., 1998). Hence, the association between NIR lab data and end use quality can be considered strong for different grain quality traits.

Each kilogram of dry maize grain contains 90 g protein, 40 g oil, 73 g starch, 2.5 g lysine, and 1.9 g methionine (Clark et al., 2006). The crop is deficient in dietary needs of essential amino acids required for monogastric animals including chicken, swine, and humans (Pollak and Scott, 2005). Fernandez et al (1994) showed that the most important limiting amino acids were lysine, threonine, tryptophan, arginine, isoleucine, valine, methionine, cysteine, phenylalanine, tyrosine, and histidine. This is because in maize, storage proteins called 'zeins', were found to account for 60-70 % of the endosperm protein (Hamaker et al., 1995), which are deficient in lysine and tryptophan content (Pollak and Scott, 2005). Hence, ultimately decreasing the quality of protein when zeins and non-zein proteins are combined.

From the farmer perspective, the quality of grains is equally important as grain yield in maize. Since maize is deficient in dietary need of essential amino acids, livestock producers spend extra money on dietary supplementation through the synthetic form of these nutrients to mitigate deficiency (Pollak and Scott, 2005). The methionine content is crucial to increase the value of poultry so does lysine content for swine feed. Protein content higher than 100 g kg^{-1} in grain helps decrease additional protein source used for mixing in animal feeds. High lysine content (>3 g kg^{-1}) and high methionine content (> 2.5 g kg^{-1}) are crucial to increase the quality of feeds. Grain oil content is valuable if it has higher values than 60 g kg^{-1} to increase caloric content in animal feed grains (Brumm and Hurburgh, 1990; Lambert, 1994).

Recently, gasoline with added ethanol has expanded worldwide (Sanchez and Cardona, 2008). This is because ethanol production is becoming an important component to boost the economy of rural areas, improving air quality as well as reducing the oil import from worldwide. Ethanol is the main biofuel in the U.S., representing 99 % of the total biofuel use (Ferrel et al., 2006). Basically three methods have been utilized to fractionate maize grain for biofuel: dry-milling, wet-milling, and alkaline processing (Sanchez and Cardona, 2008).

In the maize wet milling process, maize kernels are decomposed into starch, protein, oil and fiber using chemical, biochemical, and mechanical methods (Singh et al., 1997). The process produces more than 1000 different industrial food products including high fructose corn syrup, dextrose syrups, modified starches, lysine, paper starches, and ethanol. Extractable starch content in grain is crucial to provide the amount of starch that can be fractioned from maize kernels while conducting the wet milling process. Thus, high extractable starch in grain provides not only high starch recovery but also high process efficiencies in gluten starch separation, fiber separation, and gluten feed drying (Paulsen and Singh, 2004). Past estimates have shown that an

increase in one unit percentage concentration of extractable starch in maize grain can be worth a minimum of $1.58 to $2.36 per ton of maize (Paulsen et al., 2003). The trait is a very important in one for selection in maize germplasms (Zehr et al., 1995; Eckhoff et al., 1996; Singh et al., 2001). There has been increased interest in breeding for industrial processing of grain starch content recently, however, very few public or private breeding programs have devoted significant efforts (Pollak and Scott, 2005).

Grain quality traits are important and needed traits to move maize to marginal drought stress environments to improve the livelihood of farmers who do not have the same choices farmers have in the central U.S. Corn Belt (Carena et al., 2009). There is the need of further research on the genetic variation controlling grain quality traits in different soil water regimes in order to help breeders manage resources in breeding programs targeted for drought stress environments.

Quantitative genetics of grain quality traits in drought environments

A large number of quantitative trait loci (> 50) were found for grain starch, oil, and protein content in maize making these traits polygenic in nature (Cooks et al. 2012; Laurie et al., 2014). Mating design analyses have been used in past to study the quantitative genetics of grain quality traits in maize (Hallauer et al., 2010).

Additive genetic variances were found to be significant compared to non-additive genetic variances for grain starch, oil, lysine, and methionine content in maize studies (Sreeramulu and Bauman, 1970; Poneleit and Bauman, 1970; Darrigues et al., 2005; Bari and Carena, 2015). For grain oil, protein, and methionine content some studies showed importance of both additive and non-additive gene action (Darrigues et al., 2005; Osorno and Carena, 2008; Dudley, 2008). The presence of non-additive gene action in these traits shows a complex genetic makeup for these

traits. In the Nested Association Mapping (NAM) population, the genetic architecture of kernel composition showed the importance of additive gene action for grain starch, protein, and oil content (Laurie. 2004; Cook et al., 2012). The degree of dominance for grain starch and oil in NCII designs of ex-PVP and ND adapted lines was found to be in the partial dominance range (Bari and Carena, 2015). Positive mid-parent and high-parent heterosis was estimated for starch content and grain oil content and negative heterosis was estimated for protein content in different maize hybrids (Taboada-Gaytan et al., 2010). GCA-by-environment variance was found significant for grain protein, oil and starch contents, while SCA-by-environment variance was found not significant in a study of diallel crosses of 10 short-season maize populations (Osorno and Carena, 2008). However, the interaction variance was smaller than the GCA main effect.

The heritability of grain quality traits has been found to be variable. The broad sense heritability in half sib families in maize was estimated between 0.54 to 0.91 for grain protein content and 0.17-0.72 for grain lysine content. The heritability for grain oil content was found between 0.71 and 0.91 for grain oil content (Dudley et al., 1971). Mahan et al. (2012) reported broad sense heritability of 0.59 and 0.24 for lysine and methionine content, respectively. The narrow sense heritability for grain protein content among half sib families was found to be 0.68 (Motto, 1979). However, heritability varies with different germplasms and environments (Hallauer et al., 2010).

Starch and protein contents have shown opposite associations for total grain concentration. Significant and large negative correlations of starch and protein content in grains were found in both maize inbred lines and hybrids (Fox et al., 1992; Zehr et al., 1995; Singh et al., 2001). Significant and large correlations of methionine ($r_p = 0.95$) and lysine ($r_p = 0.76$) were found with grain protein (Mahan et al., 2012) under dryland environments. Significant and

positive correlations between lysine and protein were estimated in quality protein maize (Sreeramulu and Bauman, 1970). Also, significant and positive correlations were found not only between protein content and lysine but also between protein and oil (Dudley et al., 1971).

Historically, quantitative genetic and mutation approaches were utilized to improve grain quality traits in maize germplasms (Dudley and Lambert, 2004; Pollak and Scott, 2005). Of them, the quantitative genetic approach has been successful for improving grain quality traits, including recurrent selection and exotic germplasm incorporation (Dudley and Lambert, 2004; Osorno and Carena, 2008; Sharma and Carena, 2011; Laude and Carena, 2014,). Two maize mutants *opaque2 (O2)* and *floury2* were the most used mutants in maize for obtaining substantially higher lysine and tryptophan contents (Mertz et al., 1964; Nelson et al., 1965). However, their use was challenged because of the mutant gene being associated with soft endosperm, reduced yield, easy kernel breakage while machine harvesting, environmental fluctuation of lysine content, and less insect and disease resistance (Vasal, 2000). Introduction of *O2* modifiers (Mo2s), for converting soft endosperm to hard was found successful to develop quality protein maize (Vasal et al., 1984). Similarly, maize mutants for sweet corn sugary1 (*su1*), sugary enhancer (SE), and shrunkern2 (*sh2*) responsible for sweet corn (Schultz and Juvik, 2004) and mutant for linoleic acid1 (*ln1*) responsible for altered fatty acid ratio (Poneleit and Alexander, 1965) were discovered. However, use of these specialty mutants in breeding is limited (Cook et al., 2012).

In maize, grain quality traits are affected by the genetic makeup of plants, their growing environment and postharvest handlings (Tsai et al., 1978; Zehr et al, 1996; Cook et al., 2012). The increase of protein concentration with application of nitrogen in soil has been found important (Tsai et al., 1978; Rendig and Broadbent, 1979). The effect of relative maturity was

found significant for pattern of kernel development after endosperm cell division and starch granule formation but it was not significant for the maximum number of endosperm or starch granules formed or the kernel mass (Jones et al., 1996). A significant effect was found for grain drying temperature, soil nitrogen level, and occurrence of killing frost on ethanol concentration, grain protein and grain starch content of six maize hybrids of maturity ranging from 92 to 108 relative maturity (RM). However, when recommended practices were followed the contents were not affected (Reicks et al., 2009). Hence, this also shows the traits are more variable only in extreme environmental conditions. Strong negative correlations between grain protein and oil content while no correlation between grain oil and grain starch contents were reported in a study of 87 elite inbreds in a Chinese maize-breeding program (Chander et al., 2008). In grain sorghum, cultivars grown under different irrigation conditions, significantly affected the starch and protein contents mostly by growing environments but not by irrigation differences (Wu et al., 2008). The influence of genetic factors was found to be more important than environmental factors for grain oil concentration and its quality in maize (Jellum and Marion, 1966). In their study even though the grain oil content varied across locations and years the relative rank of hybrids or genetic stocks was found to be similar across different environmental conditions.

Future of drought resistance in maize

Further research is needed on root shoot interactions including hydraulic conductance differences in stress and non-stress environments (Comas et al., 2013). Instead of total amount of root growth, the maintenance of healthy root meristems for continual root growth could be more important for acquisition of resources from different soil layers (Robinson et al., 1991). A reduction in xylem diameter could reduce hydraulic conductivity in drought conditions, however, it could decrease yield potential in well-watered environments (Passioura, 1983; Comas et al.,

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2013). Richards and Passioura (1989) reduced the xylem vessel diameter from 65 µm to less than 55 µm through a backcross-breeding program in two Australian wheat varieties. Under drought environments the difference in yield with unselected control was between 3 and 11 %. However, the yield difference was found to be not significant under well-watered environments. The yield increase was found to be related to a high HI, biomass at maturity, and more kernels per plant.

There are very few examples of incorporation of marker-assisted selection (MAS) for breeding genetically complex traits like drought resistance (Mackill et al., 2003; Araus et al., 2008), even though numerous QTLs with small effect have been found associated with this trait (Hu and Xiong, 2014). Hence, finding new ways to phenotype drought resistance and their association with major agronomic traits holds a future of breeding drought resistance for product development. Large genetic gains were obtained for early flowering in short season environments (Carena and Wanner, 2009), which was found to be governed by numerous QTLs with small effects (Buckler et al., 2009). Flowering time, however, is a very simple trait to phenotype and obtain, as a consequence, significant genetic gain were reported (Halluer et al., 2010). Drought, however, is a very difficult trait to phenotype (Araus et al., 2012; Tuberosa, 2012) and requires a new accurate, cheaper, cost-efficient, and high throughput method of phenotyping. Hence, the future of gain in drought resistance depends on utilizing new and more efficient screening methods including selection indices for selection in breeding programs designed for improving quantitative traits like recurrent selection and exotic germplasm incorporation with unique germplasm.

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CHAPTER 2. SHORT-SEASON MAIZE DROUGHT RESISTNACE: IMPROVEMENT OF FIELD PHENOTYPING

Abstract

Development of new cultivars in dryer environments has been slow due to unavailability of reliable field phenotyping methods for drought resistance in maize (*Zea mays* L.). Root capacitance, stem diameter, brace root number, and spread width could affect drought resistance and root architecture leading to adaptation of maize to drought. This study was conducted to investigate novel *In Situ* field phenotyping methods and their genetic control to utilize them in breeding programs targeted for drought stress environment. Ninety-four partial diallel crosses from 47 diverse maize inbred lines and control checks were tested in eight water stressed (WS) and well-watered (WW) environments in years 2013 and 2014. All traits showed significantly high genetic variation (P < 0.01) both in WS and WW environments. The brace root counts ranged from 9 to 11 in WS vs. 9 to 20 in WW, the root capacitance ranged from 28 to 57 nF in WS vs. 25 to 63 nF in WW, and brace root spread width ranged from 26 to 44 mm in WS vs. 24 to 42 mm in WW. Additive genetic variances were important for brace root spread width, number of brace root count, and root capacitance. However, non-additive genetic variances were also important for root lodging and stalk diameter. Root and stalk lodging were important both in WW and WS environment to decrease grain yield. Root capacitance, as a measure of fresh root mass, was associated with brace root counts ($r_G > 0.46$, P < 0.05) in both environments. Brace root count (-59 in WS vs. -0.55 in WW) and spread width (-0.52 in WS vs -0.62 in WW) were negatively associated (P < 0.01) with root lodging. The estimates of narrow sense heritability (h^2) were higher for brace root spread width (0.23) and number of brace root count (0.24) as compared to grain yield (0.06) and root lodging (0.1) in WS environments. The visible brace root

number and spread width in maize can be exploited as an *in situ* field phenotyping method to select for root architecture leading to improvement in drought resistance in maize.

Introduction

Maize (*Zea mays* L.) is the largest crop on earth with a production of 829 million tonnes annually (FAOSTAT, 2012). The U.S. is the largest exporter of maize worldwide accounting for a total of 39 % of the world export market of 2013/14 (US Grain Council, 2013). Drought has had a devastating effect on maize production in the past and it is risking the future of maize production as well (Harrison et al., 2014; Lobell et al., 2014). In the year 2012, the reduction of maize yield due to drought in the U.S. was 21 % and 38 % in national production compared to the 2009-2011 mean levels (USDA, 2013). Worldwide loss of yield of maize due to drought was estimated to be 15 % of well-watered yield potential (Edmeades, 2013), making it one of the most important stresses in maize. Insufficient availability of water during crucial growth stages is the single most important abiotic stress factor limiting the crop expansion in western North Dakota (ND) and eastern Montana (MT) (Carena et al, 2009, Carena, 2013). The western half of the state is affected by semi-arid conditions and low annual rainfall whereas the eastern ND experiences more precipitation in normal years (Karetinkov et al., 2008). The development of new cultivars in these dryer environments is slow due to the lack of accurate phenotyping methods and the need for genetic diversity in breeding germplasms.

Extensive multienvironment testing of genetically narrow based germplasm, however, was speculated to be the reason of low genetic diversity for successful selection in temperate maize at the grain filling stage (Campos et al., 2004). Selection for yield per se has been less successful under drought conditions because of large genotype-by-environment interactions causing low heritability of grain yield (Araus et al., 2008, Lopes et al., 2011). Indirect selection

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for drought tolerance with secondary traits could be important (Bänziger and Cooper, 2001; Richards et al., 2002; Blum, 2011). There is a tremendous potential to move maize to more marginal areas with drought stress if new constitutive secondary traits and cross combinations are discovered effecting adaptation to drought environments (Monneveux et al., 2008; Araus et al., 2012).

Drought stresses at flowering and grain filling growth periods are the most critical in maize production (Edmeades et al., 1993; Blum, 2011; Araus et al., 2012). Research in maize yield under drought stress conditions has shown strong dependence on barrenness, anthesis silking interval (ASI), and kernel number per plant (Chapman and Edmeades, 1999; Campos et al., 2004). Larger stem reserves can also be exploited as important desiccation tolerance mechanism in plants (Blum, 2011). The maize stem accumulates carbohydrates between stem elongation and the beginning of kernel growth. The quantity of sugar accumulated was shown to be equivalent to 12-25 % of the final grain dry matter yield in maize (Setter and Meller, 1984). Reserves can be remobilized after flowering when many leaves start senescing to support grain filling (Blum et al., 1997). In addition, stem diameter could be associated with drought resistance in maize.

Accurate phenotyping is the major challenge in improvement of abiotic stress resistance (Araus et al., 2012; Tuberosa, 2012). Some high throughput methods have been developed for green house or lab screening (Araus and Cairns, 2014). However, very few methods have been developed for *In Situ* field phenotyping of root related traits that can be utilized in breeding. The root is an important plant part for the adaptation to specific environmental conditions. The spatial configuration of the root system, also called root architecture, is one of the most important traits to increase plant productivity under drought and N stress conditions (Blum, 2011; Lynch, 2013).

The root architecture and water capture had a direct effect on biomass accumulation and historic yield trends in maize (Hammer et al., 2009). However, field phenotyping of the root system is extremely difficult, inaccurate, and often destructive (Richards, 2008; Tuberosa, 2012). The cost-effective portable capacitance meter has shown a high correlation of root fresh mass in maize genotypes ($r^2 = 0.69$, $P < 0.001$) at flowering time in the field (van Been, 1998). However, very few studies have focused on the importance of root capacitance on the adaptation of temperate maize to drought stress.

Trachsel et al. (2011) introduced a method for field phenotyping maize root architecture, called "shovelomics". It needs excavation by removing a soil cylinder by shovel, cleaning roots, and visually scoring traits. A strong correlation ($r_p > 0.71$) was found between scored and measured trait values for brace root whorls, brace root spread width, and brace root angle in recombinant inbred lines (RILs) of maize. The shovelomics method is still very cumbersome for phenotyping adult maize plant roots, which reaches 1.5 to 2 m deep and 0.9 to 1.2 m lateral spread. This makes the excavation of an adult hybrid extremely difficult. The chance of root damage is also high in soil with high clay content or under drought environments where root systems are often very weak. The excavation and coring method has also been utilized in the past to investigate root mass and distribution (Nissen et al., 2008). The force required to pull the maize plant vertically from soil was also used to study root volume in the field (Zuber et al., 1968; kamara et al., 2002).

One of the unexplored attributes of maize root systems is the clearly visible brace root. The post embryonic roots initiated from consecutive underground and above ground nodes of the stem, called crown and brace roots, respectively, are major backbones of the maize root stock (Hocholdinger et al., 2004). The crown roots generally start to form after 10 days of germination,

whereas brace roots start around six weeks after germination. During the entire lifecycle of maize, generally 70 shoot borne roots are developed which are positioned, on average, at six whorls of underground crown roots and at two to three whorls of above ground brace roots (Hoppe et al., 1986). Brace roots form lateral roots only when they penetrate the soil, and are crucial for lodging resistance as well as for water and nutrient uptake (Guingo and Hebert, 1997; Wesley et al. 2000; Hocholdinger et al., 2004). The development of brace roots was found to decrease in moisture and heat stress (Thomison, 1995; Doussan et al, 2003; Hochholdinger, 2009) making plants vulnerable to more root lodging.

The maize root system architecture was considered to improve yield under drought stress. However, it has not been used in plant breeding program to date (Arus et al., 2012; Tuberosa, 2012). This could be one reason why there are not many field-based studies on adult plant roots and their response to heterogeneous distribution of water and nutrients in soil (Dunbabin et al., 2002; Richards, 2008; Tuberosa, 2012). The visible brace roots can be utilized as a high throughput phenotyping method in *in situ* field phenotyping if presence of genetic variation is significant. To our knowledge, this is the first study focusing on the visible number of braceroot whorls, brace root spread width, and total count of visible brace roots to improve field phenotyping of the maize root architecture. The aim of the present research is to: i) investigate brace root count, spread width, stalk diameter, and root capacitance as an *In Situ* high throughput field phenotyping method for drought resistance, i) determine heritability of traits, iii) identify phenotypic and genotypic correlations with agronomic traits important for drought stress.

Materials and Methods

<u>Plant materials</u>

A representative early maturing maize population has been considered. Forty-seven diverse inbred lines randomly chosen from the public and private sectors were utilized including NDSU maize inbred lines generated from the NDSU EarlyGEM adaptation program (Sharma and Carena, 2012), NDSU elite x elite crosses, and NDSU recurrent selection programs (Table 1). The lines were selected based on yield and grain moisture data generated under random drought conditions (eastern and northeastern ND), under drought conditions (western ND and eastern MT) and under irrigated conditions in western ND and eastern MT (Carena et al., 2009) (Table 1).

<u>Crossing scheme</u>

The 47 randomly selected maize inbred lines were crossed in a partial diallel mating design in the 2012-2013 northern New Zealand winter nursery following the circulent partials of Kempthorne and Curnow (1961). The method uses a random sample of crosses,'s', which is less than n-1, four in our case. The sampling scheme provided was by first defining a constant k, $k = (n + 1 - s)/2 = k = (47 + 1 - 4)/2 = 22$. Then, from the n inbred lines from 1 to n the following crosses were sampled.

Line i $\times$ lines $k + i, k + i + 1, \ldots\ldots, k + i - 1 + s$

……..   ………..   ……..

Line n $\times$ lines $k + n, k + n + 1, \ldots, k + n - 1 + s$

Table 1. List of inbred maize [Zea mays L.] lines used as parents for producing partial diallel crosses and their country of origin.

Pedigree	Background	Origin
LH61	[(ASA x Mo17) x Mo17] x Mo17	USA
ND203	Minnesota 13	USA
ND07-153	BS21(R-T)C8 SYN 2-86	USA
ACF47	Stiff Stalk Private	USA
PHJ40	PHB09 x PHB36	USA
NK779	CM7 x W117	USA
ND246	W755 × W771	USA
ND2004	NDSCD(M)C8	USA
ND2006	NDSBF	USA
B104	BS13(S)C5	USA
LP05	(Yugoslavian GLAMOS x B73Ht) x B73 Ht	Yugoslavia
ND2019	EarlyGEM BR52051	USA
NP2341	Non Stiff Stalk private	USA
ND2002	NDSM(M)C7	USA
ND07-255	EarlyGEM AR	Argentina
ND07-212	EarlyGEM AR	Argentina
PHG47	PH041 x MKSDTE C10	USA
ND2014	[[(GEM21xND2000)xND2000]	Argentina
ND250	W12 x W14	USA
ND291	NDSM(M)C1	USA
KMN22	Early MO17	USA
ND270	NDSL (FS)C2	USA
ND2021	CGSS(S1-S2)C5-21	Canada
ND06-189	[(ND278xND284)-34-3-1-1-1-1]	USA
ND06-85	[ND290XND291]	USA
ND2007	[(B73xMo17)]-22-1-1	USA
ND2013	NDBS1011(FR-M-S)C4	USA
ND2005	NDSM(M)C5	USA
ND265	NDSA(FS)C2	USA
ND07-226	EarlyGEM AR	Argentina
ND2009	B73 x Mo17	USA
[(Gem5 x ND200) x ND 2000)-1]-9-2-1-1-1	Early GEM BR52051	Brazil
ND06-144	CGSS(S1-S2)-91	Canada
ACLB0	Non Stiff Stalk Private	France
Il5	UQ5219 × Q114, (Exotic iod. x iod. background)	USA
ND08-53	[NDSAB(MER-FS)C13Syn1	USA
ND07-97	BS22(R-T)C8 SYN2	USA
ACF052	Non Stiff Salk Private	France
ACF49	Non stiff stalk private	France
ND290	NDSAB(MER)C5	USA
ND08-343	CGL(S1-S2)C5-43	Canada
NK807	W117 x B37	USA
ND07-228	EarlyGEM AR	Argentina
ND274	NDSF(FS)C3	USA
ND2001	NDSG(M)C19 from Minnesota#13	USA
ND2000	NDSCD(M)C8-3-2-1-1-1-1	USA
ND2032	BS22(R)C7	USA

Experimental site

The experiments were carried out in the NDSU Williston Research Extension Center Nesson Valley Irrigation Site, Williston, ND, in the USA (48°9'54" N, 103°6'32''. 4W, 590masl). Another site for our experiment was the Montana State University Eastern Agriculture Research Center, Sidney, MT, USA (47°43'48''N, 104°25'8''. 4W, 594 masl). The experiment was conducted on Nesson Valley, ND Lihen-fine sandy loam and Sidney, MT Savage Silty clay in 2013 and 2014. The water stressed (WS) and well watered (WW) experiments were laid out next to each other in both locations separated by borders and a gap. Irrigation was determined by measuring the soil water content of the top 0.6 m using a neutron probe moisture meter. This was maintained between wilting point and field capacity. The irrigation was applied with linear system sprinkler of #4 nozzle size. The schedule of irrigation is shown in Table 2. The dryland was maintained as rain fed. The precipitation amount in these locations was gathered in each of Nesson Valley and Sidney locations by the weather station situated in the research station next to the field by the North Dakota agriculture weather network (NDAWN http://ndawn.ndsu.nodak.edu/).

The moisture stress in water stressed trials was severe enough to delay silking in hybrids (Bolaños and Edmeades, 1993) and affect grain filling period with less available water. There was enough rain before silking in both water stressed and well watered experiments (Table 2). Because of this, no extra irrigation was provided during germination and stand establishment for both WS and WW trials. The target of managed stress trials was to reduce yield more than 50 % (Bänziger et al., 2000) or more than 30 % (Blum, 2011) in the WS environment compared to WW environment.

Table 2. Amount of water received (mm), grain yield mean and date of first frost in well watered (WW) and water stressed (WS) experiments in western North Dakota and eastern Montana in 2013 and 2014.

Month	Sidney WS		Nesson Valley WS		Sidney WW		Nesson Valley WW	
	2013	2014	2013	2014	2013	2014	2013	2014
May	149.0	90.2	72.9	32.8	149.0	90.2	72.9	32.8
June	105.3	28.0	92.7	61.5	105.3	59.8	92.7	61.5
July	24.3	12.2	53.1	33.8	90.4	136.4	93.7	127.8
August	104.2	131.0	26.4	61.7	199.5	176.0	110.2	115.1
September	12.7	28.9	107.4	35.6	83.0	28.9	148.1	35.6
October	27.0	2.4	61.2	5.3	27.0	2.4	61.2	5.3
Total May to October†	422.6	292.7	413.8	230.6	654.2	493.6	578.9	378.0
Mean grain yield, Mg ha^{-1}	3.2	7.6	4.0	2.2	3.2	8.6	9.1	3.1
Frost (<-1ºC) Date	4-Oct	12-Sep	5-Oct	14-Sep	4-Oct	12-Sep	5-Oct	14-Sep

†20 years normal rainfall from May to October in Sidney, MT was 275.84 mm and in Nesson valley 15 years normal was 307.84 mm (NDAWN, 2015).

Field management

In Sidney MT 100 kg urea ha^{-1} was applied across experiments and years. In Nesson Valley, ND 175 kg ha^{-1} of urea was applied in the WW trial while 34 kg ha^{-1} of urea was applied to the WS trial in 2013. In 2014 381 kg ha^{-1} urea was applied in the WW trial and 145 kg ha^{-1} urea was applied in the WS trial. The amount applied was determined based on the residual nitrogen, potassium and phosphorus present based on soil analyses and the recommended dose in dryland and irrigated environments of western ND and eastern MT (https://www.ag.ndsu.edu/crops/corn). The previous crop in both locations was barley. Weed management was done applying herbicide Moxy @109.56 ml/ha and Accent @49 ml/ha. The target plant density for the dry land and irrigated trials was 56,000 plants ha^{-1} and 78,000 plants ha^{-1}, respectively. In Nesson Valley, ND an unexpected first killing frost occurred on September 11 in 2014. In Nesson Valley, ND the crosses and check hybrids were planted in two 7.9 m rows spaced 0.76 m apart. In Sidney, MT, these were planted in 9.14 m rows spaced 0.6 m apart.

The experiment was conducted in a 10 x 10 partially balanced lattice design including 94 partial diallel crosses and six different commercial checks representing a range of relative maturities (77-88RM). Each experiment was replicated two times in each location. The WS trials were placed next to the WW trials.

Traits observed

Data on days to anthesis (days) were collected when at least 50 % of the plants in the plot were shedding pollen with anthers emerged, days to silking (days) was noted when at least 50 % of the plants in the plot were showing visible silk. Plant height (cm) and ear height (cm) were noted after flowering as distance from the ground to the terminal nodes and the node of uppermost ears, respectively, of 10 competitive plants per plot. The root lodging and stalk

lodging was noted within the week before harvest. Root lodging (%) was measured as percentage of plants leaning greater than 30° from vertical with intact stalk. The stalk lodging was measured as the percentage of plants broken below the ear. Grain moisture at harvest (g kg^{-1}) was measured by oven drying of 1000-g grain sample from each plot. It was estimated by equating the loss of grain moisture with loss in weight of sample. Grain yield (Mg ha^{-1}) was measured from shelled weight per plot adjusted to 155 g H_2O kg^{-1}. ASI (days) was calculated subtracting days to anthesis to the days to silking (Edmeades et al., 1993).

Root capacitance, stalk diameter, and brace root traits were measured a week after completion of flowering. Root capacitance was measured with a non-destructive field based method as described by vanBeem et al. (1998). For this purpose, the Extech LCR meter 380193 was used. Electrical contact with plant was established by connecting the negative electrode to the maize stem via a stainless steel needle at 6 cm above ground level on second internode of base of plant. The positive electrode was connected via a battery clamp to a copper ground rod 55 cm in length inserted into the soil to the depth of 15 cm and positioned 20 cm away from the stem base. The capacitance measurement per plant was taken after allowing five seconds for system to stable capacitance reading in nano farad scale (nF). The reading was taken after onset of rain or irrigation to ensure enough moisture was present around the root system for electrical conductance. Diameter of the first elongated stem below ear of eight competitive plants (plants from middle of the row) per plot was measured using a digital vernier caliper. The maize stalk has two sides in its roundness, longer and shorter. Short and long diameter was measured in millimeters (mm) and the average was considered the stem diameter.

The brace root spread width (mm) was measured from eight competitive plants per plot. This is measured as spread (mm) of the brace root around the stem taking three most uniform

readings randomly from three sides of each plant. Number of above ground whorls occupied with brace roots was counted visually. The number of brace roots was counted visually around the stem. The notes were taken for brace roots that were able to penetrate the soil surface to produce lateral roots. The procedure needs field to be cleaned without weeds. Whenever dead plant tissues from the surrounding field are wrapped on roots; simple hand weeder was used to remove the dead plant tissues. Data on hundred kernel weight were collected in three samples of 100 kernels randomly selected from the total kernels.

Phenotypic data analysis

Analysis of residuals showed all traits were normally distributed except for root lodging and grain moisture at harvest. Therefore, both traits were transformed by applying arcsine transformation. PROC MIXED procedure with default REML in SAS 9.4 was used to conduct combine analyses considering each location by year combination as an environment. Genotypes (partial diallel crosses and checks) were considered as fixed effects and ENV, REP (ENV), BLOCK (REP x ENV) and TRT x ENV were considered as random effects. If the genotypic means were significantly different at P < 0.05 then a combining ability analysis was carried out. The mathematical model for combining ability for a trait from the cross i x j in replicate l following Kempthorne and Curnow (1961) is shown as equation (1):

$$Yijl = \mu + r_l + g_i + g_j + s_{ij} + e_{ijl} \qquad (1)$$

Where μ is a general effect, r_l is a replicate effect; parental effects are g_i , g_j also called general combining ability (GCA), s_{ij} is the non-additive parental effects also called specific combining ability (SCA), and e_{ijl} is the plot error, where g_i, s_{ij}, e_{ijl} are independent and normally distributed with mean zero and variances $\sigma_{gca}^2, \sigma_{sca}^2, \sigma_e^2$.

The combining abilities from partial diallel crosses were computed using REML in the PROC MIXED procedure in SAS 9.4 to calculate general combining ability variances (σ_{gca}^2) and specific combining ability variances (σ_{sca}^2) as modified from the procedure described by Mohring et al. (2011) for the diallel mating design. If we consider a large random mating parental population with disomic inheritance and linkage equilibrium among gene loci, the σ_{gca}^2, σ_{sca}^2 variance components have the following genetic expectations (Lynch and Walsh, 1998) as equation (2) and (3):

$$\sigma_{gca}^2 = \sigma_A^2 + \sigma_{AA}^2 + \sigma_{AAA}^2 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad (2)$$

$$\sigma_{sca}^2 = \sigma_D^2 + \sigma_{AD}^2 + \sigma_{DD}^2 + \sigma_{DDD}^2 + \sigma_{ADD}^2 \ldots\ldots\ldots\ldots\ldots\ldots \quad (3)$$

The genetic component estimation was done by the genetic model described by Griffing (1956) model 4 method II that utilizes data from one set of F_1s without including reciprocals and parents to estimate genetic variances. Total genotypic variance (σ_G^2) was calculated as equation (4)

$$\sigma_G^2 = 2\sigma_{gca}^2 + \sigma_{sca}^2 \quad (4)$$

Without epistasis, the additive genetic variance (σ_A^2) was estimated as equation (5)

$$\sigma_A^2 = 2\sigma_{gca}^2 \quad (5)$$

σ_{sca}^2, Which is, a residual genotypic variance, and it was used to include all of the dominance and the remaining epistatic variance (Griffing, 1956) as equation (6):

$$\sigma_D^2 = \sigma_{sca}^2 \quad (6)$$

Degree of dominance ($\overline{d}$) was calculated as in the case of F = 1 as equation (7)

$$\overline{d} = \sqrt{\sigma_D^2/\sigma_A^2} \quad (7)$$

General predictability ratio (*GPR*) either due to GCA or SCA was calculated following Baker (1978):

$$GPR = 2\sigma_{gca}^2/2\sigma_{gca}^2 + \sigma_{sca}^2 \quad (8)$$

Narrow-sense heritability (h^2) for selection among parental genotypes was estimated on a plot mean basis unbiased by genotype-environment interaction. Narrow-sense heritability was estimated as equation (9) (Hallauer et al., 2010).

$$h^2 = 2\sigma_{gca}^2 / (2\sigma_{gca}^2 + \sigma_{gcaxE}^2 + \sigma_{sca}^2 + \sigma_{scaxE}^2 + \sigma_e^2) \qquad (9)$$

Broad sense (*H*) heritability was estimated with the equation (10):

$$H = 2\sigma_{gca}^2 + \sigma_{sca}^2 / (2\sigma_{gca}^2 + \sigma_{gcaxE}^2 + \sigma_{sca}^2 + \sigma_{scaxE}^2 + \sigma_e^2) \qquad (10)$$

Genetic correlations r_{gij} between traits i and j were calculated using the genotypic variance and covariance component estimates as equation (Holland, 2006) (11)

$$r_{gij} = r_{Gij} / r_{Gi} r_{Gj} \qquad (11)$$

Where r_{Gij} is the genotypic covariance between traits i and j, and r_{Gi} and r_{Gj} are the estimated genotypic standard deviations, respectively of traits i and j. The process utilizes multivariate maximum likelihood estimation in SAS PROC MIXED as described by Holland (2006). The relationships among the traits in WS and WW environments were explored using a generalized form of principle component analysis called multidimensional preference analysis. The data matrix with genotypic means as rows and traits means as columns were used for analysis. The PRIN-QUAL procedure in SAS (SAS Institute, 2015) was used to analyze data using identity transformation. The biplot generated by this procedure includes the mean principle component scores for genotypes plotted as points in the ordination space and the correlation between transformed and original data is given by eigenvectors which are plotted at end of vectors which projects from origin. The angle between vectors shows the strength of association. The right angle shows orthogonality and no association whereas other angles show the negative correlation of vectors.

Results

Irrigated and dryland precipitation and effect on trait means performances

During the growing season genotypes in Nesson Valley, ND received 29 % (in year 2013) and 39 % (in year 2014) less precipitation when compared to the amount received by fully irrigated genotypes (Table 2). The precipitation amount in Sidney, MT was 35 % (in year 2013) and 41 % (in year 2014) less than irrigated. In year 2014 the total precipitation during maize growing season was 25 % lower than the 15-year historic normal rainfall in Nesson Valley, ND and 6 % higher than the 20-year historic normal of Sidney, MT. In 2013, the total precipitation was 53 % higher in Sidney, MT compared to its 20-year historic normal and 34 % higher in Nesson Valley, ND compared to its 15-year normal.

The mean grain yield ranged from 2.20 Mg ha^{-1} in Nesson Valley , ND WS experiment to 9.08 Mg ha^{-1} in Nesson Valley WW ND experiment (Table 2). Across environment the mean grain yield was 4.26 Mg ha^{-1} in WS experiment and 6.00 Mg ha^{-1} in WW experiment. All the means for all traits were statistically significant ($P < 0.05$) (Table 3). WS reduced 29 % yield in the sample of genotypes tested compared to WW environments, which is close to the target of managed stress trials to reduce yield more than 30 % (Blum, 2011) and lower than 50 % (Banziger et al., 2000).

The mean grain yield could have varied across years in part because of occurrence of early frost in 2014, which happened on September 14th in both Sidney and Nesson Valley locations. On the other hand, early frost happened on October 4th and 5th in Sidney, MT and Nesson Valley, ND respectively during 2013 (Table 2). There was also some hail damage in 2013 Sidney, MT location as well as in 2014 Nesson Valley, ND during soft dough growing stage.

Large genetic variation for brace root spread width, brace root number, stalk diameter and root capacitance was found

Genotypes performed better in WS environment for brace root spread width (26 mm to 44 mm) compared to WW environment (24 mm to 43 mm) (Fig. 2). The cross ND2013 x ND06-36 had the largest brace root spread width of about 44 mm followed by ND2013 x KMN22 of 42 mm under WS environments while, in WW environments, AP49 x ND291 showed 43 mm followed by cross ND2013 x ND06-36 with 42 mm. Similarly, the genotype ND08-53 x ND07-226 had the smallest brace root spread width of 26 mm followed by ND203 x ND2005 with 27 mm in WS environments and ND203 x ND2005 with 24 mm under WW environments.

The performance of genotypes for the number of visible brace root counts was lower in WS environments (9 to 18) compared to WW environments (9 to 20) (Fig. 2). The number of brace root counts was highest on the hybrid ND07-228 x B104 with 18 visible brace roots followed by hybrid ND2013 x ND06-36 with 17 visible brace roots in WS environments. Hybrids ND2013 x B104 and ND2013 x ND06-36 showed 20 visible brace roots in WW trials, the largest numbers. The cross ND203 x ND2005 had the smallest number with only 9 visible brace roots in WS trials, while, in WW environments, hybrid LH61 x ND241showed 9 visible brace roots followed by ND203 x ND2005 with 10 visible brace roots.

The hybrid performance for root capacitance was higher in WW environments with a range from 63 to 25.02 nF compared to 57.39 to 27.57 nF under WS environments (Fig. 2). Root capacitance was highest in hybrid ND07-228 x B104 showing 57.39 nF followed by ND09-118 x B104 with 55.83 nF in WS environments. The best performance under WW environments was for hybrid ND07-212 x B104 showing 62.78 nF, followed by ND2013 x B104 with 53.72 nF. In WW environments capacitance was lowest in hybrid AP52 x ND250 with 27.57 nF followed by

NP2341 x ND2000 with 28.57 nF, while WS environments it was for hybrid NP2341 x ND2006 with 25.02 nF followed by NP2341 x ND2014 with 28.72 nF.
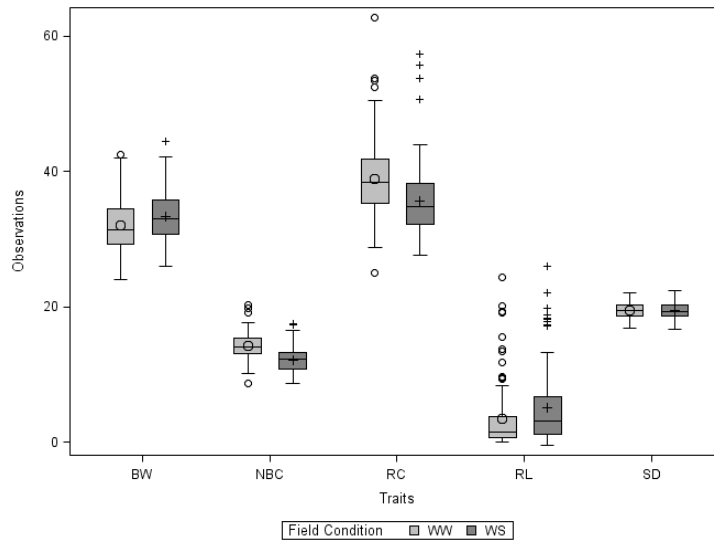
Figure 2. Box plot representing the phenotypic distribution for brace root spread width (BW), brace root counts (BC), root capacitance (RC), root lodging (RL), stalk diameter (SD) in 100 genotypes tested in well watered (WW) and water stressed (WS) environments in 2013 and 2014. Thick black bar represents median, boxplots between 25 and 75% variation, and open circles are outliers within 90% of total variation, circle or plus represent mean of population, whiskers indicate extreme data points less than 1.5 interquartile range.

The genotype performance for stalk diameter was higher under WS environments with a range of 17 to 22.36 mm compared to 16.72 to 22.02 mm under WW environments (Fig. 2). In WS environments stalk diameter was highest in hybrid ND07-212 x B104 with 22.36 mm followed by hybrid ND07-212 x LP05 with 21.59 mm, while in WW environments the cross ND07-228 x B104 had the largest diameter of 22.02 mm followed by ND07-212 x B104 with 21.54 mm. The smallest value shown under WS environments was for ND274 x II5 with 17.39 mm followed by ND08-53 x ND05-117 with a value of 17.44 mm (Table 4), while the smallest diameter was for ND274 x II5 with 16.81 mm followed by ND290 x ND05-117 with 17.14mm under WW environments (Table 5).

The largest root lodging value under WS was observed for ND203 x ND2005 with 26 % root lodging followed by ND203 x ND2001 with 22 % root lodging. In WW environments, the

largest root lodging percentage was, again, for ND203 x ND2001 with 24 % root lodging also

followed by ND203 x ND2005 with 20 % root lodging.

3a.

3b.

3c.

3d.
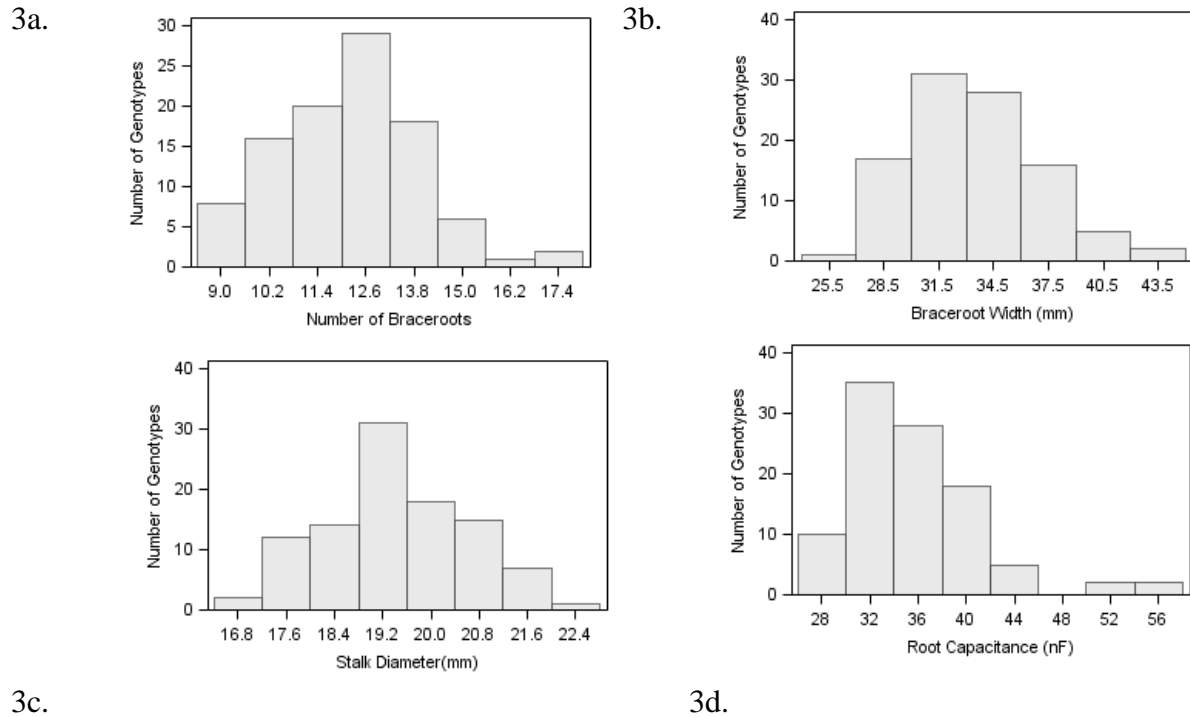
Figure 3. Histogram showing phenotypic variation of brace root and stalk traits in the 94 partial diallel crosses from 47 inbreds of maize (Zea mays. L). Data are means of eight independent measurements of plants in a plot tested in four water stressed (WS) environment replicated two times for two years.

In summary, crosses with inbred line B104 showed high brace root spread width, high

brace root count, and above average root capacitance and stalk diameter, showing consistently

highest performance in both WS and WW environments. On the other hand, crosses with ND203

showed the lowest brace root numbers and highest root lodging in WW and WS environments.

The crosses with NP2341 showed lowest root capacitance consistently in both WS and WW

environments. Similarly, ND2013 crosses showed widest brace roots in both WS and WW

environments. Trait measurements showed wide phenotypic classes in near normal distribution.

The variation was higher for number of brace root counts compared to brace root spread width

(Fig. 3a 3b, 3c, 3d).

Genetic association between traits in water stressed and well-watered environments

In WS environments, the first three principal components accounted for 38.01, 19.29, and 14.59 % of total variation (Fig. 4a, 4b), respectively. In WW environments, the three principal components accounted for 40.62 %, 25.64 % and 11.92 % respectively (Fig. 4c, 4d). Under WW environments, the traits related to flowering (days of anthesis, days of silking, and grain moisture at harvest) grouped together with the number of brace root counts, indicating a high correlation among traits. These were negatively correlated with test weight and stalk lodging. The first principal component (PCA1) showed maturity related attributes. The second principal component (PCA2) showed yield related attributes. Similar groupings can be seen under WS environment; however, the root capacitance trait has a trend to be grouped with maturity traits (Fig. 4c and 4d). This further indicates that fresh root mass can be associated with maturity in the sample studied. In WW environments, yield has shown to be more related to the maturity than in the WS environments. Also, in WW environments, the number of brace roots is grouped with plant height.

Moderate to strong correlations were observed among traits (P < 0.05). Estimates of phenotypic correlation coefficients (r_p) and genetic correlation coefficients (r_G) for WW and WS conditions are given in Table 6 and 7. Stalk diameter was positively correlated with root lodging (0.46), grain water content (0.48), and days of silking (0.46) in WS environments. However, the genetic correlations were higher under WW environments for root lodging (0.49) and grain water content (0.60), and days of silking (0.53). Also, the correlation with root lodging was better in WW environments.
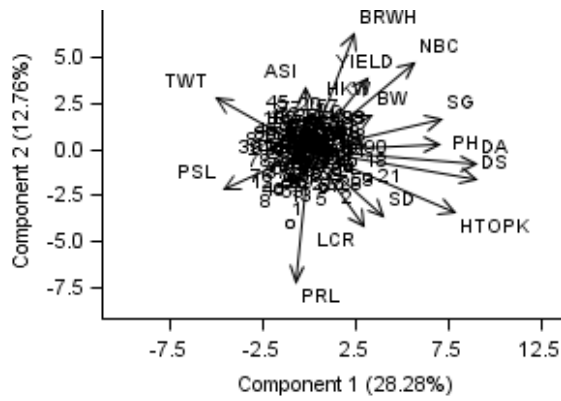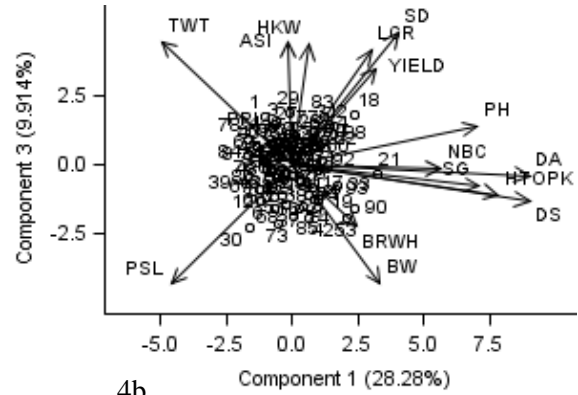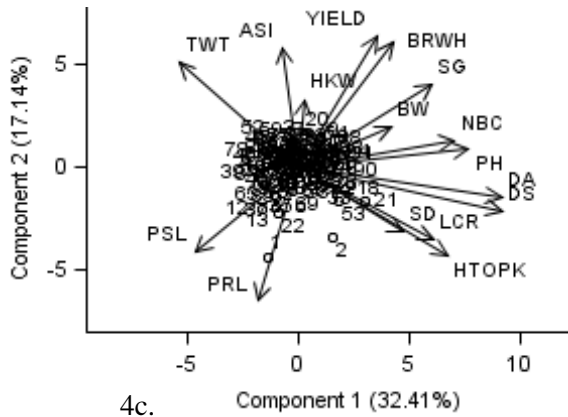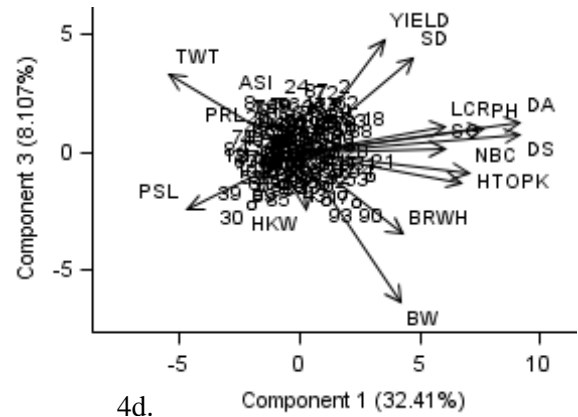
Figure 4. Biplot of Agronomic, root and stalk diameter responses of 94 partial diallel crosses from 47 inbreds of maize generated with multidimensional preference analysis for data collected on from eight a and b) well stressed, c and d) well-watered environments in western ND and eastern MT, USA from 2013 and 2014. The respective axes (x and y-axis) show the percent of variance explained by the respective principle components (PC). The abbreviations are: TWT, test weight, ASI, Anthesis silking interval, HKW, hundred kernel weight, SD, stalk diameter, LCR, root capacitance, PH, plant height, NBC, number of brace root count, DA, days of anthesis, HTOPK, grain moisture, BRWH, number of brace root whorls, BW, brace root spread width, PSL, stalk lodging percentage.

The number of brace root count was negatively correlated with root lodging (-0.59) and stalk lodging (-0.44) in WS environments. It was also positively correlated with days of silking (0.57) and brace root spread width (0.47) under the same environments. The correlation was very strong with number of brace root whorls (0.82). A similar high correlation was seen under WW environments with a decreased correlation with root lodging (-0.55) and stalk lodging (-0.33). However, the correlation was improved with days of silking (0.72) and brace root spread width

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(0.82). The improvement in correlation for brace root spread width showed the larger visible root system in field in WW environments. The genotypic correlation between brace root spread width and root lodging (-0.52) was negative while positive with days of silking (0.48) in WS environments. The correlation improved in WW environments with further negative association with root lodging (-0.62) and positive association with days of silking (0.56). The number of effective brace root whorls was highly correlated and negative with root lodging (-0.77) under both WS environment and WW environments (-0.68). The more effective whorls in WS environments showed less root lodging in WS compared to WW.

Grain yield was negatively correlated with root lodging (-0.29) and stalk lodging (-0.58) in WS environments. The correlation was more intense in WW environments for root lodging (-0.97) and stalk lodging (-0.81).

Genetic controls of agronomic roots and stalk traits in water stressed and well-watered environments

The GCA variance was significant (P < 0.05) for stalk lodging, plant height, ASI, brace root spread width, brace root count, number of brace root whorls, and root capacitance in WS environments (Table 8 and 9). In WW environments, the GCA variance was significant (P < 0.05) for grain moisture, brace root spread width, and brace root count, number of brace root whorls, root capacitance, stalk diameter, stalk lodging, and hundred kernel weight (Table 8 and 9). The significant GCA variance and not significant SCA variance for brace root spread width, number of brace root whorls, and brace root count in both WW and WS environments showed more additive gene action. Both GCA and SCA variances were significant (P < 0.05) for grain moisture, days of silking, and stalk diameter in WS environments (Table 8 and 9). Similarly, both GCA and SCA variances were significant for stalk lodging, plant height, and days of silking

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under WW conditions (Table 8 and 9). Only SCA was significant ($P < 0.05$) for grain yield in WW environments.

The GCA-by-environment interaction was significant ($P < 0.05$) for all traits in both WS and WW environments except for brace root spread width in WW environments and stalk diameter in WS environments (Table 7 and 8). The SCA-by-environment interaction was significant ($P < 0.05$) for grain moisture, grain yield, stalk lodging, days of silking, brace root spread width in WS environments for grain moisture, stalk lodging, days of silking, and number of brace root whorls and hundred kernel weight in WW environments (Table 8 and 9). The GCA-by-environment variance was smaller for all traits except for grain yield, root lodging, brace root count in WW environments and grain yield, root lodging, stalk lodging, root capacitance, and hundred kernel weight in WS environments. Similarly, SCA-by-environment interaction was higher for grain moisture at harvest, stalk lodging, and days of silking in WW environments while it was significant for only grain moisture in WS environments.

The general predictable ratio *(GPR)* exceeded 0.8 for most traits except for grain yield and hundred kernel weight in both WS and WW environments as well as stalk lodging in WW environments only (Table 8 and 9). The degree of dominance ($\overline{d}$) for all traits was estimated in the partial dominance range ($0 < d < 1$) both in WS and WW environments except for stalk lodging which showed no dominance under WS environments (Table 7 and 8). Usually, degree of dominance was increased in WS environments compared to WW except for stalk lodging, root lodging, root capacitance, ASI, and plant height.

Heritability for brace root and stalk traits were higher than grain yield and root lodging in both water stressed and well-watered environments

The narrow sense heritability (h^2) was higher for brace root spread width (0.23) in WS and WW (0.23) environments than grain yield of WS (0.06) and WW environments (0.08). The heritability was also higher than the one observed for root lodging in WS (0.11) and WW (0.10) environments. The narrow sense heritability for number of brace root count was also higher than grain yield and root lodging in WS (0.24) and WW (0.22) environments. Root capacitance narrow sense heritability was higher than yield in both WS (0.22) and WW (0.26) environments. Similar values were observed with stalk diameter for both WS (0.28) and WW (0.27) environments.

Discussion

Brace root spread width, number of visible brace roots, and stalk diameter can be utilized to increase the genetic diversity for adult plant drought resistance

The bottleneck in available phenotyping methods has decreased the pace of drought adapted cultivar development in maize (Araus et al., 2012; Carena, 2013). There has been very few research ideas applied on adult plant root and shoot attributes toward drought resistance. Most studies have focused on seminal and primary root traits as well as ASI and grain filling for drought resistance. However, this paper shows a different approach.

The genetic variability of brace root spread width, number of brace root count, stalk diameter and root capacitance was significant ($P < 0.01$) across environment in the 94 crosses of 47 inbred lines representing early maturing germplasms (Table 3). High genetic variation for root angle and branching was also reported in three RILs populations of maize (Trachsel et al., 2011).

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Table 3. Genetic variance, error variance and broad sense heritability estimates of traits measured on 94 maize [Zea mays L.] partial diallel crosses in eight managed water stressed (WS) and well-watered (WW) environments of 2013 and 2014 in western North Dakota and eastern MT, USA. The data on hundred kernel weights from four WS and WW environments.

Traits	WS			WW		
	Genetic Variance $(\sigma^2{}_g)$	Error Variance $(\sigma^2{}_e)$	Heritability (H)	Genetic Variance $(\sigma^2{}_g)$	Error Variance $(\sigma^2{}_e)$	Heritability (H)
Moisture, H_2O g kg^{-1}	3597.43*	604.14	0.69	3327.69*	806.29	0.64
Grain Yield, Mg ha^{-1}	0.16*	0.88	0.11	0.31*	1.26	0.15
Root Lodge ,%	2.12*	9.24	0.13	1.65*	7.90	0.13
Plant Height , cm	103.10*	35.87	0.62	172.03*	37.07	0.77
Days of Silking	7.59*	2.02	0.71	7.70*	1.63	0.74
ASI, days†	0.29*	1.26	0.17	0.10*	0.88	0.09
Braceroot Spread Width, mm	9.87*	21.11	0.27	11.96*	29.13	0.26
Braceroot Count	1.99*	4.95	0.26	2.12*	5.71	0.23
Braceroot Whorls	0.01*	0.04	0.20	33.27*	8.06	0.64
Root Capacitance, nF	14.37*	33.50	0.25	18.32*	31.16	0.31
Stalk Diameter, mm	0.89*	1.62	0.33	0.85*	1.90	0.30
HKW, gm ‡	0.52*	6.93	0.06	2.11*	1.28	0.47

* means were significant at 0.05 level.

†ASI, anthesis silking interval.

‡Hundere Kernel Weights

Table 4. Agronomic, root and stalk attributes of partial diallel crosses compared with commercial checks (on bottom) in water stressed environment (WS) of western North Dakota and Eastern Montana in 2013 and 2014. The crosses indicate the range of variation observed for brace root spread width.

Pedigree	Grain Moisture g/kg	Grain Yield (Mg/ha)	Root Lodging (%)	Brace Root Spread Width (mm)	Brace Root Counts (Number)	Brace Root Whorls (Number)	Root Capacitance (nF)	Stalk Diameter (mm)
ND2013xND2009	337.6	3.4	0.9	44.4	17.3	1.3	39.5	20.2
ND2013xKMN22	179.6	4.1	1.5	42.2	15.6	1.7	39.0	18.8
LH61xND246	235.0	4.5	18.4	41.1	9.2	1.2	32.9	20.5
ND07-97xND07-153	255.5	3.9	0.9	40.7	13.6	1.6	31.2	17.8
NK779xND2006	114.1	2.7	2.2	39.3	12.6	1.3	36.8	18.0
ND291 x ND2032	285.1	4.5	5.7	38.0	12.0	1.2	37.0	18.7
ND2021xIl5	174.4	4.6	1.8	36.8	12.7	1.3	38.4	19.8
ND2013xIl5	239.9	5.0	2.4	36.0	11.0	1.4	29.8	18.2
NK779xND2014	104.0	3.6	3.3	34.9	12.5	1.3	32.5	18.4
ND08-343xND07-153	209.2	4.8	0.0	33.0	13.6	1.4	33.5	19.0
PHG47xND270	137.1	4.9	0.0	31.7	10.8	1.1	36.8	18.6
ND07-212xNK807	190.6	4.5	19.9	30.8	11.5	1.3	37.4	19.1
ND08-343xND2002	188.0	4.7	3.6	30.0	11.4	1.3	43.9	21.0
ND06-144xND2006	150.0	4.3	1.5	28.9	12.1	1.1	34.0	17.8
ND265xND2001	184.8	3.7	17.2	27.5	8.8	1.2	40.6	19.8
ND08-53xND07-226	182.8	3.2	5.4	25.9	9.3	1.1	38.1	19.8
Thurston77RM	112.5	5.3	1.4	31.7	11.2	1.3	39.0	18.4
Pioneer 80RM	114.9	5.9	1.2	40.5	9.4	1.5	29.9	17.1
Syngenta 85RM	127.5	5.7	2.6	33.8	10.2	1.3	28.8	18.4
Monsanto 88RM	174.6	5.3	1.1	33.6	12.2	1.5	42.5	20.4
Mean of Experiment	187.3	4.3	5.1	33.4	12.1	1.3	35.7	19.4
LSD,0.05	47.3	1.8	15.3	9.3	4.3	0.4	11.4	2.5

Table 5. Agronomic, root and stalk attributes of partial diallel crosses compared with commercial checks in water stressed environment (WS) of western North Dakota and Eastern Montana in 2013 and 2014. The crosses indicate the range of variation observed for number of brace root count.

Pedigree	Grain Moisture g kg^{-1} H$_2$O	Grain Yield (Mg ha^{-1})	Root Lodging (%)	Brace Root Spread Width (mm)	Brace Root Counts (Number)	Brace Root Whorls (Number)	Root Capacitance (nF)	Stalk Diameter (mm)
ND02014 x B104	318.1	4.7	0.0	30.5	17.5	1.3	57.4	20.9
ND2013 x B104	446.0	2.7	0.0	36.8	16.6	1.4	55.9	21.2
ND2013 x KMN22	179.6	4.1	1.5	42.2	15.6	1.7	39.0	18.8
ND07-212 x B104	338.5	4.8	3.9	31.3	14.9	1.2	53.8	22.4
ND2021 x ND2009	291.7	3.6	0.0	33.9	14.0	1.2	30.7	20.4
ND07-255 x LP05	298.0	4.6	6.8	31.6	13.0	1.4	36.0	19.6
ND06-144 x ND2006	149.9	4.3	1.5	28.9	12.1	1.1	34.0	17.8
NK779 x ND2000	107.6	3.7	1.0	34.8	12.0	1.3	40.0	19.0
ND2013 x Il5	239.9	5.0	2.4	35.9	11.0	1.4	29.9	18.2
ND06-189 x NK807	154.5	5.5	3.5	33.4	10.9	1.2	33.3	18.6
ND265 x ND2005	133.9	3.4	18.2	30.1	10.0	1.1	31.9	17.6
LH61 x ND270	236.8	3.8	12.7	35.4	10.9	1.2	32.9	18.9
ND265 x ND2001	184.8	3.7	17.2	27.5	8.8	1.2	40.6	19.8
ND203 x ND2005	133.6	3.5	25.9	27.1	8.7	1.0	38.6	19.2
Thurston 77RM†	112.5	5.3	1.4	31.7	11.2	1.3	39.0	18.4
Pioneer 80RM	114.9	5.9	1.2	40.5	9.3	1.5	29.9	17.1
Syngenta 85RM	127.5	5.7	2.6	33.9	10.2	1.3	28.8	18.4
Monsanto 88RM	174.6	5.3	1.1	33.6	12.2	1.5	42.5	20.3
Mean of Experiment	187.2	4.3	5.0	33.4	12.2	1.3	35.7	19.4
LSD, 0.05	47.3	1.8	15.3	9.3	4.3	0.4	11.4	2.5

†, RM, relative maturity

Table 6. Genetic (below diagonal) and phenotypic (below diagonal) correlations estimated among 94 partial diallel crosses of 47 maize inbreds in water stressed (WS) environment in western North Dakota and eastern Montana in 2013 and 2014.

Trait	H₂O† g kg⁻¹	GY‡ Mg ha⁻¹	RL§ %	SL¶ %	PH# cm	DS †† days	ASI ‡‡	BW§§ mm	BC¶¶	BWH ##	RC††† nF	SD‡‡‡ mm	HKW¶¶¶ g
H₂O		-0.03	-0.28*	0.11	**0.41****	**0.68****	-0.23*	0.19	0.27**	-0.09	**0.31****	**0.32****	-0.07
GY	0.07		-0.26**	-0.13	**0.37****	0.20*	**0.30****	0.06	0.10	0.17	-0.10	-0.06	0.17
RL	0.21	**-0.29**		0.13	0.07	0.01	-0.11	-0.11	-0.50**	-0.28**	0.02	0.22*	0.07
SL	**-0.39*****	**-0.58***	0.36		**-0.31****	-0.29**	-0.10	0.01	-0.21*	-0.10	-0.08	-0.11	**-0.35****
PH	**0.58*****	0.38*	0.28	-0.30*		**0.58****	0.05	0.15	**0.31****	0.19	0.10	0.17	0.05
DS	**0.75*****	0.34	-0.01	-0.37*	**0.72*****		-0.15	0.25*	**0.36****	0.12	0.20*	0.28**	-0.08
ASI	-0.13	**0.65****	-0.11	0.10	0.13	0.01		-0.06	0.07	0.29**	0.17	-0.05	0.10
BW	**0.39*****	-0.14	**-0.52****	-0.15	0.29*	**0.48*****	-0.16		0.20*	0.23*	-0.03	-0.02	-0.07
NBC	**0.41*****	0.11	**-0.59*****	**-0.44***	0.31*	**0.57*****	0.19	**0.47****		0.26**	0.17	0.24*	-0.01
BWH	0.26	0.11	**-0.77*****	-0.21	0.37**	0.30*	**0.42***	**0.72**	**0.82*****		-0.20*	-0.14	0.15
RC	**0.56*****	-0.04	0.11	-0.10	0.30*	**0.41****	**0.36**	0.02	**0.46***	0.15		**0.48****	-0.04
SD	**0.48*****	-0.06	**0.46****	-0.21	0.24	**0.46*****	0.02	-0.03	0.25	-0.10	**0.79*****		-0.04
HKW‡	-0.20	**0.77*****	0.29	-1.21	**0.69*****	-0.17	-0.17	-0.68	-0.07	0.19	-0.32	0.42	

*, **, *** For phenotypic correlation was significant at 0.05, 0.01 and 0.001 probability levels respectively. For genetic correlations, coefficient exceeded twice, three times and four times of their standard errors, respectively.

†H₂O, grain moisture, ‡GY, grain yield, §RL, root lodging, ¶SL, stalk lodging, #PH, plant height, ††DS, days of silking, ‡‡ASI, anthesis silking Interval, §§BW, brace root spread width, ¶¶NBC, number of brace root count, ##, number of brace root whorls, †††RC, root capacitance, ‡‡‡SD, stalk diameter, ¶¶¶HKW, hundred kernel weights.

Table 7. Genetic (below diagonal) and phenotypic (above diagonal) correlations estimated from genetic variance and covariance among 94 partial diallel crosses of 47 maize inbreds in well-watered (WW) environment in western North Dakota and eastern Montana in 2013 and 2014.

Trait	H2O† g kg⁻¹	GY‡ Mg ha⁻¹	RL§ %	SL¶ %	PH# cm	DS †† days	ASI ‡‡	BW§§ mm	BC¶¶	BWH ##	RC††† nF	SD‡‡‡ mm	HKW¶¶¶ g
H2O		-0.13	-0.08	0.23*	0.41**	**0.60**	-0.16	0.1	**0.32**	0.03	**0.42**	**0.40**	-0.02
GY	-0.01		**-0.42**	**-0.36**	0.37**	0.22*	**0.38**	0.13	0.27**	**0.37**	0.08	0.13	0.05
RL	0.36*	**-0.97***		0.34**	-0.01	-0.03	-0.15	-0.20*	**-0.35**	**-0.49**	0.02	0.09	-0.16
SL	-0.28*	**-0.81***	0.61**		**-0.36**	**-0.37**	-0.13	-0.22*	-0.25*	-0.27**	-0.1	-0.01	-0.07
PH	**0.60***	0.54**	0.07	**-0.44**		0.67**	0.13	**0.35**	**0.43**	**0.32**	**0.36**	0.22*	0.09
DS	**0.72***	0.45*	0.04	**-0.43**	0.76***		-0.16	0.26**	**0.56**	0.23*	**0.57**	**0.42**	-0.09
ASI	-0.27	1.12	-0.16	-0.07	0.33	**-0.16**		-0.03	-0.02	**0.31**	-0.22*	-0.23*	0.14
BW	**0.50***	0.09	**-0.62**	-0.22	**0.59***	**0.56***	-0.09		0.23*	**0.44**	0.08	-0.14	0.09
BC	**0.46**	0.33	**-0.55**	**-0.33***	**0.61***	**0.72***	0.01	**0.49***		**0.42**	**0.47**	0.27**	-0.07
BWH	**0.27***	0.41	**-0.68***	**-0.52**	**0.48***	**0.40**	0.11	**0.82***	**0.65***		0.03	-0.03	0.17
RC	**0.60***	-0.22	0.2	**0.07**	0.41**	**0.67***	-0.19	0.13	**0.55***	0.08		**0.42**	-0.07
SD	**0.60***	-0.01	**0.49***	0.04	**0.39**	**0.53***	-0.25	-0.05	**0.41**	0.06	**0.60***		-0.06
HKW‡	-0.1	0.28	**-0.04**	**-0.49**	0.15	-0.2	0.12	-0.1	-0.21	-0.06	0.03	0.17	

*, **, *** For phenotypic correlation were significant at 0.05, 0.01 and 0.001 probability levels respectively. For genetic correlations, coefficient exceeded twice, three times and four times of their standard errors, respectively.

†H2O, grain moisture, ‡GY, grain yield, §RL, root lodging, ¶SL, stalk lodging, #PH, plant height, ††DS, days of silking, ‡‡ASI, anthesis silking Interval, §§BW, brace root spread width, ¶¶NBC, number of brace root count, ##, number of brace root whorls, †††RC, root capacitance, ‡‡‡SD, stalk diameter, ¶¶¶HKW, hundred kernel weights.

Table 8. Estimates of variance components, general combining ability variance (σ^2_{gca}), specific combining ability variance (σ^2_{sca}) and their interaction with environments (σ^2_{gca} x E and σ^2_{sca} x E), additive (σ^2_A) and dominance variance (σ^2_D), degree of dominance ($\overline{d}$) general predictability ratio (GPR) and narrow sense heritability (h^2) among 94 partial diallel crosses of 47 maize inbreds in water stressed (WS) environment in western North Dakota and eastern Montana in 2013 and 2014.

Traits	Genetic Variance and Parameter Estimates								
	σ^2_{gca}	$\sigma^2_{gca\,x\,E}$	σ^2_{sca}	$\sigma^2_{sca\,x\,E}$	$\overline{d}$	σ^2_A	σ^2_D	GPR§	h^2
H₂O, g kg⁻¹†	1627.98***	596.92***	341.47***	428.61***	0.32	3255.96	341.47	0.91	0.62
GY, Mg ha⁻¹‡	0.04	0.20***	0.07	0.22**	0.92	0.09	0.07	0.54	0.06
RL, %§	0.87	3.77***	0.38	0.99	0.47	1.74	0.38	0.82	0.11
SL, %¶	2.37**	2.38	0.00	1.95*	-	4.75	0	1	0.23
PH, cm#	68.48***	7.82*	4.06	2.4	0.17	136.95	4.06	0.97	0.61
DS ††	3.34***	0.33**	0.91**	0.68**	0.37	6.68	0.91	0.88	0.63
ASI ‡‡	0.13**	0.20***	0.04	0.02	0.39	0.26	0.04	0.87	0.15
BW, mm§§	4.23**	2.24*	1.39	3.20*	0.41	8.48	1.39	0.86	0.23
BC¶¶	0.91***	0.42**	0.17	0.24	0.31	1.82	0.17	0.91	0.24
BWH ##	0.004**	0.002*	0	0	0.4	0.01	0	0.86	0.17
RC, nF†††	6.47**	6.69**	1.43	3.59	0.33	12.95	1.43	0.9	0.22
SD, mm‡‡‡	0.37**	0.16**	0.14*	0.05	0.43	0.76	0.14	0.84	0.28
HKW, g¶¶¶	0.18	1.38**	0.16	0	0.67	0.36	0.16	0.69	0.04

*, **, *** significant at 0.05, 0.01 and 0.001 probability levels respectively.

†H₂O, grain moisture, ‡GY, grain yield, §RL, root lodging, ¶SL, stalk lodging, #PH, plant height, ††DS, days of silking, ‡‡ASI, anthesis silking Interval, §§BW, brace root spread width, ¶¶NBC, number of brace root count, ##, number of brace root whorls, †††RC, root capacitance, ‡‡‡SD, stalk diameter, ¶¶¶HKW, hundred kernel weights.

Table 9. Estimates of variance components, general combining ability variance (σ^2_{gca}), specific combining ability variance ($\sigma2sca$) and their interaction with environments (σ^2_{gca} x E and σ^2_{sca} x E), additive (σ^2_A) and dominance variance (σ^2_D), degree of dominance ($\overline{d}$) general predictability ratio (GPR) and narrow sense heritability (h2) among 94 partial diallel crosses of 47 maize inbreds in well-watered (WW) environment in western North Dakota and eastern Montana in 2013 and 2014.

Traits	Genetic Variance and Parameter Estimates								
	σ^2_{gca}	$\sigma^2_{gca\ x\ E}$	σ^2_{sca}	$\sigma^2_{sca\ x\ E}$	$\overline{d}$	σ^2_A	σ^2_D	GPR§	h2
H2O, g kg^{-1}†	1615.04***	672.37***	97.62	404.63***	0.17	3230.08	97.62	0.97	0.62
GY, Mg ha^{-1}‡	0.09	0.51***	0.13*	0.08	0.86	0.18	0.13	0.57	0.08
RL, %§	0.67	3.23***	0.32	0.44	0.48	1.34	0.31	0.81	0.1
SL, %¶	3.24**	2.07**	2.24*	2.80*	0.59	6.5	2.24	0.74	0.21
PH, cm#	109.81***	7.43**	10.93**	6.84	0.22	219.62	10.93	0.95	0.74
DS ††	3.62***	0.34**	0.45**	0.72***	0.25	7.25	0.45	0.94	0.7
ASI ‡‡	0.05	0.16***	0.02	0.11	0.41	0.09	0.02	0.85	0.07
BW, mm§§	5.36**	1.01	1.23	3.63	0.34	10.73	1.23	0.9	0.23
BC¶¶	0.99**	1.23***	0.15	0.00	0.28	1.98	0.15	0.93	0.22
BWH ##	16.15***	6.72***	0.98	4.04***	0.17	32.3	0.98	0.97	0.62
RC, nF†††	7.83**	7.72***	2.65	2.33	0.41	15.67	2.65	0.86	0.26
SD, mm‡‡‡	0.38**	0.06**	0.10	0.00	0.37	0.75	0.1	0.88	0.27
HKW, g¶¶¶	0.83**	0.50**	0.45	0.60*	0.52	1.66	0.45	0.79	0.37

*, **, *** significant at 0.05, 0.01 and 0.001 probability levels respectively.

†H$_2$O, grain moisture, ‡GY, grain yield, §RL, root lodging, ¶SL, stalk lodging, #PH, plant height, ††DS, days of silking, ‡‡ASI, anthesis silking Interval, §§BW, brace root spread width, ¶¶NBC, number of brace root count, ##, number of brace root whorls, †††RC, root capacitance, ‡‡‡SD, stalk diameter, ¶¶¶HKW, hundred kernel weights.

Similar significant genetic variation for root architectural traits including length, number, and diameter and branching of seminal, primary and nodal roots and their dry weight were found in maize seedlings grown in greenhouse (Burton et al., 2015). In our study higher brace root numbers, spread width, stalk diameter, and root capacitance were observed in hybrids derived from B104 (Tables 4 and 5), which also agrees with the root strength of B104 as described by Hallauer et al. (1997). High root lodging was associated with short-season line ND203, which showed the narrowest brace root spread width (Tables 4 and 5), confirming the weakness of this historical widely used early maturing inbred line (Hallauer et al., 2010).

Brace roots originating from first whorl were found to have similar angles to roots originating at later developmental stages from second whorls. The correlation was strong between angle of root originating from first and second whorls ($r_p = 0.66$, $P < 0.01$) (Traschsel et al., 2011). This shows the utility of the visible brace root could extend to invisible underground crown roots. In maize, an average 70 shoot borne roots developed including two to three whorls of above ground brace roots and six whorls of underground crown roots (Hoppe et al., 1986). Brace root whorls in maize RILs of three populations ranged from 1 to 2 (Traschsel et al., 2011), which is similar to the results we obtained in this study (Table 4).

The heritability of root traits had been reported to be moderate to low. This could be due to the genotype-by-environment interactions of root growth with soil type or heterogeneous available resources or variation in soil strength (Goodman and Ennos, 1999; Araus et al., 2012). Root angle and branching have shown moderate broad sense heritability from 0.21 to 0.35 (Trachsel et al., 2011). The repeatability was found to be 38.6 % for number of brace roots. This is similar to the moderate heritability of brace root spread width (0.27) and brace root counts (0.26) we found in WS environments and the one for brace root spread width (0.26) and brace

root count (0.23) in WW environments. The significant genetic diversity and moderate heritability for root traits can be utilized in breeding programs to increase the genetic diversity of adult plant drought resistance in WS environments.

Highly significant correlations were found between root capacitance readings and root fresh mass of three maize inbred lines and three maize hybrids in field measurements (van Beem et al., 1998). Root capacitance was utilized to rank genotypes based on the relative size of the root system (Messmer et al., 2011). In our sample of genotypes, although they significantly differed for root capacitance (Table 3), a weak correlation was observed with grain yield in both WS and WW environments (Table 6). Messmer et al. (2011) and Monneveux et al. (2008) also reported similar weak correlations of root capacitance with grain yield. The root capacitance was estimated to be higher in WW environments compared to WS environments, showing a high fresh root mass under WW environments, which agrees with Messmer et al (2011). The same authors found similar low heritability values for root capacitance agreeing with Lu et al. (2011). Smaller capacitance reading was also reported on early flowering genotypes in both WW and WS conditions (Messmer et al., 2011). This could be because root capacitance is associated with grain moisture content (Table 6). The results also showed that root capacitance can be a good indicator of plant vigor rather than increased grain yield. The spread of rooting length density was found to be more important than the maximum rooting depth in maize for extraction of water from soil (Yu et al., 2007). The correlation coefficients changed minimally for root capacitance across water regimes making it a less important trait for drought resistance. However, in other crops like barley, the root system size selection based on root capacitance was found to increase yield 8.1 %due to an increase of 3.9 % of root system (Svačina et al., 2013). This relationship needs to be further investigated in maize.

Stem reserves could be an important source for plants while grain filling in drought stress environments when current photosynthesis is inhibited (Blum et al., 1997). In our study, stalk diameter was found to be correlated with plant vigor related traits and root capacitance. However, it was not correlated with grain yield (Table 6) both in WS and WW environments. This may be because the stem works as a strong sink, which may compete with other sinks during kernel development (Setter and Meller, 1984). In a defoliation study, which was carried out during grain filling of tropical maize, taller genotypes with larger stem volumes did not have larger kernel weights than the shorter genotypes during stress (Edmeades and Lafitte, 1993). In other studies, however, high correlated responses were found for selection of stem diameter with grain yield in semiexotic maize population Mo17 x La Posta (Casanas et al., 2001). The correlation was positive with root lodging both in WW and WS environment showing the importance of smaller stem diameter for less root lodging. The correlation of stem diameter with other agronomic traits changed minimally in WS and WW environments of western ND and eastern MT showing less importance of the trait for adaptation to drought.

Visible brace root spread width and the number of brace roots can be utilized for selection in drought environments

The estimates of both narrow and broad sense heritability were high for brace root spread width, number of brace root count, stalk diameter, and root capacitance as compared to the important agronomic traits grain yield and root lodging (Table 3 and 7). This shows the potential genetic gain in these traits in relation to yield (Hallauer et al., 2010) under short-season drought environments. Significant ($P < 0.05$) GCA variances shown in these traits were mostly governed by additive genetic components (Table 7), increasing the potential for genetic improvement to the number of brace roots, brace root spread width, and root capacitance. Significant SCA

variances of stalk diameter showed the complex genetic make up for stalk diameter. Total GCA

variance was higher than the SCA variance for all traits except for grain yield, hundred kernel

weight, root lodging, and stalk diameter (Table 7). The significant GCA and SCA variances were

also found in the diallel cross among maize inbred lines in WS environments for grain yield,

days of silking, and plant height with only GCA variance significant for ASI (Badu-Apraku and

Oyekunle, 2012). The presence of additive genetic variance and the moderate level of heritability

shows these brace root and stalk related traits can effectively respond to selection in maize

breeding programs. The GCA variances were higher in WS environments for root lodging, stalk

lodging, and ASI while for other traits these were smaller. Similar smaller GCA variance

components were also found in WS environments compared to WW environments for grain

moisture, root capacitance, senescence, ASI, and root lodging in maize (Betran et al., 2003).

Higher GCA variance than GCA-by-environment variance for brace root width and brace root

count showed the relative importance of GCA variance for these traits (Table 7). However, the

significant GCA-by-environment interaction showed the complex nature of these traits. The root

pull resistance as a measure of root system size was found to have high additive and non-additive

gene action with significant (P < 0.01) GCA-by-environment interaction (Peters et al., 1982).

The genetic predictability ratio (GPR) close to unity (> 0.86) for brace root spread width

and brace root count in both WW and WS environments showed the larger portion of these traits

is controlled by additive gene action, whereas the value closer to 0.5 and for grain yield showed

the presence of non-additive gene action. Hence, GPR also showed the importance of additive

gene action for most of the traits studied in both WW and WS environments. The GPR was

found higher in WW environments compared to WS environments for all other traits while for

root lodging, stalk lodging, and ASI the GPR was higher in WS environments. Betran et al. (2003) also found higher GPR in WS environments compared to WW environments for ASI.

The genetic variance and values for root lodging was higher for WS environments as compared to WW environments (Table 3, Fig. 2). Root lodging has shown to be correlated with root traits like diameter of roots, the number of roots on the upper-tiered nodes, and angle of root growth (Guingo and Hebert, 1997; Wesley et al., 2000). In our study, the strong genetic correlation (r_G) of root capacitance as a measure of fresh root mass with brace root counts in WW (0.55) and WS (0.46) environments, showed the brace root count could reveal the difference in the relative size of the root system (Table 6). We found grain yield to be negatively associated with root lodging and stalk lodging both in WW and WS environments (Table 6). This showed the importance of improvement of root and stalk lodging for overall improvement of yield in WS and WW environments. The number of braceroot count and spread width was negatively correlated (r_G) with root lodging and stalk lodging in both WW and WS environments with higher negative correlation under WS environments (Table 6). Therefore, these traits can be selected against to reduce root and stalk lodging specifically in WS environments to overall increase grain yield under stressed environments.

The greater brace root spread width could also help brace roots to reach the inter row spacing, hence, utilizing water from a larger surface area in soils (Lynch, 2013). The proof of concept needs further study though. The trait could be equally important for resource acquisition of soils deficient of nitrogen and other minerals. In a study of maize under different nitrogen regimes, the number of brace roots was positively correlated ($rp = 0.73$) with grain yield in nitrogen stress environments (Trachsel et al., 2013). The morphological and physiological

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changes for drought stress were previously reported to increase yield across nitrogen stress environments (Bänziger et al., 1999).

Field phenotyping of maize root Architecture by measuring *In-situ* visible brace roots

The brace root number and the brace root spread width can be utilized as an important root architecture tool leading to drought resistance and low root and stalk lodging. The method requires very short time of counting clearly visible brace roots as well as the number of brace root whorls. The brace root spread width can be measured with a measuring scale around plant *In situ.* In very few cases it needs minimal removal of dead plant tissues wrapped around the base of plant. The visible brace root traits showed significant differences among genotypes (Table 1). These traits have a strong negative correlation with root lodging and it can be utilized to increase plant vigor in WS environments.

Conclusion

There are very few *In-situ* field phenotyping methods in maize closely related to root architecture available to phenotype a large number of genotypes in breeding programs. Root system architecture is considered a key trait when there is heterogeneous availability of soil resources like availability of water in drought stress. Although recently there has been a surge in root system studies in lab and greenhouses, there is still a lack of accurate field phenotyping of drought tolerance. Our research showed the possible exploitation of visible brace root traits for improvement of drought resistance in maize. This research has shown a new phenotyping method of maize root architecture by *In-situ* counting of visible brace root number as well as spread width measurement and their genetic control. These traits have a strong negative genetic correlation with stalk lodging and root lodging under drought environments as well as a positive correlation with plant vigor related traits, days of silking, and grain water content at harvest,

making them important traits for selection in drought environments. These traits could play an important role in moving maize to more marginal drought prone regions through selection and breeding. The correlations of stalk diameter and root capacitance were weak with important agronomic traits under drought, including lodging and grain yield. These traits are, therefore, less important in adaptation of maize to drought environments for achieving high grain yield under these conditions. The moderate to high positive relation between number of brace root count and root capacitance showed this could be important trait to categorize genotypes based on the root system size. Since these traits are not related with yield they show an independent genetic control making them more amenable to improve via index selection in recurrent selection as well as for inbred line development programs.

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CHAPTER 3. GENETIC ARCHITECTURES OF MAIZE GRAIN COMPOSITIONAL ATTRIBUTES IN THREE SOIL MOISTURE REGIMES: BREEDING IMPLICATIONS FOR DROUGHT ENVIRONMENTS

Abstract

Grain compositional attributes of total and extractable starch, oil, protein and amino acids of maize (*Zea mays* L.) are as important as grain yield for farmers because of its various end uses. The objectives of this study were to investigate the variability and genetic control of these grain compositional attributes in different water regimes and to discuss their implications for breeding maize cultivars with desired grain quality in water stressed (WS) environments. Ninety-four partial diallel crosses including 47 diverse maize inbreds and checks were tested in 12 water-stressed (WS), well-watered (WW), and random drought (RDT) environments in 2013 and 2014. The changes in mean grain extractable (< 1.33 %) and total starch (< 0.74 %), oil (< 2.2 %), cysteine (< 2.91 %) and lysine (< 2.81 %) content in WS and RDT were small while the changes in grain protein (+6.58 % in WS and +3.46 % in RDT) and methionine (+ 4.41 % in WS and -1.86 % in RDT) content were large compared to WW environments. Additive variance was most important across stresses and the largest variance was estimated in WS environments. The narrow sense heritability (h^2) was found to be high (> 0.40) for all traits in WW environments except for grain protein and its amino acids. The midparent-hybrid correlation was strong (> 0.62) for all traits across stresses except amino acids (< 0.55). The stress environments were largely associated for grain oil and total and extractable starch contents (> 0.60). However, they were less associated with grain protein content and amino acids (< 0.49). Quantitative genetic estimates and correlations varied more across stress environments for protein and amino acids contents than total starch, extractable starch, and oil content indicating selection for the latter traits can be done as part of multilocation testing for genetic improvement in WS environments.

Introduction

Maize is a major source of energy for humans and livestock. In 2013, 29.6 % of total maize production in the U.S. was processed to produce ethanol and 40.3 % for feed, 8.4 % for distillers dried grains with solubles (DDGS), 11 % for export, and the remaining 10 % for industrial uses of high fructose corn syrup, sweeteners, starch, cereals beverage/alcohol, and seeds (USDA, ERS, Feed outlook, Jan 2014). On average, a kilogram of maize grain contain 90 g protein, 40 g oil, 73 g starch, 2.5 g lysine, and 1.9 g methionine on dry matter (DM) basis (Clark et al., 2006). Maize is deficient in dietary need of monogastric animals (viz. chickens and swine) and humans for essential amino acids (Pollak and Scott, 2005). This is because in maize storage proteins called 'zeins' are found to account 60 to 70 % of endosperm protein (Hamaker et al., 1995), which are deficient in lysine and tryptophan content (Pollak and Scott, 2005). Livestock producers spend extra money on dietary supplementation through the synthetic form of these nutrients to mitigate deficiency (Pollak and Scott, 2005). High protein content (> 100 g kg^{-1}) and grain oil content (> 60 g kg^{-1}) increase value and caloric content in animal feed grains, respectively adding value to maize (Charles, 1995; Lambert, 1994). High extractable starch was found to be associated with high starch recovery, higher process efficiencies in gluten starch separation, fiber separation, and gluten feed drying and hence it is crucial for wet milling (Paulsen and Singh, 2004).

Genetic improvement for grain quality in maize has been conducted through quantitative genetic approaches and with utilization of desired grain quality mutants (Dudley and Lambert, 2004; Pollak and Scott, 2005). Quantitative genetic approaches have been successful for improving grain quality by utilizing recurrent selection and exotic germplasm incorporation with unique germplasms (Dudley and Lambert, 2004; Osorno and Carena, 2008; Sharma and Carena, 2012; Laude and Carena, 2014). Maize mutants *opaque2* (*O2*) and *floury 2* have been utilized for obtaining high lysine and tryptophan contents (Mertz et al., 1964; Nelson et al., 1965). The use of these mutants was challenged because the mutant gene is associated with soft endosperm, reduced yield, easy kernel breakage while machine harvest, high environment fluctuation in lysine content, and more pest susceptibility (Vasal et al., 1984). Later, with the introduction of *O2* modifiers (*Mo$_2$s*), the endosperm was converted to a hard one, which was crucial for

developing quality protein maize (Vasal, 2000). This was an exception as the use of specialty maize mutants is very limited for cultivar development (Cook et al., 2012).

The genetic makeup, the surrounding growing environments, and the postharvest handling of crop affects the quality of maize (Tsai et al., 1978; Zehr et al, 1996; Cook et al., 2012). Effect on grain protein, starch, and oil contents were found to be variable across environments, however, the influence of genetic factors were found to be more important than the environment (Jellum and Marion, 1966; Wu et al., 2008; Reicks et al., 2009).

Drought stress has been found crucial to reduce yield in maize (Araus et al., 2012). However, its effect on grain quality has been less studied in maize (Dwivedi et al., 2013). The U.S. drought of 2012 reduced national maize yield by 21 % and production by 38 % compared to the 2009-2011 mean levels (USDA, 2014). Worldwide, the loss of maize yield because of drought equals 15 % of well-watered yield potential every year (Edmeades, 2013), making it one of the important abiotic stress limiting grain yield (Araus et al., 2012). Short-season drought is also an important abiotic stress factor limiting maize grain production in western North Dakota (Carena, 2013). The western half of North Dakota (ND) and eastern Montana (MT) is affected by semi-arid conditions with low annual rainfall whereas eastern ND receives more rainfall in normal years (Karetinkov et al., 2008).

Screening for grain quality has increased in breeding programs with utilization of nondestructive, fast, and accurate near infrared reflectance (NIR) techniques (Alander et al., 2013; Huang et al., 2008). NIR is used to measure organic substances like protein, starch, oil, extractable starch, fermentable starch, and amino acids like methionine, cysteine, and lysine in grains of maize (Orman and Schumann, 1991; Paulsen et al., 1999; Paulsen and Singh, 2004; Bastianelli et al., 2007). The correlations between NIR screening data and end use quality were found to be strongly related and positive in maize for wet milling starch from laboratory and NIR screened total starch ($r_p = 0.9$) and between NIR screened protein content and gluten in maize (Zehr et al., 1995; Dijkhuizen et al., 1998).

Studies on sets of maize cultivars grown in the last 80 years showed, in general, decreasing protein content, increasing starch content, and no significant change in grain oil content (Scott et al.,

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2006). Similar changes were also found in other studies across genotypes (Duvick et al., 2004; Galais et al., 2008). Therefore, there is a need for breeding to improve not only quantity but also quality of grain. Increasing maize grain yield in drought stress environments has been an important objective of breeding programs (Araus et al., 2011; Blum, 2011; Carena, 2013). However, generation of information on variability and genetic control of grain compositional attributes in drought stress environments are equally important but least studied. This is crucial for development of cultivars with both high grain yield and quality in drought stress environments. The objectives of this study were 1) to determine the genetic variability of grain compositional attributes including grain protein, oil, total starch, extractable starch, methionine, cysteine, and lysine in three water regimes; 2) to estimate the genetic control and mode of gene action for grain quality attributes in different water regimes; 3) to estimate the genetic correlations of grain quality attributes across environments; 4) to discuss breeding implications of improving grain quality attributes in short-season breeding programs moving maize west to drier areas.

Materials and Methods

Plant materials

Fourty seven diverse inbred lines (Table 1) were randomly chosen from public and private maize breeding programs. This included NDSU inbreds developed by NDSU EarlyGEM incorporation program (Sharma and Carena, 2012), elite x elite crosses, and lines extracted from recurrent selection programs (Laude and Carena, 2014) for grain quality and grain yield. The 47 inbred lines were crossed in a partial diallel mating design utilizing circulent partials scheme of Kempthorne and Curnow (1961).

Test environments

The experiments were carried out in the NDSU Williston Research Extension Center Nesson Valley Irrigation Site, Williston, ND, USA (48º9'54" N, 103º6'32''. 4W, 590 masl), the Montana State University Eastern Agriculture Research Center, Sidney, MT, USA (47º43'48''N, 104º25'8'' .4W, 594 masl), the Fargo NDSU research site in main campus, ND, USA (46º 53'49''. 2N, 96º 48' 43''. 2W, 274 masl) and the NDSU Prosper Research Station, ND, USA (47º0'7''. 2N, 97º6'54'', 284 masl).

Table 10. Amount of Water received (mm), means of grain yield, grain compositional attributes in g kg^{-1} of dry matter in twelve well-watered (WW), water stressed (WS) and random drought (RDT) experiments in eastern North Dakota, western North Dakota and eastern Montana in 2013 and 2014.

Month	Sidney WS		NessonValley WS		Sidney WW		NessonValley WW		Fargo RDT		Prosper RDT	
	2013	2014	2013	2014	2013	2014	2013	2014	2013	2014	2013	2014
May	149	90.2	72.9	32.8	149	90.2	72.9	32.8	141.1	49.8	105.2	52.1
June	105.3	28	92.7	61.5	105.3	59.8	92.7	61.5	199.3	140.3	192.5	107.2
July	24.3	12.2	53.1	33.8	90.4	136.4	93.7	127.8	26.5	34.1	20.1	33.3
August	104.2	131	26.4	61.7	199.5	176	110.2	115.1	12.2	37.1	50.5	60.5
September	12.7	28.9	107.4	35.6	83	28.9	148.1	35.6	106.4	51.3	92.5	46.7
October	27	2.4	61.2	5.3	27	2.4	61.2	5.3	112.2	7.7	84.3	9.1
May to October	422.6	292.7	413.8	230.6	654.2	493.6	578.9	378	597.6	320.2	545.1	308.9
Yield, Mg ha^{-1}	3.2	7.6	4	2.2	3.2	8.6	9.1	3.1	4.8	5.5	6.3	4.3
Extract Starch	601	614.7	653.8	601.9	610	623.6	656.4	614.4	598.4	636.4	619.4	634.2
Methionine	2.4	2.3	2.1	2.6	2.4	2.1	2	2.6	2.5	2	2.2	2.3
Protein	113.4	104.8	86.6	119.1	110.5	97.4	78.3	111.6	124	91.5	102.2	93.8
Oil	44.4	42	50	41.6	45.6	41.1	54.7	40.6	42.8	46.5	45.9	47.5
Total Starch	688.4	699.2	710.6	686.1	690.1	706.2	716.2	692.6	686	709.9	714.1	704.8
Cysteine	2.4	2.2	2.5	2.7	2.3	2.1	2.5	2.7	2.5	2.3	2.1	2.5
Lysine	3.2	3.1	2.9	3.3	3.2	3	2.7	3.3	3.3	3	3	3

20 years normal rainfall from May to October in Sidney, MT is 275.84 mm while for 15 years normal it is 307.84 mm on Nesson Valley and 25 year normal rainfall for Fargo was 426.212 mm and it was 459.486 mm for Prosper (NDAWN, 2015).

Water Stressed (WS) trials were managed in order to have moisture stress severe enough to delay silking and affect grain filling in maize hybrids (Bolaños and Edmeades, 1993). Rain before silking was sufficient enough for all the stress environments (Table 10), not requiring supplemental irrigation during germination and stand establishment. Trials were managed in such way that the reduction in yield would be more than 50 % in WS environments (Bänziger et al., 2000). The year 2014 was drier compared to year 2013 (Table 10).

Soil types were Lihen-fine sandy loam for Nesson Valley, ND; Savage Silty clay soil for Sidney, MT; Fargo-Ryan silty-clay for Fargo, ND; and Bearden silty clay loam soil for Prosper, ND. The irrigation was applied with linear system sprinkler of #4 nozzle size. The schedule of irrigation is shown in Table 10. The precipitation amount in these locations was gathered by North Dakota agriculture weather network (NDAWN) (http://ndawn.ndsu.nodak.edu/ accessed 17 July, 2015).

Experimental designs and field management

Evaluation trials of genotypes was conducted on random drought (RDT) conditions in eastern ND, USA (Prosper and Fargo), and well watered (WW) and water stressed (WW) conditions of western ND, USA (Nesson Valley) and eastern Montana, USA (Sidney), for two years. The WW and WW experiments were placed next to each other in Nesson Valley, ND and Sidney, MT, separated by border rows. The experiment was conducted in a 10 x 10 partially balanced lattice design including 94 partial diallel crosses and six different commercial best checks representing a range of relative maturities. Each experiment was replicated two times in each location. Parents were also tested in an inbred trial conducted in a 7 x 7 partially balanced lattice design including 47 inbred lines and two commercial checks in two replicates in Prosper and Fargo.

The fertilizer was estimated based on the residual N, P and K in soil after soil sample analysis and recommended dose in WS and WW environments of eastern and western ND (https://www.ag.ndsu.edu/crops/corn accessed 17 July, 2015). In Sidney, both in WW and WS environments 100 kg ha^{-1} urea was applied. In dryland trials 56,000 plants ha^{-1} was the plant density

targeted. In irrigated conditions 78,000 plants ha^{-1} was maintained. In eastern ND (Prosper and Fargo), the plant population was maintained at 78,000 plants ha^{-1}. The previous crop was soybean.

Agronomic trait observations

Data were collected for grain moisture at harvest (H$_2$O g kg^{-1}) by a moisture blade in the combine harvester in Prosper and Fargo, ND, while in Nesson Valley, ND and Sidney, MT it was measured by oven drying 1000-g of grain plot samples. Grain yield (Mg ha^{-1}) was measured from shelled weight per plot adjusted to 155 g H$_2$O kg^{-1}. Days to anthesis (days) was noted when at least 50 % of the plants in the plot were shedding pollen with anthers emerged, days to silking (days) was noted when at least 50 % of the plants in the plots were showing visible silks in all stress environments. Anthesis silking interval (ASI) (days) was estimated subtracting the days to anthesis to the days to silking (Bolaños and Edmeades; 1996). Hundred kernel weights were collected in three samples of 100 kernels randomly selected from the total kernels. Plant height (cm) and ear height (cm) data were collected on plot samples of 10 plants as distance from the ground to the terminal nodes and node of uppermost ears respectively after flowering. Test weight (Kg hl^{-1}) was measured with test weight chamber in combine harvester.

Evaluation of grain compositions

500 gm of maize grain samples were collected from each plot while harvesting. The grain samples were dried to lower the grain moisture to less than 5 % in dryers. The relative grain protein, oil, starch, methionine, cysteine, and lysine content data were estimated using OMEG analyzer G^{TM} (UV-VIS NIR Spectrometer) from Bruins instruments. The measurements were based on the calibration provided by the Iowa Grain Quality lab at Iowa State University. The extractable and fermentable starch contents were measured through the Infratec^{TM} 1241-grain analyzer from FOSS A/S (NIR Spectrometer). The measurement of these traits was based on calibrations and equipment provided by Monsanto.

Statistical analysis

PROC MIXED with default REML in SAS 9.4 (SAS Institute, 2015) was used to conduct combine analyses considering each location by year combination as a separate environment. Genotypes

were considered as fixed effects and env, rep (env), block (rep x env) and trt x env were considered as random. Combining ability analyses were carried out for traits when means were significantly at $P < 0.05$. The model given by Kenpthorne and Curnow (1961) was used for combining ability analyses of partial diallel crosses of i x j in replicate l .

$$Yijl = \mu + r_l + g_i + g_j + s_{ij} + e_{ijl} \tag{12}$$

Where μ is a general effect, r_l is a replicate effect; parental effects are g_i , g_j also called general combining ability (GCA), s_{ij} is the non-additive parental effects also called specific combining ability (SCA), and e_{ijl} is the plot error, where g_i, s_{ij}, e_{ijl} are independent and normally distributed with mean zero and variances $\sigma^2_{gca}, \sigma^2_{sca}, \sigma^2_e$.

The combining ability analysis was computed using REML in PROC MIXED procedure in SAS 9.4 to estimate general combining ability and specific combining ability variances. The codes were modified from the procedure described by Mohring et al. (2011) for diallel mating design. If we consider a large random mating parental population with disomic inheritance and linkage equilibrium among gene loci, the $\sigma^2_{gca}, \sigma^2_{sca}$ variance components estimated by the mixed model defined have the following genetic expectations (Lynch and Walsh, 1998).

$$\sigma^2_{gca} = \sigma^2_A + \sigma^2_{AA} + \sigma^2_{AAA} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots \tag{13}$$

$$\sigma^2_{sca} = \sigma^2_D + \sigma^2_{AD} + \sigma^2_{DD} + \sigma^2_{DDD} + \sigma^2_{ADD} \quad \ldots\ldots\ldots\ldots\ldots\ldots \tag{14}$$

The Grifing model 4 method II (Grifing, 1956) was used to estimate the genetic components from the data set of partial diallel crosses not including reciprocals and parents and considering parents as random. Total genotypic variance (σ^2_G) was estimated as equation (15)

$$\sigma^2_G = 2\sigma^2_{gca} + \sigma^2_{sca} \tag{15}$$

Considering absence of epistasis, the additive genetic variance (σ^2_A) was estimated as equation (16)

$$\sigma^2_A = 2\sigma^2_{gca} \tag{16}$$

Based on Griffing (1956), the residual variance σ^2_{sca} included all the non-additive or dominance variance (σ^2_D) considering absence of epistatic variance, which is expressed as equation (17)

$$\sigma^2_{D=} \sigma^2_{sca} \tag{17}$$

Importance of GCA was calculated by general predictability ratio (*GPR*) estimated as by Baker (1978) as equation (18)

$$\text{GPR} = 2\sigma^2_{gca}/2\sigma^2_{gca} + \sigma^2_{sca} \tag{18}$$

Narrow-sense heritability (h^2) for selection among parental genotypes was estimated on a plot mean basis unbiased by genotype-by-environment interaction (Hallauer et al., 2010) as equation (19)

$$h^2 = 2\sigma^2_{gca}/(2\sigma^2_{gca} + \sigma^2_{gcaxE} + \sigma^2_{sca} + \sigma^2_{scaxE} + \sigma^2_e) \tag{19}$$

Broad sense (H) heritability was estimated with the equations (20)

$$H = 2\sigma^2_{gca} + \sigma^2_{sca}/(2\sigma^2_{gca} + \sigma^2_{gcaxE} + \sigma^2_{sca} + \sigma^2_{scaxE} + \sigma^2_e) \tag{20}$$

Genetic correlations r_{gij} between traits i and j were estimated utilizing the genotypic variance and covariance component estimates as described by Holland (2006) as equation (21)

$$r_{gij} = r_{Gij}/r_{Gi}r_{Gj} \tag{21}$$

Where r_{Gij} is the genotypic covariance between traits i and j, and r_{Gi} and r_{Gj} are the estimated genotypic standard deviations respectively of trait i and j. The correlation of the grain quality traits for inbred lines per se and their hybrids were estimated by regressing F1 hybrid values on midparent values (Betran et al., 2003). The Pearson correlation coefficient and their significance were estimated by PROC CORR procedure in SAS 9.4. The generalized principle component analysis, also called multidimensional preference analysis, was used to study the relationship among the traits in different moisture regimes and among the environments for different traits. The PRIN-QUAL procedure in SAS 9.4 was utilized to analyze data utilizing identity transformation. The procedure generates the biplot (SAS Institute, 2015).

Results

Relative moisture stress across environments, means of grain yield and quality

Genotypes in Nesson Valley, ND WS experiments received 29 % and 39 % less water in years 2013 and 2014, respectively compared to Sidney, MT WW trials. Similarly, genotypes in Sidney, MT WS experiments received 35 % and 41 % less water in years 2013 and 2014, respectively when compared to

the Sidney, MT WW trials. Fargo, ND received 9 % and 35 % less water than Sidney, MT WW in years

2013 and 2014, respectively. Prosper, ND received 16 % and 37 % less water than Sidney, MT WW

experiment in years 2013 and 2014, respectively. The precipitation in Sidney, MT was 53 % and 6 %

higher than the historic normal (of 20 years) in years 2013 and 2014, respectively. The precipitation was

34 % higher in Nesson Valley, ND than the historic normal (of 15 years) in 2013 and 25 % lower than

historic normal (of 15 years) in year 2014 (NDAWN, 2015). In Fargo, ND precipitation was 40 % higher

in 2013 and 25 % lower in 2014 than the historic normal of 25 years. In Prosper, ND the precipitation was

19 % higher in 2013 and 33 % lower in 2014 than the historic normal of 25 years (Table 10).

      All traits showed near normal distribution as confirmed from residual analysis. The mean grain

yield of hybrids was reduced by 29 % in WS environments compared to the well-watered environments.

The decrease was closer to the 30 % reduction in grain yield in drought stress as described by Blum

(2011), however, it was smaller than the 50 % reduction in grain yield in WS as described by Bänziger et

al. (2000). The mean yield of hybrids was reduced by 13 % in RDT environment compared to WW

environments. The variation in ASI was higher in WS compared to RDT and WW conditions. The yield

variation was highest in WW followed by RDT and least in WS environments (Fig. 5). The higher

variation for ASI in WS compared to WW showed drought was present in WS environment during

flowering time (Bänziger et al., 2000).

      The genotypic variation was significant (P < 0.01) for grain yield, grain oil, protein, starch,

extractable starch, methionine, cysteine and lysine content among hybrids in each environment (Table

11). The mean of grain methionine was 4.41 % higher in WS and 1.86 % lower in RDT compared to WW

environments. The mean of grain cysteine was 2.03 % higher in WS and 2.91 % lower in RDT compared

to WW environments. The mean of grain lysine was 2.81 % higher in WS and 0.94 % lower in RDT

environments. The means in grain protein content were 6.58 % higher in WS environments while only

3.46 % in RDT compared to WW environments. On the other hand, changes in grain starch and oil

contents were different and minimal. Grain oil showed 2.18 % lower in WS and 0.38 % higher in RDT

compared to WW environments. The change in extractable starch was 1.32 % in WS and 0.65 % in RDT
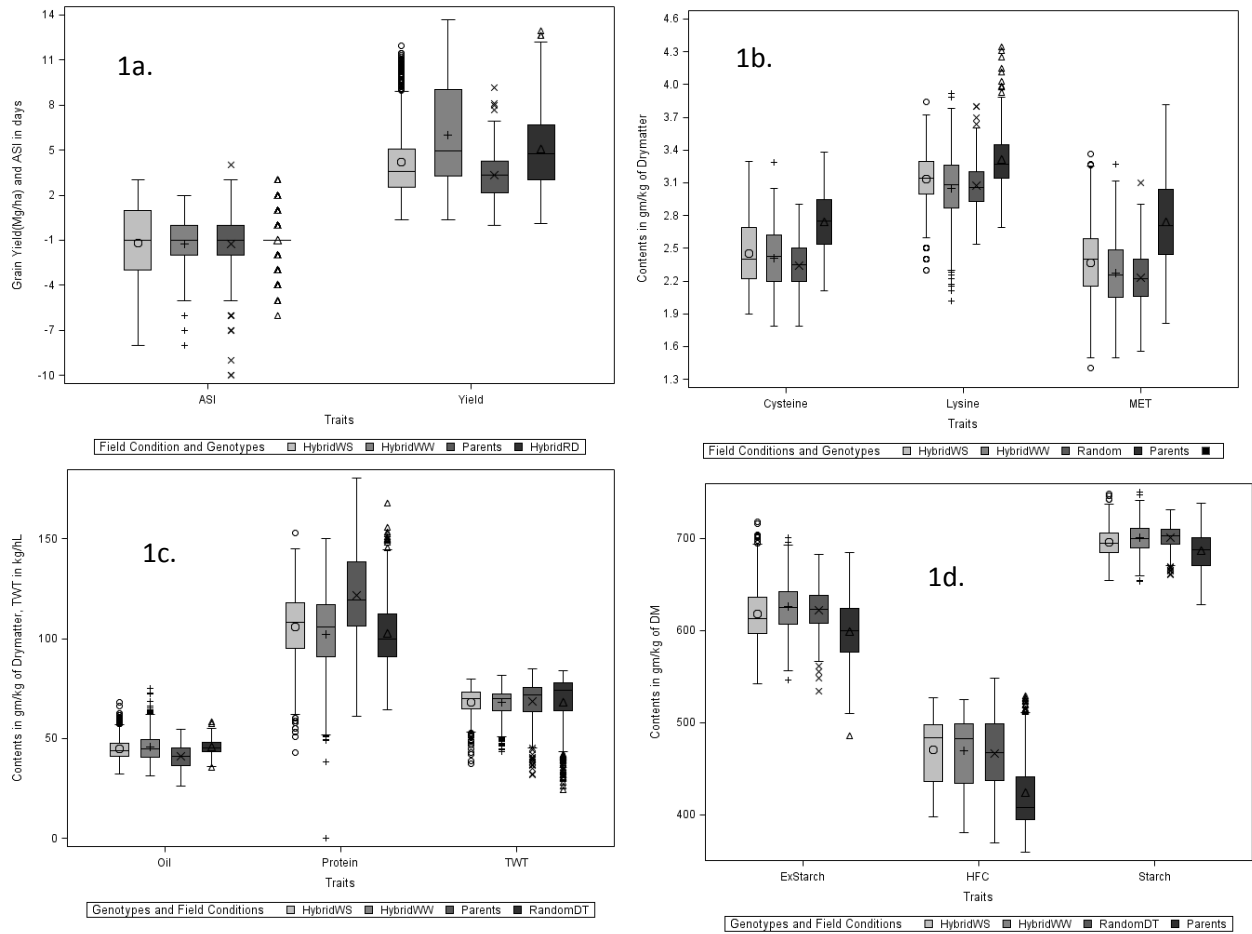
Figure 5. Box plot representing the phenotypic distribution for (a) anthesis silking interval (ASI), grain yield (yield), (b) amino acids cysteine, lysine and methionine (MET), (c) grain oil, protein, and test weight (TWT), (d) grain extractable starch (ExStarch), fermentable corn (HFC), and starch in 94 partial diallel cross from 47 parents in water stressed (WS) and well-watered (WW) and random drought (DT) environments in 2013 and 2014. Thick black bar represents median, boxplots between 25 and 75% variation, and open circles are outliers within 90% of total variation, circle or plus represent mean of population, Whiskers indicate extreme data points less than 1.5 interquartile range.

while for total starch 0.74 % lower in WS and 0.35 % higher in RDT compared to WW environments

(Fig. 5).

Genetic variance and heritability estimates across stresses

The GCA variance was significant (P < 0.05) for all grain quality traits in all three moisture

regimes (Table 15). The SCA variance was significant for grain oil and cysteine content in WW

environments. The general predictable ratio (GPR) was higher than 0.9 for all traits across environments

except for grain cysteine content at 0.80 in WW environment showing the importance of additive genetic action for all the traits. The significant SCA variance in grain oil and cysteine content in WW environments showed importance of non-additive gene action for the trait. The GCA variance was highest in WS environments for grain starch, oil, protein, extractable starch, and amino acid contents. The same variance was lowest in RDT environments except for lysine content which was lowest in WW environments (Table 15). The degree of dominance was highest in WW environments for grain cysteine amino acid and oil content. Degree of dominance was highest for grain protein content in WS environments and for grain starch, methionine, and extractable starch content in RDT environments. Highest degree of dominance for starch traits on RDT showed more complex gene action for these traits.

Narrow sense heritability (h^2) estimates for starch, protein, oil, methionine, and extractable starch contents were equal to or higher than 0.40 in WS and WW environments. In RDT, heritability was 0.37 for starch and 0.36 for extractable starch contents. The highest heritability was estimated for starch content (0.56) in WW environments. The essential aminoacids cysteine and lysine showed low heritability of 0.2-0.25 across stress environments. The narrow sense heritability was highest in WS environments for grain extractable starch and methionine amino acid content and it was highest in WW environments for grain protein, oil and, grain starch contents. The narrow sense heritability was highest for lysine and cysteine contents in RDT environments.

Variance for GCA-by-ENV was significant for all the traits across three soil moisture regimes. The variance for SCA-by-ENV was significant for all the traits except cysteine and lysine. In this case, it was significant for lysine and methionine content, starch, oil, protein, and extractable starch in WW environments. The variance of SCA-by-ENV was not significant for any trait in RDT environments.

Phenotypic and genotypic correlation coefficients among grain compositions

Highly significant and positive genetic (r_g) and phenotypic (r_p) correlations (P < 0.05) were estimated between amino acids lysine, cysteine, and methionine (Table 14). The coefficient was above 0.8 (r_A and r_P) in WW, RDT, and WS environments. Protein showed a genetic correlation of > 0.87 with

grain methionine content across stresses. An opposite relationship was estimated between starch and protein in all three moisture regimes. The negative correlation was equal > -0.85 between these two compositions in grains. Oil showed independent relationships with very low correlations with most traits. Extractable starch content showed a strong positive correlation with total starch content in grain with a genotypic correlation of > 0.79 across environments (Table 14).

The biplot analysis showed that the relationship between compositional attributes is mostly influenced by change in grain yield than agronomic traits (Fig. 6). In WS environments, the first principle component (PC1) accounted for 34 % variation while the second component (PC2) showed 19 % variation. In WW environments the PC1 accounted for 33 % and the PC2 accounted for 21 % of the phenotypic variation. In RDT, PC1 accounted for 40 % and PC2 accounted for 19 % of the variation.

In the parental trials PC1 accounted for 38 % and PC2 accounted for 23 % variation. In WS environments grain protein, amino acids and grain oil grouped together opposite to extractable and total starch content. Grain moisture and days of silking showed to be independent from grain quality traits. Grain yield, ASI, and hundred-kernel weight were grouped together with starch contents. A similar relationship can be seen in WW environments. In both cases, PC1 showed grain protein and related traits while PC2 showed grain starch, yield, and related traits. In the case of RDT environments a similar relationship can be seen, however, grain yield was correlated with grain moisture, days of silking, plant height and test weight. In this case, the PC1 was related with grain yield and starch related traits and PC2 accounted for protein related traits. When inbred parents were considered it showed that starch, protein, oil, and lysine contents grouped together while yield grouped together with methionine and cysteine. Grain moisture at harvest and days of silking were related with extractable starch content.

Correlations and efficiency of indirect selection across stresses

Significant ($P < 0.001$) positive phenotypic correlations were found between the RDT environments and the two managed WW and WS environments for grain quality traits (Table 12). The correlations for grain oil and total starch and extractable starch contents were strong (> 0.60) between
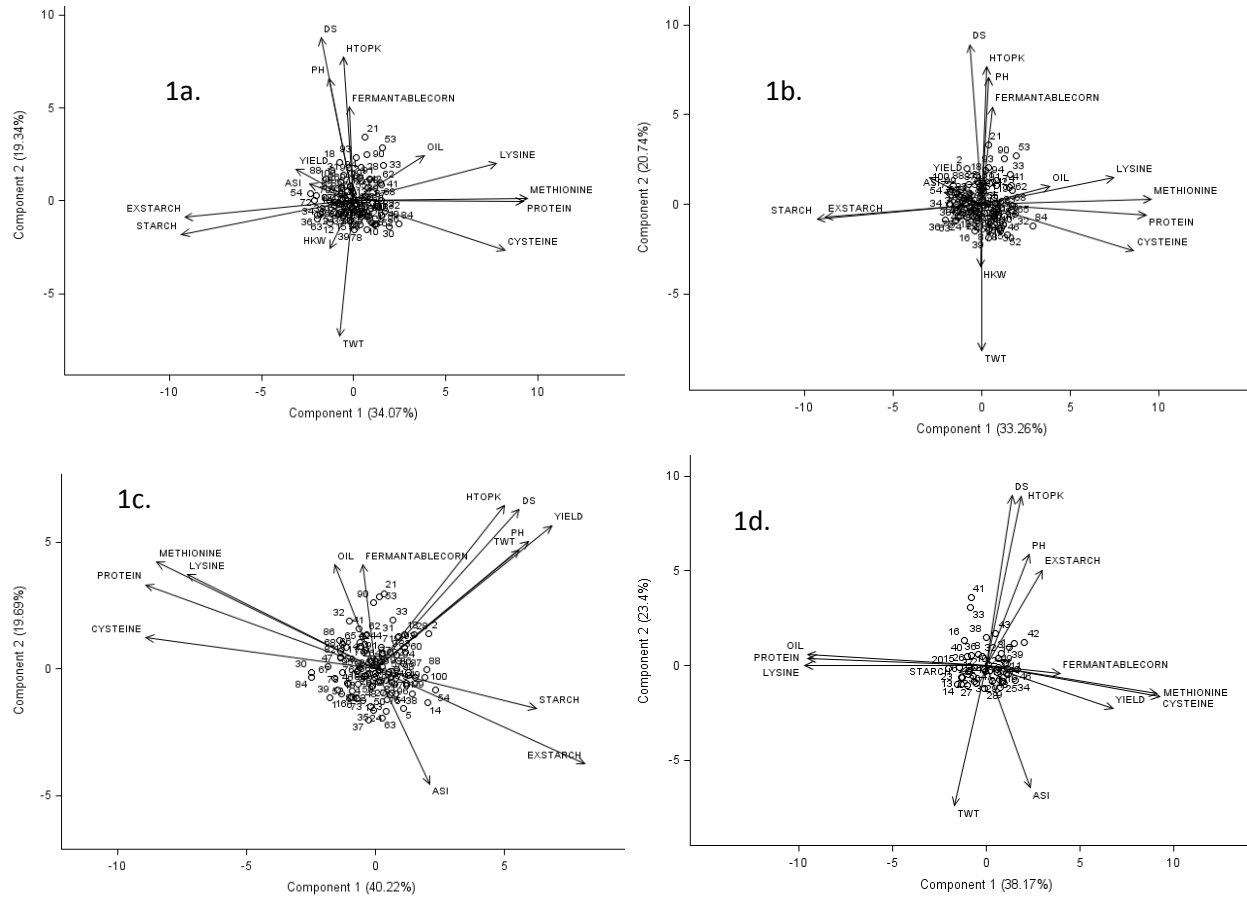
Figure 6. Biplot of agronomic (DS, days of silking, HTOPK, grain moisture, PH, plant height) and grain quality attributes (EXSTARCH, extractable starch) in (a) water stressed (WS), (b) well-watered (WW), (c) random drought (RDT), and (d) inbred parents for 94 partial diallel crosses from 47 inbreds of maize generated with multidimensional preference analysis for data collected from 12 water stressed and well watered environments in eastern North Dakota (ND), western ND and eastern Montana, USA from 2013 and 2014. The respective axes (x and y-axis) shows the percent of variance explained by the respective principle components (PC).

RDT and the two managed stress environments. The correlations for protein, cysteine, lysine, and

methionine were moderate to weak (< 0.49).

Relationship between inbred per se in random drought and hybrids across stresses

The correlation between midparent (inbreds) in RDT and offspring (hybrid) across WS, WW, and

RDT environments for grain compositional traits were significant and positive ($P < 0.0001$). However,

grain yield was only significant and positive ($r_p = 0.375$, $P < 0.01$) between midparent (inbreds) and

hybrids for WW environments. The correlation was high for extractable starch (0.67 in WS, 0.70 in WW,

0.61 in RDT), grain protein (0.71 in WS, 0.67 in WW and moderate of 0.47 in RDT), grain oil (0.73 in WS, 0.70 in WW and 0.67 in RDT) total grain starch (0.73 in WS, 0.70 in WW, 0.67 in RDT) across stress environments (Table 13). The correlation between midparent and hybrids for grain amino acids including cysteine, lysine, and methionine was moderate to low (< 0.55). However, the correlation for these traits and grain yield in RDT environments was not significant (Table 13).

Discussion

Genetic variation, estimation of genetic parameters and heritability

The presence of additive and non-additive gene action leads to the choice of breeding methods and resource management for successful cultivar development (Halluer et al., 2010). The estimation of genetic parameters with diallel mating designs including a limited number of parents has been criticized due to potential lack of distribution of genes in the parental lines (Baker, 1978; Hallauer et al., 2010). Utilization of a large number of diverse parents can help improve genetic parameter estimation and interpretations (Kempthorne and Curnow, 1961; Hallauer et al., 2010). In our study, all traits showed the importance of additive gene action compared to non-additive gene action except grain oil and cysteine in WW environments where non-additive gene action was also important. As a consequence, intra-population recurrent selection with the use of trait indices could be important to improve these traits. Many studies found the presence of higher additive genetic variance compared to non-additive genetic variance for grain starch, oil, lysine, and grain methionine content in maize (Poneleit and Bauman, 1970; Sreeramulu and Bauman, 1970; Darrigues et al., 2005; Bari and Carena, 2015). Other studies showed the importance of both additive and non-additive gene action for grain oil and protein content in maize (Dudley, 2008; Osorno and Carena, 2008). The presence of non-additive gene action for grain oil and cysteine content in our sample might imply a complex genetic makeup for these traits. In each environment, the degree of dominance was found to be in the range of partial dominance for most of the grain compositional traits. Partial dominance for grain starch and oil was also found with short-season ex-PVP and ND adapted lines (Bari and Carena. 2015).

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Table 11. Genetic variance, error variance and broad sense heritability estimates of grain compositional traits in g kg^{-1} of dry matter measured on 94 maize [Zea mays L.] partial diallel crosses in water stressed (WS) and well watered (WW) environments of 2013 and 2014 in eastern North Dakota, western North Dakota and eastern MT, USA.

Traits	WS			WW			RDT		
	σ^2_g	σ^2_e	H	σ^2_g	σ^2_e	H	σ^2_g	σ^2_e	H
Extractable Starch*	202.84	102.41	0.54	157.70	78.62	0.51	135.19	196.30	0.39
Starch*	70.01	25.79	0.59	63.65	26.67	0.58	41.41	58.96	0.39
Protein*	52.84	30.60	0.49	47.63	27.46	0.48	38.63	56.12	0.39
Oil*	8.29	6.41	0.51	8.60	3.47	0.58	5.09	5.22	0.45
Methionine*	0.02	0.02	0.45	0.02	0.01	0.43	0.01	0.02	0.33
Cysteine*	0.01	0.02	0.24	0.01	0.02	0.24	0.01	0.00	0.23
Lysine*	0.01	0.02	0.28	0.01	0.02	0.19	0.01	0.02	0.25

* means were significant at 0.05 probability level.

Table 12. Phenotypic Correlation of grain quality traits (gm kg^{-1} of dry matter) between random drought (RDT) and managed stress trials of well-watered (WW) and water stressed (WS) among 94 partial diallel crosses from 47 maize inbreds.

ENV	Ext. starch	Total Starch	Protein	Oil	Methionine	Cysteine	Lysine
WS	0.60***	0.65***	0.50***	0.69***	0.33**	0.34**	0.29**
WW	0.63***	0.619***	0.41***	0.73***	0.32**	0.32**	0.23*

*, **, *** For phenotypic correlation were significant at 0.05, 0.01 and 0.001 probability levels respectively.

Table 13. Phenotypic Correlation of Midparent (inbreds) -offspring (hybrid) for grain yield (Mgha^{-1}) and grain quality traits (gm kg^{-1} of drymater) at random drought (RDT) (Prosper and Fargo,ND, USA) and water stress (WS) well-watered (WW) (Nesson Valley, ND and Sidney , MT, USA) environments in a circulent partial diallel among 47 maize inbreds.

ENV	Yield	Ext.Starch	Total Starch	Methionine	Protein	OIL	Cysteine	Lysine
WS	0.05	0.67***	0.73***	0.56***	0.72***	0.65***	0.44***	0.25*
WW	0.38**	0.71***	0.71***	0.48***	0.67***	0.70***	0.30**	0.11
RDT	-0.13	0.62***	0.67***	0.05	0.47***	0.77***	-0.04	-0.14

*, **, *** For phenotypic correlations were significant at 0.05, 0.01 and 0.001 probability levels respectively.

Table 14. Genetic (below diagonal) and phenotypic (above diagonal) Correlations of grain compositions in g kg^{-1} of dry matter in 94 partial diallel crosses of 47 maize inbreds in wellwatered (WW), waterstressed (WS), random drought (RDT) and inbred parent experiments in eastern, western North Dakota and eastern Montana in 2013 and 2014.

Environments	Extractable Starch	Total Starch	Protein	Oil	Methionine	Cysteine	Lysine
WW Experiments							
Extractable Starch		0.79***	-0.72***	-0.33**	-0.59***	-0.28**	-0.45***
Total Starch	0.78**		-0.90**	-0.71**	-0.82**	-0.31**	-0.43***
Protein	-0.70**	-0.88***		0.21	0.90**	0.41***	0.44***
Oil	-0.38**	-0.54***	0.42**		0.23	0.07	0.12***
Methionine	-0.87***	-0.58***	0.67***	0.15		0.84***	0.82***
Cysteine	-0.73	-0.81**	0.91**	0.27*	0.92**		0.74***
Lysine	-0.94**	-0.66**	0.71**	0.09	0.92**	0.62**	
WS Experiments							
Extractable Starch		0.82***	-0.71***	-0.15	-0.67***	-0.30**	-0.48***
Total Starch	0.86**		-0.89**	-0.64**	-0.83**	-0.46***	-0.33**
Protein	-0.83**	-0.85***		0.07	0.87**	0.46***	0.31**
Oil	-0.39**	-0.40***	0.28*		0.18	0.25*	-0.07
Methionine	-0.94**	-0.68***	0.69***	0.17		0.78***	0.68***
Cysteine	-0.90	-0.80**	0.86**	0.22	0.91**		0.41***
Lysine	-0.91**	-0.80**	0.79**	0.24	0.91**	0.71**	
RDT Experiments							
Extractable Starch		0.82***	-0.76***	-0.34**	-0.54***	-0.43***	-0.42***
Total Starch	0.97**		-1.21**	-0.73**	-0.97**	-0.44***	-0.40***
Protein	-0.81**	-0.87***		0.27**	0.93	0.60***	0.54***
Oil	-0.30*	-0.55***	0.19		0.12	0.32**	0.33**
Methionine	-0.9**	-0.54***	0.71***	0.33**		0.97***	0.92***
Cysteine	-0.82**	-0.98**	0.96**	0.06	0.91**		0.93***
Lysine	-0.92**	-0.74*	0.84**	0.14	0.91**	0.83**	
Inbred (Parents) Experiments							
Extractable Starch		0.87***	-0.85***	-0.17	-0.90***	-0.84***	-0.79***
Total Starch	0.91**		-0.95**	-0.43*	-0.88**	-0.89***	-0.71***
Protein	-0.90**	-0.94***		0.14	0.95**	0.957***	0.63***
Oil	-0.20	-0.41**	0.18		0.07	0.05	0.07
Methionine	-0.94**	-0.86***	0.94***	0.03*		0.95***	0.62***
Cysteine	-0.90**	-0.91**	0.97**	0.12	0.97**		0.61***
Lysine	-0.84**	-0.76**	0.73**	0.07	0.66**	0.69**	

*, **, *** For phenotypic correlations were significant at 0.05, 0.01 and 0.001 probability levels respectively. For genetic correlations, coefficient exceeded twice, three and four times of their standard errors, respectively.

Table 15. Estimates of variance components, general combining ability variance (σ^2_{gca}), specific combining ability variance (σ^2_{sca}) and their interaction with environments (σ^2_{gca} x E and σ^2_{sca} x E), additive (σ^2_A) and dominance variance (σ^2_D), degree of dominance ($\overline{d}$) general predictability ratio (GPR) and narrow sense heritability(h^2) among 94 partial diallel crosses of 47 maize inbreds in random drought (RDT), wellwatered (WW) and water stressed (WS) environment in eastern North Dakota, western North Dakota and eastern Montana in 2013 and 2014 (the negative estimates were converted to zero).

Traits	σ^2_{gca}	$\sigma^2_{gca\ x\ E}$	σ^2_{sca}	$\sigma^2_{sca\ x\ E}$	σ^2_A	σ^2_D	GPR	$\overline{d}$	h^2
WS Environment Experiments									
Ext. Starch†	96.68***	62.63***	9.46	22.91*	193.38	9.46	0.95	0.05	0.49
Total Starch	34.07***	16.43***	1.87	9.72**	68.14	1.87	0.97	0.03	0.56
Protein	25.43**	16.85***	1.97	10.67**	50.87	1.97	0.96	0.04	0.46
Oil	3.84***	1.51***	0.61	1.37**	7.67	0.61	0.93	0.08	0.44
Methionine	0.01**	0.007***	0.00	0.003*	0.02	0.00	0.96	0.04	0.42
Cysteine	0.004*	0.002**	0.00	0.00	0.01	0.00	0.92	0.09	0.21
Lysine	0.003*	0.004***	0.00	0.00	0.01	0.00	0.90	0.11	0.23
WW Environment Experiments									
Ext. Starch	75.87***	44.11***	5.95	26.99**	151.75	5.95	0.96	0.04	0.49
Total Starch	30.59***	12.57***	2.48	6.33**	61.17	2.48	0.96	0.04	0.56
Protein	23.59***	12.54***	0.45	12.45**	47.19	0.45	0.99	0.01	0.47
Oil	3.84***	1.49***	0.91*	1.29**	7.69	0.91	0.89	0.12	0.52
Methionine	0.007**	0.006***	0.00	0.004**	0.02	0.00	0.94	0.07	0.40
Cysteine	0.003*	0.002**	0.001*	0.00	0.01	0.00	0.80	0.16	0.19
Lysine	0.002*	0.003**	0.00	0.003*	0.01	0.00	0.96	0.04	0.18
RDT Environment Experiments									
Ext. Starch	63.40***	16.23**	8.40	0.00	126.80	8.40	0.94	0.07	0.36
Total Starch	19.79***	6.51**	1.83	0.00	12.01	1.83	0.96	0.15	0.37
Protein	18.83***	5.36**	0.96	0.00	37.67	0.96	0.98	0.03	0.38
Oil	2.34**	1.009***	0.39	0.09	4.70	0.39	0.92	0.08	0.41
Methionine	0.006**	0.002**	0.00	0.00	0.01	0.00	0.92	0.08	0.30
Cysteine	0.003**	0.0008*	0.00	0.00	0.01	0.00	1.00	-	0.23
Lysine	0.003**	0.001*	0.00	0.00	0.01	0.00	1.00	-	0.25

*, **, *** For significant at 0.05, 0.01 and 0.001 probability levels respectively.
† Ext. Starch, grain extractable starch content

Non-significance of SCA variance for quality traits showed the heterosis could not be effective for improvement in these traits. This result could have been obtained because of defined heterotic group has not been exploited for grain quality improvement in maize. The heterotic pattern was empirically designed for exploitation of non-additive gene action and discovery of superior hybrid cultivars in maize, mainly for grain yield (Hallauer et al., 2010). GCA-by-environment was found significant for all grain quality traits across water regimes indicating that the environment affected GCA effects of these lines, which is in agreement with Pixley and Bjarnason (1983). However, GCA variances were higher than the GCA-by-environment variances for all traits across all environments, except for grain lysine content in WS environments.

Narrow sense heritability (h^2) estimates were high for grain total and extractable starch contents and oil content, moderate for grain protein and methionine, and low for grain cysteine contents across three water regimes. But they could have been biased by many sources (Table 15). Genetic makeup, the surrounding growing environments, and postharvest handling of crop have influenced maize grain quality traits (Cook et al., 2012; Tsai et al., 1978; Zehr et al, 1996). Sometimes, structured source populations or incomplete grain filling due to early frost can produce bias (Zehr et al., 1996). Grain protein and amino acid contents were found to be more influenced by agronomic practices than grain starch and oil contents (Mason and Mason, 2008). The estimate of broad sense heritability for half sib families derived from modified protein maize synthetics for grain protein content was estimated between 0.54 and 0.91 and for lysine content it was 0.17 to 0.72, while the heritability was high of 0.73 to 0.91 for grain oil content (Dudley et al., 1975). Mahan et al. (2014) found different narrow sense heritability estimates for lysine (0.12), methionine (0.24), protein (0.48), oil (0.79), and starch content (0.46) in quality protein maize germplasms. However, Motto (1979) estimated the narrow sense heritability for protein content among half sib families to be 0.68. The relatively high heritability estimate for major grain quality traits and their high additive genetic variances show potential for rapid progress from selection in these traits (Hallauer et al., 2010).

The narrow sense heritability was found high in WS environments for grain extractable starch, starch, and methionine contents (Table 15). The narrow sense heritability was higher for grain oil, protein, extractable starch, and starch contents for WW environments. For lysine and cysteine contents it was higher in RDT environments. For grain yield, the heritability was found highest in WW environments and lowest under RDT conditions (Weber et al., 2012). This shows the different compositional attributes behave differently in different environments. The increase in narrow sense heritability with increasing stress conditions was also described by Ward (1994), which can be seen with the traits we observed. However, this research also shows this may not apply for all traits. Higher narrow sense heritability under WS environments for grain extractable starch and starch content could have high selection response in these environments. These traits are especially important for wet milling and ethanol production in rural areas (Scott and Pollack, 2005; Carena, 2013).

Correlations for grain quality traits across stress environments

Our study showed consistent high but opposite nature of correlation between grain protein and starch contents in all different water regimes (Table 14). Therefore, it shows the challenge to select for higher grain protein and starch content together. Significant and negative correlations between starch and protein contents in grains were also found in maize inbred lines and hybrids (Zehr et al., 1995; Singh et al., 2001). The correlation was similar to the coefficients provided in literature for grain quality traits (Halauer et al., 2010).

Grain protein and methionine amino acid contents had high correlations in all environments. However, even though the genetic correlation was high for grain protein with lysine and cysteine in RDT environments, the same correlation was moderate to low in WW and WS environments. High correlations of methionine (0.95) and lysine (0.76) were found with grain protein (Sreeramulu and Bauman, 1970; Mahan et al., 2014) and between grain protein and oil (Dudley et al., 1971). This shows the selection for methionine and lysine contents could increase the overall grain protein content in maize. It could also be possible to select for grain protein and grain oil together to increase the value of grain. However, our

results warn us that special attention should be paid to genetic background and the type of environment used for selection.

Utilizing inbred line information for hybrid performance for grain quality traits

There was a significant correlation (r_p) between midparent and hybrid values for each grain quality trait in all environments except for grain lysine and cysteine contents (Table 13). In similar studies for grain yield in maize a low correlation was estimated under severe WS environments (Betran et al., 2003). This shows some of the grain compositional traits may act different than grain yield. In maize, a positive mid-parent heterosis was estimated for starch content and a negative heterosis was estimated for protein content in different maize hybrids (Taboada-Gaytan et al., 2010). However, in our sample of short-season maize genotypes, the correlation was positive for grain protein content across environments (Table 13). The high additive gene action for grain protein, grain oil, total starch, and extractable starch (Table 15) along with a high mid parent to hybrid correlation (Table 13) may indicate possible utilization of inbred line information for predicting hybrid development across environments. Parent-offspring correlation was found to increase with increasing extremity of environmental conditions (Ward, 1994). This shows the need of caution in data interpretation from correlation studies.

Relevance of managed stress trials for selecting grain quality traits

The significant ($P < 0.05$) and high positive correlation ($r_p > 0.60$) of grain oil, starch, and extractable starch across environments (Table 12) along with high narrow sense heritability (h^2), significant GCA and additive gene action, high GPR and partial dominance in low range, showed that simultaneous selection for different stress regimes could be possible for these traits. However, since the correlation is not very strong, there is the possibility of discarding some genotypes that may have desirable grain quality in managed stress environments when selection is done in RDT. The similar correlation estimates (genotype and phenotypes) for grain starch, oil, protein, and extractable starch across stress environments implies that similar physiological mechanisms and genes are involved for partitioning these grain quality components (Eisen and Saxton, 1983). Some of the changes in genetic

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correlations of these traits across stresses could have been caused by the genetic structure and history of selection of the inbred lines utilized in this study (Falconer and Mackay, 1996). Presterl et al. (2003) and Banziger et al. (1997) found significant and positive correlations for yield between low nitrogen and high nitrogen environments. Gallais et al. (2008) showed the greatest efficiency of indirect selection in high N-input environments. The result showed managed stress environment are required to improve the grain yield. However, this may or may not apply to grain quality traits as they could be selected as part of multilocation testing. The correlation between RDT and managed stress environments was moderate to low for grain protein (< 0.50), methionine (< 0.33), cysteine (< 0.34), and lysine content (< 0.28). The narrow sense heritability was also moderate and variable for grain protein and methionine content and low in cysteine and lysine contents across environments. The differences found in performance between midparent and hybrids (Table 10) for grain protein and amino acids including cysteine, methionine, and lysine across environments and the low correlations between RDT and manages stress environment indicate the need of different breeding programs for different stresses for these grain quality attributes, at least for short-season maize genotypes. Using locally adapted germplasm and selection in target environments was found to be an effective strategy to increase productivity of crops in less-favored areas (Ceccarelli et al., 1998; Weber et al., 2012).

Conclusion

Quantitative genetics approaches have been successful to improve grain quality in maize germplasms through long-term breeding programs. Grain quality traits including grain protein, total starch, oil, extractable starch, methionine, cysteine and lysine have potential to boost the rural economy through addition of commodity value. The study showed that genetic parameter estimates were different across water regimes for grain protein, methionine, cysteine and lysine while similar for grain oil, starch, and extractable starch contents. Highest GCA variance was found for all quality traits in WS environments. The correlation between RDT and managed stress environments was found strong for grain oil, starch, and extractable starch contents. The high narrow sense heritability, genetic predictability ratio, and partial dominance of low level, showed that simultaneous selection for different stresses is possible

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for these grain compositional attributes with the risk of losing few lines. However, the low correlation between RDT and managed stress environments with moderate to low narrow sense heritability showed need of selection in target environments for grain protein and amino acid contents. High midparent-hybrid correlation for grain extractable starch and oil contents, across stress environments, showed the utilization of parent per se information for desired grain quality in hybrid across environments could be efficient. However, for grain protein and amino acids the moderate to low correlations in managed stress and RDT environments showed a high influence of the environment. Grain oil, starch, and extractable starch contents, being an important trait for wet milling and ethanol utilization for various maize end uses, showed consistent genetic control across stresses and high variability in WS environments. Therefore, these traits could be utilized in the future for high genetic gain expectations. Predominance of additive variance in all compositional attributes and considering that grain yield is an important trait influencing grain composition, reciprocal recurrent selection seems to be crucial for combining genetic gain in grain yield and quality under drought stress.

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CHAPTER 4. GENERAL CONCLUSIONS

High Throughput *In-Situ* Field Phenotyping of Maize Root Architecture with Visible Brace Root Scoring

Maize cultivar development in drought environments has been slow due to unavailability of reliable and non-destructive field phenotyping methods. This is especially important for maize adult plant root phenotyping in the field where root systems grow below ground with many axes as well as they are highly affected by soil type or heterogeneous available resources in soil or by the soil strength (Goodman and Ennos, 1999; Blum, 2011; Araus et al., 2012; Lynch, 2013). The variability and genetic control of drought resistance in maize showed, in our study, that the brace root number and the spread width could be utilized for high throughput selection in drought environments.

The new phenotyping method includes traits with relatively high variability ($P < 0.0001$) in both well watered (WW) and water stressed (WS) environments in the sample of short-season genotypes tested. Genotypes for brace root spread width ranged from 24 mm to 44 mm, while the range for number of visible brace root counts was from 9 to 20 brace roots. Therefore, the visible brace root number count (VBRNC) and the visible brace root spread width (VBRSW) can be phenotyped with a method of scoring.

Several advantages were found for VBRNC and VBRSW. These traits showed higher broad and narrow sense heritability than important agronomic traits root lodging and stalk lodging as well as grain yield in both WS and WW environments. In addition, the narrow sense heritability was found to be higher in WS environments for both traits (Table 8 and 9). Additive genetic variance was predominance in these traits with significant ($P < 0.01$) GCA variance and non-significant SCA variances in both WS and WW environments. The genetic predictability

ratio (GPR) was also high (> 0.86) in both WW and WS environments. The presence of additive gene action and moderate narrow sense heritability showed the potential genetic gain will be higher if these traits are used for phenotyping. As a consequence, a pool of germplasm with overall bigger root systems can be accurately developed targeting at short-season WS environments (Hallauer et al., 2010). The moderate genetic correlation between root capacitance and brace root counts in both stress environments (0.55 in WW and 0.46 in WS) showed VBRNC could help differentiate root systems based on size.

We hereby introduce a new method for drought resistance phenotyping in maize with *In Situ* brace root count and spread width measurement in the field. VBRNC and VBRSW traits are easy to measure for high throughput data collection. Data collection is fast, similar to measurement of plant height (around two minutes per plot). The number of visible brace roots is counted and the spread width is measured with a measuring scale as total spread from stem. Brace root width (mm) is proposed from eight competitive plants (plants from middle of the row) per plot (Fig 1a, 1b, 1c and 1d). This is measured as spread (mm) of the brace root around the stem taking three most uniform reading randomly from three sides of each plant (Fig 1a). The number of above ground whorls occupied with brace roots is counted visually. Also, the number of brace roots is counted visually around stem. Data for brace root include those that are able to penetrate the soil surface to produce lateral roots. The procedure needs to have the field without weeds. If the dead plant tissues from the surrounding field are wrapped on roots, simple hand weeder can be used to remove the dead plant tissues. A difference can be clearly distinguished in the data for brace root counts and width in the (Fig. 7b, 7c, 7d, and 7e). The difference in the brace root number and spread width shows a scoring method can be developed based on the phenotypic classes among the roots to show the difference in root system (Fig 7e).
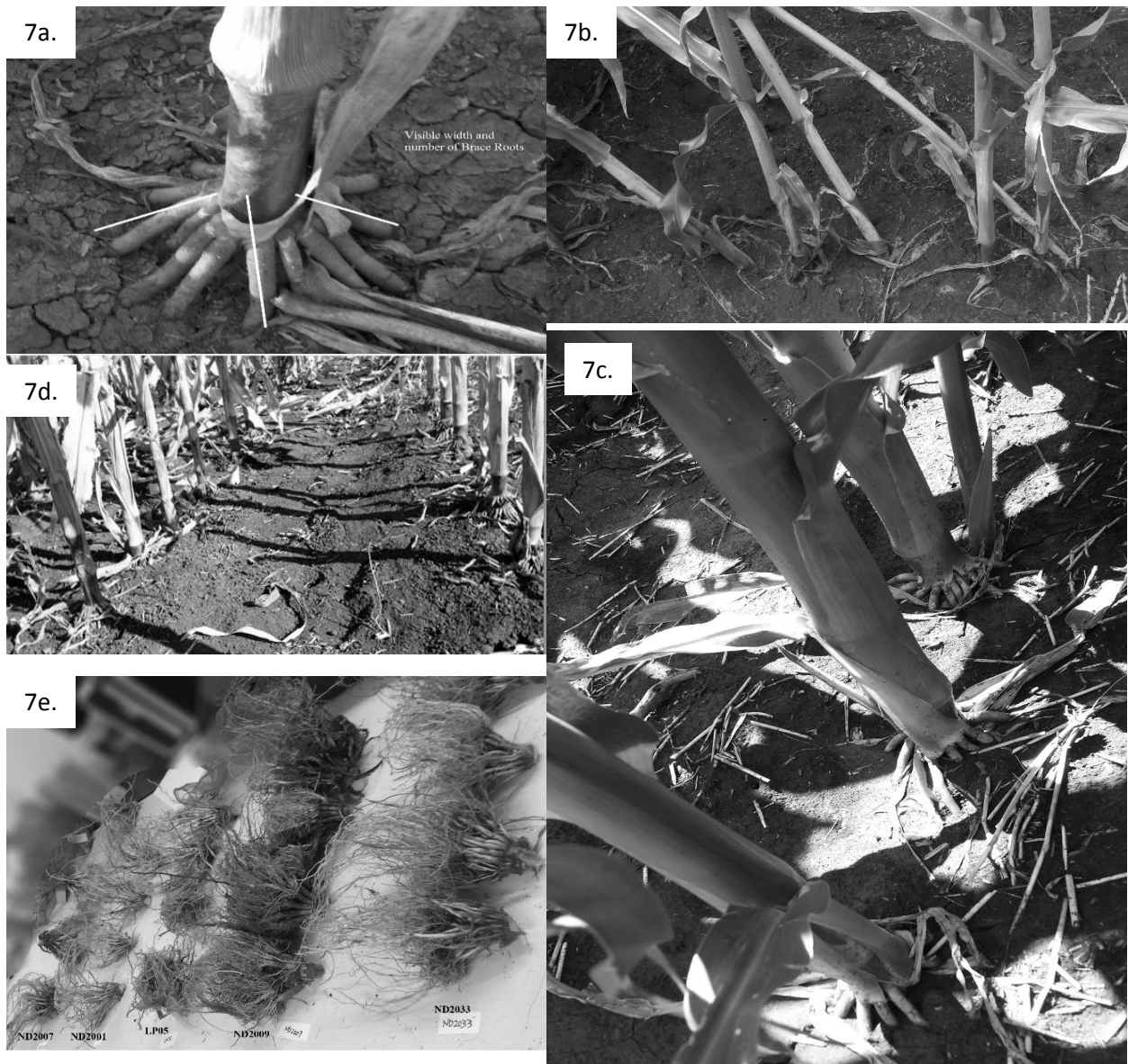
Figure 7. Visible Brace root traits in field and laboratory, a) three visible brace root traits were assessed on In Situ field condition: number of visible brace root count (VBRC), visible brace root spread width (VBRSW) and number of whorls occupied by brace roots (BRWH), b) In Situ visible brace root traits in poor performing cross, c) In Situ visible brace root traits in moderate performing cross, d) In Situ visible brace root traits in better performing cross, e) difference in visible brace root and the secondary roots in five distinct maize inbreds (ND2007, ND2001, LP05, ND2009 and ND2033).
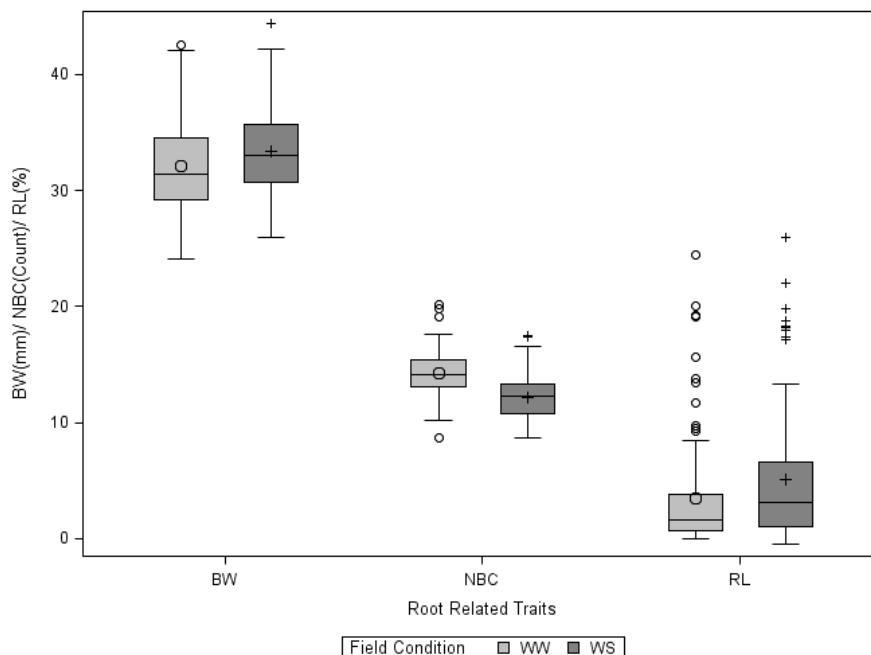
Figure 8. Box plot of the phenotypic distribution for brace root width (BW), brace root counts (BC) in 94 genotypes tested in well watered (WW) and water stressed (WS) environments in 2013 and 2014. Thick black bar represents median, boxplots between 25 and 75% variation, and open circles are outliers within 90% of total variation, circle or plus represent mean of population, Whiskers indicate extreme data points less than 1.5 interquartile range.

The distribution of the traits showed the various phenotypic classes more amenable for quantitative genetic data analysis (Fig. 3).

In WS environments, the biplot analysis for number of brace root counts showed that the three principle components accounted for 44 %, 12 % and 12 %, respectively (Fig. 9). For brace root spread width, the three principle components accounted for 43 %, 13 % and 11 %. The environment has shown a strong association (Fig. 9a and 9b). The association between environments showed traits to be important in WW and WS environments.

Cluster analysis showed that crosses including B104, ND2013, ND2009, ND2014, and ND07-212 grouped together, which also has highest number of brace root counts. Similarly ND203, ND2001, ND08-53, PHG47, and ND246 grouped together with the lowest number of brace root counts

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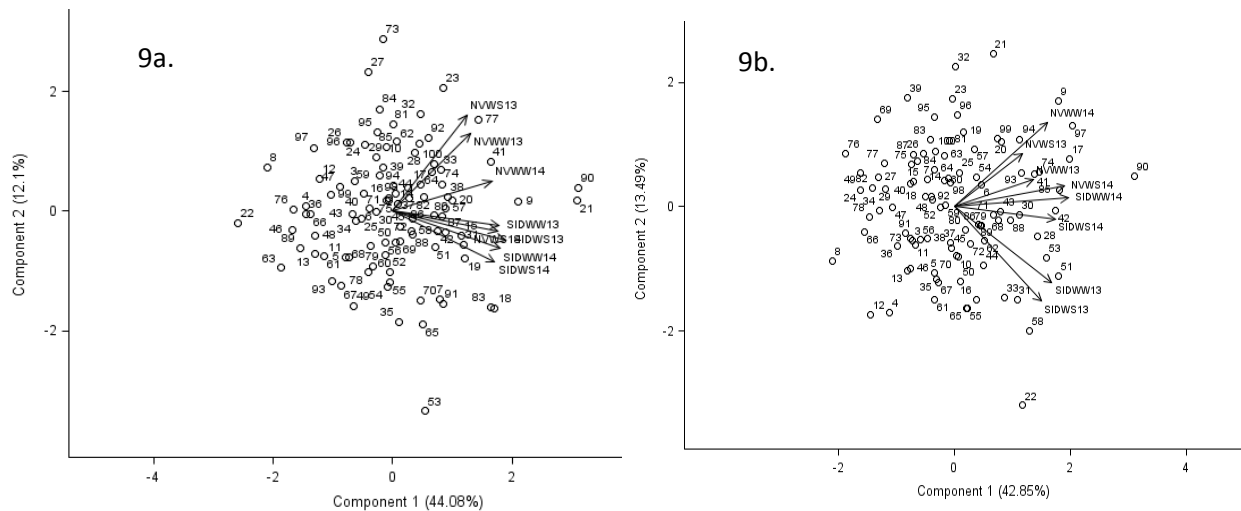
Figure 9. Distribution of testing environments for number of a) visible brace root count and b) visible brace root spread width: nesson valley 2013 and 2014 in water stressed and well water environments (NVWS13, NVWS2014, NVWW13, NVWW14 respectively),sidney 2013 and 2014 in water stressed and well-watered (SIDWS13, SIDWS14, SIDWW13, SIDWW14 respectively) in the orthogonal panel of the principle components analysis of the 94 partial diallel crosses from 47 inbreeds of maize and the percent contribution of each axis to total variability.

Five distinct groups showed the possibility of developing a five point score for these traits (Fig. 10). In case of brace root spread width, crosses including ND2009, ND2013, ND2004, and ND2007 showed the largest brace root spread width. The crosses from lines ND203, ND2001, ND2000, and NP2341 had the smallest brace root spread width. Based on our sample a five point score could also be important for brace root spread width (Fig. 11). Since brace root spread width and brace root count have moderate (0.47 in WS vs 0.49 in WW) significant (P < 0.01) genetic correlations in WW and WS environments, a combined five point score can be developed ranging from 1 to 9. A similar five-point score was also developed by Trachsel et al. (2010) for brace root number and angle for excavated roots. The scoring can be carried out visually observing the root system size comparing the spread width and number of brace root differences with integrated brace root number and spread width scoring visually.

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Measurement of the visible brace root diameter is also a suggested trait to include to investigate drought resistance in water stress environments. Based on the short-season germplasm evaluated, the larger the brace root diameter the deeper and stronger are later roots leading to increased resistance to root lodging and higher grain yield in WS environments. The new score system needs to be validated. These traits can be easily exploited in breeding programs targeted at cultivar development for drought stress environments, affecting root architecture leading to drought resistance with a non-destructive method. New populations can be developed combining the root traits and other agronomic characters in useful maize germplasm. A new population (NDSSR) has been developed by the North Dakota State University maize breeding program backcrossing ND203 as recurrent parent to the lines with highest number of brace roots, B104, as donor parent to develop early lines with strong root system for short season drought resistance (data not shown).

Relevance of Managed Stress Environment for Genetic Improvement of Grain Quality Traits in Drought Stress

The genetic architecture of the grain compositional traits across different water regimes showed the importance of additive gene action for most traits. The midparent-hybrid correlation, environmental correlation across stresses, and narrow sense heritability were relatively high for grain starch, extractable starch, and grain oil content while it was weak for protein and amino acid traits. The results could be crucial in the choice of improvement programs as well as the management of resources for grain quality improvement in drought environments. Our results showed that total starch, extractable starch, and grain oil do not need management of stress environments while for grain protein and amino acids we do need to control stress environments for genetic improvement of these grain quality traits under drought environments.

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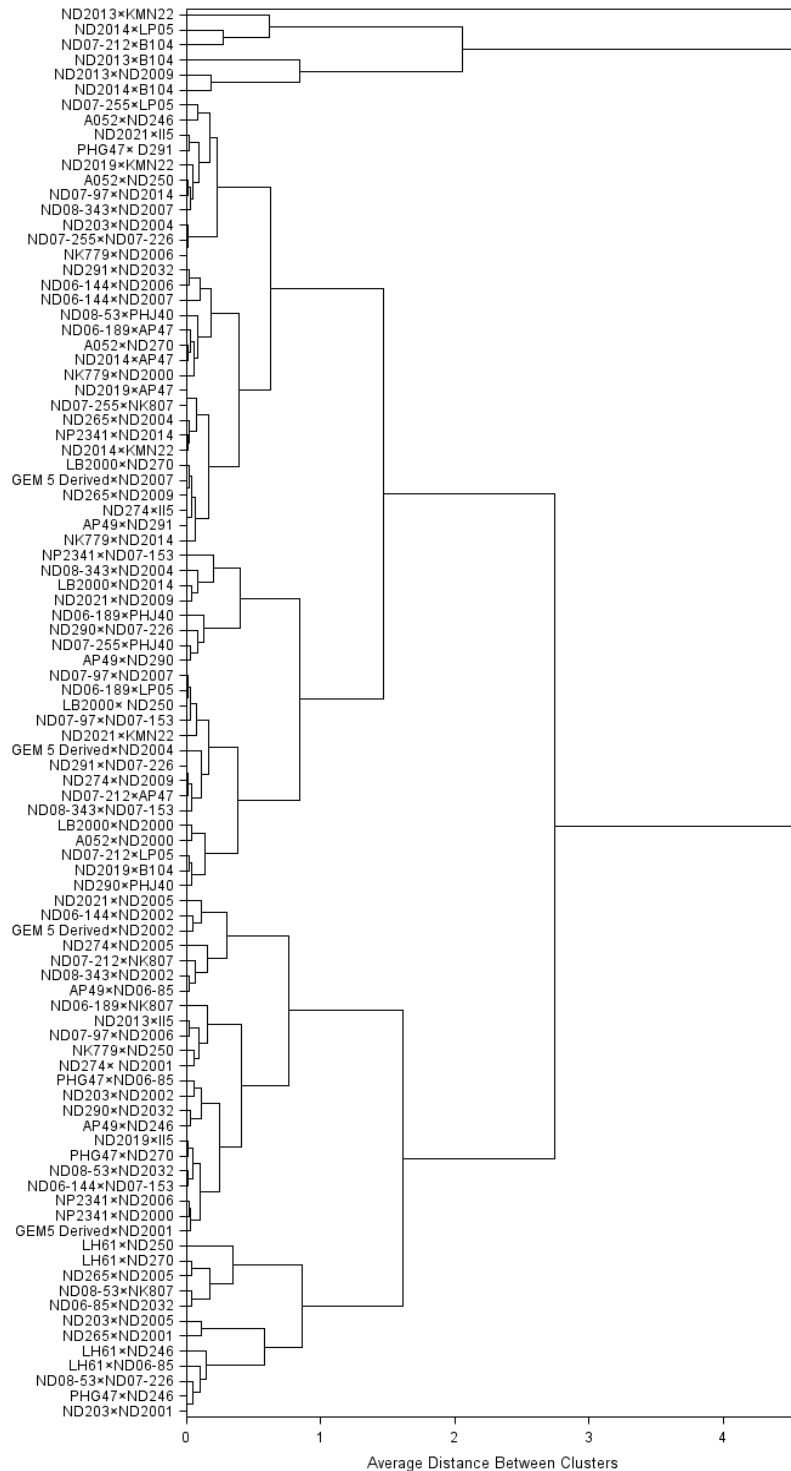
Figure 10. Cluster analysis conducted by using Euclidian distance as dissimilarity coefficient and average distance as grouping methods. Dendrogram was developed with the average of the number of visible brace root count (VBRC) in 94 partial diallel cross from 47 inbred parents across four water stressed environments of Sidney, Montana, USA and Nesson Valley, North Dakota, USA.

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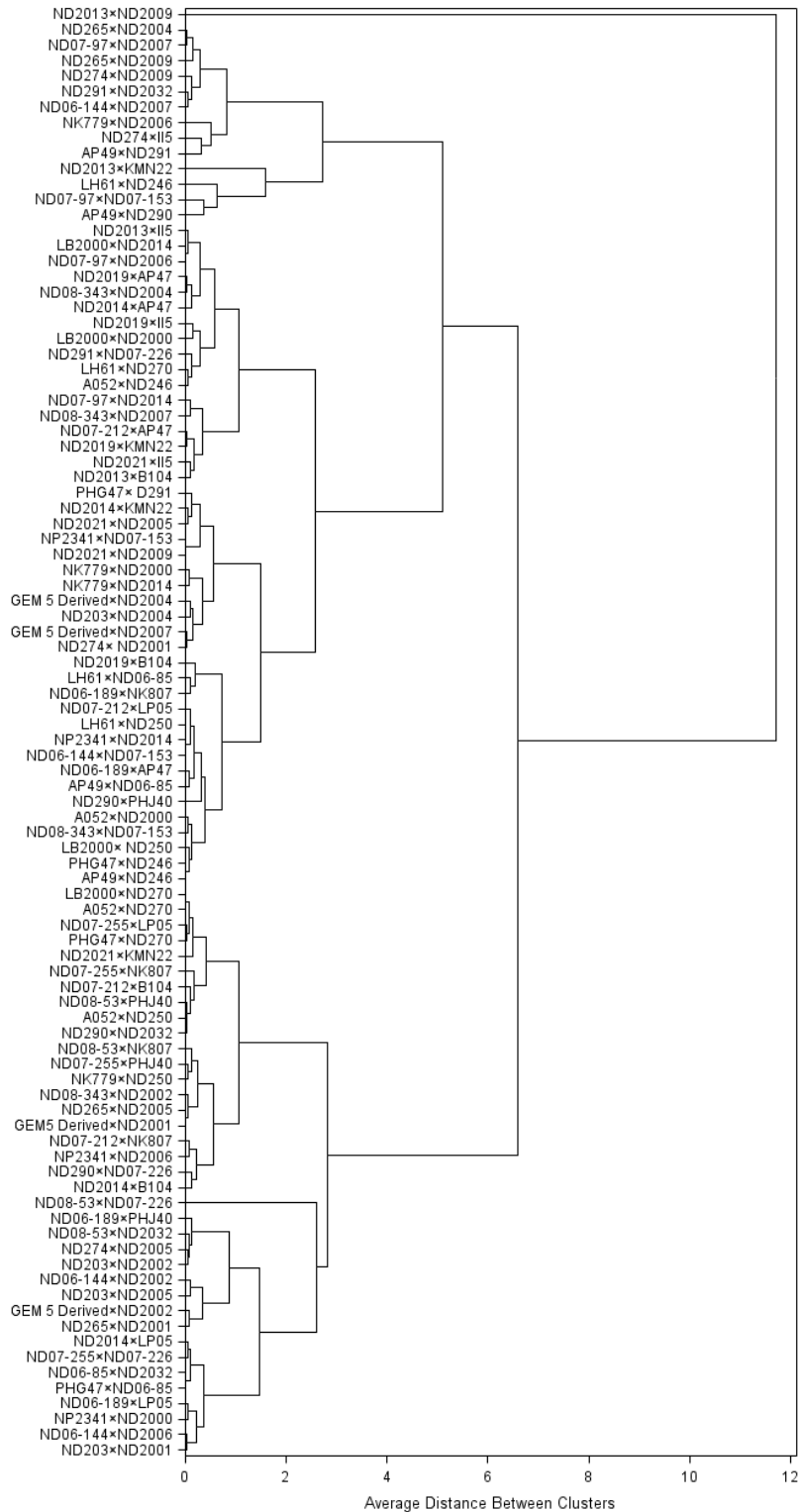
Figure 11. Cluster analysis conducted by using Euclidian distance as dissimilarity coefficient and average distance as grouping methods. Dendrogram was developed with the average of the visible brace root spread width measurements (VBRSW) in 94 partial diallel cross from 47 inbred parents across four water stressed environments of Sidney, Montana, USA and Nesson Valley, North Dakota, USA.

Grain yield was one of the crucial traits to influence grain quality as it is controlled by both additive and non-additive gene action in our study and previous studies in maize (Hallauer et al., 2010). Grain quality was controlled largely by additive gene action. The quantitative genetic parameter estimates indicated the reciprocal recurrent selection with unique germplasm choice, will be crucial for genetic improvement of grain yield and quality under drought stress environments.

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APPENDIX

Table A1. Grain moisture (H2O kg^{-1}) at harvest adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

| | | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
Entry	Pedigree	NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	122.8	.	200.1	.	.	333.1	162.2	330.6	165.7	130.2	79.8
2	ND2014×B104	.	353.5	.	.	.	.	407.3	166.5	411.1	160.5	216.8	171.5
3	GEM5Derived×ND2001	186.5	107.6	219.5	191.7	.	.	205.7	96.2	211.5	83.2	116.1	128.8
4	ND265×ND2001	173.6	218.9	269.9	271.7	.	.	226.8	127.9	281.0	96.5	119.6	119.6
5	AP49×ND246	222.8	126.2	261.3	421.6	.	.	331.8	151.6	344.2	128.2	169.3	149.3
6	ND274×ND2001	188.2	106.5	271.0	178.8	.	114.5	227.3	107.2	301.8	94.8	99.9	123.0
7	ND290×PHJ40	188.1	92.9	221.7	128.0	121.0	115.0	171.9	76.7	179.3	66.3	117.3	124.7
8	ND203×ND2005	163.3	103.8	185.3	114.2	162.5	117.5	187.6	83.3	215.7	63.3	113.1	110.4
9	AP49×ND290	214.9	128.5	230.2	169.5	138.0	113.0	275.4	83.9	292.5	58.5	145.8	131.0
10	NK779×ND2014	152.2	70.7	175.2	79.6	113.5	107.5	145.9	53.7	170.7	46.3	99.7	111.0
11	ND290×ND2032	208.3	197.4	258.9	284.3	132.5	116.5	230.2	113.0	249.4	92.7	132.2	139.4
12	ND203×ND2002	192.6	138.2	212.3	197.7	122.5	119.5	242.0	116.7	299.0	109.0	123.2	102.6
13	PHG47×ND246	186.3	132.8	248.1	134.9	129.0	78.5	327.4	109.9	344.3	123.8	92.6	123.4
14	AP49×ND06-85	210.9	231.0	228.5	306.7	122.5	122.0	237.5	93.3	242.9	75.3	123.1	110.2
15	ND290×ND07-226	191.6	93.5	221.4	105.2	121.0	114.5	174.4	82.4	204.1	74.9	117.8	120.9
16	NK779×ND2000	157.5	65.6	178.1	66.9	101.5	96.5	154.9	59.9	148.7	54.8	105.9	125.6
17	AP49×ND291	220.4	182.3	236.3	315.0	133.5	116.0	299.0	122.7	281.2	110.8	143.8	145.8
18	ND07-212×B104	350.6	444.3	398.4	463.6	168.0	138.5	387.7	176.8	221.1	145.2	178.6	162.0
19	ND2021×ND2009	327.2	434.1	347.8	470.1	141.0	112.0	280.1	116.2	323.9	114.0	143.3	141.6
20	NP2341×ND07-153	230.9	173.8	231.8	218.8	113.5	113.5	271.0	122.4	278.1	103.7	145.7	143.1
21	ND2013×B104	437.0	604.4	422.2	.	208.0	127.0	462.3	287.3	463.7	243.6	258.0	190.4
22	LH61×ND246	212.7	184.0	269.0	272.8	119.0	86.5	363.5	178.7	402.8	200.4	121.5	131.0
23	ND08-343×ND07-153	226.0	195.0	250.9	272.4	140.5	117.0	272.9	139.3	271.2	135.8	145.8	145.8
24	GEM5Derived×ND2002	180.6	122.6	216.8	138.2	115.5	109.0	171.5	94.4	184.2	93.5	110.8	124.7
25	ND06-189×NK807	177.8	146.7	206.2	220.5	114.5	103.5	208.0	81.2	227.4	77.3	111.0	116.9
26	ND2021×ND2005	170.6	137.9	196.4	198.3	116.5	114.5	206.5	75.9	186.0	76.9	141.1	142.1
27	NP2341×ND2000	163.6	99.1	191.1	149.7	108.0	111.0	170.6	61.2	151.5	52.9	117.5	99.8
28	ND06-144×ND2007	361.2	382.9	361.2	417.4	164.0	119.0	358.8	187.8	369.4	180.6	235.4	164.0
29	ND08-343×ND2002	216.3	203.4	225.6	308.6	148.0	116.0	203.1	116.4	208.2	122.4	128.0	140.1
30	NK779×ND2006	149.6	68.4	163.6	91.1	104.5	109.0	157.1	85.8	153.9	62.6	91.4	67.6
31	ND2019×B104	229.5	331.6	237.1	384.5	126.5	111.5	374.5	154.4	392.2	143.2	210.1	153.8
32	ND2021×KMN22	199.8	115.5	210.4	217.5	120.0	117.0	238.2	80.9	251.2	57.4	129.1	118.9
33	ND08-343×ND2007	356.0	434.6	374.7	584.9	161.0	155.0	376.6	227.4	394.1	181.1	206.9	163.7
34	PHG47×ND06-85	179.1	95.8	228.6	355.6	111.0	108.5	173.7	67.3	174.6	46.1	109.9	113.6
35	ND203×ND2004	185.3	70.8	236.0	100.3	116.5	95.0	193.1	98.7	298.3	85.3	62.6	118.7

Table A1. Grain moisture (H2O kg^{-1}) at harvest adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued)

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	213.2	312.4	254.2	368.8	134	127.5	249.2	102.7	260.4	116.2	175.3	145
37	A052×ND246	165.2	90.2	199.4	107.5	106	110.5	236.8	99.3	232.9	77.5	89.1	76.2
38	A052×ND2000	186.3	136.4	218	161	121	110	172.5	90.1	192.8	76.4	119	129.3
39	NK779×ND250	152.9	83.7	194.9	129.6	119	119.5	180.8	75	219.6	67.2	94.6	85.4
40	NP2341×ND2006	167.7	93.2	192.5	110.5	135.5	109	177.3	99	176.8	73.8	116	112.5
41	ND2013×KMN22	216.2	133.5	217.3	349.1	137.5	111	294.3	76.5	312.6	80.2	114.7	114.8
42	ND07-97×ND07-153	295.5	195.7	333.2	318.2	147.5	129.5	377.6	147.7	387.1	120.8	145.2	139.9
43	ND06-144×ND07-153	259.8	230.7	282.5	340.4	148	133.5	290.5	178.6	316.5	147.7	152	158.7
44	ND2014×KMN22	181.4	147	208.9	235.9	119	114.5	223.6	74.4	234.1	66.3	120	125.1
45	LB2000×ND2000	146.1	57.2	192.3	136.3	108.5	109	148.5	66.3	144.7	70.6	129.2	114.8
46	ND265×ND2005	177.9	103.1	200.5	156.7	116.5	117	174.5	79.4	188.3	62.7	110.3	129.5
47	ND274×ND2005	181.9	86.4	211.2	167	108.5	113.5	170.6	66.5	166.8	64.3	104.7	121.2
48	ND08-53×NK807	174.5	169	196.8	270.3	121.5	113.5	218.8	93.4	236.2	72.3	113.6	104.4
49	ND06-144×ND2002	226.6	269.2	260.7	381.7	131.5	119.5	236.7	93.3	232.5	97.9	130.7	141.5
50	PHG47× D291	208.9	143.2	247.3	226.8	121.5	112	192.6	80.8	247.3	65.7	132.6	99
51	ND265×ND2009	280.1	275.5	287	378.4	144.5	109.5	243.1	129	290	130.3	138.4	152.8
52	LB2000× ND250	177.4	51	207.4	98.5	119	109	183.8	95.9	178.6	79.3	116	133.9
53	ND07-97×ND2007	418.6	488.8	419.7	.	193	152.5	456.7	198	465.4	226.1	269.3	192.7
54	ND2014×AP47	219.7	237.5	234.6	314.2	135.5	117.5	291.8	226.6	288	86.1	151.3	135.1
55	ND06-189×AP47	204.9	130.7	228	227.3	118	120	207.3	83.1	220.2	63.8	117	112.8
56	NP2341×ND2014	178.8	106.1	208.7	178.6	112.5	137	159.8	71.5	172.8	73.4	127.1	117.5
57	ND08-343×ND2004	206.2	193.9	237.4	230.1	131	122	168.7	115.7	241.3	107.3	126.5	138.7
58	ND265×ND2004	179.4	112.8	225.5	186.6	126.5	123.5	161.6	101.1	178.2	85.6	127.3	124.9
59	ND08-53×PHJ40	163.5	103.2	203.9	103.9	114.5	89	179.9	67.4	202.5	64.7	114.5	122.5
60	GEM5Derived×ND2007	296.2	274.8	330.9	370.7	151	123	249.9	121.9	316.7	122.5	160.9	155.5
61	LH61×ND250	218.4	184.6	246.2	295.9	122	117	309.7	122.1	341.8	122.3	170.5	129.5
62	ND2019×KMN22	201.1	135.3	203.1	270.5	120	115.5	307.9	69	232.4	64	117.5	120.1
63	LH61×ND06-85	198.4	186.2	219.9	280.6	115.5	105	262.3	96.9	307.7	125.7	92.4	124.4
64	GEM5Derived×ND2004	191.5	72.1	213.8	143.4	120	111	179.4	89.6	198.3	81.9	122.4	117.8
65	ND07-97×ND2014	241.7	168.3	272.7	255.7	116.5	115.5	228.3	89.3	309.5	91.9	121.6	137
66	ND08-53×ND2032	214.5	272	253.9	314.1	136	169	293.3	107.4	327.6	99.6	142.7	150.7
67	PHG47×ND270	167	101.9	230.1	170.7	108.5	90.5	223.5	55.2	210.1	79.1	104.6	109.4
68	ND07-97×ND2006	219.6	85.7	229.7	265.7	120	110.5	314.2	111.7	330	100.5	133.9	156.6
69	ND07-255×ND07-226	187.2	162.5	264.6	242.7	125	123	241.5	134.3	315.3	117.8	152.1	147.7
70	ND07-212×NK807	220	237.9	210.2	323.7	124.5	104	217.5	92	222	82.3	113.5	136.7

Table A1. Grain moisture (H2O kg^{-1}) at harvest adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	202	223.4	218.9	309.9	121	111	199.6	80.2	245.9	69	110.1	127.3
72	ND07-212×AP47	216.8	207.6	220.7	293.8	125.5	130	284.3	112.1	329.5	92.6	147.1	138.5
73	A052×ND270	198	133.4	230.1	203.7	112.5	111	170.2	82.8	199.3	74.4	110.4	95.3
74	ND274×ND2009	209.1	144.7	363.5	254.1	123	110	277.3	118.9	341.4	108.6	132.9	126.1
75	A052×ND250	192.8	134.7	253.9	180.7	131	114.5	267.7	136.4	226.6	123.7	114.7	135.3
76	ND08-53×ND07-226	191.7	100.8	229.6	192.6	110	90.5	218.2	225.7	273.7	82.4	139.3	150.5
77	ND07-255×PHJ40	211.1	134.5	238.8	245.2	128.5	115	206.9	90.4	231.2	84.2	165.2	134.2
78	ND06-144×ND2006	174.1	101.6	212.4	177.4	112.5	123.5	242.6	82.3	214.6	74.2	114	126.9
79	ND291×ND2032	266.4	324.8	294.3	418.6	152	112.5	267.9	269.4	323.4	123.3	144.6	166
80	ND291×ND07-226	202.6	93	235.3	212.8	121.5	115	210.4	114.6	252.1	111.1	125.6	123
81	ND07-255×NK807	199.8	236.7	247.3	319.5	135	116.5	265	131.2	271.5	123.9	126.9	139.1
82	ND06-189×PHJ40	178.6	88.4	206.6	117.7	118	112.5	186.2	70.9	196.1	58	107	115.7
83	ND2014×LP05	244.3	298.6	233.5	355.2	165	130	281.1	95.2	279.9	77.5	143.8	138.5
84	LB2000×ND270	166.9	83.9	198.9	106.1	109	81	175.2	73.1	170.5	50.7	110.3	94.4
85	ND274×Il5	189.1	112.1	228.3	212	120.5	104	199.2	65.5	196.7	69.7	106	115.1
86	LB2000×ND2014	169	78	205.5	121.6	107	117	148.2	71.2	165.3	73.9	110.1	116.8
87	ND07-212×LP05	214.4	284.6	271.7	393	125.5	123	348.8	105.5	340.3	109.2	135	146
88	ND2019×AP47	244.1	281.2	238.8	342.5	164	115	335.5	100.4	344.7	110.5	159.9	146.2
89	LH61×ND270	252.7	203.3	331.2	294.9	134	137	312.8	170.6	353	196	96.5	110.3
90	ND2013×ND2009	389.4	369.7	378.2	522.6	163	117	427.3	173.8	449.2	159.8	219.4	175.3
91	ND06-189×LP05	238.5	182.4	252.9	264.9	201	110.5	376.4	99.9	336.4	103.2	122.9	128.7
92	ND07-255×LP05	319.7	335.5	321.7	400.3	140	130	392.1	143.3	413.5	147.2	157	153.4
93	ND2013×Il5	205.5	270.7	241	396.1	140.5	108	393	86.3	402.8	67.4	137.3	132.2
94	ND2019×Il5	209.6	138.9	225.5	275.4	136	109.5	311.1	70	335.4	73.6	124.3	126.5
95	**Thurston 77RM†**	170.3	73.5	194.3	93.2	111.5	108.5	140.6	60.4	149.6	57.5	106	112.2
96	**Pioneer 79RM**	166.6	47.4	204.1	103.6	114.5	113	151.1	71.7	150.7	63.1	118.1	114.9
97	**Pioneer 80RM**	170.1	67.9	190.3	123	113	109	160.2	59.4	183.2	45.4	104.5	113.6
98	**Thurston 82RM**	201.2	111.2	213.8	214.4	128	107	146.9	71	154.1	66.5	115.9	113.8
99	**Syngenta 85RM**	168.8	101.4	210.3	212.5	114	117.5	156.7	69.6	159.9	59.3	113	112.4
100	**Monsanto 88RM**	194.6	175	225.8	316.5	116.5	107	234.7	98.2	267.1	85	144.9	129.4
	Experimental Mean	213.3	176.9	243.3	245.5	128.9	114.9	247.6	109.6	263.1	97.3	132.4	129.3
	CV%	7.3	11.5	6.6	16.4	18.2	13	8.9	30.7	12.8	14.4	18	12.4
	LSD,0.05	30.8	40.4	22.6	56.3	32.8	21	43.7	66.7	47.2	19.7	33.3	22.5
	Error Variance	241.3	414.2	261.6	1616	548.2	224.1	484.3	1129.4	1137	197.1	566.3	257.1

† RM, relative maturity

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Table A2. Grain yield (Mg ha^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	2.1	.	1.8	.	.	1.9	6.4	1.9	4.6	1.8	0.6
2	ND2014×B104	.	3.9	.	.	.	.	1.1	9.2	1.9	10.1	6.5	6.6
3	GEM5Derived×ND2001	2.7	3.2	8.4	3.6	.	.	2.8	9.9	3.9	11.8	7.2	3.7
4	ND265×ND2001	3.7	3.3	6.2	2.7	.	.	1.7	6	2.3	10.6	3.2	1.5
5	AP49×ND246	1.3	0.3	3.8	.	.	.	1.6	6.9	2.9	8.5	3.6	2.5
6	ND274×ND2001	2.9	2.8	7.5	2.7	.	6.7	2.3	8.6	2.4	10.1	2.6	1.6
7	ND290×PHJ40	3.9	4.2	9.2	4.6	5.4	4.6	2.3	8.2	4.1	8.9	5.2	4.1
8	ND203×ND2005	3.4	3.1	8.3	2.7	5.3	5.3	1.8	5.4	3	6.7	2.8	2.4
9	AP49×ND290	3.7	2.4	7.4	3.6	5.6	9.1	1.9	9.9	2.8	11.6	7.1	6.7
10	NK779×ND2014	2.5	3.7	8.3	2.6	3.3	2.3	2.4	5.7	3.8	6.3	3	2
11	ND290×ND2032	4	4	9.1	3.4	4.9	5.9	1.9	5.9	3.6	6.6	6.2	4.4
12	ND203×ND2002	3.4	1.7	7.4	2.1	3.9	3.8	1.8	5.1	1.7	4	2.1	1.2
13	PHG47×ND246	3.7	3.5	7.8	4	1.8	4.5	1.8	8	3.2	5.9	1.6	1.3
14	AP49×ND06-85	3.6	2.5	10	2.3	5.9	5.1	2.5	8.8	2.3	10.7	7.4	2.1
15	ND290×ND07-226	3.8	3.4	9	3.4	2.8	3.4	2.8	7.1	2.9	7.5	3.1	3.4
16	NK779×ND2000	3.1	3.2	8.7	3.4	1.8	7.5	2.7	5.5	4.2	6	4.2	1
17	AP49×ND291	4.1	2.5	9.2	2.6	4.6	8.8	2.1	5.9	2.1	8.7	6.6	5.7
18	ND07-212×B104	4.3	2.8	6.3	3.5	6.6	7.8	2.3	9.8	3.6	11.6	8.2	10.5
19	ND2021×ND2009	3.5	1.7	8.5	1.1	6.1	5.7	2.2	7	1.9	11.1	7.8	6.5
20	NP2341×ND07-153	3.9	3.1	9.5	3	4.3	9.3	2.8	7.8	3.4	10	3.8	4.5
21	ND2013×B104	2.6	1.3	5.8	.	3.8	4.1	0.9	6.2	1.2	8.6	5.8	7.8
22	LH61×ND246	3.3	4.3	8.9	3.6	3.9	6.5	2	8.5	2.1	6	2.5	1.1
23	ND08-343×ND07-153	4.5	2.6	9.6	2.4	6.2	5.9	2.3	9.4	3.7	8	6.8	3.2
24	GEM5Derived×ND2002	4.6	3.2	8.7	3.5	4.6	4.7	3.2	5.3	3.3	8	4.8	2.4
25	ND06-189×NK807	3.8	4.7	10.2	4.3	5.5	4.7	2.4	11.3	4	9.9	6.5	1.6
26	ND2021×ND2005	3.7	2.2	9.2	2.4	4.7	7.3	2.5	7.5	3.6	9	6.1	4.5
27	NP2341×ND2000	4.9	3.2	9	3.6	3.8	10.8	2.7	8.5	4.1	9.5	4.9	2.4
28	ND06-144×ND2007	5.3	1.7	8.6	1.3	5.8	3	2.6	6.6	2.3	12.7	7.6	9.8
29	ND08-343×ND2002	4.5	2.3	9	2	7	3.8	3.1	9	3.7	10.6	7.7	3.5
30	NK779×ND2006	3.7	1.7	7.4	1.7	2.2	6.1	2.5	2.8	4.7	3	1.3	0.4
31	ND2019×B104	4.8	3.9	11.5	3.4	8.3	6.7	1.9	8.1	2.1	10.3	8.1	7.8
32	ND2021×KMN22	3.6	2.4	8.3	1.4	4.4	8.6	2.4	5.6	4.3	10.1	6.6	6
33	ND08-343×ND2007	3.4	0.8	8	0.8	6.7	3.5	1.9	6.3	2.5	8.7	8.7	7.3
34	PHG47×ND06-85	3.4	2.3	8.3	3.4	3.6	3	1.7	7.3	3	8.1	4.3	1.9
35	ND203×ND2004	3.3	3.3	8.3	3.5	3.9	7	2.3	7.4	2.5	6.7	0.3	1.9

Table A2. Grain yield (Mg ha^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	4.3	4	11.1	3.7	5.8	1.4	2	9.6	2.7	9.8	6.6	4.9
37	A052×ND246	3.8	3.1	7.4	3.4	3.4	8.5	1.8	7.2	3.1	5.1	1.4	0.6
38	A052×ND2000	5.3	4.2	10.4	3.1	5.2	3.6	3.3	7.4	4.2	12.5	7.8	3.1
39	NK779×ND250	2.8	2.2	7.2	2.3	2.8	6.1	2.7	5	3.4	3.5	1.9	1.3
40	NP2341×ND2006	3.7	3.1	8.8	2.8	4.5	8.1	2.7	5.1	3.8	8.9	4.5	3.6
41	ND2013×KMN22	3.9	1.4	9.2	1.8	2.9	5.9	1.9	8.8	2.8	10.1	7.4	6.4
42	ND07-97×ND07-153	4.9	2.3	9.1	1.5	5.8	6.1	1.4	7.2	2.6	7.4	4.9	5.6
43	ND06-144×ND07-153	3.7	2.6	9	2.2	6.4	8.6	3.2	8.5	4.4	9.5	6.2	4.5
44	ND2014×KMN22	4.7	3.1	10.8	2.1	3.4	6.4	1.6	7.6	3.1	12.1	6.3	6.9
45	LB2000×ND2000	4.2	4.1	10	3.8	4.1	3.6	3.1	6.4	5.3	6.1	5.9	4.2
46	ND265×ND2005	3.8	3.1	8.5	3	3.2	2.6	2.1	4.9	3.1	7.5	2.9	3.9
47	ND274×ND2005	3.8	3.6	7.3	3.8	2.2	5.4	1.9	8.9	3.3	6.5	3.1	3.8
48	ND08-53×NK807	4	2.7	8.1	2.2	3.5	6.8	2.2	9.7	3.2	10.1	3.5	1.7
49	ND06-144×ND2002	4.5	2.6	9.5	4	5.4	4.8	2.3	9	4.4	10.9	7.3	4.7
50	PHG47× D291	3.9	3.2	8.2	3.3	3.6	7.6	2.8	6.3	3	6.3	6.1	1.5
51	ND265×ND2009	3.3	2.9	9.6	2.5	2.5	2.9	1.3	6.4	2	7.8	3.6	2.5
52	LB2000× ND250	3.9	3.5	9.1	4	2.9	5.6	2.8	3.7	3.9	4.1	3.1	4
53	ND07-97×ND2007	4.5	1	7.5	.	6.3	10.4	0.8	8.4	1.4	7.7	7	5.6
54	ND2014×AP47	4.5	4.1	11.1	3.3	6.9	9.7	2.1	6.9	3.1	11.4	9.8	5
55	ND06-189×AP47	5.9	3.7	10.7	4.3	3.6	7.1	2	8.3	3	11.3	6.3	5.4
56	NP2341×ND2014	3.5	3	9.4	2.8	3.4	6.3	2.4	4.2	3.1	7.8	5.3	4.8
57	ND08-343×ND2004	5.5	2.3	10.2	2.5	4.5	5.7	2.3	9.5	2.9	8.1	5.5	6.5
58	ND265×ND2004	4.7	4.1	9.3	2.9	4.5	6.2	1.6	6.9	3.2	5.9	3.8	1.5
59	ND08-53×PHJ40	4	3.4	9.9	5.1	4.7	8.5	2	8.1	4.6	10.1	3.7	3
60	GEM5Derived×ND2007	4.1	3.6	10.4	2.7	9.6	5.1	1.9	11.5	3.1	11.3	8.8	9.9
61	LH61×ND250	3.6	3	9.6	3.5	2	8.4	1.8	5.7	2.7	6.5	5.1	3
62	ND2019×KMN22	4.9	4.1	10.4	3.7	6.6	2.8	2.2	9.6	3.2	9.9	6.7	5.8
63	LH61×ND06-85	3.7	3.4	8.7	3.8	5	7.1	1.8	7.2	2.4	5	1.8	1.5
64	GEM5 Derived×ND2004	4.8	3.6	10	3.4	3.5	6.6	2.9	8.1	3.9	8.6	5.2	4.2
65	ND07-97×ND2014	3.5	3.5	8	2.6	5	4.9	2.3	8.8	2.5	7.3	3.9	2.9
66	ND08-53×ND2032	4	2.1	7.8	2.9	5	2	1.6	4.6	2.3	7.8	5.7	5.1
67	PHG47×ND270	4.2	4	8.5	5.5	4.3	6.7	1.8	9.5	2.8	7.8	4	1.4
68	ND07-97×ND2006	4.1	3.1	9.4	2	3.5	4.7	1.9	6.4	2.9	8	4.3	3.9
69	ND07-255×ND07-226	3.4	2.7	8.5	3	4.9	4.8	1.8	3.9	3	4.9	3.9	3.6
70	ND07-212×NK807	3.3	2.2	9.4	3.9	7.2	9.1	2.5	9.9	3.9	10.8	5.7	4.5

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Table A2. Grain yield (Mg ha^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	5.2	3.9	9.5	2.9	5	9.2	2.1	7.1	3.2	10	7.2	7.4
72	ND07-212×AP47	5.3	4.2	11.3	4	5.1	2.6	2.7	9.7	3.2	10.7	7.5	5.2
73	A052×ND270	4.1	3.8	8.2	4.8	2.5	4	2.5	6.1	3.8	5	2.3	1.3
74	ND274×ND2009	3.8	2.9	8	2.9	4.7	6.9	1.9	9.7	1.7	10.6	5.4	2.8
75	A052×ND250	4.4	4.2	10.3	3.6	3.6	2.9	2.4	7.6	3.7	6.9	3.7	3.6
76	ND08-53×ND07-226	3.8	2.9	7.8	3.3	1.8	5.4	2.2	3.9	3.3	7.4	4.8	3.9
77	ND07-255×PHJ40	4.5	3.9	9.4	4.2	6.1	6.6	2.5	8.1	3.7	8.2	4.8	5.1
78	ND06-144×ND2006	5	4	9.4	3.6	3	6	2.5	6.2	3.3	7.6	5.5	3.7
79	ND291×ND2032	4.1	3.2	9.4	3.6	4.7	5.3	2.5	8	2.5	9.6	7.1	5.1
80	ND291×ND07-226	4.4	3.6	9.9	3.6	4.1	4.4	2.1	6	4.1	8.4	6.4	2.4
81	ND07-255×NK807	4.2	4.2	9.4	3.9	5.9	3.6	2.4	5.7	3.2	9.7	5.8	8.1
82	ND06-189×PHJ40	3.7	4.8	10.4	5.1	5.2	5.5	3	10	3.5	9.6	4.3	3.4
83	ND2014×LP05	4.2	2.6	9	2.5	4.9	2.8	2.1	9.7	3.9	12.9	10.6	8.2
84	LB2000×ND270	3.7	4	9.5	4.4	1.7	3.3	2.7	5	3.7	4.5	2.8	1.6
85	ND274×Il5	4.1	4.5	9.6	4.5	5.4	8.9	2.2	8.2	3.4	9.5	5.2	2.8
86	LB2000×ND2014	3.9	3.8	11.1	4.1	4.1	5.5	2.8	5.1	3.8	7.8	6.6	5.2
87	ND07-212×LP05	3.5	2.8	9.5	1.5	6.2	10.3	1.9	9.9	4.2	10.2	9.6	4.2
88	ND2019×AP47	5.5	3.9	11.3	4.3	7.6	3	1.5	10.5	2.9	9.8	7.5	7.1
89	LH61×ND270	3.4	2.4	6.8	4.4	3.7	10	1.6	7.6	1.6	5.9	1.5	1.2
90	ND2013×ND2009	3	2.8	7.2	1.1	5.1	7.3	1.1	6.5	1.9	9.8	8.1	9.8
91	ND06-189×LP05	4	3.6	11	3.5	5.2	9.3	1.2	9	3.3	12.1	7.9	2.4
92	ND07-255×LP05	3.7	2.3	10.4	2.6	6.1	11.8	2.2	10.2	2.4	7.6	9.5	9
93	ND2013×Il5	5	3	10	4.1	8.4	10.8	1.5	10.6	1.7	10	8.6	7.9
94	ND2019×Il5	4.9	4.3	10.6	5	6.4	5.3	1.9	9.1	2.1	7.5	9.5	3.2
95	**Thurston 77RM**	4.4	4.5	9.7	3.5	5.3	9.7	2.8	9.5	3.4	8.5	5.2	4.5
96	**Pioneer 79RM**	3.9	4.2	9.7	3.6	5.1	7	2.9	8.4	4.2	7.8	7.8	5.3
97	**Pioneer 80RM**	4.5	3.7	9.7	3.8	5.2	8.1	3.5	11.9	3.6	10.1	6	6.3
98	**Thurston 82RM**	4.6	3.3	9.8	3.8	8.6	11.1	2.2	7.8	2.8	7.2	8.6	6.2
99	**Syngenta 85RM**	5.3	3.6	12.2	4.3	6	12.2	2.5	11.3	3.1	10.8	6.9	5.8
100	**Monsanto 88RM**	5.9	4.7	13	5.3	7.6	10.7	2.8	7.9	4.9	10.4	10.7	9.8
	Experimental Mean	4	3.2	9.1	3.2	4.8	6.3	2.2	7.6	3.1	8.6	5.5	4.3
	CV%	15.1	16.4	13	21.9	32.5	27.9	20.1	20.8	21.5	18.9	25.2	32.2
	LSD,0.05	1.2	1	1.6	1	2.2	2.4	0.9	3.1	0.9	2.3	1.9	1.9
	MSE	0.4	0.3	1.4	0.5	2.4	3	0.2	2.5	0.5	2.6	1.9	1.9

Table A3. Grain Test weight (Kg hl^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	69.6	.	69.3	.	.	57.5	73	58.8	71.9	37.5	.
2	ND2014×B104	.	67.5	.	62.1	.	.	52.8	72.8	47.4	71.5	69.4	69.9
3	GEM5Derived×ND2001	72.6	68.1	73.7	67.8	.	.	61.2	71.2	60.8	70.8	72.9	58.6
4	ND265×ND2001	72.9	71.8	76.5	71.2	.	.	60.4	74	55	72.7	53.8	39.3
5	AP49×ND246	.	70.1	63.9	66	.	.	57	69.8	56.2	73.3	56.3	54.4
6	ND274×ND2001	72.2	69.4	70	69.7	.	82.2	59.9	73	58	72.3	66.6	34.9
7	ND290×PHJ40	69.2	73.2	75.8	74	67.6	75.3	65	74.4	62.4	74	70.4	62
8	ND203×ND2005	75.3	72.2	74.5	72.2	73.4	82.5	64.8	73.4	64.7	73.9	52.2	37.4
9	AP49×ND290	.	72.6	74.5	73.4	69	85.5	62.9	74.9	64.9	75.2	77.3	79.4
10	NK779×ND2014	54.4	69.1	75.6	70	57.6	57.9	66.6	74.4	62.7	72.1	52.4	41.2
11	ND290×ND2032	79.2	75.1	71	73.4	79	65.7	66.1	76.4	66.1	76.3	79.6	79.4
12	ND203×ND2002	.	70.3	69.2	69.4	70.7	78.5	59.9	71.1	58.6	70.3	46.9	40.9
13	PHG47×ND246	67.7	69	69.5	69.7	42.9	.	56.1	71.1	54.7	68.6	44.7	52.4
14	AP49×ND06-85	69.4	68.6	70.7	67.5	73.2	59.6	63.7	71.7	62.5	71.8	75.7	46.8
15	ND290×ND07-226	71.6	70.9	74.6	72	57.7	68.1	68.4	73.1	67.1	72.7	59	72.4
16	NK779×ND2000	70.4	69.6	76.4	70.6	35.3	61.6	65.9	73.5	64.1	73.3	63.6	36.6
17	AP49×ND291	.	68.8	69.4	68.4	63.8	79.9	60.6	73	59.5	72.5	75.8	77.9
18	ND07-212×B104	57.3	64	59.4	61.9	70.8	74.2	57	71.7	51.9	73.3	72.1	71.8
19	ND2021×ND2009	66.9	66	74.1	66.5	72.4	76	60.4	68.5	59.4	69.3	74	72.1
20	NP2341×ND07-153	70.6	70.9	74	70	55.8	64.8	61.5	73.7	60.2	72.4	64.8	76.2
21	ND2013×B104	70	59.9	56	60.3	68.3	61.5	42.6	64	43.9	65.1	64.9	67.2
22	LH61×ND246	71.9	70.1	76.6	69.7	71.6	77.7	53.7	72.2	49.7	71	45.4	43.9
23	ND08-343×ND07-153		70.6	72.3	69.7	76.5	77.3	64.4	75.6	63.3	73.4	77.1	69.4
24	GEM5Derived×ND2002	71	70.6	71.2	70	73.7	76.7	63.5	70.6	62.9	70	74.9	52.8
25	ND06-189×NK807	66.9	72	74.6	70.4	76.3	79.1	61	72.6	61	72.1	75.6	37.8
26	ND2021×ND2005	72.8	70.7	76.5	70.3	74.5	62	63.4	73.1	62.5	72.7	73.7	74.4
27	NP2341×ND2000	73.9	72.6	72.8	72.5	56.9	77.3	64.7	74.7	61.1	73.1	76	49.3
28	ND06-144×ND2007	.	66.9	61.5	66.3	73	76	60.5	72.2	61.2	72.1	71.1	73.2
29	ND08-343×ND2002	.	70.4	74	70	73	78.5	66.3	74.3	64.6	73.7	76.9	69.3
30	NK779×ND2006	.	64.4	70.8	64.7	38.4	74.8	63.3	72.2	62.4	72.1	29.1	.
31	ND2019×B104	74.5	68.9	72.8	66.8	74.9	75.2	54.7	68.4	56.9	68.8	69.6	69.4
32	ND2021×KMN22	77.2	73.8	75.1	73.1	75.3	82.1	62.2	71.5	63.5	72.2	75.7	78.6
33	ND08-343×ND2007	67.2	66.5	60.4	65	73	72.8	60.5	69.6	58.5	72.1	73.8	74.3
34	PHG47×ND06-85	70.5	68.7	67.5	69.7	61.6	77.6	60.8	71.5	60.5	69.9	74.9	50.2
35	ND203×ND2004	.	70.3	70.1	69.8	68.5	79	58.8	73.2	56.2	70.8	.	45.1

Table A3. Grain Test weight (Kg hl^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	73.2	70.3	74.8	67.5	78.3	79.5	63.3	74.3	63.8	73.6	71.3	74.1
37	A052×ND246	61.1	68.5	70.7	68.7	52.1	55.6	60.9	71.3	59.3	69.3	41.5	.
38	A052×ND2000	74.9	72.2	73.9	71.6	74.8	80.5	65.7	73.7	63.1	72.9	77	69.8
39	NK779×ND250	.	72.6	75.5	73.7	52.9	72.1	66.8	75.5	64.7	73.9	32.7	35.9
40	NP2341×ND2006	70.3	68.8	69	68.1	71.7	76.5	60.1	74.1	59.2	71.1	74.3	67.9
41	ND2013×KMN22	70.2	70.8	78.8	68.1	62.5	77.3	58.6	70.2	56.2	68	76.9	73.5
42	ND07-97×ND07-153	68.3	70.3	68.7	66.2	73.5	72.9	56.4	71.8	54	70.4	75.5	75.9
43	ND06-144×ND07-153	75	73.7	68.2	72.8	77.3	74.3	66.5	76.5	64.5	75.9	77.5	78.2
44	ND2014×KMN22	79.7	74.3	72.6	73.8	61.4	83.3	64.4	74.6	65.1	74.4	78.7	78.7
45	LB2000×ND2000	75.9	71	75.9	73.2	72.4	81.6	66.1	74.8	61.7	71.8	77.8	67.3
46	ND265×ND2005	.	71.5	76	70.3	61.1	69.1	63.4	73.6	62.9	73.1	52.8	56.8
47	ND274×ND2005	75.8	70.7	74.9	71.3	37.8	64.8	65.2	74.7	65.5	73.4	58.2	69.1
48	ND08-53×NK807	74.8	72.8	73.3	74.1	65	79.8	65.8	75.9	64.1	75.2	58.7	29.9
49	ND06-144×ND2002	69.7	72	72.6	70.6	76.3	83.1	65.8	77	66.2	76.2	80.1	79.3
50	PHG47× D291	71.7	69.7	65.7	69.2	70.8	78.9	65.2	72.2	62.3	71.9	76.1	42.8
51	ND265×ND2009	60.9	70	66.9	65.6	61.1	72.8	59.9	70.3	58.4	71.5	60.7	45.6
52	LB2000× ND250	50.4	74.9	76.3	74.4	53	.	69.1	77.9	68.2	76.1	50.1	70.4
53	ND07-97×ND2007	64.8	60.8	61.9	63.8	71	68.9	42.4	68.5	46.4	65	70.8	70.3
54	ND2014×AP47	75.1	71.7	70.3	70.1	74.8	80.2	60.2	73.7	57.3	71.7	75	72.8
55	ND06-189×AP47	74.8	70.5	72.5	69.8	55.8	78.9	58	69.6	57.6	69.1	73	74.5
56	NP2341×ND2014	63.1	72.7	73.9	73.5	67.5	80.5	63.7	73.4	62	73.4	76.6	80.1
57	ND08-343×ND2004	73.2	70.9	69.7	69.5	56.3	81	61.6	74.1	59.3	71.7	78.8	77.9
58	ND265×ND2004	74.2	72.4	72.1	72.3	71.3	80.4	62.6	74.4	57.8	73.4	68	34.9
59	ND08-53×PHJ40	72.8	71.8	79.6	72.8	55.5	84.4	66.3	75	66.6	73.5	61.3	56.3
60	GEM5Derived×ND2007	71.8	68.6	66.9	66.6	72.6	73.2	60.5	72.3	57.1	71.3	75.1	73.6
61	LH61×ND250	72.7	71.1	71.9	69.6	43	62.4	59.6	74.3	59.4	73.9	74.4	57.8
62	ND2019×KMN22	76.5	72.2	74.2	71.5	75	83.9	59.4	73.4	60.3	71.6	77.6	76.5
63	LH61×ND06-85	70.9	71.9	69.1	70	67.9	47.8	60.8	72.2	59.9	72.1	36.3	38.2
64	GEM5 Derived×ND2004	73.4	69	79	70.3	58.7	83.5	62.5	73	59.3	70.9	75.9	64.5
65	ND07-97×ND2014	77.2	74.4	68.8	71.9	76.4	85	60.6	75.4	59.6	73.4	66.1	58.4
66	ND08-53×ND2032	79.4	72.8	76.1	72.5	75	72.3	61.5	76.1	63.9	77.4	80.8	73.3
67	PHG47×ND270	70.9	68.5	68	69.3	72	69.1	58.6	69.1	58.7	68.1	56.9	36.4
68	ND07-97×ND2006	74.4	68.2	71.2	68.7	63.2	80	53.1	71.5	53.3	71.1	72.6	72.8
69	ND07-255×ND07-226		70.7	73.7	69.9	73.3	71.7	63.3	73	61.9	71.8	71.2	69.4
70	ND07-212×NK807	76	71.3	71	70	74.1	77	65.1	74.7	61.7	73.7	79.6	77.3

Table A3. Grain Test weight (Kg hl^{-1}) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	72.7	71.1	74.4	69.3	72.8	77.5	63.7	70.5	62.1	70.5	74.7	75.3
72	ND07-212×AP47	76.3	71.9	78.4	71.9	63.8	79	60.6	71.5	56.8	72.6	72.8	75.3
73	A052×ND270	69.3	68.7	72.8	70.6	46.9	52.5	60.5	68.1	60.3	69.1	42.2	28
74	ND274×ND2009	60.9	66.2	69.1	66.3	74.2	78.8	53.9	68.9	53.9	67.3	72.6	52.9
75	A052×ND250	74	71	70.4	71.6	69.5	82.2	62.6	73.2	62.6	72.2	68.5	76.4
76	ND08-53×ND07-226	75.1	71.9	73.2	70.9	36.2	.	68.9	73.6	67.5	74.7	75.6	61.8
77	ND07-255×PHJ40	72.9	70.7	67.9	71.2	76.4	79.9	61.3	74.4	55.2	72.9	72.1	71.1
78	ND06-144×ND2006	71.5	71.6	71.6	72.8	63.3	81	64.8	77.7	64.9	76.9	78.8	71.6
79	ND291×ND2032	67	68.8	68	67.8	63.5	82.8	65.3	76.4	60.3	75.7	79.7	75.2
80	ND291×ND07-226	73.6	70.3	70.9	70.3	71.4	79.4	63.7	73.7	64.5	73.5	77.4	47.4
81	ND07-255×NK807	71.9	71.3	73.8	70.9	76.2	71	61.9	73.4	59.6	72.5	75.6	76.8
82	ND06-189×PHJ40	76.1	68	73.1	70.3	76.7	75.2	60.6	70.6	59.6	70.2	68.6	54
83	ND2014×LP05	72	72.3	73.5	70.3	73.1	74.3	65.9	75	65.2	75.7	77.6	78.3
84	LB2000×ND270	64.7	71	76.6	71	42	.	63.5	73.7	62.7	73.6	52.1	25.6
85	ND274×Il5	57.9	68.3	71.4	68.8	74.3	56.5	61	70.8	59.7	70.1	77	43.9
86	LB2000×ND2014	68.7	71.4	76.1	72.2	68.3	83.4	63.3	73.7	58.9	71.6	75.8	65.2
87	ND07-212×LP05	.	71.8	76	69.4	74.5	68.4	59.8	73.5	56.4	72	77.7	78.1
88	ND2019×AP47	73.8	69.2	77.2	68.2	75.2	79.1	55.3	70.3	56.6	69.4	69.9	72.4
89	LH61×ND270	70.1	69	65.5	69.7	62.6	77.2	53.3	71.1	53.5	71	29.7	35.1
90	ND2013×ND2009	70.9	64.9	60.2	60.7	69.5	72.2	49	66	48.4	65.4	72.2	68.3
91	ND06-189×LP05	66.9	67.3	67.9	67.4	68.4	75.3	53.7	69.8	55.1	69.3	73.2	47.3
92	ND07-255×LP05	66.1	68.4	71	68.4	70.9	78	57.2	70.7	56.5	69.9	74.8	73.8
93	ND2013×Il5	68.7	67.1	66.4	65.6	73.1	77.9	47.4	68.9	44.7	67.6	71.3	71.9
94	ND2019×Il5	67.3	68.3	68.8	66.9	73.4	80.2	54.9	71.3	50.1	68.2	76	63.1
95	**Thurston 77RM**	72.8	68.4	71.8	70.1	74.8	80.4	64.9	72.4	60	70.4	76.1	64.1
96	**Pioneer 79RM**	73.7	69.6	71.9	69.1	75.9	81.7	60.2	71.3	56.7	69.1	74.7	77.8
97	**Pioneer 80RM**	67.8	67.2	71.8	68.7	72.4	75.8	58.3	70.5	54	67.6	72.9	75.2
98	**Thurston 82RM**	70	64.3	67.7	64.7	72	76.8	51.8	65.4	51.3	61.6	72.2	72.8
99	**Syngenta 85RM**	62.5	67.8	69.6	67.5	74.4	77	55.2	68.5	54	66	73.5	75.8
100	**Monsanto 88RM**	68.9	66.9	.	65.3	71.3	74.5	56.2	68.6	57.2	67.3	74.7	70.1
	Experimental Mean	70.6	69.9	71.5	69.4	66.9	75	60.7	72.5	59.3	71.6	68.1	62.5
	CV%	8.1	1.4	4.7	1.8	15.7	10.3	2.6	1.7	2.9	1.5	13	19.1
	LSD,0.05	11.4	1.9	4.7	1.7	14.7	10.8	3.1	2.4	2.4	1.5	12.4	16.7
	MSE	33	0.9	11.3	1.5	110.9	59.7	2.5	1.5	3	1.1	78.8	143

Table A4. Root lodging (%) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	64.5	.	69.6	.	.	5	-0.1	6.2	0	0.5	0
2	ND2014×B104	.	-0.4	.	11.3	.	.	2.3	-0.5	0.8	0	4.6	0
3	GEM5Derived×ND2001	0	15.2	-0.2	10	.	.	0	0.1	0	0	3.1	0
4	ND265×ND2001	7.3	60	1.1	47.9	.	.	2	0.1	1.6	0	0.5	0
5	AP49×ND246	14.6	49.1	13.9	61.9	.	.	5.2	0.1	1	0	4.8	0
6	ND274×ND2001	0	0	-0.6	0.7	.	8.2	1	0.2	0	0	-1	0
7	ND290×PHJ40	0	1.8	-0.1	1.5	1.3	16.4	1	0.1	0.8	0	2.8	0
8	ND203×ND2005	2.9	75.1	-0.6	66.9	6.3	14	11	14.4	10.9	2.9	19	12.5
9	AP49×ND290	0	8.3	-0.5	3.1	0	19	0	0	0	0	-1.6	0
10	NK779×ND2014	0	9.6	0.5	0.2	1.3	32.9	1.9	1.6	0	0	-1.4	0
11	ND290×ND2032	0	2.1	-0.4	9.6	1.4	25.1	0	2.8	0	0	0.9	0
12	ND203×ND2002	6.3	64.7	-0.1	58.6	4.2	75.2	0	1.4	3.9	0	-1.3	55.4
13	PHG47×ND246	0	40.5	0.2	38.2	4.5	44.6	0	0.1	0	0	2.4	0
14	AP49×ND06-85	0	36.3	-0.1	20.1	4.8	64.3	0	0.1	1	0	-0.4	0
15	ND290×ND07-226	1.7	11.2	0.7	1.3	0	40.9	0	0.1	0	1.9	0.7	0
16	NK779×ND2000	0	4	-0.2	-1.1	0	70	0	0.2	0.9	0	-0.6	0
17	AP49×ND291	0.9	14.7	-0.1	20.4	1.6	47.1	0	0.2	0	0	1	0
18	ND07-212×B104	7.5	8.7	2.9	9.8	17.9	24.4	0	0.1	1	0	6.3	0
19	ND2021×ND2009	0	0.8	-0.1	1.2	2.2	40.6	0	0	0	0	-1.2	0
20	NP2341×ND07-153	3.3	9.2	0	1.7	0	20.4	0	1.5	0	0	5.1	7.6
21	ND2013×B104	0	0.6	1.6	4	3.7	15.4	0	-0.2	0	0	1.8	0
22	LH61×ND246	0	63.2	0	64.9	5.6	22.7	9.3	0.7	10.2	1.4	2.2	6.3
23	ND08-343×ND07-153	0	-0.5	0.3	2.3	3.1	10.8	0	0	0	0	3.6	0
24	GEM5Derived×ND2002	2.7	40.4	0.1	21.2	4.2	35.5	0	2.3	4.5	0	0.5	0
25	ND06-189×NK807	0	13.2	0.9	0.9	0	20.1	0	0	0.9	0	4.1	0
26	ND2021×ND2005	0.9	24.3	0	13.5	1.2	38.1	0	0.1	1	0	0.3	0
27	NP2341×ND2000	0	32.7	-0.4	1.8	5.6	31.4	0	0	0	0	1.8	0
28	ND06-144×ND2007	0	50.5	0.9	36.1	0	23.8	0	-0.1	0	0	14.1	0
29	ND08-343×ND2002	3	10.1	0.1	12.6	7.4	28	1.1	-0.1	0	0	7.1	0
30	NK779×ND2006	0	5.1	0.8	3	0	22.2	1	2.3	0	0	-0.1	0
31	ND2019×B104	0.9	19.5	2.6	11.5	0	42.3	0	-0.1	0	0	15	0
32	ND2021×KMN22	0	3.1	0.8	7.6	0	4	0	5.3	0	0	-1.7	0
33	ND08-343×ND2007	17.3	34.3	2.6	13.7	9.1	5.7	0	1.8	0	0	12.1	0
34	PHG47×ND06-85	7.3	11.5	0.3	19.8	0	69.2	1.4	2	0	0	-0.8	0
35	ND203×ND2004	0	16.5	0.6	24.5	0	42.6	3.8	0.1	0.7	1.7	0.2	0

Table A4. Root lodging (%) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	0	45.7	0.2	13	11.7	33.2	0	0.2	0	1.4	27.3	0
37	A052×ND246	0	26.6	8.2	9	0	85.3	4.4	0.1	1	0	0.5	0
38	A052×ND2000	0	2.2	0.1	-1.2	5.4	21.4	0	2	0	0	-1.5	5.8
39	NK779×ND250	0	3.4	0.3	0.3	0	17.8	0	0	0	6.3	-1.6	0
40	NP2341×ND2006	0	8.4	0.4	15.5	0	31.8	0	0	0	0	2.2	0
41	ND2013×KMN22	0	0.2	0.9	-0.4	2.4	9.8	1	1.6	0	0	1.3	0
42	ND07-97×ND07-153	0	4.2	0.3	-1	0	21	0	-0.5	0.9	0	-0.9	0
43	ND06-144×ND07-153	0	1.6	0.6	6.8	2	7.7	0	0.1	0	0	1.6	0
44	ND2014×KMN22	0	8.5	0.3	11.6	0	40	0	0.1	0.8	0	-0.1	0
45	LB2000×ND2000	0	-0.4	0.6	-2.1	0	2.2	0	0.1	0	0	6.3	0
46	ND265×ND2005	2.8	67.5	1.8	29.4	5.8	53.5	0	2.2	5.1	2.9	9.8	6.5
47	ND274×ND2005	0	0.9	-0.2	-2.5	1.3	28	0	0.1	0	1.8	1.3	0
48	ND08-53×NK807	0	15.6	6	10.9	0	27.6	0	0	0	0	1.9	0
49	ND06-144×ND2002	0	6.3	2.2	-0.7	1.5	44	0	4.6	0	0	5.1	0
50	PHG47× D291	0	8	0.8	-0.2	2.8	45.7	0	0	0	0	-0.7	0
51	ND265×ND2009	1	17.6	-0.5	16	0	50.5	0	-0.2	0	0	6.9	0
52	LB2000× ND250	0	6.5	-0.2	-1.6	0	48.9	0	-0.6	0	0	1.2	0
53	ND07-97×ND2007	0	28.4	3.9	29.4	9.2	18.2	0	0	2.8	0	3.6	0
54	ND2014×AP47	0	7.5	2.1	6.2	1.6	26.4	0	1.6	0	0	2	0
55	ND06-189×AP47	0	1.7	0.1	4.2	0	4.4	1.1	-0.1	0	0	1.8	0
56	NP2341×ND2014	0	12.7	1.4	12	2	46.1	0	1.8	0	0	1.8	0
57	ND08-343×ND2004	0	-1	-0.7	-2.5	0	11.9	1.1	0	0	0	2.1	0
58	ND265×ND2004	5.3	5.3	-0.3	-0.4	2.7	32.9	1	-0.1	0	0	0.1	0
59	ND08-53×PHJ40	0	20	-0.2	5.2	1.3	45.7	0	-0.2	0	0	8.7	0
60	GEM5Derived×ND2007	3.6	14.9	0.9	8.3	0	47.5	0	-0.1	0.8	0	11.7	0
61	LH61×ND250	0	17	1.1	5.5	1.4	10.1	0	-0.1	0	0	2.9	0
62	ND2019×KMN22	0	11.3	0	6.9	2.3	21.6	2.2	-0.5	0	0	6.4	0
63	LH61×ND06-85	0	37.8	0.3	33.7	5	63.7	0	0	0	0	3.3	0
64	GEM 5 Derived×ND2004	0	12.9	0	0.5	0	19.4	0	0	0	0	1.6	0
65	ND07-97×ND2014	0	-1.1	0.3	2.4	0	3.5	1.2	0	0.7	0	3.9	0
66	ND08-53×ND2032	5.9	26.7	-0.1	22.6	5.8	45.7	6.2	0.1	1.6	0	9.1	0
67	PHG47×ND270	0	-1.6	-0.5	0.8	0	56	1.1	0.1	0	0	2.9	0
68	ND07-97×ND2006	0	5.8	-0.1	3.6	0	16.2	0	0	0	0	11.2	0
69	ND07-255×ND07-226	0.8	13.5	0	7.9	4.9	86.2	0	1.9	0.7	0	7.7	0
70	ND07-212×NK807	33.9	41.8	0.6	2.1	0	56	2	1.6	1.5	1.2	12	19.5

Table A4. Root lodging (%) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	0	5.3	-0.3	8.7	0	24.3	0	2.2	0	1.4	1.5	0
72	ND07-212×AP47	1.7	14.4	-0.1	3.8	0	43.4	0	25.7	0	0	21.3	0
73	A052×ND270	0	1.6	0.2	3.8	0	23.3	0	0.5	0	0	0.7	0
74	ND274×ND2009	0	13.9	0	4	0	77.4	0	0.5	0	0	-1	0
75	A052×ND250	0	1	0.3	5.3	0	0	0.9	0.5	0	0	0.1	0
76	ND08-53×ND07-226	0	20.2	0.9	20.2	0	83.5	0	0.5	0	0	10.8	0
77	ND07-255×PHJ40	0	6.1	-0.5	-0.1	0	22.1	1.1	0.5	0.9	0	7.4	0
78	ND06-144×ND2006	0	5.4	-0.2	9.1	0	21.7	0	0.4	0	0	-0.3	0
79	ND291×ND2032	0	25	0	4.7	4.2	44.1	0	0.3	0	1.2	0.6	0
80	ND291×ND07-226	0	4.9	0.1	1	0	58.1	0	0.4	1	0	-1.6	0
81	ND07-255×NK807	0	7.5	3.1	8.8	1.4	38.2	0	-0.2	0	0	5.3	0
82	ND06-189×PHJ40	0	7.8	2.9	2.7	0	41.9	0	-0.6	0	0	-3.2	0
83	ND2014×LP05	13.8	11.6	11.5	27.2	28.7	54.8	0	0	6.2	2.3	40.6	0
84	LB2000×ND270	0	3.7	0.3	1.5	3.2	67.7	0	0	2.9	0	-2.3	0
85	ND274×Il5	0	1.1	0.7	3.1	0	21.7	0	0	0	1.3	-1.3	0
86	LB2000×ND2014	0	0.9	0.3	0.6	0	42.3	0	0.1	0	0	-1.4	0
87	ND07-212×LP05	23.3	51.3	7.6	38.8	4.6	51.7	0	0	7.1	0	19.6	0
88	ND2019×AP47	0	11.6	0.2	1.2	0	45.9	0	1.6	0	0	2	0
89	LH61×ND270	4.3	45.7	0.4	4.1	1.9	5.2	1.1	-0.1	9.3	0	-3.1	0
90	ND2013×ND2009	0	3.8	0.5	5.6	0	48.1	0	-0.1	0	0	-2.9	0
91	ND06-189×LP05	0	3.4	-0.1	0.5	13.9	21.6	0	2.6	0	0	1.6	0
92	ND07-255×LP05	15.3	10.8	0.1	-1.4	2.8	19.4	0.9	-0.5	0	0	14.3	0
93	ND2013×Il5	0	8.8	0.4	1.1	0	2.8	0	0.1	0	0	3.3	0
94	ND2019×Il5	2.6	48.3	6	2.2	0	1.8	0	1.4	0	0	2.5	0
95	**Thurston 77RM**	0	4.5	0.5	-0.4	0	0	0	0	0	0	1.3	0
96	**Pioneer 79RM**	0	47	0.1	4.9	0	2.6	1	1.6	0	2.9	4	0
97	**Pioneer 80RM**	0	0.3	-0.3	10.4	1.3	11.4	0	3.2	0	2.4	1.6	0
98	**Thurston 82RM**	0	-1.3	0	-0.2	0	13.6	0	0	0.8	0	-0.4	0
99	**Syngenta 85RM**	0	9.7	0.1	2.4	0	11	0	-0.1	0.7	0	-0.5	0
100	**Monsanto 88RM**	0	1.7	0.3	0.5	1.3	13.9	0	1.9	0	0	-0.3	0
	Experimental Mean	1.9	16.5	0.9	11	2.3	32.1	0.7	0.9	0.9	0.3	3.8	1.1
	CV%	255.9	83.3	255.9	90.7	188.5	69.9	349	423.1	321.4	405.8	138.3	354.1
	LSD,0.05	9.9	27.3	3.4	13.9	6.1	31.4	5	7.9	4.1	1.9	7.3	5.6
	MSE	24.8	189.5	5.9	98.8	19	503.5	6.4	16	8.4	1.8	27.4	16.2

Table A5. Stalk lodging (%) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	25	.	9.2	.	.	16.4	9.5	15	40.6	56.8	49.9
2	ND2014×B104	.	0	.	-0.7	.	.	4.9	5.4	6.8	4.1	12.3	60.4
3	GEM5Derived×ND2001	0	13	3.4	7	.	.	7.8	5.1	11.3	7.6	2.3	81.3
4	ND265×ND2001	3.2	28.1	33.7	8.1	.	.	27.9	9.8	26.3	9.1	24.7	91.2
5	AP49×ND246	3.5	4.1	5.4	17	.	.	47.2	9.4	30	7.9	64.1	99
6	ND274×ND2001	19.2	20.7	1.6	19.8	.	13.5	48.5	8.1	27.6	6.9	7.4	91.1
7	ND290×PHJ40	0	9.1	-1.4	7.5	2.7	0	9.4	4.7	6.5	8.7	3.4	46.5
8	ND203×ND2005	3.6	11.3	-0.7	4.1	30.2	50	38.3	1.7	20.4	9.3	8.3	70.2
9	AP49×ND290	3.4	21.3	3.4	3.9	44	9.3	5.7	4	3	3	22.8	28.1
10	NK779×ND2014	0.9	42.4	11.5	52.8	17.2	8.9	17.3	7.1	13.8	24.7	10.4	90.3
11	ND290×ND2032	0	4.2	1.4	0.4	3.8	11.2	3.5	4.8	9.8	-1.6	0	57
12	ND203×ND2002	19.2	18.2	10.9	41.2	32.3	2.5	58.1	11.4	90.9	39.2	91.4	43.5
13	PHG47×ND246	12.7	51.6	15.3	44.1	92.3	3.2	22.1	11.7	18.5	16.1	43.3	96.7
14	AP49×ND06-85	4.1	7	8.2	6.9	17.8	0.5	12.7	6.1	15.9	-2.4	6.8	85.9
15	ND290×ND07-226	1.9	24.4	4.8	32	27.6	8.1	9.3	16.8	7.2	27	3.3	51
16	NK779×ND2000	8	18.8	4.5	26.4	47.9	0.5	5.8	6	14.9	18.6	1.3	97.1
17	AP49×ND291	3.8	8	7.6	7.2	14.9	0	13.2	9	19.4	24.5	24.3	84
18	ND07-212×B104	0	1.5	7.8	1.2	36.5	49.3	0	4.4	5	-0.3	3.8	53.5
19	ND2021×ND2009	0	0	1.7	4.8	12.8	7.6	12.4	3.9	10.7	2.3	8.3	90.2
20	NP2341×ND07-153	0	3.8	0.4	3.4	41.9	4.6	5.9	1.4	6.1	18.1	5.9	69.1
21	ND2013×B104	0.8	2.9	0.7	9.5	29.7	6.2	4.5	0	2.5	-0.3	0	25.5
22	LH61×ND246	0	11.5	8.5	11.3	18.2	28	9.5	10.3	25.6	20.5	49.6	86.7
23	ND08-343×ND07-153	2.7	7.9	4.1	2.3	9.2	19.4	27.2	3.1	17.5	6	7.4	95.8
24	GEM5Derived×ND2002	0	10.2	1.5	18.4	16.7	23.7	15.8	8	17.5	8.8	4.1	85.7
25	ND06-189×NK807	8.1	5	1.8	4.1	12.8	24.8	20.6	7.1	12.4	6.4	6.3	94.3
26	ND2021×ND2005	0	2.7	0.4	7.9	3.6	15.8	3.1	3.1	12.2	2.8	1.3	88.9
27	NP2341×ND2000	0	3.5	-0.4	1.8	17.5	16.2	5.1	1	6.7	2.6	10.5	97.5
28	ND06-144×ND2007	0	0	1.7	2.4	6.1	64.3	4.1	3	7.1	5.8	4.3	77.2
29	ND08-343×ND2002	1.1	10	4.9	8.9	11.1	51.7	14.3	3.7	16.8	1.1	3.5	82.9
30	NK779×ND2006	1.8	49.3	3.1	52.6	3.4	6.3	18.2	1.7	6.9	38	12.9	78.3
31	ND2019×B104	5.1	3.8	3.9	2.1	3.7	23.8	5.4	6.3	12.7	-2	16.3	60.4
32	ND2021×KMN22	0	7.1	0.8	7.9	1.5	14.3	2.9	4.5	6.8	-1.8	2.5	73
33	ND08-343×ND2007	0	0	6.1	3.2	27.3	39.9	5.6	6.7	23.8	3.1	2.6	80.1
34	PHG47×ND06-85	6.4	24.7	3.4	18.4	11.4	3.5	22.9	14.7	13.3	9.2	6.6	91.8
35	ND203×ND2004	5.3	32.3	9.5	21.3	31.6	16.3	31	14.9	48.3	22.8	91.7	99.9

Table A5. Stalk lodging (%) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	1	6.2	0.6	4.1	15.8	20	11.2	4	16.7	1.1	11.4	49.2
37	A052×ND246	6.2	18.4	7.8	46	62.6	0.2	64.1	18.7	61.3	44	74.9	98.4
38	A052×ND2000	11.5	8.5	3.7	10.6	22.1	29.2	8.8	7.8	18.9	4.5	1.1	79.5
39	NK779×ND250	0	49.4	0.6	34.4	17	0	7.8	18.1	10.9	48	5.9	87.4
40	NP2341×ND2006	0	0	2.2	8.6	0	19.2	9.8	0	18.7	0.5	3.7	49.2
41	ND2013×KMN22	0	0.4	0.8	-0.8	2.6	-1.8	6.7	15.5	5.1	-0.1	0	20.8
42	ND07-97×ND07-153	0	1.5	2.3	0.8	1.5	4.1	14.1	0	9	4	5.9	67.3
43	ND06-144×ND07-153	0	0	1.1	14.3	17.1	3.5	3.4	2.7	5.7	1	1.4	56.4
44	ND2014×KMN22	0	2.4	1.2	1.6	26.3	27.1	2.1	0	5.5	2.8	0	70.9
45	LB2000×ND2000	0	16.3	5.9	24.1	1.3	13	1.1	0	7.9	7	22.3	68.4
46	ND265×ND2005	8.3	2.7	3.9	8.2	14.6	3.9	7.5	8	7.7	3.4	10.9	87.3
47	ND274×ND2005	6.1	6.8	7.8	11.3	29.5	12.5	18.2	3.8	11.6	3.8	0	38.5
48	ND08-53×NK807	1.9	0	0	5.9	64.7	33.1	34.5	4.2	16.9	6.6	24.7	91.1
49	ND06-144×ND2002	0	1.2	0.1	8.1	18.3	16.3	17.8	1.7	36.3	1.6	6.1	94.6
50	PHG47× D291	4.8	16.8	-0.2	14.5	24	10.7	6.4	11.7	18.1	14.5	9.3	87.3
51	ND265×ND2009	19.2	21.9	8.9	7.9	82.6	16.6	54	22.2	27.3	16.3	41.7	97.6
52	LB2000× ND250	0	21.7	0.9	14.1	2.9	8.9	4.2	4.9	8.8	11.4	1.4	60.9
53	ND07-97×ND2007	0	0	2.7	0.1	21.2	32.9	-0.6	0	12.9	0.7	2.4	72.1
54	ND2014×AP47	4.9	1.3	5.6	3	8.2	11.7	11.6	8	1.9	7.4	6.1	78.4
55	ND06-189×AP47	0	15.1	3.9	4.2	60.2	32.3	5.2	3.1	2.8	1.4	14.1	62
56	NP2341×ND2014	2.6	2.9	-0.1	2.5	18.4	12.3	21.9	0	7.3	5	14	72.2
57	ND08-343×ND2004	0	3.9	6.5	12.4	57.4	0.4	19.7	0	13.7	3.5	8.5	54.5
58	ND265×ND2004	3.6	19.7	1.2	2.6	28.4	19.8	28.8	13.1	7.6	4.8	8.4	90.6
59	ND08-53×PHJ40	0	8.6	0.7	7.6	39.7	0.8	21.2	3.8	11.8	6.5	14.4	81.8
60	GEM5Derived×ND2007	0	9.3	2.9	8.4	0	33.2	14.4	0	13	4.3	9.4	74.7
61	LH61×ND250	2.3	9.8	2.3	4.6	4.6	0	7.3	1.8	6.3	1.2	2.4	73.7
62	ND2019×KMN22	0	0	0.4	0.8	9.5	3.4	7.5	1.3	5	3.6	0	41.8
63	LH61×ND06-85	0	0	4.1	2.9	17	2.8	11	2.6	3.1	22	21.9	84.7
64	GEM5 Derived×ND2004	0	7.8	5	6.7	16	12	5.4	0	14.7	1.6	0	57.9
65	ND07-97×ND2014	0	9.1	0.1	6.2	5.6	12.5	11.4	0	6.4	6.5	13.7	69.6
66	ND08-53×ND2032	0.9	4.5	0.8	2.7	17.3	14.2	19	1.7	5.1	1.8	14.1	81.1
67	PHG47×ND270	0	35.1	1	1.7	6.4	13.8	24.5	0	10.7	8.6	0	71
68	ND07-97×ND2006	0.9	6.4	2	13.2	6.3	2.6	10.7	1.6	13	-0.1	2.7	47.7
69	ND07-255×ND07-226	4.3	15.9	4.8	11.8	21.4	0	12.7	13.5	19.6	7.8	14.5	85.9
70	ND07-212×NK807	12.4	9.5	2.3	5.9	52.2	13.2	17.5	1.4	15.1	1.3	30.7	75

Table A5. Stalk lodging (%)adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	0	0	2.2	0.9	11.1	15.4	10.5	1.4	14.3	-0.6	9.1	56.2
72	ND07-212×AP47	5.1	5.8	4.9	4.8	22.4	0.9	14.4	0	22.5	5.7	11.3	89.5
73	A052×ND270	2.7	3.4	8.1	7.7	20.5	22.5	37.6	13.8	34.6	28.5	5.4	78.3
74	ND274×ND2009	36.8	45.1	9.1	40.6	10.3	0	13.2	1.6	18.4	3.5	21.1	76.2
75	A052×ND250	0	15.7	0.3	22	11.1	7.1	24.2	9.2	8.8	7.3	6.1	59.4
76	ND08-53×ND07-226	15.2	17.3	1.7	7.5	57.9	0	28.9	9.2	2.9	12	17.4	86.2
77	ND07-255×PHJ40	0	3.4	1.1	8.5	5.5	14.8	7.4	1.7	5.8	2	15.3	55.5
78	ND06-144×ND2006	0	4.5	-0.7	4.8	0	14.2	3.6	0	17.7	-0.5	0	67.5
79	ND291×ND2032	0	1.9	-0.2	5.9	13.5	20.8	12.2	2.8	13	3.2	0	48.7
80	ND291×ND07-226	0	12	-0.4	30.1	26.8	7.8	12	23	13.9	6.7	1.2	85.8
81	ND07-255×NK807	8.3	1	4.5	2.6	22.7	29.2	4.5	5.2	8.8	2.5	10	89.5
82	ND06-189×PHJ40	3.4	2.6	5.8	2.7	1.7	12.4	2.9	4.9	12.5	4	2.4	78.7
83	ND2014×LP05	6.3	0	3.9	3.1	20.6	22.3	2.2	14.5	3.5	8.9	2.5	100.3
84	LB2000×ND270	6.2	17.3	3.7	10.3	23.7	0.8	7.9	6.6	17.7	29.9	10.5	76.7
85	ND274×Il5	4.5	7	3.4	9.9	2.8	9.4	28.9	3.9	8.8	4.7	1.2	77.4
86	LB2000×ND2014	4.4	15.9	-0.6	5.4	11.5	7	11.2	3	6	1.8	2.3	83.7
87	ND07-212×LP05	26.5	6.4	1.5	8.8	49.4	10	8.5	6.5	1.3	5.2	11	101
88	ND2019×AP47	0.9	5	0.7	4.5	8.5	18.2	11	1.7	5.6	0.1	13	82.3
89	LH61×ND270	0	1.3	1.8	9	1.9	30.5	11.7	0	6	6.6	6.6	89.1
90	ND2013×ND2009	0.9	3.9	0.1	4.9	0	6.7	2.7	0	6.2	1.4	11.3	11.1
91	ND06-189×LP05	2.9	8.8	3	11.4	12.1	27.7	17.7	2.7	12.9	0.7	18.8	98.3
92	ND07-255×LP05	2.5	3.8	0.9	5.3	21.1	19.3	11.4	3.1	19.5	1.3	6.2	74.5
93	ND2013×Il5	0	1.3	-0.3	0.2	5.1	11.9	9.2	1.3	19.5	-0.4	2.8	35.9
94	ND2019×Il5	2.5	8.5	5.3	3.3	2.8	53.1	14.2	1.4	5.7	1.5	7.2	49.9
95	**Thurston 77RM**	0	2.6	0.1	6	0	4.7	9.2	4	1.4	0.4	0	57.7
96	**Pioneer 79RM**	0	0	0.2	0.4	0	2.3	1.1	1.5	0.6	0.3	1.3	36.2
97	**Pioneer 80RM**	0	22.2	-1	7.2	2.6	0.1	2.4	0	8.6	1.2	2.5	37.5
98	**Thurston 82RM**	0	1.3	0.1	3.6	0	3.6	7.3	0	5.2	-0.2	0	35.2
99	**Syngenta 85RM**	0	1.3	-0.3	0.5	11.8	26.3	4.6	0	2.3	-0.1	12.5	60.8
100	**Monsanto 88RM**	1	1.3	-0.6	3.5	2.6	0	4	0	4.5	1.1	0	60.3
	Experimental Mean	3.4	10.4	3.3	10.1	19.1	14.3	14.1	5.3	13.5	7.8	12.3	71.7
	CV%	147.2	83.7	129.5	53	93.1	96.9	67.1	118.7	70.5	88.8	89.5	24.5
	LSD,0.05	10	17.2	5.9	7.5	24.9	19.4	18.8	12.4	13.4	9.7	15.4	24.6
	MSE	25.4	75.3	18.1	29	317.5	191.5	90	39.1	91.2	48.3	120.5	309.4

Table A6. Ear height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	79.2	.	93.7	.	.	87.1	73.9	100.5	92.5	83.9	99.4
2	ND2014×B104	.	91.1	.	107.1	.	.	114.3	81.8	125.9	117	108.5	145.8
3	GEM5Derived×ND2001	49.8	75.1	94.7	89.7	.	.	93.6	75.5	102.6	92.8	71.9	100.3
4	ND265×ND2001	70.9	89.9	101.3	100.3	.	.	102.9	74	110.1	104	84.6	123
5	AP49×ND246	86.8	99.2	131	105.8	.	.	115.3	92.6	117.5	110.4	103.7	129.3
6	ND274×ND2001	71.8	87.9	92.6	91.9	.	78.3	91.2	81.2	98	97	75.9	103.9
7	ND290×PHJ40	64.1	91.1	88.2	99.3	86.3	81.8	102	77.9	111.6	105.1	81.1	121.3
8	ND203×ND2005	61	88.2	88	84	103	86.2	84.9	73.6	98.8	98.1	83.8	104.9
9	AP49×ND290	74.5	98	89.9	108.2	99.6	100.3	107	86.9	114.4	99.4	93.1	125
10	NK779×ND2014	51.3	75.2	93.7	71.6	95.5	76.1	81.1	67.3	97.8	85.6	72.2	88.9
11	ND290×ND2032	40.8	71.5	77.4	72.1	74.5	76.2	83.4	56.2	83.6	75.3	65.5	89.1
12	ND203×ND2002	49.9	77.4	100.7	83.6	90.5	95.8	79.9	64.4	88.9	78.8	68.8	91.5
13	PHG47×ND246	56.6	84.8	92.2	92.9	99.3	92.1	88.9	78.5	92.4	101.4	73.8	110
14	AP49×ND06-85	79.4	106	113	107	119.2	116.5	102.2	82.3	121.9	119.8	92.2	132.5
15	ND290×ND07-226	50.3	77.9	87.5	76.7	83.8	80.7	78.6	59.4	85	80.2	59.8	82.7
16	NK779×ND2000	46.1	73.1	82.4	72.6	76.8	71.8	77.8	60.5	91.8	76.3	65.3	81.4
17	AP49×ND291	74.4	103.8	99.2	105.8	91.5	104.1	111.1	81	119.7	111.1	105	131.2
18	ND07-212×B104	72.7	100.2	98.7	113.5	106	102.2	105.9	82.9	121.8	117.9	99.4	131.4
19	ND2021×ND2009	69.5	89.5	105.2	101.6	99	101.4	95.8	71.7	110.7	106.4	79.7	111.7
20	NP2341×ND07-153	64.4	101.2	101.9	106.8	95.5	106.9	112.4	83.6	124.8	108.9	100.5	121.3
21	ND2013×B104	66.9	102.6	117.8	109.2	107.8	99.4	101.7	77.8	113	116.1	109.6	128.9
22	LH61×ND246	58.4	77.4	92.1	84.1	91.3	82.5	84.7	67.4	94.3	90.1	67.7	90.8
23	ND08-343×ND07-153	77	100	103	101.7	102.8	97.5	100.2	86.6	107.3	108.4	86.8	118.6
24	GEM5Derived×ND2002	52.9	70.2	80.9	72.3	82.3	81.5	81.3	52.3	87.3	80.1	66.8	88
25	ND06-189×NK807	66.2	91.6	105.4	92.2	102.8	100.4	99.9	82.5	101.7	102.3	87.9	110.3
26	ND2021×ND2005	72.5	85.1	96.3	89.4	99.3	91.5	94.1	78.8	108.5	96.4	83.9	103.7
27	NP2341×ND2000	60.3	84.8	90.1	95.6	85.5	96.3	93.4	68.3	106.3	90.4	95.3	108
28	ND06-144×ND2007	84.9	103.4	111.4	117	113	107.4	104	89.2	135.2	121.7	100.5	122.7
29	ND08-343×ND2002	54	81.4	89.5	74.2	99.8	94.3	88.4	66.8	101.6	86.5	72.3	86.5
30	NK779×ND2006	54.5	73.2	90.1	70.3	68.3	69.3	70.7	46.1	81.7	64.4	66.9	75.6
31	ND2019×B104	81	97.7	123.9	106.8	107	107.3	110.1	84.6	135.6	116.3	120	148.3
32	ND2021×KMN22	55.2	83.1	100	86.7	88.5	87.1	88	73.8	88.7	80	81.5	92.8
33	ND08-343×ND2007	71.5	100.6	108	111	111.8	111.4	108.6	73.2	112.4	109.6	87.7	106.6
34	PHG47×ND06-85	65.7	89.5	93.8	93.1	86.3	102.6	91.9	61.7	95.4	79.8	82.9	101.3
35	ND203×ND2004	49.1	83.2	92.6	92.5	87.3	83.5	92.8	71.1	92	93.2	72.3	107.3

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Table A6. Ear height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	63.1	69.7	92.2	87.5	85.5	89.9	90.7	65.4	100.4	84.6	95.5	100.7
37	A052×ND246	61.4	86.1	93.8	93.9	83.8	88.4	95.5	72.4	99.7	90.8	69.9	100.7
38	A052×ND2000	72	93.7	95.8	98.4	88.3	88.8	95.9	68.5	109.9	93.9	80.9	111.4
39	NK779×ND250	47.8	65.2	67.5	65.7	71.3	69	76	54.1	84.7	72.2	63.9	80.3
40	NP2341×ND2006	61.4	85.7	92.2	88.9	95.5	99.7	91.1	59.7	116.4	93.9	87.5	109.6
41	ND2013×KMN22	53.3	74.7	95.4	78.5	77	78.4	82.9	70.9	98.5	85.1	84.4	94.9
42	ND07-97×ND07-153	66.5	109.1	114	106.5	94.5	105.2	95.1	75.1	118.4	92.6	80.4	110.4
43	ND06-144×ND07-153	59.3	92.2	90.5	103.6	97.3	91.2	93.7	70.8	114.6	108.6	80.4	103.4
44	ND2014×KMN22	63.7	90.9	105.1	93.5	102	99.5	93.3	73.2	108.6	95.6	76.6	103.6
45	LB2000×ND2000	61.3	81.4	84.5	79	79.3	72.6	73.1	55.9	83.7	75	84.4	93.1
46	ND265×ND2005	64.8	85.7	108.4	95.8	98	94.8	91.3	76.4	99.8	97.3	81.4	113.5
47	ND274×ND2005	54.9	87.2	99	86.4	87.5	85	87.3	80.7	94.9	90.8	76.1	98.8
48	ND08-53×NK807	62.5	90.6	103.5	107.1	96.3	95.4	101.7	85.6	111.3	104.9	88.5	109.3
49	ND06-144×ND2002	57	89.4	100.5	90	110.8	104.3	97.4	82.9	114.9	106.9	79.8	111.4
50	PHG47× D291	51.1	83.6	84.7	77.3	84.3	85.1	84	54.8	90.5	83.7	70.4	87.2
51	ND265×ND2009	67.9	96.2	116.7	96.6	109	106.3	101.3	81.4	118.2	105.8	86.2	116.6
52	LB2000× ND250	49.8	74.1	88.3	78.3	82.8	91.6	86.3	53.5	95.3	68	71.8	85.8
53	ND07-97×ND2007	78	100.8	129.8	106.5	100.3	107.4	111.1	95.2	118	120.6	90.8	115.1
54	ND2014×AP47	89.5	109.5	124.9	111.5	108.3	115.1	105.4	88.2	125	126.1	94.4	132.3
55	ND06-189×AP47	70.7	88.9	103.4	97.9	99.8	99.5	100	81.1	108.9	105	88.8	118.3
56	NP2341×ND2014	54.9	97.6	99.5	103.1	99.8	105.9	103	70.4	117.2	101.8	99.3	119.2
57	ND08-343×ND2004	70	88.3	92.1	83	95.3	93.9	94	74.4	106.8	92.3	71.7	107.7
58	ND265×ND2004	59.3	92.6	99.6	84.4	95.5	97.5	84.4	73.8	108.7	95.6	84.2	114.1
59	ND08-53×PHJ40	65.1	84.7	105.3	92.6	101.8	96.2	107.8	83.1	107	105.7	82	119
60	GEM5Derived×ND2007	74.5	98.2	106	93.4	92.3	110.4	106.6	88.7	115.7	103.1	93	106.6
61	LH61×ND250	48.6	67.5	84.4	64.2	84.3	79.4	77	62.7	87.7	78.6	64.9	83.1
62	ND2019×KMN22	75.5	94.9	103.8	106.2	110.3	100.7	92	83.1	104.6	115.3	85.5	109.3
63	LH61×ND06-85	58.7	78.4	84.2	82.5	88.3	87.4	80.5	72.2	86.1	84.1	70.9	88.6
64	GEM 5 Derived×ND2004	58.5	77	89.8	84.3	90.3	83.4	79.6	64.7	97.8	81.1	71.8	101.3
65	ND07-97×ND2014	60.6	88.9	94.3	94.2	89.3	90.1	98	75.9	106.4	97.9	86.7	104
66	ND08-53×ND2032	55.6	67.9	73.9	75	87	83.7	85.6	65.4	91.7	79.6	70.4	89.9
67	PHG47×ND270	38.4	66.6	73.7	61.1	80.5	64.5	65.2	54.4	68.7	68.8	64.4	73.2
68	ND07-97×ND2006	51.8	82.7	98.8	83.8	79.8	82.6	94.1	62.3	103.5	86.1	72.6	97.4
69	ND07-255×ND07-226	60.6	69.8	88.9	90.2	84.8	92	79.7	60.4	93.6	81.9	75.3	93
70	ND07-212×NK807	64.7	84.6	119	107.1	110.8	99.2	97.5	90.3	118.2	118.6	93.1	110.4

Table A6. Ear height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	73.4	98.6	111.5	107.1	105.5	105.6	108.5	86.4	127	110.2	99.6	117.1
72	ND07-212×AP47	90.8	100.6	118.6	108.5	114	101.6	105.9	89.8	125.2	108.4	108.5	129.3
73	A052×ND270	49.7	63.7	74	71.4	74.8	65.9	80.5	60.7	78.4	71	60.7	84.8
74	ND274×ND2009	66.8	92.4	109.4	104.4	98	96.4	86.5	78.4	110.3	100.2	87.8	107.8
75	A052×ND250	66.4	85.9	93.8	76.4	78.8	82.5	85.4	67.8	98	88.1	75.7	88.3
76	ND08-53×ND07-226	59.7	74	85	87.1	82.3	85.4	91.3	59.9	95.8	86.7	85.2	93.9
77	ND07-255×PHJ40	67	90.7	106	102	99.8	91.7	98.9	78.3	114.9	102.2	95.4	109
78	ND06-144×ND2006	63.2	79.6	101.1	85.7	82.5	86.3	83	56.3	98.5	79	69.6	89.7
79	ND291×ND2032	49.7	63.6	89.2	85.8	98.5	91	86.9	66.8	99.1	90	65.1	91.3
80	ND291×ND07-226	50.3	72.6	81.3	81.7	80	84	86.2	55.7	94.8	90	81.9	86.1
81	ND07-255×NK807	79.5	90.3	115.6	97.4	107	98.6	98.4	80.1	116.6	105.7	90.2	114.4
82	ND06-189×PHJ40	61.1	85.8	102.2	86.4	91	88.4	87.9	76.5	100	94.6	80.8	102.1
83	ND2014×LP05	85.3	110.2	127.7	120.5	105.8	116.9	106.1	91.4	129.2	124	102	138.7
84	LB2000×ND270	48.1	59.9	72.5	65.3	86.5	72.6	61.2	51.1	73.4	69.6	52.7	78.4
85	ND274×Il5	79.7	91.6	106.2	103.2	94.3	92.8	97.3	77.5	108.6	97.8	82	99.4
86	LB2000×ND2014	61.3	82	98.8	85.7	82.8	87.7	88	63.8	105.6	85.4	78.5	99.8
87	ND07-212×LP05	87.8	100.6	114.7	105.1	105	108.2	98.5	84.8	117	117.9	103	127.8
88	ND2019×AP47	95.7	107.6	135	121	113.3	117.1	110.9	96	136.9	127	106.2	152.5
89	LH61×ND270	44.7	55.2	77.1	64.1	60	66.5	62.6	55.1	74.7	68.5	55.4	76.4
90	ND2013×ND2009	75.3	97.9	125.4	104.3	91.3	101.7	104.9	72.5	124.4	108.5	102	122.7
91	ND06-189×LP05	73.5	101.1	113.2	105.2	107.5	104.7	94.8	79.1	120.9	113.7	97.4	117.1
92	ND07-255×LP05	79.2	99.1	128.6	108.4	108.8	105.3	102.3	80.5	114.2	98.7	92.3	117.9
93	ND2013×Il5	77.3	101	93.8	110.5	100	99.8	102.4	83.4	114.9	120.8	99.9	130.4
94	ND2019×Il5	80.2	104.2	134.1	126.3	107.5	114.8	113.4	104.6	136.9	131.5	109.6	149.4
95	**Thurston 77RM**	54.5	82.4	77.4	77.2	79.8	71.9	81.8	64.5	92.3	73.4	70	89.1
96	**Pioneer 79RM**	63.3	93.1	100.5	91.7	93.8	92.8	94.5	78.8	112.4	100.5	88	105.8
97	**Pioneer 80RM**	73.6	94.3	92.1	93.1	96.5	92.8	102.3	89.8	114	108	94.2	119.6
98	**Thurston 82RM**	76	100.6	109.4	101	95.5	93.5	103.4	81.5	109.4	115.1	86.8	121
99	**Syngenta 85RM**	67.3	84.9	99.8	99.9	98.3	96.4	92.5	70.3	110.7	102.8	80.6	109.1
100	**Monsanto 88RM**	69.3	90.9	101	97.8	94	85.8	96.1	67.2	109.9	94.6	77.7	102.2
	Experimental Mean	64.6	87.3	99.3	93	93.9	92.8	93.4	73.6	105.7	96.9	83.5	107
	CV%	11	5.4	7.3	6.2	9.8	5	5.9	9.2	4.9	6.3	7.6	5.9
	LSD,0.05	14.1	9.4	10.2	8.1	12.8	6.5	11	13.5	7.2	8.6	8.9	8.8
	MSE	50.8	22.3	53.2	33.2	84.2	21.6	30.6	46.1	26.5	37.6	40.1	39.3

Table A7. Plant height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	167.8	.	195.7	.	.	191	155.3	227.7	189	183.7	222.4
2	ND2014×B104	.	193.4	.	209.7	.	.	224.1	164.9	243.6	223.6	208.6	264.5
3	GEM5Derived×ND2001	124.6	165.3	193	190.3	.	.	189.3	153.2	214.8	186.8	167.7	222.1
4	ND265×ND2001	156.3	178	203	190.3	.	.	197.4	146.2	222.2	193.6	183.8	239
5	AP49×ND246	168.3	192.6	220.6	209.5	.	.	225.3	179.4	244.8	206.3	195.9	260.7
6	ND274×ND2001	157.8	181	196.9	188.2	.	185.8	183.4	160.2	219.8	183.1	165.5	225.9
7	ND290×PHJ40	157.6	191.2	200.9	206.4	189.4	188.5	205.9	162.4	235.6	204.7	175.5	254.2
8	ND203×ND2005	163.2	191.4	205.9	197.4	206	196.4	209.3	163.8	236	201.9	191.5	250
9	AP49×ND290	176.4	200.7	203.8	216.8	206.7	221.2	209.1	172.4	245.6	211.7	196.2	260.8
10	NK779×ND2014	136.5	170	196.4	176.8	204.5	184.1	183.2	152.5	212.9	179.5	173.2	218.6
11	ND290×ND2032	144.5	186.8	199.9	200.2	195.5	200.3	187.5	142.1	222.1	197.3	185	235.4
12	ND203×ND2002	136.3	177.8	209.1	187	199.1	203.8	184.8	151.4	206	181.5	172.7	214
13	PHG47×ND246	154.4	183.1	210.3	203.3	208.4	201.5	195.5	172.2	219.7	200.7	182.8	244.4
14	AP49×ND06-85	171.5	196.7	222.4	212.3	219.6	220.3	208.1	162	239.6	214.5	190.1	258.8
15	ND290×ND07-226	145.3	177.7	191.5	181.8	195	190.3	181.5	138.7	203.7	175.9	159.7	210.4
16	NK779×ND2000	129.3	165.8	186.6	179	181	179.7	178.6	139.5	209.2	168.4	168.1	208.4
17	AP49×ND291	169.9	207.5	215	216.2	208.8	218.9	222.9	165.4	250	218.1	212	271.8
18	ND07-212×B104	172	202	217.5	226.5	214.4	217.3	222.8	175.8	257.4	224	212	262.6
19	ND2021×ND2009	182.2	207	237.2	215.6	224	223.8	214.5	159.9	256	224.6	191.7	266.1
20	NP2341×ND07-153	162	203.3	207.7	221.9	201.9	216.5	224.9	170	260.8	211.9	207.7	258.2
21	ND2013×B104	156.3	193.6	241.9	206.5	213.4	208.5	210.4	162.9	248	224.8	212.9	251.2
22	LH61×ND246	151.2	181.2	202.5	190.5	198.6	186.3	191	145.9	221.3	187.9	173.3	227.1
23	ND08-343×ND07-153	184.5	212.4	217.8	216.4	218.4	222.8	219.4	180.5	253.6	218.2	202.1	258.4
24	GEM5Derived×ND2002	141.9	165.8	191.1	169.5	180.3	183.9	192.6	126.5	204.9	170.9	157	216.3
25	ND06-189×NK807	160.4	192.2	215.7	200.7	201.2	204.1	210.7	169.7	235	205.3	185.1	244.7
26	ND2021×ND2005	174.2	192.4	217.3	207.8	212.7	213.3	222.3	166.7	243.8	203.9	188.4	253.2
27	NP2341×ND2000	150	180.5	193.5	196.4	189.5	193.7	192.5	143.7	229.3	181.8	190.6	237.1
28	ND06-144×ND2007	197.6	205.8	233.2	228.5	218.9	223.3	221.9	185.3	264	239.7	207.6	263.1
29	ND08-343×ND2002	152.5	188.6	209.9	192.4	215.2	209.6	206.2	158.4	233.6	191.3	178.6	226.9
30	NK779×ND2006	149.1	171.2	202.2	179.6	182.6	185.3	181.8	117.8	215.6	167.6	181.8	212.4
31	ND2019×B104	179.7	202.9	247.9	221.1	206.1	213.6	219.1	183.8	262.5	228.1	216.3	271.1
32	ND2021×KMN22	156.9	197.2	226.8	220.8	210.3	223.7	223.7	169.2	254.4	199.2	208.7	262.2
33	ND08-343×ND2007	180.4	204.1	236.3	229.9	218.3	242.9	220.1	168.7	247.6	221	205.3	255.1
34	PHG47×ND06-85	151.3	180.5	201.8	190.3	181.8	204.2	192.7	139.5	208.5	174.5	178.6	226.7
35	ND203×ND2004	138	188.2	202.2	205.2	207.9	202.8	203.9	142.7	228.1	193.2	172.2	245.1

Table A7. Plant height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	158.8	181.2	211.5	205.1	204.9	199.6	203	149.2	231.6	188.2	201.8	238.6
37	A052×ND246	153.9	179.5	197.7	193	186.2	193.3	205	156.4	218.1	182.6	168.5	227.7
38	A052×ND2000	162	182.3	200.5	199.5	191.4	190.7	193.9	142.6	226	185.5	169	236.5
39	NK779×ND250	136.4	156.8	165.6	161.2	168.7	161.7	176.4	135.2	209.2	165.3	151.2	203
40	NP2341×ND2006	156.7	186.9	203.2	201.4	200.6	207.7	193	130.6	242.2	194.7	185.2	243.6
41	ND2013×KMN22	169	189.2	235.8	203.5	185.7	207.7	206.6	168	240.7	196.5	198.8	248
42	ND07-97×ND07-153	167.1	207.3	233	216	198.4	218.8	204.4	163.9	231	192.1	182	242.9
43	ND06-144×ND07-153	159.7	193	205.8	216.8	203.2	202.2	213.6	164.1	244.8	215.3	192.9	235.5
44	ND2014×KMN22	173.8	193.8	241.3	202.9	212.4	219.6	205.7	162.4	246.1	209.6	192.2	261.6
45	LB2000×ND2000	154.6	178.3	187.4	195.6	187.8	184.9	192.1	129.4	215.3	171.3	193.3	229.8
46	ND265×ND2005	156.1	180.1	220	205.6	204.8	196.2	198.2	153.7	223.5	193.1	171.9	245.3
47	ND274×ND2005	137.4	183.9	198.2	192.2	191.5	180.9	201.1	166.3	222.3	198	173.4	230.6
48	ND08-53×NK807	169	199.7	223.5	221	209.9	201.3	216.1	181	249.4	217.4	189.8	257.6
49	ND06-144×ND2002	148.2	181.7	208.8	204.9	211.3	213.3	203.6	162.1	234.3	211.7	180.1	240.4
50	PHG47× D291	146.5	187.2	204.2	186.5	195.9	193	201.2	133.2	215.8	185.3	182.8	227.7
51	ND265×ND2009	157.4	186.7	230.7	208.3	215.6	216.4	202.7	170.9	239.3	213.1	190.1	251
52	LB2000× ND250	144.2	163	196.4	181.3	175.3	193.8	184.3	125.3	219.5	158.2	168.2	214.3
53	ND07-97×ND2007	177.5	189.7	242.2	213.8	210.8	227.2	204.7	181.3	241.5	227.3	193.3	249
54	ND2014×AP47	168.9	199	226.7	199.2	206.5	221.3	209.8	166.1	245.3	219.5	184.9	242.6
55	ND06-189×AP47	158.9	182.8	206.8	199.4	200.9	208.6	202	163.8	233.4	200.7	177.8	242.7
56	NP2341×ND2014	140.2	181.2	206.4	202.9	198.2	203.2	192.8	132.6	235.7	186.5	186.6	244
57	ND08-343×ND2004	169	197.1	220.6	201	209.9	217.4	199.1	160.5	249.5	200.1	189.6	254.8
58	ND265×ND2004	145.4	188.4	215.1	193.3	205.3	208.1	191.7	158.2	240.3	196.8	184.5	250.9
59	ND08-53×PHJ40	163.5	181.9	222.2	198.2	204.9	199.1	204.2	166.2	236.8	201.4	175.3	249.9
60	GEM5Derived×ND2007	172.1	195.4	217.1	197.8	200.1	224.2	207.1	173.6	241.7	201.2	193.3	252.7
61	LH61×ND250	130.7	156.1	187.6	163.5	190.2	180	168.8	138.9	209.5	164.1	149.2	203.7
62	ND2019×KMN22	192.6	204.5	244	222	216.1	223.1	207.6	179.2	250.6	236.7	203.4	262.3
63	LH61×ND06-85	138.6	165.9	188.2	178.9	178.7	187.8	177.6	149.5	184.8	170.7	156.4	203.4
64	GEM5 Derived×ND2004	149.8	184.7	200.5	196.3	199.4	194.9	192.2	146.8	225.2	176.8	173.8	242
65	ND07-97×ND2014	141.3	171.8	195.6	188.4	180.3	188.9	188	150	218.1	189.9	171.6	224.9
66	ND08-53×ND2032	168.8	179.9	203.9	198.3	206.8	210.1	203.6	160.7	237.8	205.7	185.2	241.9
67	PHG47×ND270	134.9	165.5	184.2	168.4	182	170.7	171.9	143.7	193.8	166.6	167.5	219.3
68	ND07-97×ND2006	144	178.3	214.7	190.7	181.4	183.4	195	138.8	225.5	183	170.2	223.3
69	ND07-255×ND07-226	156.7	172	194.1	189.2	185.8	194.9	182.8	137.4	200.6	174.6	167.9	216.8
70	ND07-212×NK807	157.7	187.5	238.4	211.9	211.9	207.1	208.9	185.6	246.6	226.9	193.4	255.4

Table A7. Plant height (cm) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	179.4	205.4	243.4	219.9	229.9	229.1	227.9	185.7	264.4	229	212.4	267.3
72	ND07-212×AP47	181.2	195	225.3	208.9	218.6	204.4	206.7	173.1	239.3	203.9	202.4	252.2
73	A052×ND270	139.6	162.4	177.5	175.7	176.9	171.4	183.9	135.8	193.3	163.2	158	209.1
74	ND274×ND2009	171.4	200.8	230.8	214.7	216.3	216	203.5	175.1	241.4	217	204.5	255
75	A052×ND250	150.2	168	185.4	173	176	179.5	188.4	136.1	211	169.4	167.1	210.4
76	ND08-53×ND07-226	165	179.4	201.2	200.9	198	188.4	196.5	139.9	226.2	182.6	188	231.4
77	ND07-255×PHJ40	159.8	182.3	210.2	198.3	201.5	191.3	203.5	156.3	229.5	193.5	191.5	236.9
78	ND06-144×ND2006	159.4	181.3	210.7	191.9	186.6	193.7	175.1	135.2	223.7	177.5	179.7	223.2
79	ND291×ND2032	155.3	175.8	213.1	207	219.2	207	203.7	161.1	229.6	201.3	178.4	241.7
80	ND291×ND07-226	149.6	177.4	201.4	193.2	190.6	190.9	191.8	126	223.6	184.6	179.1	226.1
81	ND07-255×NK807	172.6	189	227	204.1	211.6	204.8	207.6	159.7	242.5	208	192.3	241.4
82	ND06-189×PHJ40	151.5	179.4	211.9	188.7	185.5	183.6	192.9	151	221.6	187.7	179.3	231.2
83	ND2014×LP05	169.6	208.8	237.9	224.7	217.3	209.8	196.6	176.6	244.3	222.7	207.1	258.9
84	LB2000×ND270	148.9	160.9	196.2	172.9	184.5	175.4	169.7	131.6	211.5	167.4	161.9	219.3
85	ND274×Il5	176	196.9	221.5	217.5	204.4	207	205.6	166.6	234.8	205.1	184.8	240.9
86	LB2000×ND2014	156.5	177.2	211.4	195.2	184.2	192.3	187.2	135.1	230.4	180.9	181.9	235.6
87	ND07-212×LP05	187.1	199.6	228.3	215.3	207.4	211.5	189.5	168.8	249.8	219	202.1	263.2
88	ND2019×AP47	184.4	200.9	252.3	224.9	211.8	219.9	208.1	180	258	227.7	196.3	261
89	LH61×ND270	130.8	145.3	184.5	162.8	155.7	163.4	159.9	135	191.4	159.5	152.1	200
90	ND2013×ND2009	180.4	202	249.5	215	201.6	216.9	201.3	163.4	244.1	225.6	208.8	259.6
91	ND06-189×LP05	162.8	199	228.6	210.7	212.7	210	187.8	161.8	245.1	209.8	198.6	248.4
92	ND07-255×LP05	179.2	194.6	248.2	213.7	211.9	204.8	205.4	164.9	236.5	203.7	187.3	247.3
93	ND2013×Il5	172.7	192.2	203.5	211.3	210.7	221	203.6	180.1	241.9	229.4	200.1	256.9
94	ND2019×Il5	174.3	199.6	249.8	223.2	220.1	231.1	219.2	195.4	263.6	238.2	215	269.1
95	**Thurston 77RM**	168.1	196.6	200.4	205.3	209.3	206.8	210.8	162.4	242.7	189.9	193.3	250
96	**Pioneer 79RM**	152.7	190	208.7	199.5	196	196.5	196.9	157.2	235.4	190.1	187.4	235.7
97	**Pioneer 80RM**	169.2	185.9	190.7	195.7	191	195.7	214.2	166.1	244.4	197.3	182.4	248.3
98	**Thurston 82RM**	187.5	204.4	244.5	222.2	218.2	221.9	220	174.3	256.6	224.7	201.4	277.3
99	**Syngenta 85RM**	168	189.9	230.3	215.1	203.8	212.1	213.8	165.4	252	220.8	193.4	262.9
100	**Monsanto 88RM**	174.3	200.2	229.2	213.8	218.2	208.6	214.5	156.3	242	207.1	191.1	256.4
	Experimental Mean	159.9	186.5	213.1	201	201	202.8	200.4	157.5	232.7	198.5	185.7	241.3
	CV%	6.7	2.8	4.5	2.9	4.7	2.9	4.2	6.5	2.3	3.7	4.1	1.8
	LSD,0.05	21.3	10.3	13.4	8	13.3	8.3	16.7	20.2	7.6	10.4	10.8	6.2
	MSE	114.9	27	91.8	32.9	90.7	35.5	71.1	104.2	29.5	55.3	59.3	19.6

Table A8. Days of An thesis (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	64.4	.	65.6	.	.	64.5	59.5	63.5	58.7	66.5	62.9
2	ND2014×B104	.	74.4	.	74.5	.	.	71.9	68	72	69.7	76	71.4
3	GEM5Derived×ND2001	64.4	68.2	57.3	66.4	.	.	65	62.5	64	62.6	63	64.3
4	ND265×ND2001	63.7	67.2	63.3	68.1	.	.	66.9	64	66	64	67	64.8
5	AP49×ND246	73.5	75.1	73.8	67.6	.	.	65.8	61.5	65.5	62	66.5	67.4
6	ND274×ND2001	58.6	62.7	55.7	61.4	.	66.6	64.9	58.5	64	61.8	60.5	62.9
7	ND290×PHJ40	62.6	68.8	60.9	66.8	61	65.9	65.8	61.5	65	62	63	65.5
8	ND203×ND2005	55.8	61.9	57.8	61.1	64.5	62.8	63.9	57.5	63.5	60	66	63.8
9	AP49×ND290	64.2	71.4	64.6	70.1	66	66.8	68.1	63	67.5	63.5	71	68.3
10	NK779×ND2014	58	61.7	55.7	61.8	61	62.4	64.5	57.5	64	58.4	60	61.8
11	ND290×ND2032	58.1	65.1	57.6	66	60	65.1	65.3	61.5	65.5	60	61	63.6
12	ND203×ND2002	58.8	63.6	56.4	64.9	60.5	63.3	62.7	57.5	62.5	59	61	63.1
13	PHG47×ND246	64.4	67	59.2	65.2	61	66.3	66.3	60	65	63.3	63.5	65
14	AP49×ND06-85	64.7	69.4	62.3	69.4	63.5	69.2	67.2	63	66	63.5	67.5	67
15	ND290×ND07-226	61	62.8	58.2	62.9	58.5	61.3	64.6	59.5	63.5	58.7	60	62.6
16	NK779×ND2000	57.1	59.9	54.6	61.2	56	59.5	63.7	57.5	63	57.5	60	62.1
17	AP49×ND291	65.1	72.5	62.8	72.1	62	69.8	68.1	65.5	67.5	64.8	71	67.2
18	ND07-212×B104	68.2	73.1	66.7	73.5	62.5	70.7	71.2	65.5	71	64.7	71.5	69.4
19	ND2021×ND2009	68.1	71.6	65	73.4	65.5	66.2	67.4	63.5	67	63.7	67.5	67.9
20	NP2341×ND07-153	62.5	66.4	61.1	67.2	60.5	63.8	66.8	62.5	64.5	64.6	68	64.4
21	ND2013×B104	73.4	76.1	71.7	75.2	67	75.3	74	71.5	73	69.2	76	72.9
22	LH61×ND246	61.6	63.6	59	64.1	60	63.5	64.9	59.5	65.5	59.7	63.5	63.9
23	ND08-343×ND07-153	59.2	65.5	55.8	65	58	62	64.4	58	63.5	61	62	64.4
24	GEM5Derived×ND2002	59	68.9	57.4	67.7	61.5	65.4	64.4	60	62.5	61.4	66.5	64.9
25	ND06-189×NK807	61.8	64.8	59.3	65.7	61.5	62.5	65.8	62	65	62.9	63	63.9
26	ND2021×ND2005	60.4	66.9	61.2	66	62.5	63.7	66.9	61	66	60.2	64	66
27	NP2341×ND2000	59.4	66	56.9	66.4	60	62.5	65.2	61	64	61	60.5	63.6
28	ND06-144×ND2007	64.5	71.1	63.3	69.7	65.5	67.4	66.9	65.5	68	66.4	73.5	66.8
29	ND08-343×ND2002	59.9	64.6	57.1	66.2	60	63.4	64.1	57.5	62.5	59.9	61	63.8
30	NK779×ND2006	54.3	58.9	52.7	59.9	55	56.5	64	58	63	57.3	64.5	60.8
31	ND2019×B104	65	71	64.8	71.4	62.6	71.8	68.9	67	69.5	67	71	71.1
32	ND2021×KMN22	62.7	69.5	57.1	70.3	61.6	66	67.3	61.5	66.5	61.6	69.5	64.6
33	ND08-343×ND2007	64.3	72.9	64	72.1	64.1	69	67.9	65.5	66	64.9	69	67.1
34	PHG47×ND06-85	65	68.8	61	68.3	59.1	65.4	65.9	62.5	66	63.3	67.5	64.5
35	ND203×ND2004	62.3	65.7	58.9	64.8	58.1	62	65.2	60	63.5	59.8	62.5	64.1

Table A8. Days of An thesis (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	58.9	65.3	58.9	64.1	60.6	64.7	64.8	59	64	59.1	72	63.7
37	A052×ND246	61.4	65.9	60.5	65	60.1	64	66.2	59.5	65	60.8	62	64.7
38	A052×ND2000	64.1	70	62.9	69.4	62.5	64.9	66.9	64.5	66	61.8	63.5	66
39	NK779×ND250	54.5	60	51.8	59.8	55.6	62.9	64	57	63	57.8	59	61.5
40	NP2341×ND2006	59.8	65.8	58.4	65.1	62.5	63.5	64.4	60	63	59.7	66.5	64
41	ND2013×KMN22	67	71.6	65.2	71	61.5	68.1	68.5	63.5	68.5	62.2	69	69
42	ND07-97×ND07-153	64.2	68.6	61.5	67	60	65.8	66.4	61	67	61.7	63.5	64
43	ND06-144×ND07-153	59.8	62	55.9	65.3	56.5	61.8	63.5	60	63.5	61.1	61	62.5
44	ND2014×KMN22	64.6	71.4	63.9	71	65	70.2	70	63.5	69	64	67	66.9
45	LB2000×ND2000	58.4	60.8	56.3	62.5	57	59.8	62.8	60	63.5	59.4	65	62
46	ND265×ND2005	61.5	65.9	59.2	64.8	62	63.5	66.9	61	65.5	60.3	64	65.1
47	ND274×ND2005	59.9	63	57.4	62.7	59	64.3	65.3	60	65	61.5	60	63.6
48	ND08-53×NK807	61.6	67.1	61.3	66	61.5	64.2	66	63	65.5	63.4	63.5	63.9
49	ND06-144×ND2002	63	68.6	58.7	66.5	64	64.2	65.6	63	65	61.9	63.5	65.4
50	PHG47× D291	63.9	68.9	61.2	68.8	63.5	68.8	66.5	62	67.5	61.3	67.5	65.4
51	ND265×ND2009	66	73.1	64.4	71.8	67	68.4	67.2	65	67.5	66.3	68	67.6
52	LB2000× ND250	55.2	60.6	54.1	62.7	57	63.1	63.1	59	63.5	59.8	60	62.1
53	ND07-97×ND2007	65.3	74.5	66.5	72.6	65	72.1	70.7	64	71	67.7	72.5	69.5
54	ND2014×AP47	66	73	65.5	72.3	67	68.5	68.6	65	67	67.6	68	68.5
55	ND06-189×AP47	64.3	70.8	63.4	70.8	63	66.1	68	64	66.5	64.1	67	67.6
56	NP2341×ND2014	63	68.4	58.9	67.5	60.5	64.8	66.6	61.5	65	62.4	67.5	64.1
57	ND08-343×ND2004	58.9	68.1	57.6	65.9	63.5	62.1	66.5	60	64.5	61.6	63	65.2
58	ND265×ND2004	60.6	70.2	63	69.3	60.9	64	67.2	63.5	67	64.1	70	65.9
59	ND08-53×PHJ40	62	67.1	62.8	66.8	63	65.5	67.3	62	66	63.1	65	65.9
60	GEM5Derived×ND2007	65.8	71.5	62.9	73	64	67.1	67.2	63.5	66.5	65.5	67.5	66.9
61	LH61×ND250	60.1	65.5	56.4	65.9	62	63.5	65.5	61	65.5	60.7	61	64
62	ND2019×KMN22	65.8	73.5	65.7	74.3	64.5	69.3	70.4	63	70	65.2	67.5	69.5
63	LH61×ND06-85	59.9	62.9	56.5	63.6	59.5	64.2	65.5	59	64.5	59.6	61.5	63.9
64	GEM 5 Derived×ND2004	60.1	68.8	58.6	68.3	60.5	63.7	65.5	62.5	66	61.5	67.5	63.9
65	ND07-97×ND2014	61.9	63.4	59	64.8	60	64.2	66.8	60	68	60.9	63	64
66	ND08-53×ND2032	59.1	67.3	62.9	67.1	61	65.4	67.9	63.5	66.5	61.3	65	65
67	PHG47×ND270	60.5	66.4	57.6	66	60	65.7	65.8	59	64.5	59	63	64.1
68	ND07-97×ND2006	60.2	64	58	65.9	59	61.7	65.5	58.5	64.5	60.9	68	63.8
69	ND07-255×ND07-226	64.6	66	62.9	64.8	62	63.6	66.6	60	66.5	61.4	69.5	65.8
70	ND07-212×NK807	65.9	68.8	61.4	69.6	61	67.3	67	62.5	68	64.3	63	65.9

Table A8. Days of An thesis (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	65.2	71.4	62.9	73.7	63.5	67.7	67.6	67	67.5	65.5	67	67.4
72	ND07-212×AP47	64.4	70.9	63.7	72.1	65	67.4	68.5	65	67	65.6	73.5	69.4
73	A052×ND270	62	66.8	59.5	66	59.5	64.9	66.6	61	65.5	59.9	63.5	65.3
74	ND274×ND2009	66.3	70.8	65.1	69.6	66.5	67.3	67	64	67	64.3	68	67.8
75	A052×ND250	58.1	63.6	59	64.1	61.5	61.9	66.9	61	65.5	63.3	62	64.4
76	ND08-53×ND07-226	60.2	64.2	60.9	65.9	61	64.6	67	61	66	62.1	68.5	63.9
77	ND07-255×PHJ40	64.7	67.3	61.1	69.8	60.5	63.4	66.4	61	65	61.4	73.5	65
78	ND06-144×ND2006	56.2	61	55	61.7	56	57.8	63.5	57	63	58.3	59.5	61.7
79	ND291×ND2032	64.8	71.4	62.9	69.1	63.5	67.3	66.7	61.5	65	62.3	64	63.8
80	ND291×ND07-226	60.6	63.2	58.9	64.9	60	62.4	66.6	62.5	65.5	60.2	63	63.8
81	ND07-255×NK807	61.2	67.6	61.3	66.1	61.5	67.6	66.2	64	66	63.1	64	65.2
82	ND06-189×PHJ40	59.9	67.1	61.1	66.1	60	64.4	66.6	62.5	66	62.1	63.5	64.2
83	ND2014×LP05	68.5	74	64.5	74.9	67.5	70.3	68.6	68	67.5	66.9	70	69.2
84	LB2000×ND270	54.8	59.4	56	61.6	60.4	59.8	65.6	58	64	56.8	61	57.1
85	ND274×Il5	63.1	65.8	59.4	68.1	61	66.3	67	63	66	62.8	63	64.2
86	LB2000×ND2014	59.2	62.9	56.9	63.4	59	62	65.6	59	63.5	60.2	63.5	63.8
87	ND07-212×LP05	65.2	71	64	72.8	64.9	70.3	67.9	64	66.5	63.4	68.5	66.8
88	ND2019×AP47	66.8	74.1	65.4	74.1	63.4	70.8	69.6	68	70.5	68.3	73.5	70.1
89	LH61×ND270	65.7	67.6	58.8	66.1	61.4	65.2	65.3	59.5	65.5	62.8	61.5	64.6
90	ND2013×ND2009	70.6	74.9	67.9	73.9	63.9	71.4	73.7	71	72.5	68.2	76.5	73.1
91	ND06-189×LP05	65	69.2	63	67.6	68.5	66	68.5	64	66.5	62.4	68	66.2
92	ND07-255×LP05	68.2	71.3	63.3	71.6	63.5	67.7	66.4	62	66	63.4	67.5	66.7
93	ND2013×Il5	69.8	74.6	65	73.9	66.5	70.7	71	68	71	66.8	74.5	70.7
94	ND2019×Il5	66.6	73.6	65.7	73.1	66	69.1	71.9	69	71.5	68.1	70	71.1
95	**Thurston 77RM**	60.9	68	59.6	67.1	59.5	62.7	64.8	62	65.5	63.6	63	64.7
96	**Pioneer 79RM**	58.5	66.6	58.5	64.9	60	62.4	65.9	60	64.5	63.5	67	64.3
97	**Pioneer 80RM**	62.9	68.2	63	66.3	61.5	65.2	65.8	60	65.5	62.7	63.5	64.8
98	**Thurston 82RM**	67.1	73.8	65.1	73.6	65.4	65.1	67.9	67.5	67.5	68.6	69	68.1
99	**Syngenta 85RM**	64	71.7	62.9	71.6	62.5	64.6	67.6	65	66	66.1	68	68.1
100	**Monsanto 88RM**	65.9	72.6	63.5	72.4	65	68.7	68.5	63.5	66.5	68.5	66.5	67.6
	Experimental Mean	62.6	67.8	60.8	67.7	61.8	65.4	66.7	62.1	66	62.6	65.9	65.5
	CV%	3	2.3	2	1.3	3.7	2.1	1.2	2.2	1	2.1	5.2	1.6
	LSD,0.05	3.8	3.1	1.7	1.3	3.2	2	1.6	2.7	0.9	1.8	4.8	1.5
	MSE	3.6	2.4	1.5	0.8	5.2	2	0.7	1.9	0.4	1.7	11.8	1.1

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Table A9. Days of Silking (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	67	.	68	.	.	63	60.2	65	61.6	67	62.8
2	ND2014×B104	.	75.4	.	76.1	.	.	70.9	69.4	73	72.1	78.5	71.2
3	GEM5Derived×ND2001	64.3	68.9	56.3	66.6	.	.	63.9	63.5	66	62.7	64	62.8
4	ND265×ND2001	63	69.9	62.3	69.8	.	.	66	65.4	67	64.1	67.5	65.6
5	AP49×ND246	73.3	70.1	73.3	68.9	.	.	64.9	65.3	66.5	64.9	65	65.8
6	ND274×ND2001	58.1	64.9	54.8	64.8	.	67.4	64	60	66.5	63.8	61	62.4
7	ND290×PHJ40	64.7	69.5	60.3	67.7	65	67	64.9	61.9	66	62.1	65	67.3
8	ND203×ND2005	58.1	65.6	56.2	65.6	65.5	64.2	63	59.5	64.5	62.4	66.5	63.7
9	AP49×ND290	65.2	74.6	63.5	74.3	66.5	69.8	67	66.6	68.5	68	74	68.1
10	NK779×ND2014	59.3	64.4	55.2	66.5	63.5	62.7	63.5	58.7	65	59	63	62.7
11	ND290×ND2032	61.6	69.1	57.6	68.6	64.5	69	64.1	64.6	66.5	61.3	64.5	64.6
12	ND203×ND2002	61.3	66.5	55.4	66.2	61	64.3	61.6	58.3	63.5	59.3	62	62.1
13	PHG47×ND246	64.2	69.9	58.7	67.3	62.5	67.4	65.1	62.5	66	66.9	63.5	65.1
14	AP49×ND06-85	64.9	73.5	61.2	71.5	65	71.6	66.1	66.9	67	67.7	69	67.4
15	ND290×ND07-226	61.6	68.5	57.7	68.3	64	64.9	63.5	63.3	64.5	61.2	64	63.1
16	NK779×ND2000	58.4	63	53.7	63.5	58	61.4	62.1	59.5	64	58.6	62	62.3
17	AP49×ND291	65	74	61.7	72.9	64.5	69.5	67.1	66.9	68.5	66.9	72.5	66.6
18	ND07-212×B104	68.9	76.2	65.6	76.2	64	72.2	70.1	70.5	72	69.2	75	70.1
19	ND2021×ND2009	68.5	75.1	63.9	74.9	67	66.8	66.2	68.1	68	66.2	70	69.5
20	NP2341×ND07-153	63.1	68	60.1	68.1	62	64.7	65.1	63.6	66	66.8	69	64.6
21	ND2013×B104	73.7	81.1	71.2	81.4	71	77.7	72.9	73.5	74	72	80	74.1
22	LH61×ND246	62.9	68	59	67.5	61	66.5	63.9	63.6	66.5	62.5	64.5	64.6
23	ND08-343×ND07-153	58.8	67.5	55.3	66	59	63.6	63.4	60.3	64.5	62.6	64	63.1
24	GEM5Derived×ND2002	58	70	55.3	67.7	60.5	66.3	63	62.2	66	63	64.5	62.9
25	ND06-189×NK807	61.7	67.5	58.3	67	63	62.6	64.9	63.1	66	64.8	63	63.6
26	ND2021×ND2005	62.6	72	61.4	70.2	64.5	65.6	66	65.3	67	62.7	65.5	67.3
27	NP2341×ND2000	60.6	67.6	56.4	66.6	62	62.7	64.4	63.2	65	63	62	62.6
28	ND06-144×ND2007	66	74.2	62.3	74	68.5	68.9	66	72.8	69	67.8	75	68.1
29	ND08-343×ND2002	59.1	66.7	55.1	67.2	60	64	62.5	57.9	63.5	62.4	61.5	63
30	NK779×ND2006	55.7	62.5	52.7	61.8	57.5	58.9	62.5	62.4	64	58.5	65.5	62.1
31	ND2019×B104	65.8	73.5	63.9	73.8	63.5	73.7	68	67.2	71	70.9	72.5	71.7
32	ND2021×KMN22	65	71	56.7	71.9	63.5	67.5	66.4	66.4	67.5	63.3	72	66.1
33	ND08-343×ND2007	65.9	73.9	63	73	66	70.5	66.4	70.5	67	66	71.5	68.7
34	PHG47×ND06-85	65.1	70.9	60.5	69.7	61	66.7	65	62.9	67	64.9	68	64.5
35	ND203×ND2004	63.3	67.4	58	69	60.5	63.6	64.4	60.8	65	63.2	63	64.7

Table A9. Days of Silking (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	60.7	69.5	58	67.2	62.5	66.6	64	62.1	65	60.6	73.5	64.3
37	A052×ND246	63.8	70.5	59.5	69.6	61.5	64.7	65.4	62.4	66.5	65.4	62.5	64.7
38	A052×ND2000	65.1	73.1	61.9	71.4	64.5	66.4	66	68.5	67	64.7	64.5	66.6
39	NK779×ND250	58.7	63.1	51.7	63.1	58	64.5	62.5	58.2	64	60.2	59.5	62.5
40	NP2341×ND2006	59.4	66.4	57.9	66.3	64	62.9	63	61.2	64.5	60.3	66.5	63.6
41	ND2013×KMN22	67.4	74.6	64.2	74	64	69.8	67.5	66.4	69.5	66.7	71	69.8
42	ND07-97×ND07-153	65.2	72.5	60.5	69.1	63	68.1	65.5	63.1	68	64.1	66	65.8
43	ND06-144×ND07-153	60	65.9	55.8	66.7	58	63.7	61.9	61.7	64.5	63.2	63	63.3
44	ND2014×KMN22	64.2	74.3	62.8	74.4	67.5	70.4	68.5	64.6	70	67.2	71	66.6
45	LB2000×ND2000	59	63.5	55.3	66.2	59.5	61.2	61.4	62.5	64.5	61.5	66.5	62.4
46	ND265×ND2005	62.8	71	58.3	67.9	63.5	65.2	66	63.2	66.5	62.4	66.5	66
47	ND274×ND2005	61.9	67	57.3	66.8	60	65.3	64.4	62.6	66	64.7	61.5	63.4
48	ND08-53×NK807	62.2	69.7	60.2	67.6	62	64.5	65	64.7	66.5	66.5	65	64.3
49	ND06-144×ND2002	63.9	70.1	57.5	69.3	66	64.6	64.1	63.3	66.5	64.5	63.5	64.7
50	PHG47× D291	64.5	70.9	60.2	71.5	64.5	68	65	65.9	68.5	64.6	68.5	65.3
51	ND265×ND2009	66	73.5	63.4	74	68	69.8	66.1	66.7	68.5	70	71.5	68
52	LB2000× ND250	56.7	62.5	54.2	65.1	58	64.6	61.1	60.9	63.5	62	60	62
53	ND07-97×ND2007	65.1	79.9	66	75.2	68	75.7	71.1	69.5	72	71.1	77.5	71.5
54	ND2014×AP47	64.8	74	64	73.8	67.5	68.9	67.2	65.5	68.5	68	69	67.8
55	ND06-189×AP47	65.6	72.9	63	72.7	64	67.2	67	67.4	67.5	69.9	67.5	67.6
56	NP2341×ND2014	64.4	70	59	69.3	61	66.2	65.6	64.1	66.5	64.8	68.5	64.7
57	ND08-343×ND2004	59	69	57	66.6	65	62.8	65.6	61	66	62.1	64.5	66.1
58	ND265×ND2004	62.3	72.6	61.9	70.1	63.5	65	66.1	64	68	66.9	71.5	67
59	ND08-53×PHJ40	64.4	69.6	61.7	69.8	64	66.6	66.2	63.2	67	64.4	66.5	66.9
60	GEM5Derived×ND2007	66.1	71.9	61.9	76	65.5	68	66.1	65.2	67.5	66.5	69	67
61	LH61×ND250	62.5	69.9	55.5	69.7	66.5	66.9	65.5	62.3	66.5	64.9	63.5	65
62	ND2019×KMN22	65.7	74.9	64.9	76.3	65.5	70.2	69.5	67.5	71	69.9	70	70
63	LH61×ND06-85	64.1	68.3	56.6	69.3	61.5	67.3	64.4	61.1	65.5	62	65	64.5
64	GEM 5 Derived×ND2004	59.3	69.8	57.6	69	62	64.5	64.5	63.6	67	62.9	68.5	64.3
65	ND07-97×ND2014	64	69.7	59.1	68.9	64	66.9	65.9	63	69.5	65.7	66.5	66.6
66	ND08-53×ND2032	62.3	70.3	62.2	68.5	62.5	66.4	67	65.7	68	64.6	69	66.2
67	PHG47×ND270	61.4	68.9	57.2	66.9	60.5	66	64.4	60.1	65.5	60.4	64	63.1
68	ND07-97×ND2006	60.3	67	57.6	67.3	61.5	62.7	64.5	61.2	65.5	62.7	69.5	64.5
69	ND07-255×ND07-226	64.4	71	61.9	69	63.5	65.3	65.6	62.8	67.5	64.3	71	66.4
70	ND07-212×NK807	67	71.8	60.5	71.2	61.5	68.2	66	63.8	69	67.3	64	66

Table A9. Days of Silking (days after planting) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	65.7	73.5	61.9	73.7	66	69.1	66.5	69.2	68.5	66.9	66.5	67.8
72	ND07-212×AP47	64.5	73	63.2	72.3	66.5	68.9	67.5	67.4	68	66.9	73.5	68.3
73	A052×ND270	62.3	71.4	58.5	69.9	63.5	66.5	65.5	64	66.5	62.5	65	66.3
74	ND274×ND2009	67	72.5	64	73.1	68	68.2	66	65	68	64.9	69	66.1
75	A052×ND250	58.3	69	58.5	67.9	64	63.6	65.9	63.4	66.5	65.7	63.5	65.9
76	ND08-53×ND07-226	62.6	70.5	60.5	70.1	63.5	66	66	64.6	67	66.1	72	66
77	ND07-255×PHJ40	65.2	68	60	70	62	64.6	65	62.5	66	61.4	76	65.4
78	ND06-144×ND2006	53.9	63.6	53.5	63.3	58.5	57.3	62.5	59	64	59.2	60	61.8
79	ND291×ND2032	66.2	73.6	61.7	71	65	67	65.1	62.7	66	64.8	65.5	64.7
80	ND291×ND07-226	60.8	68.4	58.9	69.2	64	63.4	65.5	65.7	66.5	62.4	65	64.3
81	ND07-255×NK807	63.7	70.1	60.4	68.4	61.5	66.6	65.1	65.8	67	65.4	64.5	65.2
82	ND06-189×PHJ40	62.4	70	60.2	69.5	60.5	67.4	65.6	65	67	63.4	64	64.1
83	ND2014×LP05	68.7	75.5	63	75.5	68.5	72	67	68.6	69	69	72	69.2
84	LB2000×ND270	55.4	63.5	55	66.2	61.5	61.2	63.1	59.6	65	58.4	62	57
85	ND274×Il5	64.2	69.5	58.9	70.5	62	67.6	66	65	67	64.3	63.5	64.7
86	LB2000×ND2014	60	67	56.5	67.2	61.5	64	64.6	62.7	64.5	65.2	64.5	63.9
87	ND07-212×LP05	65.1	72.6	63	74.1	66.5	71.7	67	66.1	67.5	66	69.5	68.2
88	ND2019×AP47	67.4	76.2	64.4	75	67	70.8	68.6	69.1	71.5	70.8	75	70.2
89	LH61×ND270	66.6	73.2	59.2	68.7	62	67.5	63.6	61.3	66.5	63.3	65.5	67.5
90	ND2013×ND2009	70.7	78.5	66.8	77.3	66.5	72.4	72.6	71.3	73.5	71.4	79	73.2
91	ND06-189×LP05	66.6	73.1	62	71.6	71.5	67	67.4	69.8	67.5	66.9	67.5	66.2
92	ND07-255×LP05	68.4	73	62.3	74.2	65.5	68.8	65.4	64	67	64.9	67.5	66.6
93	ND2013×Il5	68.7	76.4	64	74.8	68	70.9	69.9	69.1	72.5	69	76	70.2
94	ND2019×Il5	66.9	76	64.6	75	66	69.6	69.9	69.5	73	70.4	71	70.5
95	**Thurston 77RM**	61.7	68.5	58.6	67.8	60.5	61.9	63.8	63.4	66.5	67.3	63	65.2
96	**Pioneer 79RM**	59.5	67	57.2	66	60.5	62.4	64.4	62.2	66	66.7	67.5	63.8
97	**Pioneer 80RM**	63.1	68.5	62	68.9	62	66	64.4	62.5	66.5	65	63.5	65.2
98	**Thurston 82RM**	66.4	73.7	64.1	73.7	66.5	66.2	66.9	68.1	69	69.3	70	69.1
99	**Syngenta 85RM**	64.5	72.6	61.9	72.9	63.5	64.8	66.5	66.2	67	67.8	69	67
100	**Monsanto 88RM**	66.2	73	62.5	73.6	65.5	69.3	67.4	64.3	67.5	69.9	65.5	67.6
	Experimental Mean	63.4	70.5	60	70	63.6	66.6	65.6	64.3	67.1	64.9	67.4	65.8
	CV%	3	1.6	2	1.6	4.3	2.5	1.3	2.4	1	2.8	5.2	1.7
	LSD,0.05	3.8	2.2	1.7	1.6	3.8	2.4	1.7	3.1	1	2.6	4.9	1.6
	MSE	3.7	1.2	1.5	1.3	7.5	2.9	0.8	2.4	0.5	3.4	12.4	1.2

Table A10. Anthesis Silking Interval (days beteween anthesis and silking) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	-2.9	.	-2.1	.	.	1.5	-0.7	-1.5	-2.5	-0.5	-0.5
2	ND2014×B104	.	-1.3	.	-1.5	.	.	1	-1.2	-1	-2.5	-2.5	-2.5
3	GEM5Derived×ND2001	0.1	-0.8	1	-0.4	.	.	1.1	-0.9	-2	0	-1	-1
4	ND265×ND2001	0.8	-2.9	1	-1.5	.	.	0.9	-1.4	-1	0	-0.5	-0.5
5	AP49×ND246	0	-1.8	0.5	-1.1	.	.	1	-3.9	-1	-3	1.5	1.5
6	ND274×ND2001	0.6	-2.5	1	-3.5	.	-0.9	0.9	-1.4	-2.5	-2	-0.5	-0.5
7	ND290×PHJ40	-2.1	-0.9	0.5	-1	-4	-1.3	0.9	-0.4	-1	0	-2	-2
8	ND203×ND2005	-2.2	-3.9	1.5	-4.5	-1	-1.5	1	-2	-1	-2.5	-0.5	-0.5
9	AP49×ND290	-1.1	-3.5	1	-4	-0.5	-3.1	1	-3.5	-1	-4.5	-3	-3
10	NK779×ND2014	-1.1	-2.9	0.5	-4.5	-2.5	-0.4	1	-1.3	-1	-1	-3	-3
11	ND290×ND2032	-3.2	-4	0	-2.6	-4.5	-3.9	1.1	-3.4	-1	-1	-3.5	-3.5
12	ND203×ND2002	-2.6	-2.9	1	-1.5	-0.5	-0.9	1	-0.9	-1	-0.5	-1	-1
13	PHG47×ND246	0.3	-3	0.5	-2.3	-1.5	-1	1.2	-2.5	-1	-3.5	0	0
14	AP49×ND06-85	0	-4	1	-2	-1.5	-2.4	1	-4	-1	-4	-1.5	-1.5
15	ND290×ND07-226	-0.8	-5.5	0.5	-5.4	-5.5	-3.7	1.1	-4.1	-1	-2.5	-4	-4
16	NK779×ND2000	-1.2	-3.1	1	-2.4	-2	-1.9	1.5	-2	-1	-1	-2	-2
17	AP49×ND291	0.1	-1.5	1	-0.9	-2.5	0.2	1	-1.5	-1	-2	-1.5	-1.5
18	ND07-212×B104	-0.5	-3.1	1	-3	-1.5	-1.5	1	-5.1	-1	-4.5	-3.5	-3.5
19	ND2021×ND2009	-0.3	-3.6	1	-1.5	-1.5	-0.6	1.1	-4.6	-1	-2.5	-2.5	-2.5
20	NP2341×ND07-153	-0.4	-1.5	1	-1	-1.5	-0.9	1.6	-1.5	-1.5	-2.5	-1	-1
21	ND2013×B104	0	-5	0.5	-6.1	-4	-2.3	1	-2	-1	-2.5	-4	-4
22	LH61×ND246	-1.3	-4.5	0	-3.5	-1	-2.8	1	-4	-1	-3	-1	-1
23	ND08-343×ND07-153	0.5	-2	0.5	-1.4	-1	-1.4	1.1	-2.1	-1	-1.5	-2	-2
24	GEM5Derived×ND2002	1.2	-1.1	2	0	1	-0.7	1.4	-2.2	-3.5	-1.5	2	2
25	ND06-189×NK807	0	-2.5	1	-1.5	-1.5	-0.1	1	-1.2	-1	-2	0	0
26	ND2021×ND2005	-1.9	-5.1	0	-4.4	-2	-1.8	0.9	-4.2	-1	-2.5	-1.5	-1.5
27	NP2341×ND2000	-1.1	-1.6	0.5	-0.4	-2	-0.2	0.9	-2.2	-1	-2	-1.5	-1.5
28	ND06-144×ND2007	-1.2	-3.1	1	-4.5	-3	-1.3	1	-7.3	-1	-1.5	-1.5	-1.5
29	ND08-343×ND2002	0.9	-2.1	2	-1	0	-0.4	1.5	-0.3	-1	-2.5	-0.5	-0.5
30	NK779×ND2006	-1.2	-3.5	0	-2	-2.5	-2.3	1.5	-4.6	-1	-1.5	-1	-1
31	ND2019×B104	-0.5	-2.5	1	-2.2	-1	-1.8	1	-0.3	-1.5	-3.5	-1.5	-1.5
32	ND2021×KMN22	-2.4	-1.5	0.5	-1.6	-2	-1.3	0.9	-4.8	-1	-2	-2.5	-2.5
33	ND08-343×ND2007	-1.5	-1	1	-0.9	-2	-1.4	1.6	-5	-1	-1	-2.5	-2.5
34	PHG47×ND06-85	0.2	-2.1	0.5	-1.1	-2	-1.2	0.9	-0.5	-1	-1.5	-0.5	-0.5
35	ND203×ND2004	-1.1	-1.5	1	-4.1	-2.5	-1.6	1	-1	-1.5	-3.5	-0.5	-0.5

Table A10. Anthesis Silking Interval (days beteween anthesis and silking) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	-1.5	-4.1	1	-3	-2	-1.8	0.9	-3	-1	-1.5	-1.5	-1.5
37	A052×ND246	-2.2	-4.6	1	-4.5	-1.5	-0.7	0.9	-3	-1.5	-4.5	-0.5	-0.5
38	A052×ND2000	-0.7	-3.1	1	-2.1	-2	-1.3	0.9	-4.1	-1	-3	-1	-1
39	NK779×ND250	-4.1	-3.1	0	-3.1	-2.5	-1.4	1.5	-1.1	-1	-2.5	-0.5	-0.5
40	NP2341×ND2006	0.8	-0.6	0.5	-1.1	-1.5	0.7	1.5	-1.4	-1.5	-1	0	0
41	ND2013×KMN22	-0.4	-3	1	-2.7	-2.5	-1.8	1	-2.8	-1	-4	-2	-2
42	ND07-97×ND07-153	-1.3	-3.9	1	-2.1	-3	-2.3	1	-1.8	-1	-2.5	-2.5	-2.5
43	ND06-144×ND07-153	-0.4	-4	0	-1.4	-1.5	-1.9	1.6	-1.4	-1	-2	-2	-2
44	ND2014×KMN22	0.3	-3.1	1	-3	-2.5	-0.3	1.4	-1	-1	-3	-4	-4
45	LB2000×ND2000	-1	-2.5	1	-3.5	-2.5	-1.6	1.5	-2.5	-1	-2	-1.5	-1.5
46	ND265×ND2005	-1.4	-5.1	1	-3	-1.5	-1.8	0.9	-2	-1	-2	-2.5	-2.5
47	ND274×ND2005	-2.1	-4	0	-4	-1	-1.2	0.9	-2.5	-1	-3	-1.5	-1.5
48	ND08-53×NK807	-0.6	-2.6	1	-1.5	-0.5	-0.3	1	-1.5	-1	-3	-1.5	-1.5
49	ND06-144×ND2002	-1	-1.6	1	-2.6	-2	-0.4	1.5	0	-1.5	-2.5	0	0
50	PHG47× D291	-0.6	-2	1	-2.6	-1	0.7	1.5	-3.9	-1	-3.5	-1	-1
51	ND265×ND2009	-0.3	-0.4	1	-2.1	-1	-1.4	1	-1.8	-1	-3.5	-3.5	-3.5
52	LB2000× ND250	-2.1	-1.9	0	-2.5	-1	-1.4	1.9	-1.8	0	-2.5	0	0
53	ND07-97×ND2007	-0.3	-5.4	0.5	-2.8	-3	-3.5	-0.5	-5.4	-1	-3.5	-5	-5
54	ND2014×AP47	0.9	-1	1.5	-1.5	-0.5	-0.4	1.4	-0.5	-1.5	-0.5	-1	-1
55	ND06-189×AP47	-1.8	-1.9	0.5	-1.9	-1	-1.2	0.9	-3.5	-1	-6	-0.5	-0.5
56	NP2341×ND2014	-1.7	-1.5	0	-1.9	-0.5	-1.4	0.9	-2.4	-1.5	-2.5	-1	-1
57	ND08-343×ND2004	-0.4	-1	0.5	-0.9	-1.5	-0.8	0.8	-1	-1.5	-0.5	-1.5	-1.5
58	ND265×ND2004	-2	-2.5	1	-1	-2.5	-0.9	0.9	-0.5	-1	-3	-1.5	-1.5
59	ND08-53×PHJ40	-2.9	-2.5	1	-3	-1	-1.1	1	-1	-1	-1.5	-1.5	-1.5
60	GEM5Derived×ND2007	-0.5	-0.5	1	-3	-1.5	-0.9	1	-1.9	-1	-1.5	-1.5	-1.5
61	LH61×ND250	-2.4	-4.4	1	-3.6	-4.5	-3.4	0	-1.4	-1	-4	-2.5	-2.5
62	ND2019×KMN22	-0.2	-1.4	1	-2	-1	-0.9	1	-4.4	-1	-5	-2.5	-2.5
63	LH61×ND06-85	-4.3	-5.4	0	-5.9	-2	-3	1.1	-2.1	-1	-2.5	-3.5	-3.5
64	GEM 5 Derived×ND2004	0.8	-1	1	-0.5	-1.5	-0.9	0.9	-1.1	-1	-1.5	-1	-1
65	ND07-97×ND2014	-2.4	-5.9	0	-4	-4	-2.7	1	-3.1	-1.5	-5	-3.5	-3.5
66	ND08-53×ND2032	-3.3	-3	1	-1.5	-1.5	-0.9	0.9	-2.1	-1.5	-3.5	-4	-4
67	PHG47×ND270	-1	-2.5	0.5	-1	-0.5	-0.3	1.4	-1.1	-1	-1.5	-1	-1
68	ND07-97×ND2006	-0.1	-3	0.5	-1.5	-2.5	-1	1	-2.7	-1	-2	-1.5	-1.5
69	ND07-255×ND07-226	0	-5	1	-4	-1.5	-1.6	1	-2.7	-1	-3	-1.5	-1.5
70	ND07-212×NK807	-1	-3	1	-1.5	-0.5	-0.9	1	-1.5	-1	-3.5	-1	-1

Table A10. Anthesis Silking Interval (days beteween anthesis and silking) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	-0.3	-2.1	1	0	-2.5	-1.5	1.1	-2.4	-1	-1	0.5	0.5
72	ND07-212×AP47	-0.2	-2	0.5	-0.5	-1.5	-1.5	1	-2.4	-1	-1.5	0	0
73	A052×ND270	-0.3	-4.6	1	-4.3	-4	-1.6	1.1	-3	-1	-2.5	-1.5	-1.5
74	ND274×ND2009	-0.6	-1.7	1	-3.4	-1.5	-0.9	1	-1.1	-1	-0.5	-1	-1
75	A052×ND250	-0.4	-5.1	0.5	-3.9	-2.5	-1.8	1	-2.6	-1	-2.5	-1.5	-1.5
76	ND08-53×ND07-226	-2.3	-6.2	0.5	-4.4	-2.5	-1.5	1	-3.5	-1	-4	-3.5	-3.5
77	ND07-255×PHJ40	-0.5	-0.7	1	-0.4	-1.5	-1.4	1.4	-1.6	-1	0	-2.5	-2.5
78	ND06-144×ND2006	2.3	-2.7	1.5	-1.9	-2.5	0.5	1	-2.1	-1	-1	-0.5	-0.5
79	ND291×ND2032	-1.4	-2.2	1	-2	-1.5	0.4	1.6	-1.1	-1	-2.5	-1.5	-1.5
80	ND291×ND07-226	0	-5.1	0	-4.5	-4	-1	1	-3.5	-1	-2.5	-2	-2
81	ND07-255×NK807	-2.2	-2.5	1	-2.1	0	1	1	-1.9	-1	-2	-0.5	-0.5
82	ND06-189×PHJ40	-2.5	-3	1	-3.5	-0.5	-3	1	-2.4	-1	-1.5	-0.5	-0.5
83	ND2014×LP05	-0.2	-1.5	1.5	-0.9	-1	-1.6	1.6	-0.5	-1.5	-2	-2	-2
84	LB2000×ND270	-0.5	-4.1	1	-4.5	-1	-1.5	2.4	-1.5	-1	-1.5	-1	-1
85	ND274×Il5	-1.2	-3.5	0.5	-2.5	-1	-1.3	1	-2	-1	-1.5	-0.5	-0.5
86	LB2000×ND2014	-0.6	-4.1	0.5	-4	-2.5	-2	0.9	-3.5	-1	-5	-1	-1
87	ND07-212×LP05	0.2	-1.6	1	-1.5	-1.5	-1.4	0.9	-2	-1	-2.5	-1	-1
88	ND2019×AP47	-0.4	-2.1	1	-1	-3.5	-0.1	1	-1.1	-1	-2.5	-1.5	-1.5
89	LH61×ND270	-0.8	-5.6	-0.5	-2.5	-0.5	-2.2	1.5	-1.6	-1	-0.5	-4	-4
90	ND2013×ND2009	0.2	-3.5	1	-3.5	-2.5	-1	1	-0.4	-1	-3.5	-2.5	-2.5
91	ND06-189×LP05	-1.5	-3.9	1	-3.7	-3	-1	1.1	-5.9	-1	-4	0.5	0.5
92	ND07-255×LP05	-0.3	-1.8	1	-2.6	-2	-1	1	-1.9	-1	-1.5	0	0
93	ND2013×Il5	1	-1.8	1	-0.9	-1.5	-0.1	1.2	-1	-1.5	-2	-1.5	-1.5
94	ND2019×Il5	-0.3	-2.4	1	-1.6	0	-0.5	2	-0.6	-1.5	-2	-1	-1
95	**Thurston 77RM**	-1	-0.4	1	-0.5	-1	0.7	1.1	-1.6	-1	-3.5	0	0
96	**Pioneer 79RM**	-0.9	-0.5	1.5	-1	-0.5	0	1.5	-2	-1.5	-3	-0.5	-0.5
97	**Pioneer 80RM**	-0.1	-0.4	1	-2.5	-0.5	-0.9	1.5	-2.6	-1	-2	0	0
98	**Thurston 82RM**	0.8	0.1	1	-0.1	-1	-1.1	1	-0.6	-1.5	-0.5	-1	-1
99	**Syngenta 85RM**	-0.6	-1	1	-1.1	-1	-0.2	1.1	-1.1	-1	-1.5	-1	-1
100	**Monsanto 88RM**	-0.2	-0.4	1	-1.1	-0.5	-0.6	1.1	-1	-1	-1.5	1	1
	Experimental Mean	-0.8	-2.7	0.8	-2.3	-1.8	-1.2	1.1	-2.2	-1.1	-2.3	-1.4	-1.4
	CV%	-154.5	-40.2	66.8	-40.8	-65	-65.9	35.3	-60.6	-30.1	-63.2	-75	-75
	LSD,0.05	2.5	2.2	0.7	1.3	1.6	1.1	0.8	2.7	0.5	2.1	1.5	1.5
	MSE	1.5	1.2	0.3	0.9	1.3	0.7	0.2	1.8	0.1	2.2	1.2	1.2

Table A11. Grain Extractable Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	597.4	.	612.2	.	.	589	617	602.7	629.1	625.3	641.4
2	ND2014×B104	.	616.9	.	623.2	.	.	610.3	643.2	613	654.4	647.9	650.5
3	GEM5Derived×ND2001	656.5	606.5	658.7	625.9	.	.	610.1	627.2	622.1	638.3	652.2	646.5
4	ND265×ND2001	666	599.8	671.6	605.7	.	.	600.1	606.1	596.9	620	619.3	633
5	AP49×ND246	644	616.2	655.6	626.6	.	.	625	640.4	619.1	644.2	647.2	658.5
6	ND274×ND2001	670	605.1	656.7	617.6	.	639.8	578.5	618.6	594.5	614.7	628.8	637.5
7	ND290×PHJ40	666.5	599.9	676.5	606.2	589	611.8	611.4	628.3	637.3	626.9	655	639.5
8	ND203×ND2005	631	591.9	655.8	600.3	614.5	591.6	599.6	610.4	621	610.7	620.6	637.5
9	AP49×ND290	668	611.3	668.8	617.6	615	629.8	623.4	631.5	643.4	630.8	622.9	647
10	NK779×ND2014	657.5	601.4	652.7	610.6	585.5	639.1	581.7	600	610.6	604.6	623.2	620.5
11	ND290×ND2032	653	597.3	658.3	606.2	583.5	611.5	610.1	605.3	629.1	623.4	626.8	630
12	ND203×ND2002	667.5	617.3	640.5	611.7	592.5	621.4	638.1	632	645.9	637.8	627.9	652.6
13	PHG47×ND246	666	600.4	670.8	609.4	590.5	632.2	604.7	626	619.5	632.2	639.2	652.5
14	AP49×ND06-85	664	628.7	681.2	630.7	632.5	647.3	636.2	647.4	634.3	648.5	650.3	659.5
15	ND290×ND07-226	673.5	600.3	656.6	604.7	596.5	643.6	618	625.7	620.6	618.1	615.7	621
16	NK779×ND2000	657	607.5	677.2	619.2	584	653.6	600.1	601.9	629.4	593.1	629.3	643.5
17	AP49×ND291	668.5	628.8	676	635.8	607.5	634.6	643.9	645.1	636.2	650.8	666	669
18	ND07-212×B104	636.5	610.8	647.3	616.3	603	619.5	628.7	651.6	626.9	650.6	648.1	648
19	ND2021×ND2009	640	552.2	644.3	568.2	606	622	618.5	617.7	636	628.2	640.4	642.5
20	NP2341×ND07-153	669	618.8	673.8	630.2	589	591.6	597.7	625.3	613.5	643.5	653.2	648.5
21	ND2013×B104	589.5	597.8	644.5	600.4	584.5	615.2	577.3	628.3	579	636.4	614.9	615.4
22	LH61×ND246	677.5	611.3	655.8	617.3	594	624	577.1	626.5	594.3	639.2	636	635.5
23	ND08-343×ND07-153	634.5	585.4	650	583.1	611.5	621	616.4	603	628.4	625.1	644.7	625
24	GEM5Derived×ND2002	659.5	625.7	672.5	632.3	609	638	627.9	635.4	643.2	642.8	650.4	638
25	ND06-189×NK807	668.5	596.3	638.4	603.8	595	607.5	577.2	594.7	591.5	597	634.3	608
26	ND2021×ND2005	620	590.4	646	599.8	594.5	599	595.8	590.9	600.4	607	625.9	625
27	NP2341×ND2000	673	602.8	680.8	610.9	582	638	596.2	616.1	612.6	621.2	639.1	633.5
28	ND06-144×ND2007	621	565.7	621.1	594.4	623	631.7	608.4	598.1	628.4	625	620.7	627
29	ND08-343×ND2002	634	592.1	651.1	596.3	605.5	595.7	631.7	617.7	627.4	637.1	649	642
30	NK779×ND2006	621.5	588.3	650.6	605.3	554.5	635	583.9	578.8	627.5	589.4	610.2	609.4
31	ND2019×B104	643.5	595.9	637	600.8	604	625.4	606.8	631.6	617.8	625.3	630.4	635
32	ND2021×KMN22	613.5	576.8	642.3	579.3	576.5	609.9	592.1	593.8	602.1	602.1	616.5	595.5
33	ND08-343×ND2007	612	551.5	637.5	555	612	605.7	599.4	583.8	594.2	620.5	626.3	629.5
34	PHG47×ND06-85	682	626.8	678.4	632.3	561	.	631.4	633.2	627	649.2	658.9	654.5
35	ND203×ND2004	660	599.4	661.9	605.3	590.4	616.3	615.2	619.5	638.3	643.4	641.8	651.5

Table A11. Grain Extractable Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	656	622	660	632.3	605.6	617.9	638.8	630.8	644.2	642.4	627.9	637
37	A052×ND246	655.5	618.9	680.8	624.9	598	621.3	613.1	633.9	637.4	639.1	642.1	.
38	A052×ND2000	664	610.3	655.6	615.9	627	618.6	629.9	627.5	647.7	626.9	664.7	645.5
39	NK779×ND250	645.5	607.7	663.6	604.3	579	611.5	612.7	613.1	627.7	623.5	634	606.6
40	NP2341×ND2006	670	593.8	675	608.7	587	621.4	591.4	566.6	602.8	621.3	642.8	636
41	ND2013×KMN22	598.5	586.1	615.7	590.9	573	616.6	573.5	597.1	586.2	594	604.4	601
42	ND07-97×ND07-153	649	601.1	647.4	595.9	596.5	607.9	593.8	612.4	591	615.8	637	636.5
43	ND06-144×ND07-153	626	586.2	653.7	605.6	595	605.2	631.6	599.8	637.6	623.2	641.3	637
44	ND2014×KMN22	655	599.5	645.6	604.4	587	610.8	604.6	596.8	618.4	603.4	632.4	629
45	LB2000×ND2000	686	577.6	659	595.9	566.5	614.6	594.4	582.1	612.2	598.6	624.8	631
46	ND265×ND2005	645.5	605.7	663.1	608.4	587	617.9	583	589.8	595.1	604.1	628.9	635.5
47	ND274×ND2005	659	607.6	681.4	622.2	579	612.6	580.8	605.9	577.3	608.8	616.6	613.5
48	ND08-53×NK807	646.5	595.6	660.7	605	598	611.6	613.1	598.5	615	607.1	637.2	615
49	ND06-144×ND2002	678	611.9	669.7	604.4	611	630.6	623.4	607.6	637.6	626.7	640.5	645
50	PHG47× D291	694	639.1	670.2	647.4	622	628.4	613.1	621.6	625.6	645.5	650.3	666.4
51	ND265×ND2009	683	612.4	677.7	593.7	615.5	591	605	629.8	614	638.4	658.5	649
52	LB2000× ND250	618	588.4	613.4	599.1	572	608	593.9	596.6	602.3	606.3	629.1	630
53	ND07-97×ND2007	615.5	572.5	625.2	572.5	591	627	560.2	599	571.9	601.6	616.9	625.4
54	ND2014×AP47	695	641.8	685.1	633.6	643.5	652.5	641.6	660	631.2	666.8	682.1	673
55	ND06-189×AP47	664.5	621.4	658	628.6	588.5	572	596.5	622.8	602.5	624.6	654.4	637.5
56	NP2341×ND2014	657	600.5	653.1	614.1	581	632	565.5	599	601.3	614.1	630.5	626
57	ND08-343×ND2004	651.5	575.9	656.9	611.2	609.5	617	616	610.1	627.1	630.3	629.7	640
58	ND265×ND2004	652	611.3	674.2	609.7	612.5	607	607.2	620.7	623.8	622	630.8	635.5
59	ND08-53×PHJ40	640.5	588.7	643.2	600.1	594.5	.	602.5	619.8	607.4	619.1	617.6	619.5
60	GEM5Derived×ND2007	642	608.4	664.7	601.6	621.5	621	611.7	619.8	628.9	633.9	643.9	645.5
61	LH61×ND250	678	590	657.4	603.3	589.5	613	596.2	610.4	621.1	620.3	638.6	631
62	ND2019×KMN22	627.5	580.5	658.7	600.3	622.5	662.7	585	583.1	596.4	585.6	615.7	606.5
63	LH61×ND06-85	679.5	625.6	665.9	636.5	622.5	618.8	624.3	636.1	624.5	639	655.9	642.5
64	GEM 5 Derived×ND2004	644	596.9	664.8	618.8	619.5	636.7	615.8	609.5	626.3	629.7	644.6	648
65	ND07-97×ND2014	662	573.2	635.3	596.3	581	591.3	575.6	587.3	602.1	593.4	621.5	607.5
66	ND08-53×ND2032	613.5	583.6	640.4	591.8	603.5	593	598.7	596.1	612.4	598.4	615.6	608.5
67	PHG47×ND270	681	582	661.2	601.2	590.5	.	577	610.2	614.2	614.6	626.8	617
68	ND07-97×ND2006	620.5	572	651.5	591.4	570.5	.	580.3	598.3	573.9	611.4	630.9	621
69	ND07-255×ND07-226	641.5	604.8	678.5	611.3	617.5	617.1	621.6	616.9	631.5	633.5	635.7	641
70	ND07-212×NK807	671	598	669.9	623.3	617	632	616.3	626.4	631	632.3	643.9	641

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Table A11. Grain Extractable Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	662	613.3	663.8	618.1	604	615.4	602.1	612.2	626.6	615.5	638.7	627.5
72	ND07-212×AP47	693.5	617.8	688	627.1	619.5	644.4	648.4	660.4	642.4	661.8	662.8	659
73	A052×ND270	670.5	607.9	656.8	617.3	591.5	614.4	596.8	622.9	629.9	611.7	642.5	637.5
74	ND274×ND2009	683.5	616.8	649.2	616.1	600.5	636.4	583.2	614.3	586.2	620.4	639.7	626.5
75	A052×ND250	674	620.8	656.6	632.1	616	633.7	640.6	638.6	647	643.1	658.1	634
76	ND08-53×ND07-226	663.5	591	653.7	601.1	598.5	613.4	606.6	608.9	616.9	616.6	640.7	622
77	ND07-255×PHJ40	641.5	600.8	667.5	594.2	598	627.2	605.5	610	617.2	624.8	636.8	631.5
78	ND06-144×ND2006	643.5	592.8	639.3	603.7	559	585.4	600.2	590.6	614.9	595.6	633.5	626
79	ND291×ND2032	664.5	629.9	650.8	632.6	611.5	622.9	606	626.2	628.4	635.7	647.2	643.5
80	ND291×ND07-226	659	616.3	663.3	632.6	620.5	618.8	608.8	608.2	646	640.5	648.5	640.5
81	ND07-255×NK807	662.5	604.6	653.4	606.1	612	645	631.1	607.7	630.1	634.5	646.1	640
82	ND06-189×PHJ40	647	585.6	642.6	595.1	573.5	614.6	575.4	595.9	593.4	610.9	618.7	608
83	ND2014×LP05	651	603.7	658.9	612.3	616.5	624	619.7	626.8	634	631.7	642.5	653
84	LB2000×ND270	638.5	557.5	623.3	569.6	567	565	566.7	575.8	575.8	563.9	596.6	609.5
85	ND274×Il5	687.5	639.6	678.2	642.5	597.5	623.5	593.5	621.6	602.6	626.2	645.5	637
86	LB2000×ND2014	654.5	573.7	643.3	596.6	557.5	590.6	559.6	575.3	593.5	601.2	616.1	618.5
87	ND07-212×LP05	663	595.6	650.6	597.6	630	629	617.4	629.9	620.7	639.4	644.3	641.5
88	ND2019×AP47	683.5	625.6	678.9	637.2	623	651.7	636.2	651	638	645.7	677.4	660.5
89	LH61×ND270	627	572.4	636.4	614	589	611	565.5	613.6	585	608.8	630.7	614.4
90	ND2013×ND2009	621.5	599.6	616.9	598.5	574.5	599.1	574.7	615.6	589	619.6	630	621
91	ND06-189×LP05	632.5	591.3	632.3	593.7	590	619.4	577.5	600.4	591	615.2	636.5	623
92	ND07-255×LP05	639.5	599.3	652.5	606.7	626	593.4	617.3	628.6	633.3	642.6	648.1	657
93	ND2013×Il5	640	620.4	642.3	625.9	622	618.4	571.6	620.6	567.9	618.4	621.8	626.5
94	ND2019×Il5	671.5	617.8	657.7	628.7	625.5	617.4	599.6	609.6	608.2	626.6	638.5	632
95	**Thurston 77RM**	651	605.3	645.6	612.2	583.5	607.4	581.4	611.3	597.5	629.4	629.9	633
96	**Pioneer 79RM**	657.5	580.5	651.7	604.2	585	621.4	585	601.6	599.3	624.9	623.5	618.5
97	**Pioneer 80RM**	684	600.3	666	612.8	578.5	627.3	579.8	611.7	590.1	620.1	622.6	625
98	**Thurston 82RM**	653	589.8	662.8	609.3	596.5	622	535.6	623.3	556.3	609.3	647.3	635
99	**Syngenta 85RM**	675.5	614.2	662.3	633.7	601	644.5	574.9	640.9	597.9	634.9	642.5	658
100	**Monsanto 88RM**	646.5	608.8	654.8	633.7	617	634.4	576.1	628.4	622.4	638.7	648.3	640
	Experimental Mean	653.8	601	656.4	610	598.4	619.4	601.9	614.7	614.4	623.6	636.4	634.2
	CV%	2.4	1	2	1.2	3.1	2.2	1.4	1.3	1	1.1	1.6	1.4
	LSD,0.05	31.6	12.2	26.4	15	37.3	26.6	16.1	16.1	12.4	13.7	19.9	17.7
	MSE	253.7	37.8	176.5	57.1	353.2	180.3	66.2	65.9	39.3	47.6	100.6	79.8

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Table A12. Total Grain Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	692.2	.	696.5	.	.	676.6	703.5	688.5	706.6	699	709.4
2	ND2014×B104	.	697.7	.	692.8	.	.	694	710.9	697.8	719	713.4	716.7
3	GEM5Derived×ND2001	709.8	687.4	710.6	697	.	.	689.2	700.2	699.4	709.7	717.8	705.4
4	ND265×ND2001	720.7	694.5	732.3	695.6	.	.	683.7	692.8	685.4	704.5	701	707.3
5	AP49×ND246	711	699.6	717.9	697.6	.	.	706.3	716.6	708.1	721.6	717.1	724.4
6	ND274×ND2001	714.1	681.6	704.9	686.6	.	713.9	669.5	695	676.2	693.8	691.4	697.2
7	ND290×PHJ40	730.4	693.7	732.5	692.5	680.4	713.9	690	708.5	702.9	714.9	720.7	712.5
8	ND203×ND2005	692.1	688.9	710.9	690.4	698.4	700	680.4	692.3	687.7	700.9	701.5	701.3
9	AP49×ND290	723.6	699.5	727.7	702.6	693.4	704.9	698.1	712.1	703.1	714	700.7	709.2
10	NK779×ND2014	696.4	689.7	708.6	685	677.8	711	676.4	696.2	691	697.4	697.1	695.8
11	ND290×ND2032	715.7	694.6	720.6	696.7	687.2	712.5	687.3	702.8	698.8	711.1	711.1	704.4
12	ND203×ND2002	721.2	698.2	716	700.5	684.2	717.5	713.3	712.2	713	713.9	702	719
13	PHG47×ND246	717.5	684.4	714.4	689	667.2	725.5	681.7	700.3	694.3	704.6	698.6	709.3
14	AP49×ND06-85	722.9	709.3	736.5	707.5	711.3	729	709.1	721.8	703.7	726	726.4	723.4
15	ND290×ND07-226	710.9	684.6	716.2	684.4	674	712.9	691.7	706.5	689	703.9	698.5	690.5
16	NK779×ND2000	702.6	693.9	716.4	699.8	680.2	725.9	689.2	696.5	701.7	700.6	704.9	702.1
17	AP49×ND291	725	703.9	730.7	702.8	691.5	709.9	701.6	715.3	698.8	723.4	723.9	720.1
18	ND07-212×B104	706.4	683.3	707.7	685.9	693.1	719	696.9	710.9	696.8	715.6	713.8	707.9
19	ND2021×ND2009	708.9	659.9	708.1	664.6	684.4	701	687.7	697	689.6	705.1	710.7	709.1
20	NP2341×ND07-153	715.5	691.1	717.8	693.7	674.8	714.9	678.8	699	680.5	709.6	715.3	706.6
21	ND2013×B104	685.8	687.1	710.8	687.6	681.4	704.5	682.4	706.6	691.8	710.6	700.2	702.7
22	LH61×ND246	723.2	700.3	721.8	700.6	691.9	725.9	681.4	712.5	691.7	719.1	716.3	712.5
23	ND08-343×ND07-153	700.6	672.3	700.9	672.1	688.5	716.9	685.4	687.3	690.5	698.7	714.1	696.7
24	GEM5Derived×ND2002	733.9	704.5	725.2	707	694.6	736.9	706.4	714.8	709.8	718.1	716.5	707.6
25	ND06-189×NK807	720.2	689.7	711.1	691.4	666.9	728	675.6	689.4	686.8	694.2	706.2	694.8
26	ND2021×ND2005	697.3	678.2	701.9	681.6	679.6	712.9	674.7	686.7	683	694.6	703.7	697.5
27	NP2341×ND2000	725.1	692.8	721	695.4	676.8	722	683.8	700.8	696.1	709	716.5	704.3
28	ND06-144×ND2007	702.4	674.2	700.1	679.6	698.8	706	692.3	691.4	697.7	712.2	699.3	706.1
29	ND08-343×ND2002	714.7	679.7	716	678.1	692.8	706.5	706.3	702.2	702.8	715.8	719.4	712.2
30	NK779×ND2006	692.5	682.1	702.9	685.7	664.5	705.9	681.4	686.1	702.8	691.6	690.6	688
31	ND2019×B104	716.1	688	710	683.5	688.3	722	688.3	707.2	699.5	704.1	708	707.8
32	ND2021×KMN22	699.6	670.5	705.9	671	676.8	716	677.2	689.2	681.7	697.8	699.7	691.4
33	ND08-343×ND2007	683.4	660.4	699.9	656.1	691.3	696	681.2	682.9	683.7	704.9	704.3	704
34	PHG47×ND06-85	724.6	704.3	738.8	706.3	665.3	.	702.3	717.4	701	720.4	722.7	718.5
35	ND203×ND2004	723	693.1	725.5	695.2	690	711.5	704.1	707.5	715.1	721.7	714.8	721

Table A12.Total Grain Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	721.3	713.1	721.2	714.2	697.9	715	713.5	722.1	719.5	727.1	714.2	717.8
37	A052×ND246	711.4	699.1	729.6	703.9	687	723	697.1	710.2	711.7	714.2	709.3	719.5
38	A052×ND2000	722.6	697.6	723.7	697.7	699.3	701.9	707.5	704.5	708.2	712.5	729.7	712.1
39	NK779×ND250	701.4	687.8	702.6	689.2	677.4	706	680	703.4	686.6	700.7	702.7	688.3
40	NP2341×ND2006	719.5	681.7	725	683.4	681	718.5	680.1	669.6	689.7	706.3	712.3	708.5
41	ND2013×KMN22	691.4	683.4	705.9	681	688.7	714.9	670.3	695.8	675.5	695.8	698.6	697.6
42	ND07-97×ND07-153	702.6	678.6	704.8	672.9	677.3	697	670.8	686	670.2	692.1	704.4	699
43	ND06-144×ND07-153	693.8	681.6	712.9	686.6	687.6	699	694.6	690	699.9	705.5	715.6	703.2
44	ND2014×KMN22	715.7	690.3	711.6	691.8	679.1	712	686.4	691.5	687.8	697.9	706.8	702.6
45	LB2000×ND2000	715.4	676.1	715.3	684.8	666.6	709.9	685.5	682.8	694.5	700.3	707.3	696.4
46	ND265×ND2005	710.3	693.1	713.7	688.9	681.7	714.5	668.4	687.9	674.1	695.8	711.5	701.9
47	ND274×ND2005	703.5	681.3	712	691.8	669.3	704.9	657.1	686.2	654.9	687.9	696.5	683.4
48	ND08-53×NK807	709	690.1	727.8	688.4	696.3	711.9	690.4	693.8	696.9	702.9	715.5	692.6
49	ND06-144×ND2002	723.2	696.9	738.7	691.1	698.7	736.9	704.7	706	710.6	716.2	724.2	715.3
50	PHG47× D291	724.4	703.4	730.9	702.6	689.2	721.5	683.3	695	691.4	712.7	713.1	711.9
51	ND265×ND2009	724.9	691.7	729.9	684.7	693	712.9	678.3	703.4	688.8	713.3	718.2	712.9
52	LB2000× ND250	689.1	679.7	690.1	682.8	662.7	719.9	675.1	688	677.5	696.1	705.2	699.7
53	ND07-97×ND2007	673.9	678.8	699.8	660.9	682.7	723.9	679.1	689	690.5	689.1	700.1	698.6
54	ND2014×AP47	727.7	703.3	728.9	699.1	705.3	732.5	699.5	717.4	698	720.7	726.6	720.8
55	ND06-189×AP47	706.4	690.9	714.1	694.3	677.8	689.9	676.8	686.6	685.7	703.4	708.3	701.7
56	NP2341×ND2014	726.9	692	713.3	690.4	676.1	730.9	670.7	697.3	684.7	705.4	714.9	704.7
57	ND08-343×ND2004	707.9	668.7	720.6	694.9	689.8	714.9	705.4	700.5	703.2	709.4	713.3	715.1
58	ND265×ND2004	725	698.7	733.8	691.1	697.1	714.9	693.9	704.3	704.7	714.9	711.9	714.8
59	ND08-53×PHJ40	715.6	682	712.3	686.7	689.4	.	687.5	707.4	693.4	704.6	705.3	700.8
60	GEM5Derived×ND2007	706.6	679.5	715.1	675.4	697.4	717.9	690.9	699.5	694.4	707.6	709.5	709.7
61	LH61×ND250	722.5	682.1	714.4	690.8	686.5	717.5	682.9	699.9	686.8	708.6	713	699.6
62	ND2019×KMN22	699	678.9	720	679.3	692.3	713.9	669.7	686.2	672.6	690.2	694.3	692.2
63	LH61×ND06-85	733.1	708.5	730.1	709.4	704.1	730.1	703.5	717	705.9	722.1	726.6	710.2
64	GEM 5 Derived×ND2004	718.3	691.2	720.9	694.2	695.6	708.9	697.1	694.8	700.7	710.9	720.3	716.2
65	ND07-97×ND2014	712.9	674.7	711.5	679.2	678.1	701.5	673.9	685.8	681.1	691.1	708.4	693.3
66	ND08-53×ND2032	706.1	684.9	711	691.3	697.8	710	685.7	698.3	693.5	700.7	706.8	696.2
67	PHG47×ND270	707.5	671.7	719.7	686.8	673.4	.	667.8	692.9	688.2	693.7	700.9	689.8
68	ND07-97×ND2006	699.6	675.2	712.6	674.9	670.9	.	678.5	692.8	677.1	698.9	707.9	688.4
69	ND07-255×ND07-226	703.1	683.6	711.9	682.1	688.3	709	686.4	691.1	685.4	704.6	703.5	697.9
70	ND07-212×NK807	725.1	688.3	733.4	696.6	696.7	719	697.2	706.3	702.3	711.9	719.1	707.5

Table A12.Total Grain Starch (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	714.4	693.2	722	692.3	683.1	700.9	678.2	694.6	687.1	700	709.4	700.8
72	ND07-212×AP47	730.6	696.7	726.4	690.3	690.2	719.5	701.6	715.2	697.5	720.2	719.5	711.9
73	A052×ND270	717.1	694.4	722.4	700.7	680.2	710.9	690.7	702.8	708.4	695.8	712.7	703.1
74	ND274×ND2009	706.4	684	690.2	681.5	685.1	705.9	668.8	687.5	672.2	691.6	701.4	693.7
75	A052×ND250	708.2	702.3	710.8	704.9	693.3	715.5	693.9	703.8	704.2	710.1	720.8	702
76	ND08-53×ND07-226	710.1	681.9	709.3	683	682.5	712.9	688.4	694.9	684.1	701.4	709.5	695.8
77	ND07-255×PHJ40	703.9	683.5	722.6	681.6	680.9	712	688.7	695.5	692.8	702.9	711.7	705.7
78	ND06-144×ND2006	692.6	693.9	708.6	691.4	666	712.9	692.1	699	696.7	703.1	712.3	706
79	ND291×ND2032	722.1	706.2	725.2	707.6	696	712	689.1	715.3	704.9	718.9	725	713.9
80	ND291×ND07-226	715.7	694.1	715.8	695.1	692.5	712.5	687.4	690.4	695	709.3	715.2	699.5
81	ND07-255×NK807	709.9	693.5	720.4	692	688.8	704.9	693.7	698.5	702.2	711	710.2	711.1
82	ND06-189×PHJ40	695.4	684	704.7	685.2	676.7	707.5	673.3	685.7	685.5	698.9	691.4	692.4
83	ND2014×LP05	711.3	680.9	719.5	684.2	691.4	726.9	687.7	703.4	695.8	707.6	712.4	708.7
84	LB2000×ND270	685.4	663.4	694.3	671.8	678.9	709.1	668.8	680.3	670.5	674.7	686.1	686.8
85	ND274×Il5	704.7	700.6	710.6	701.6	685.3	714.5	671.4	698.8	669.9	700.5	705.7	697.8
86	LB2000×ND2014	709.6	674.9	708.5	685.1	666.6	704	670.9	687.7	686.1	701.6	705.4	696.1
87	ND07-212×LP05	715.9	673.6	717.1	673.9	694.7	704.9	684.1	699.8	691.1	709.8	716.9	710.8
88	ND2019×AP47	719.2	694.3	717.5	693.9	700.8	728	692.5	708	693.6	705.6	721.2	708.4
89	LH61×ND270	710.5	674.4	721.1	694.7	685.3	715.9	678	702.6	682.2	703.8	708.9	700.9
90	ND2013×ND2009	689.3	682.1	693.7	680.1	672.7	694	676.1	696.7	680.1	699.5	700.8	694.6
91	ND06-189×LP05	695	682.5	700.1	680.5	695	703	666.1	687.1	678.9	699.2	703.5	692.7
92	ND07-255×LP05	692.6	675.5	705.6	679.2	690.9	706.9	686.4	698.9	695.6	707.2	711.8	712
93	ND2013×Il5	697.8	699.8	710	699.8	700.9	713.9	668.8	696.1	677.1	702.7	706.7	703.8
94	ND2019×Il5	701.3	698.6	714.5	694.4	694.5	707.9	680.2	692.6	680.6	702.4	710.3	698.3
95	**Thurston 77RM**	707.5	694.8	713.8	699.8	677.3	725.9	681.1	698.7	688.8	706.1	707.5	705.3
96	**Pioneer 79RM**	723.9	689.9	726.5	693.8	695.9	714.9	694.6	700.6	706.2	710.9	717.8	712
97	**Pioneer 80RM**	722	695.9	728.7	699.7	686.4	723	699.4	704.6	709.2	712.5	708.6	711.2
98	**Thurston 82RM**	714.3	690.4	732.2	697.3	696.2	730	677.3	702	690.1	708.2	719.4	713.3
99	**Syngenta 85RM**	723.4	697.6	727.3	701.9	685.1	728.5	681.2	711.5	698.8	713.8	719.9	715.6
100	**Monsanto 88RM**	709	702.2	732.2	705	699.9	727.9	689.7	709.7	704.7	716.9	720.1	718.3
	Experimental Mean	710.6		716.2	690.1	686	714.1	686.1	699.2	692.6	706.2	709.9	704.8
	CV%	1.1		1.1	0.6	1.6	1.4	0.6	0.6	0.5	0.5	0.8	0.7
	LSD,0.05	15.3		15.6	8.5	21.8	19.2	8	8.8	6.4	7.6	11.4	9.2
	MSE	59.4		61.7	18.5	120.9	93.4	16.1	19.5	10.5	14.5	32.9	21.7

Table A13. Grain Oil (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	41.9	.	40.1	.	.	39.9	40	37.2	39.3	42.8	39.8
2	ND2014×B104	.	41.3	.	44.6	.	.	38.4	40.9	36.4	40.3	47.6	44.6
3	GEM5Derived×ND2001	45.8	43.2	50.9	45.5	.	.	41.6	40.9	38.7	37.6	41.7	47.4
4	ND265×ND2001	39.1	39.7	48.4	41	.	.	33.3	36.2	33	35.1	44	44.8
5	AP49×ND246	43.1	40	46.9	42	.	.	37.4	38.3	36.5	39.4	43.6	39.5
6	ND274×ND2001	46.6	44.5	56	45.9	.	41.8	45	40.6	43	39.6	43.8	44.7
7	ND290×PHJ40	41.1	37.9	50.9	41.5	40.1	41.3	34.1	38.3	31.8	37.6	41.9	46.6
8	ND203×ND2005	49.1	47.6	57.3	46.2	42.5	46.1	46.7	47.4	47	45.6	49.8	52.4
9	AP49×ND290	49.7	38.6	52.9	39.8	44.2	46	38.5	36.8	40.1	37.3	45.7	47
10	NK779×ND2014	51.7	42.1	52.2	46.5	44.1	44.7	47.8	43.4	44.9	41.1	46.2	51.7
11	ND290×ND2032	45	42.5	55.1	43.8	39.3	44.2	38.3	39	35.2	38.1	43.8	46.6
12	ND203×ND2002	53.6	45.9	49	45.4	43.5	44.4	38.8	42	41.1	40.4	46.2	44.9
13	PHG47×ND246	50.4	45.6	56.4	44.7	43.8	43.6	39.5	47.3	38.7	43.9	46.8	47.1
14	AP49×ND06-85	48.9	45.3	55.2	44.1	41.7	44	40.9	39.6	41.5	38.5	43.6	45
15	ND290×ND07-226	54.4	42.9	58.5	47.2	44.4	46.1	42.2	43.1	42.5	43.3	48.6	50.4
16	NK779×ND2000	46.9	41.8	54	44.6	44.5	45.6	46.5	43	44.9	43.3	48.5	51.1
17	AP49×ND291	47.3	37.6	52.3	40.6	43.4	42.8	39.3	36.8	38.4	34.6	41.4	45.6
18	ND07-212×B104	49.8	44.4	55.9	46.7	43.3	51.4	43.3	43.4	41	42.7	44.9	47.6
19	ND2021×ND2009	57.9	45.8	63.5	46.7	42.3	46.3	42.4	41.4	43.7	40.8	46.6	48.9
20	NP2341×ND07-153	49	45.8	61.6	47.3	45.3	44.3	47.7	46.2	47.9	46.4	49.2	52
21	ND2013×B104	56.9	48	62.9	48	45.8	55.1	38.9	41	36	44.4	48.9	46.9
22	LH61×ND246	49.1	42.4	51.7	41.6	40.8	43.7	41	39.9	39.9	37.5	37.9	43.3
23	ND08-343×ND07-153	50.6	46.4	58.4	45.2	47.5	51.6	43.7	47	42.4	45.6	50.2	52.3
24	GEM5Derived×ND2002	42.6	44.2	50.8	44.3	39.4	41.3	36.8	38.6	37.4	38.7	42.2	45.9
25	ND06-189×NK807	55.4	49.1	52.4	48.2	44.6	45.4	45.3	44.1	45.1	44.8	50.6	48.8
26	ND2021×ND2005	44.2	45.8	54.1	46	42.6	43.5	45.8	41.6	44.5	42.8	46.1	51.6
27	NP2341×ND2000	45.6	43.3	50.7	40.9	42.2	42.5	42.3	39.6	43.7	38.6	44.2	51.5
28	ND06-144×ND2007	60.2	52.5	61.6	51.4	44.1	56.8	43.4	47	47.3	43.8	54.2	48.8
29	ND08-343×ND2002	45.7	46.1	53.2	45.2	42.8	43.2	36.4	42.2	38.4	41.7	45.7	45
30	NK779×ND2006	42.2	42.3	51	41.2	39.4	46.7	36.9	39.1	38.4	39.7	43.9	46
31	ND2019×B104	43.7	46.5	50.1	45.8	43.2	45	42.2	40.3	37.7	41	47.6	43
32	ND2021×KMN22	46.2	42.8	48.7	43.6	39.2	43.3	42.5	38.3	42.2	40	44.8	46.1
33	ND08-343×ND2007	62.9	50.2	70	51	43.6	59.3	47.8	47.4	43.7	45.2	53.8	45.8
34	PHG47×ND06-85	50.1	42.4	53.8	45.1	47.8	44.6	37.7	42.1	39.1	41.2	46.7	46.5
35	ND203×ND2004	49.7	42.9	49.2	42.1	43.1	43.3	36.5	41.9	36	37.8	45.6	45.2

Table A13. Grain Oil (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	46	41.9	55	45.8	40.4	46	40.3	40.1	36.7	38.9	47.9	46.1
37	A052×ND246	44	40.3	55.9	41.6	41.5	42.4	39.1	45.3	36.7	40.9	43.1	45.9
38	A052×ND2000	47.6	44.3	52.4	46.5	43.2	50.5	39	43.2	41.9	42.7	42.1	47.9
39	NK779×ND250	46.8	46.9	60.2	49.1	47.2	49.2	47.5	45.6	44.9	44.8	50.3	55.5
40	NP2341×ND2006	46	39.8	51.2	42.1	42.4	42.4	40.7	41.6	37.8	39.3	46.4	45.2
41	ND2013×KMN22	50.3	45.5	58.3	47.7	41.6	43.3	43.2	42	42.9	42.6	47.7	50.3
42	ND07-97×ND07-153	56.9	45.6	62.6	45.5	46.2	49.2	43.8	44.8	41.3	42.5	49.9	47.8
43	ND06-144×ND07-153	54.8	47.7	60.3	49.4	49.1	48.8	44.3	46.8	43.8	45.5	50.4	52.2
44	ND2014×KMN22	44.3	41.9	51.3	42.9	39.8	41.6	40.8	39.4	39.3	37.2	42.6	47.6
45	LB2000×ND2000	58.2	48.3	55.2	47.7	48.8	46.5	47.6	45	44.4	43.2	51.6	52.5
46	ND265×ND2005	44.7	42.8	50.9	44.6	39.9	42.6	41.3	39.7	40.7	38.3	42.7	47.1
47	ND274×ND2005	53.6	49.1	59.3	45.1	49.2	46.3	52	46.8	50.2	44.3	51	52.6
48	ND08-53×NK807	45.7	43.1	52.9	44.1	41.8	44.1	41.1	44.3	41.9	43.9	44.7	47.5
49	ND06-144×ND2002	56.7	45	56.3	47.6	42.9	45.7	40.2	39.4	40.5	41.1	46.7	46.1
50	PHG47× D291	54	40.8	55.4	42.2	43.6	46.8	41.1	43.4	37.2	39.6	50.1	47.7
51	ND265×ND2009	51.1	42.7	53.3	42.6	37.7	46.2	40.7	38.3	36.8	36.7	43.9	43.3
52	LB2000× ND250	58.4	50.3	59.4	49.7	53	49.2	49.9	46.2	47.2	45.2	50.1	54.1
53	ND07-97×ND2007	63.9	48.6	59.9	48.1	42.6	49.3	39.9	42.8	35.9	41.4	49.4	46.6
54	ND2014×AP47	50.2	40.7	52.2	44.5	36.5	44	41.5	36.8	39.9	36	42.7	45.6
55	ND06-189×AP47	47	45.1	50.8	45.4	43.6	48.9	40.8	41.5	40.1	41.5	45.4	48.1
56	NP2341×ND2014	44.6	45.5	53.8	46.2	44.9	45	42.3	41	42.2	41.4	47.4	46.7
57	ND08-343×ND2004	53.4	46.3	53	43	41.4	46.3	32.5	43.4	32	39	46.4	44.4
58	ND265×ND2004	37.8	40.9	48.7	42	40.2	45.2	32.9	36.8	32.6	35	41.6	42.9
59	ND08-53×PHJ40	42.9	43.2	49.3	45.8	38.8	41.9	35.7	39.1	33.9	41.4	43.9	44.2
60	GEM5Derived×ND2007	51.3	47.8	62.4	49.8	39.5	48.3	43.8	42.2	42.5	41.9	48.3	47.3
61	LH61×ND250	52.6	47.6	55.5	47.9	42.7	48.1	46.2	41.9	45.8	40.9	46.3	49.1
62	ND2019×KMN22	47.8	43.4	52.7	47.3	39.8	42.9	43.6	38.7	41.8	37.9	44.4	46.6
63	LH61×ND06-85	49	42.8	47.3	46.4	41.9	44.6	41.4	40.6	39.7	36.8	43.3	43.7
64	GEM 5 Derived×ND2004	42.8	39.4	48.7	43.8	42.7	44	36.8	39.1	36.4	36.5	43.2	44.2
65	ND07-97×ND2014	56	46.9	53.3	49.5	41	43.9	41.8	42.9	44.2	40.5	46.3	47.7
66	ND08-53×ND2032	42.1	39.2	53.6	41.6	41.3	44.9	36.5	37.5	39.3	39.2	44.8	43.4
67	PHG47×ND270	58.4	44.2	62	49	44.7	45.8	47.6	46.9	42.5	43.6	49.4	50
68	ND07-97×ND2006	47.2	41.1	54.5	43.2	40.8	48	39.1	39.9	36.8	40.3	45.7	45.9
69	ND07-255×ND07-226	50.3	50.8	62.6	49.9	44.7	47.9	44.7	45.8	47.7	44.8	50.9	51.3
70	ND07-212×NK807	47.4	45	48.9	46.4	41.9	46.1	42.3	40.6	41.6	41.7	47	47.7

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Table A13. Grain Oil (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	51.2	44.6	55.5	43.3	42.7	43.4	45.8	43	41.9	43.1	46.1	48.8
72	ND07-212×AP47	49.6	42.6	52.2	46	41.8	46.5	42.2	37.9	42.6	39.1	43.4	45.1
73	A052×ND270	58.4	42.9	56	47.6	42.4	41.8	40.3	42.8	38.9	43	45.3	51.6
74	ND274×ND2009	59	45.4	73.8	51.9	41.8	46	51	45	48.7	46.2	50	50.8
75	A052×ND250	51.6	43.2	61.4	45.3	44.4	49.3	45.8	46.1	42.8	44.6	44.1	51.9
76	ND08-53×ND07-226	51.7	46.2	57.7	49	45.2	44.2	42.5	43.2	45.5	44.6	51.1	45.4
77	ND07-255×PHJ40	49.9	43.4	55.7	46.2	43.8	44.3	39.1	40.1	39.1	40.5	47.5	45.8
78	ND06-144×ND2006	49.6	43.5	52.7	45.6	42.3	45	36	41.8	36.9	40.9	47.8	46.5
79	ND291×ND2032	51.9	42	47.3	42	40.8	44.3	34.3	35.5	33.6	36.1	41.1	41.9
80	ND291×ND07-226	45.9	43.2	53.8	47.3	43.8	45.3	39.2	41.3	42.1	41.6	46.4	48.8
81	ND07-255×NK807	48.1	47.1	51.8	48.2	44.8	46.2	43.6	41.6	43.1	42.7	46	46.8
82	ND06-189×PHJ40	55.4	49.5	55.6	47.5	42.2	46.6	42	43.6	40	41.1	49.7	48.4
83	ND2014×LP05	53.5	46.8	51.6	47.2	43.3	48.8	42.9	42.1	43.4	42.1	49.3	50.8
84	LB2000×ND270	58	49.6	57.5	48.8	43.6	46.1	49	43.8	47.9	44.4	48.8	52.8
85	ND274×Il5	51.7	44.5	57.2	46.4	43.5	44.4	45.6	44.9	43	42	45.6	49.7
86	LB2000×ND2014	54.1	47.7	55.4	48.7	44.8	47.8	45.4	45	42	42.3	49.4	50.5
87	ND07-212×LP05	45.5	47.7	58.5	46.9	44.4	50.5	46.1	44.4	46.2	42.8	48.3	51.2
88	ND2019×AP47	51.8	42.7	54.9	45.4	42.1	44.8	42.5	37.5	40	40.3	44.1	45.1
89	LH61×ND270	49.9	47.3	60.2	48.9	42.8	46.5	43.4	41	42.2	39.7	45.8	45.8
90	ND2013×ND2009	61.5	49.3	65.1	50.5	45.3	56.4	45	42.9	45.4	43.9	52.9	50.1
91	ND06-189×LP05	53.5	46.5	61.6	49	42.9	48	49.7	49.7	49.8	46.1	52.7	50.3
92	ND07-255×LP05	58.7	46.4	61.1	47.9	43.8	49	42.6	44.3	43.8	43.6	48.9	45.9
93	ND2013×Il5	53	47.9	54	50	44.4	47.6	42.6	44.1	39.6	44.7	50.6	49.7
94	ND2019×Il5	56.1	44.7	49.1	47	43.6	47	41.3	40.3	37.5	39.7	45.6	49.6
95	**Thurston 77RM**	48.1	42.9	49.8	42.7	42.8	43.4	39.5	44.8	37.5	40.3	45.1	48
96	**Pioneer 79RM**	43.4	43	45.1	43.3	40	45.2	36.3	45.9	35.3	43.6	47.1	47
97	**Pioneer 80RM**	50	39.6	43.2	40.6	39.3	40.5	36.5	41.6	31.8	40.4	44.2	43.7
98	**Thurston 82RM**	45.1	37.9	46.6	36.2	36.7	40.6	31.6	38.9	28.3	35.5	39.5	43.1
99	**Syngenta 85RM**	44.4	42.1	47.1	45.7	38.4	41.4	37.4	39.7	33.9	39	46	47.8
100	**Monsanto 88RM**	44	44.4	50.2	46.6	41.1	42.3	36.7	39.2	40.3	38.6	48.1	43
	Experimental Mean	50	44.4	54.7	45.6	42.8	45.9	41.6	42	40.6	41.1	46.5	47.5
	CV%	8	3.6	4.7	3.7	6.4	5.2	4.3	4.3	3.8	3.8	4.1	3.6
	LSD,0.05	8	3.2	5.1	3.3	5.5	4.7	3.6	3.6	3.1	3.1	3.8	3.4
	MSE	16.2	2.6	6.7	2.8	7.6	5.6	3.2	3.2	2.4	2.5	3.6	3

Table A14. Grain Protein (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	113.9	.	109.3	.	.	128	103.2	120.1	98.1	106.9	97.4
2	ND2014×B104	.	106.4	.	106.7	.	.	113	93.9	105.2	87.4	84.2	86.5
3	GEM5Derived×ND2001	98.5	115.5	96.6	106.3	.	.	119	104.7	108.7	99.7	89	94.6
4	ND265×ND2001	85.5	111.7	68	109	.	.	133.5	115.4	127.6	105.1	103.6	94
5	AP49×ND246	94.1	102	84.7	100.4	.	.	100	84	94.5	83	86.7	81.6
6	ND274×ND2001	83.4	116.7	82.1	110.2	.	96.4	131.5	106.2	122.5	107.4	114.4	103.1
7	ND290×PHJ40	68	113	64.1	114.3	132.7	104.7	122	97.7	107.6	91.3	84.6	86.9
8	ND203×ND2005	106	110.1	82.1	107.7	112.5	114.8	119.5	105.9	108.7	98.1	97.9	91.9
9	AP49×ND290	74.6	108.3	67.8	105.1	114.5	97	112	96.4	103.7	94.6	102.8	90.3
10	NK779×ND2014	108.8	114.5	89	116.3	130.3	98.8	122	104.3	112.5	106.9	105.2	99.5
11	ND290×ND2032	83.4	109.5	75.3	107.4	129.9	106.1	117	105.5	109.2	96.8	96.2	96.2
12	ND203×ND2002	79.3	103.5	85.2	99.8	124.4	97.7	97.4	91.7	93.8	89.6	101	81.9
13	PHG47×ND246	77	115.7	81.2	114.8	143.3	108.5	127	97	111.3	96.5	104.8	90.6
14	AP49×ND06-85	72	91.4	61.1	91	98.3	84.3	95	83.2	96.7	79.3	78.7	76.7
15	ND290×ND07-226	86.1	116.2	78.3	117	136.7	101.9	112	97.3	111.1	97.7	105.4	110.4
16	NK779×ND2000	96.5	107.4	81.1	104.7	130.4	106.2	114	106	99.6	102.1	95.9	92
17	AP49×ND291	75	103.7	71.1	103.8	116.6	90.1	105	96.5	107.7	88.5	81.1	80.2
18	ND07-212×B104	86	113.8	87.2	110.8	117.1	94.9	109.5	90.7	104.8	88.3	91.5	92.6
19	ND2021×ND2009	79.2	140.4	84.4	141.1	126.8	106.2	115.5	109.2	111.3	99.9	90.7	86.3
20	NP2341×ND07-153	77.3	108.7	74.6	106.4	133.5	107.1	122	101.1	117.1	87.2	81	84.9
21	ND2013×B104	94.9	105.8	75.6	111.2	126.1	91.4	114	94.9	104.5	84.8	97.4	96
22	LH61×ND246	77.8	97.8	78.5	98	118.8	98.4	123.5	91.6	109.7	85.1	89	88.3
23	ND08-343×ND07-153	92.9	131.9	94	136.6	116.6	105	121	114.4	114.2	102.4	83.8	97.8
24	GEM5Derived×ND2002	65	100.1	77	95.8	120.2	88.4	106.5	96.1	101.5	88.4	90.6	94.4
25	ND06-189×NK807	75.5	106	84.1	105.8	142.5	98.7	125	111.8	116	104.2	88.4	101.9
26	ND2021×ND2005	103.4	122.6	95	120	132.3	117.1	125.5	121.9	124	109.1	99.2	94.7
27	NP2341×ND2000	76.4	112.4	73.5	112.6	135.2	97	117	108.9	106	99	87.7	91.2
28	ND06-144×ND2007	82.4	118.5	81.5	111.6	109.2	89.8	106	105.6	93.2	87.3	90.9	93.6
29	ND08-343×ND2002	86.6	125.2	85.8	123.4	117.3	115.7	108	104.6	105.6	88.3	82.7	89.2
30	NK779×ND2006	109.8	124.5	92	121.2	151.8	100.3	131.5	125.5	104.9	112.2	114.6	116.4
31	ND2019×B104	82.8	108.5	87	116.3	120.5	98.5	115	96.7	109.4	99.6	91.7	99.2
32	ND2021×KMN22	103.1	138	96.4	136.6	141.2	112.8	128.5	124.3	125.1	110.4	105.8	111
33	ND08-343×ND2007	95.3	137.1	82.9	139.2	118.5	100.6	120.5	117.6	121.1	96.2	88.7	97.4
34	PHG47×ND06-85	73.3	97.8	58.8	94.4	137.4	89.6	108	82.9	109.4	81.5	78.8	81
35	ND203×ND2004	70.4	108.7	68.5	103.3	116.9	103.3	105.5	95	94.8	85	88.6	79.1

Table A14. Grain Protein (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	78.3	88.3	75.3	84.1	116.1	94.6	94	83.7	88.4	81.4	84.6	80.9
37	A052×ND246	89.8	101.6	63.3	95.2	121.2	94	112	85.7	98.4	84.8	93.8	78.1
38	A052×ND2000	73.3	104.7	64.4	103.6	108.6	94.7	101.5	98.9	93	90.1	75	84.8
39	NK779×ND250	97.5	113.4	89.1	109.5	133.5	109.1	124.5	98.9	118	99.6	95.6	103.8
40	NP2341×ND2006	80.6	126.2	72.8	123.7	128.8	102.8	130.5	139.2	119.3	99	87.4	92.2
41	ND2013×KMN22	110.4	117.2	84.1	114.8	124.8	107.9	132	112.3	123.5	107.6	101.7	97.1
42	ND07-97×ND07-153	88.7	121.7	80.5	129.2	130.6	112.6	135	116.5	134.2	111.4	94.9	99.7
43	ND06-144×ND07-153	102.9	121.3	79.5	111.3	114.8	111	108	108.8	103.2	94.2	82.9	89.8
44	ND2014×KMN22	86.9	119.5	91.4	115.5	135.2	116	121	120	121	114.1	102.1	98.5
45	LB2000×ND2000	80	122.8	80.1	114.9	137.6	110.5	113	120.1	108.5	104.5	89.7	98
46	ND265×ND2005	84.9	108.5	81.5	111.7	133.2	106	140.5	122.3	134.5	109.4	94.5	95.5
47	ND274×ND2005	85.9	113.3	74.9	107.3	135.5	109.7	137	109.3	136	108.8	100.4	111.8
48	ND08-53×NK807	90.9	114.9	66.5	114.7	115.1	101.5	117	107.5	102.7	97.1	88.1	106.1
49	ND06-144×ND2002	72.6	106.1	56.7	111.1	111.4	94.8	107	105	94.6	91.1	77.1	85.4
50	PHG47× D291	70.7	100.4	57.9	98.3	119.8	101.7	128	110.4	126.4	93.4	83.3	84.9
51	ND265×ND2009	70.1	112.2	68.5	121.9	122.8	106.6	130	103.8	118	94.8	85.7	88.3
52	LB2000× ND250	101	117.2	98.5	112.8	139.4	101.4	125	114.5	126.6	105.6	95.4	92.7
53	ND07-97×ND2007	106.7	118.9	83	137.3	128.1	105.7	124.5	111.8	111.6	114.5	96.8	100.2
54	ND2014×AP47	65.2	103.1	68.4	103.6	112.3	94.3	110	97	109	89.4	78	79.7
55	ND06-189×AP47	93.2	112.4	78	108	132.6	112.4	130.5	110.1	123.4	101.3	93.4	95.5
56	NP2341×ND2014	68.6	110.1	81.4	109.8	131.2	97	133	110.3	121.4	100.1	85.2	95.8
57	ND08-343×ND2004	84.7	133.9	72.4	112.3	119.9	99	111.4	104.8	114.9	95.5	88.6	87.9
58	ND265×ND2004	77.7	108.5	64.5	112.8	114.4	105.4	120.5	103	106.6	97.8	95.8	87.3
59	ND08-53×PHJ40	86.8	119.6	85.2	114.7	126	101.8	123	98	120.6	94.4	100.2	103.2
60	GEM5Derived×ND2007	84.5	120.4	76.9	121.9	116.4	95	112	106.4	106.9	97.7	89.1	90.3
61	LH61×ND250	76.9	115.5	77.2	103.8	122	103.9	113.5	100.5	107.6	93.4	89.1	95.7
62	ND2019×KMN22	107.7	125	78.2	119.2	122.3	113.5	138	127.6	131.7	124.7	113.4	108.5
63	LH61×ND06-85	65.9	97.2	68.7	86.3	104.4	95.5	99	85.4	99.2	87.1	78.4	92.2
64	GEM 5 Derived×ND2004	84.9	118.4	77.6	106.5	110.8	100.5	112	112.2	108.1	98	84.6	85.4
65	ND07-97×ND2014	88	131	82.7	121.9	136.6	102.7	134.5	121.8	119	118.3	96.7	107.4
66	ND08-53×ND2032	95.4	120.9	86.6	115.2	114.2	112.8	125.5	113	115	108.2	99.6	109.6
67	PHG47×ND270	88.9	128.2	68.6	111.3	134	110.7	138.5	102.4	114.6	106.6	97.3	107.1
68	ND07-97×ND2006	93.9	140.3	83.7	131.7	141.8	107	135	115.7	137.2	108.4	96.4	114.6
69	ND07-255×ND07-226	96.6	115.4	77.4	116.1	120.6	108.3	116.5	110.7	113.2	99.5	95.5	98.8
70	ND07-212×NK807	73.7	114.2	67.1	104.3	112.8	95	111	100.5	101	92.3	81.9	90.6

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Table A14. Grain Protein (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	86	110.8	73.6	115.4	127.6	106.0	124.5	110.9	117.0	103.5	94.9	98.0
72	ND07-212×AP47	71.4	111.3	74.1	112.8	121.6	95.1	107.5	96.0	106.1	89.3	85.2	89.5
73	A052×ND270	78.1	108	71.6	95.3	128.2	106.7	119.5	93.8	102.1	102.7	88.3	89.4
74	ND274×ND2009	85.6	117.7	85.5	109.1	127.1	105.6	123.5	107.6	118.0	99.1	96.6	99.3
75	A052×ND250	88.7	103.5	82.6	97.5	115.7	95.9	107.0	93.2	101.9	88.4	83.9	91.7
76	ND08-53×ND07-226	89.0	121.2	88.5	118.2	126.2	110.0	118.5	110.9	115.9	101.3	88.4	107.1
77	ND07-255×PHJ40	95.1	122.5	73.5	124.8	127.3	99.2	118.0	112.8	111.5	102.2	87.8	96.7
78	ND06-144×ND2006	108.9	113.6	85	111.3	145.9	109.9	124.0	108.6	114.6	105.5	89.2	94.8
79	ND291×ND2032	81.2	92.4	77.8	94.6	116.1	103.1	125.0	98.6	108.1	92.1	82.0	91.3
80	ND291×ND07-226	82.9	112	77.0	105.9	117.1	101.6	125.5	120.4	111.4	97.4	87.2	99.3
81	ND07-255×NK807	84.6	107.5	69.7	105.4	116.9	97.2	107.5	108.0	97.5	89.4	91.4	87
82	ND06-189×PHJ40	100.5	113.5	89.1	112.3	137.3	105.1	136.0	113.7	121.6	104.7	106.7	105.2
83	ND2014×LP05	85.7	118.7	76.1	115.8	117.6	99.3	116.5	100.5	108.6	97.6	84.6	86.4
84	LB2000×ND270	104.2	130.9	93.5	123.5	131.0	114.9	127.5	118.2	124.0	124.5	114.6	105.9
85	ND274×Il5	90.8	98.7	81.7	96.0	125.1	109.1	125.5	100.8	122.4	100.3	99.5	98.2
86	LB2000×ND2014	86.6	126.3	88.0	114.7	143.1	110.5	129.0	116.5	119.4	102.7	94.2	99.4
87	ND07-212×LP05	82.7	126.2	73.0	124.8	111.6	97.2	118.5	102.5	109.0	92.6	81.6	82.6
88	ND2019×AP47	82.2	111.2	80.1	105.8	110.4	94.2	114.0	103.2	112.1	98.9	82.3	93.2
89	LH61×ND270	80.8	118.9	63.8	99.6	122.3	102.6	118.0	94.2	112.6	97.0	90.2	96.1
90	ND2013×ND2009	94.0	109.2	94	107.9	132.6	101.6	120.5	104.6	109.9	98.8	90.0	101.5
91	ND06-189×LP05	96.2	116.1	90.9	115.6	117.2	100.3	130.0	108.7	114.0	99.1	89.0	100.9
92	ND07-255×LP05	98.1	122.1	82.4	115.9	115.6	107.1	116.0	101.3	102.6	88.4	84.8	87.2
93	ND2013×Il5	97.2	95.8	82.9	95.5	106.3	108.3	118.5	103.1	112.6	95.8	89.1	91.0
94	ND2019×Il5	92.7	101.5	86.3	103.2	113.4	101.3	121.0	116.9	120	106.7	94.9	98.9
95	**Thurston 77RM**	89.8	101.3	82.4	99.6	131.0	107	122.5	99.5	117.4	92.0	95.8	91.6
96	**Pioneer 79RM**	82.2	107	69.3	104.9	113.7	90.4	110.5	95.2	99.9	81.9	78.7	82.4
97	**Pioneer 80RM**	85.2	107.8	72.3	100	125.1	97.0	105.5	96.2	99.9	85.3	91.5	88.4
98	**Thurston 82RM**	86.7	114.4	66.4	109.4	117.5	98.6	128.0	90.9	118.1	83.6	85.9	82.5
99	**Syngenta 85RM**	84.4	107.5	70.1	97.8	128.5	88.8	123.0	88.4	112.1	87.2	77.8	79.3
100	**Monsanto 88RM**	89.0	97.3	65.3	91.5	106.6	88.1	117.0	94.2	98.9	85.0	74.5	81.4
	Experimental Mean	86.6	113.4	78.3	110.5	124	102.2	119.1	104.8	111.6	97.4	91.5	93.8
	CV%	9.1	3.7	10.2	3.8	7.8	6.9	3.6	4.8	3.2	4	6.8	5.3
	LSD,0.05	15.6	8.3	15.8	8.2	19.3	14	8.6	9.9	7	7.7	12.3	9.8
	MSE	62.1	17.5	63.2	17.2	94.7	49.6	18.9	25.1	12.5	15.1	38.3	24.5

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Table A15. Grain Methionine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	2.4	.	2.4	.	.	2.9	2.3	2.8	2.1	2.3	2.4
2	ND2014×B104	.	2.3	.	2.3	.	.	2.7	2	2.7	1.9	1.9	2.3
3	GEM5Derived×ND2001	2.3	2.5	2.1	2.2	.	.	2.6	2.2	2.5	2.1	1.9	2.1
4	ND265×ND2001	2.1	2.4	1.8	2.4	.	.	2.9	2.6	3.1	2.3	2.1	2.2
5	AP49×ND246	2.3	2.4	2.2	2.3	.	.	2.3	2.1	2.5	1.9	2	2.1
6	ND274×ND2001	2	2.5	2	2.4	.	2	2.9	2.4	2.8	2.3	2.3	2.4
7	ND290×PHJ40	1.9	2.5	1.7	2.4	2.7	2.3	2.7	2.3	2.6	2.1	1.9	2.2
8	ND203×ND2005	2.6	2.4	2.1	2.5	2.3	2.4	2.6	2.3	2.6	2.1	2.2	2.2
9	AP49×ND290	2	2.3	1.9	2.4	2.4	2.1	2.4	2.2	2.2	2.1	2.3	2.1
10	NK779×ND2014	2.4	2.5	2.1	2.6	2.5	2.1	2.8	2.5	2.6	2.4	2.2	2.4
11	ND290×ND2032	2.2	2.5	1.9	2.4	2.6	2.3	2.7	2.4	2.6	2.3	2.2	2.3
12	ND203×ND2002	1.9	2.2	2.1	2.3	2.6	2.2	2.1	2	2.1	2	2.2	2
13	PHG47×ND246	2	2.5	2	2.4	2.9	2.3	2.7	2.2	2.5	2.1	2.1	2.2
14	AP49×ND06-85	1.9	2	1.6	2.2	2.1	1.8	2.2	2	2.4	1.9	1.8	1.9
15	ND290×ND07-226	2.1	2.6	1.9	2.6	2.8	2.1	2.5	2.2	2.6	2.2	2.2	2.6
16	NK779×ND2000	2.3	2.4	1.9	2.3	2.7	2.2	2.4	2.4	2.3	2.2	1.9	2.2
17	AP49×ND291	1.9	2.3	1.8	2.2	2.3	2	2.4	2	2.5	1.9	1.8	2
18	ND07-212×B104	2.2	2.5	2.1	2.5	2.5	2.1	2.4	2	2.4	1.9	2	2.3
19	ND2021×ND2009	2	3	2	2.9	2.6	2.2	2.4	2.3	2.4	2.1	1.9	2.2
20	NP2341×ND07-153	1.8	2.2	1.7	2.2	2.7	2.2	2.6	2.2	2.6	1.9	1.7	2
21	ND2013×B104	2.4	2.3	2.1	2.4	2.6	2.2	3	2.1	2.9	2	2.2	2.5
22	LH61×ND246	2	2.4	2	2.3	2.4	2.1	2.8	2	2.7	2	1.9	2.3
23	ND08-343×ND07-153	2.2	2.8	2.2	2.7	2.3	2.1	2.6	2.3	2.5	2.1	1.8	2.3
24	GEM5Derived×ND2002	1.8	2.1	1.9	2.2	2.4	1.9	2.5	2	2.3	1.9	1.9	2.3
25	ND06-189×NK807	1.9	2.3	2.1	2.3	2.7	2.1	2.8	2.4	2.6	2.3	1.9	2.4
26	ND2021×ND2005	2.4	2.7	2.2	2.6	2.6	2.5	2.7	2.6	2.6	2.3	2.1	2.3
27	NP2341×ND2000	1.9	2.5	1.9	2.5	2.6	2.1	2.7	2.3	2.5	2.2	1.9	2.2
28	ND06-144×ND2007	2.1	2.6	2.2	2.6	2.1	1.9	2.4	2.3	2.3	2	1.9	2.2
29	ND08-343×ND2002	2	2.5	2.1	2.7	2.4	2.5	2.3	2.2	2.4	2	1.8	2.1
30	NK779×ND2006	2.5	2.6	2.2	2.6	3.1	2.1	3	2.7	2.5	2.5	2.3	2.7
31	ND2019×B104	2.1	2.4	2.2	2.5	2.4	2	2.6	2.2	2.6	2.2	2	2.4
32	ND2021×KMN22	2.3	2.9	2.4	2.9	2.9	2.4	2.8	2.6	2.7	2.4	2.3	2.6
33	ND08-343×ND2007	2.3	3	2.1	3.1	2.4	2.2	2.5	2.5	2.7	2.1	2	2.3
34	PHG47×ND06-85	1.9	2.2	1.6	2.1	2.8	2	2.4	1.9	2.4	1.9	1.7	2
35	ND203×ND2004	2	2.4	1.9	2.3	2.5	2.2	2.5	2.2	2.2	2	1.9	2

Table A15. Grain Methionine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	2.1	2.1	1.9	2	2.5	2.1	2.1	2	2.1	1.9	1.9	2.1
37	A052×ND246	2.2	2.3	1.7	2.2	2.5	2.1	2.5	2	2.3	1.9	2	2
38	A052×ND2000	1.9	2.3	1.8	2.3	2.2	2	2.3	2.2	2.2	2	1.7	2.1
39	NK779×ND250	2.2	2.3	2	2.3	2.7	2.1	2.5	2.1	2.5	2.1	2	2.4
40	NP2341×ND2006	2	2.7	1.8	2.6	2.7	2.1	2.9	3.1	2.7	2.3	1.9	2.2
41	ND2013×KMN22	2.7	2.5	2.2	2.5	2.6	2.2	3.1	2.3	2.9	2.4	2.2	2.4
42	ND07-97×ND07-153	2.1	2.5	2	2.6	2.5	2.3	2.7	2.3	2.9	2.3	1.9	2.3
43	ND06-144×ND07-153	2.4	2.6	2	2.4	2.4	2.3	2.2	2.4	2.2	2	1.8	2.1
44	ND2014×KMN22	2.1	2.5	2.2	2.4	2.6	2.4	2.6	2.6	2.6	2.5	2.1	2.4
45	LB2000×ND2000	2	2.7	2	2.5	2.8	2.3	2.6	2.7	2.5	2.3	1.9	2.4
46	ND265×ND2005	2.1	2.4	2	2.4	2.6	2.2	3	2.5	2.9	2.4	2	2.3
47	ND274×ND2005	2.2	2.5	1.8	2.3	2.8	2.2	2.9	2.4	3	2.4	2.1	2.6
48	ND08-53×NK807	2.3	2.5	1.8	2.5	2.3	2.2	2.5	2.4	2.4	2.1	1.9	2.5
49	ND06-144×ND2002	1.9	2.4	1.7	2.3	2.3	2.1	2.3	2.3	2.2	2	1.8	2.1
50	PHG47× D291	1.8	2.1	1.7	2.1	2.3	2.1	2.6	2.2	2.6	2	1.7	2
51	ND265×ND2009	1.8	2.3	1.8	2.5	2.5	2.3	2.6	2.2	2.6	2	1.8	2.1
52	LB2000× ND250	2.3	2.5	2.3	2.4	2.7	2.2	2.6	2.5	2.7	2.3	1.9	2.2
53	ND07-97×ND2007	2.4	2.6	2	2.8	2.6	2.2	3	2.5	2.9	2.4	2.1	2.4
54	ND2014×AP47	1.7	2.1	1.7	2.2	2.1	2	2.2	1.9	2.4	1.8	1.6	1.9
55	ND06-189×AP47	2.1	2.2	1.9	2.2	2.5	2.5	2.8	2.5	2.7	2.2	1.9	2.2
56	NP2341×ND2014	1.9	2.5	2.1	2.5	2.7	2.1	3.1	2.5	2.7	2.2	1.9	2.4
57	ND08-343×ND2004	2.1	2.9	1.9	2.3	2.4	2.1	2.6	2.2	2.5	2.1	2	2.2
58	ND265×ND2004	2	2.4	1.8	2.5	2.4	2.3	2.7	2.4	2.6	2.1	2.1	2.3
59	ND08-53×PHJ40	2.2	2.6	2.1	2.5	2.5	2.2	2.7	2.3	2.8	2.3	2.2	2.5
60	GEM5Derived×ND2007	2.1	2.5	1.9	2.5	2.3	2	2.4	2.3	2.4	2.1	1.9	2.2
61	LH61×ND250	1.9	2.4	2	2.2	2.5	2.1	2.5	2.2	2.4	2.1	1.9	2.3
62	ND2019×KMN22	2.4	2.6	2	2.5	2.4	2.4	2.9	2.7	3	2.7	2.4	2.6
63	LH61×ND06-85	1.7	2	1.9	2	2.1	2.1	2.2	1.9	2.3	2	1.8	2.3
64	GEM 5 Derived×ND2004	2	2.4	1.9	2.4	2.3	2.2	2.6	2.6	2.5	2.2	1.8	2.1
65	ND07-97×ND2014	2.1	2.7	2.1	2.5	2.8	2.1	2.8	2.6	2.7	2.6	2.1	2.5
66	ND08-53×ND2032	2.4	2.7	2.2	2.6	2.4	2.4	2.7	2.5	2.6	2.4	2.2	2.6
67	PHG47×ND270	1.9	2.7	1.7	2.3	2.7	2.3	2.8	2.2	2.6	2.2	1.9	2.4
68	ND07-97×ND2006	2.3	2.7	2	2.8	2.8	2.2	2.8	2.4	3.1	2.3	2.1	2.7
69	ND07-255×ND07-226	2.2	2.3	1.9	2.5	2.3	2.1	2.5	2.4	2.4	2.1	2	2.3
70	ND07-212×NK807	1.8	2.5	1.7	2.3	2.3	2.1	2.4	2.2	2.4	2.1	1.8	2.2

Table A15. Grain Methionine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	2.1	2.4	2	2.4	2.6	2.2	2.7	2.4	2.6	2.2	2	2.3
72	ND07-212×AP47	1.7	2.3	1.8	2.3	2.4	2	2.2	2	2.3	1.9	1.8	2.1
73	A052×ND270	1.8	2.3	1.9	2.2	2.5	2.2	2.5	2.1	2.3	2.2	1.8	2.1
74	ND274×ND2009	1.9	2.2	2.1	2.3	2.5	2.2	2.7	2.3	2.7	2.2	1.9	2.3
75	A052×ND250	2	2.1	1.9	2	2.3	2	2.3	2	2.1	1.9	1.7	2.1
76	ND08-53×ND07-226	2.2	2.6	2.1	2.5	2.6	2.3	2.6	2.4	2.5	2.2	2	2.5
77	ND07-255×PHJ40	2.3	2.5	1.9	2.5	2.6	2.1	2.6	2.4	2.6	2.2	2	2.3
78	ND06-144×ND2006	2.7	2.4	2.1	2.5	3.1	2.4	2.6	2.5	2.6	2.3	2	2.4
79	ND291×ND2032	2	2.1	2	2.1	2.4	2.2	2.8	2.1	2.5	2	1.9	2.2
80	ND291×ND07-226	2.1	2.4	2	2.2	2.3	2.2	2.6	2.5	2.5	2.1	1.9	2.3
81	ND07-255×NK807	2.2	2.1	1.9	2.2	2.3	2.2	2.4	2.3	2.2	1.9	1.9	2.1
82	ND06-189×PHJ40	2.3	2.4	2.2	2.5	2.7	2.2	2.9	2.5	2.8	2.3	2.2	2.5
83	ND2014×LP05	2	2.4	1.9	2.3	2.4	2.2	2.4	2.2	2.3	2.1	1.8	2
84	LB2000×ND270	2.5	2.9	2.4	2.7	2.6	2.4	2.8	2.6	2.9	2.6	2.4	2.5
85	ND274×Il5	2.1	2	2	2	2.5	2.3	2.8	2.1	3	2.2	2	2.2
86	LB2000×ND2014	2.1	2.6	2.1	2.4	2.9	2.4	3.1	2.6	2.7	2.3	2.1	2.4
87	ND07-212×LP05	2	2.7	1.9	2.7	2.2	2.1	2.5	2.2	2.4	2	1.8	2.1
88	ND2019×AP47	2	2.3	1.9	2.2	2.3	1.9	2.3	2	2.5	2.1	1.8	2.2
89	LH61×ND270	2	2.5	1.8	2.1	2.4	2.1	2.8	2.1	2.8	2.2	1.9	2.3
90	ND2013×ND2009	2.3	2.4	2.3	2.6	2.8	2.2	2.8	2.3	2.6	2.2	1.9	2.5
91	ND06-189×LP05	2.2	2.5	2.2	2.4	2.5	2.1	2.9	2.2	2.6	2.1	1.9	2.4
92	ND07-255×LP05	2.2	2.6	2	2.5	2.2	2.3	2.5	2.1	2.4	2	1.8	2.1
93	ND2013×Il5	2.3	2.2	2.1	2.1	2.3	2.3	3.1	2.4	2.9	2.2	2	2.3
94	ND2019×Il5	2.1	2.3	2	2.3	2.3	2.1	2.8	2.5	2.8	2.3	2	2.3
95	**Thurston 77RM**	2.2	2.3	2	2.3	2.7	2.3	2.9	2.3	2.8	2.2	2	2.3
96	**Pioneer 79RM**	2	2.5	1.8	2.4	2.5	2	2.8	2.2	2.6	2	1.8	2.2
97	**Pioneer 80RM**	2	2.4	1.9	2.3	2.7	2.2	2.7	2.2	2.7	2.1	2	2.2
98	**Thurston 82RM**	2.2	2.5	1.9	2.4	2.4	2.1	3.3	2.3	3	2.2	1.9	2.1
99	**Syngenta 85RM**	1.9	2.2	1.8	2	2.6	1.9	2.9	2	2.6	1.9	1.7	1.9
100	**Monsanto 88RM**	2.2	2.2	1.9	2.1	2.1	2	2.7	2.1	2.2	2	1.7	2.1
	Experimental Mean	2.1	2.4	2	2.4	2.5	2.2	2.6	2.3	2.6	2.1	2	2.3
	CV%	8.1	4.7	7.7	4.1	7.8	8.2	4.8	4.7	3.8	4.4	6.3	4.6
	LSD,0.05	0.3	0.2	0.3	0.2	0.4	0.4	0.3	0.2	0.2	0.2	0.2	0.2
	MSE	0	0	0	0	0	0	0	0	0	0	0	0

Table A16. Grain Cysteine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	2.3	.	2.4	.	.	2.9	2.2	2.9	2.2	2.6	2.7
2	ND2014×B104	.	2.2	.	2.3	.	.	2.7	2.1	2.6	2	2.2	2.4
3	GEM5Derived×ND2001	2.7	2.4	2.7	2.2	.	.	2.7	2.2	2.5	2.1	2.2	2.4
4	ND265×ND2001	2.7	2.4	2.5	2.3	.	.	3	2.5	3	2.3	2.4	2.5
5	AP49×ND246	2.7	2.4	2.8	2.3	.	.	2.5	2.1	2.5	1.9	2.3	2.4
6	ND274×ND2001	2.6	2.4	2.4	2.4	.	2.0	2.9	2.4	2.9	2.3	2.6	2.7
7	ND290×PHJ40	2.1	2.4	2.4	2.3	2.7	2.2	2.8	2.2	2.7	2.1	2.3	2.4
8	ND203×ND2005	2.9	2.4	2.7	2.3	2.2	2.3	2.8	2.3	2.8	2.2	2.4	2.6
9	AP49×ND290	2.6	2.3	2.5	2.3	2.5	2.1	2.7	2.2	2.6	2.1	2.4	2.4
10	NK779×ND2014	3.2	2.4	2.5	2.5	2.5	2.1	2.9	2.3	2.7	2.3	2.5	2.5
11	ND290×ND2032	2.5	2.4	2.6	2.3	2.5	2.3	2.9	2.3	2.7	2.2	2.4	2.6
12	ND203×ND2002	2.7	2.2	2.4	2.2	2.6	2.1	2.5	2.1	2.4	2.1	2.4	2.4
13	PHG47×ND246	2.6	2.4	2.7	2.4	2.9	2.3	2.8	2.2	2.6	2.1	2.5	2.6
14	AP49×ND06-85	2.3	2.1	2.4	2.2	2.1	1.9	2.5	2	2.5	2.0	2.1	2.3
15	ND290×ND07-226	2.8	2.5	2.5	2.5	2.8	2.1	2.7	2.2	2.7	2.2	2.4	2.6
16	NK779×ND2000	2.8	2.3	2.5	2.2	2.4	2.1	2.6	2.2	2.5	2.1	2.3	2.5
17	AP49×ND291	2.3	2.3	2.5	2.2	2.4	2.0	2.6	2.0	2.7	1.9	2.2	2.3
18	ND07-212×B104	2.1	2.5	2.4	2.4	2.5	1.9	2.6	2.0.	2.6	2	2.3	2.4
19	ND2021×ND2009	2.4	2.8	2.5	2.7	2.6	2.1	2.7	2.3	2.6	2.1	2.3	2.5
20	NP2341×ND07-153	2.2	2.3	2.6	2.3	2.6	2.2	2.7	2.2	2.6	1.9	2.1	2.3
21	ND2013×B104	2.2	2.3	2.6	2.3	2.5	1.9	2.8	2.1	2.7	2	2.4	2.5
22	LH61×ND246	2.7	2.2	2.6	2.3	2.4	2.1	2.8	2.1	2.7	2.1	2.4	2.6
23	ND08-343×ND07-153	2.3	2.6	2.8	2.5	2.4	2.1	2.6	2.3	2.6	2.1	2.2	2.4
24	GEM5Derived×ND2002	1.9	2.1	2.6	2.1	2.4	1.9	2.5	2.1	2.5	2.0	2.3	2.6
25	ND06-189×NK807	2.5	2.2	2.7	2.2	2.7	2.1	2.7	2.3	2.6	2.2	2.2	2.5
26	ND2021×ND2005	2.5	2.4	2.8	2.5	2.5	2.3	2.8	2.4	2.7	2.3	2.3	2.5
27	NP2341×ND2000	2.4	2.4	2.5	2.4	2.6	2.1	2.7	2.2	2.6	2.1	2.2	2.4
28	ND06-144×ND2007	2.3	2.4	2.5	2.5	2.4	1.9	2.6	2.3	2.5	2.1	2.3	2.3
29	ND08-343×ND2002	2.1	2.4	2.7	2.5	2.4	2.3	2.6	2.1	2.5	2.0	2.2	2.3
30	NK779×ND2006	2.6	2.5	2.7	2.5	2.7	2.1	3	2.5	2.6	2.3	2.5	2.8
31	ND2019×B104	2.2	2.3	2.4	2.4	2.4	2.0	2.7	2.1	2.7	2.1	2.3	2.4
32	ND2021×KMN22	2.3	2.7	2.8	2.7	2.6	2.3	2.8	2.4	2.7	2.3	2.4	2.5
33	ND08-343×ND2007	2.3	2.7	2.6	2.7	2.4	2.0	2.7	2.3	2.8	2.1	2.3	2.5
34	PHG47×ND06-85	2.6	2.2	2.3	2.1	2.6	2.0	2.6	2	2.6	2.0	2.1	2.3
35	ND203×ND2004	2.4	2.3	2.3	2.2	2.4	2.2	2.6	2.2	2.5	2.0	2.3	2.3

Table A16. Grain Cysteine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	2.3	2.1	2.5	2.2	2.4	2.1	2.4	2.0	2.4	1.9	2.2	2.3
37	A052×ND246	2.8	2.3	2.5	2.3	2.5	2.0	2.6	2.0	2.5	2	2.5	2.4
38	A052×ND2000	2.2	2.2	2.0	2.1	2.3	2.0	2.5	2.1	2.5	2	2.0	2.4
39	NK779×ND250	2.4	2.3	2.7	2.3	2.4	2.1	2.7	2.1	2.6	2.1	2.4	2.6
40	NP2341×ND2006	2.6	2.6	2.6	2.6	2.5	2.1	2.9	2.7	2.7	2.2	2.3	2.5
41	ND2013×KMN22	2.8	2.4	2.6	2.3	2.4	2.2	2.9	2.2	2.8	2.2	2.3	2.4
42	ND07-97×ND07-153	2.5	2.5	2.7	2.5	2.6	2.2	2.8	2.3	2.9	2.3	2.2	2.6
43	ND06-144×ND07-153	2.7	2.5	2.7	2.4	2.4	2.2	2.6	2.3	2.5	2.1	2.2	2.5
44	ND2014×KMN22	2.4	2.4	2.7	2.3	2.5	2.3	2.7	2.4	2.8	2.3	2.3	2.5
45	LB2000×ND2000	2.7	2.5	2.6	2.4	2.6	2.2	2.6	2.4	2.6	2.2	2.2	2.6
46	ND265×ND2005	2.4	2.3	2.8	2.4	2.6	2.2	3.0	2.4	2.9	2.4	2.3	2.4
47	ND274×ND2005	2.6	2.5	2.7	2.3	2.8	2.2	3.0	2.3	3.0	2.4	2.4	2.7
48	ND08-53×NK807	2.6	2.3	2.5	2.3	2.2	2.1	2.8	2.3	2.6	2.1	2.3	2.6
49	ND06-144×ND2002	2.7	2.3	2.5	2.2	2.4	2.1	2.5	2.2	2.5	2	2.1	2.3
50	PHG47× D291	2.7	2.2	2.1	2.3	2.5	2.1	2.9	2.2	2.8	2.1	2.1	2.4
51	ND265×ND2009	2.3	2.3	2.5	2.4	2.5	2.2	2.8	2.2	2.8	2.1	2.2	2.4
52	LB2000× ND250	2.5	2.5	2.6	2.4	2.7	2.2	2.8	2.4	2.9	2.3	2.4	2.5
53	ND07-97×ND2007	2.8	2.4	2.3	2.6	2.5	2.1	2.8	2.4	2.8	2.3	2.3	2.5
54	ND2014×AP47	2.1	2.2	2.2	2.2	2.3	2.0	2.5	2	2.6	2	2.0	2.3
55	ND06-189×AP47	2.2	2.2	2.1	2.2	2.5	2.3	2.8	2.4	2.7	2.1	2.3	2.4
56	NP2341×ND2014	2.0	2.3	2.6	2.4	2.5	2.0	2.9	2.4	2.7	2.2	2.2	2.5
57	ND08-343×ND2004	2.6	2.6	2.3	2.2	2.4	2.1	2.7	2.2	2.7	2.2	2.3	2.3
58	ND265×ND2004	2.2	2.3	2.5	2.4	2.5	2.3	2.8	2.3	2.7	2.2	2.3	2.5
59	ND08-53×PHJ40	2.3	2.5	2.4	2.4	2.3	2.2	2.8	2.3	2.8	2.2	2.4	2.6
60	GEM5Derived×ND2007	2.2	2.4	2.5	2.4	2.4	1.9	2.7	2.2	2.6	2.1	2.2	2.4
61	LH61×ND250	2.6	2.3	2.6	2.2	2.5	2.1	2.7	2.3	2.6	2.2	2.4	2.5
62	ND2019×KMN22	2.6	2.4	2.5	2.4	2.4	2.3	2.9	2.4	2.9	2.4	2.4	2.6
63	LH61×ND06-85	2.4	2.1	2.3	2.1	2.2	2.1	2.5	2.0	2.6	2.1	2.3	2.5
64	GEM 5 Derived×ND2004	2.1	2.4	2.3	2.3	2.5	2.1	2.6	2.4	2.6	2.2	2.1	2.3
65	ND07-97×ND2014	2.7	2.5	2.3	2.5	2.7	2.1	2.9	2.4	2.8	2.4	2.4	2.7
66	ND08-53×ND2032	2.4	2.5	2.6	2.4	2.5	2.3	2.9	2.4	2.7	2.2	2.3	2.6
67	PHG47×ND270	2.8	2.6	2.4	2.2	2.7	2.3	2.8	2.2	2.7	2.2	2.3	2.6
68	ND07-97×ND2006	2.3	2.5	2.6	2.6	2.7	2.2	2.8	2.4	2.9	2.3	2.4	2.8
69	ND07-255×ND07-226	2.4	2.2	2.5	2.5	2.4	2.1	2.7	2.3	2.7	2.1	2.3	2.5
70	ND07-212×NK807	2.4	2.3	2.2	2.3	2.4	2.1	2.6	2.2	2.6	2.1	2.1	2.4

Table A16. Grain Cysteine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| Entry | Pedigree | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	2.6	2.2	2.6	2.4	2.6	2.2	2.7	2.3	2.7	2.1	2.2	2.4
72	ND07-212×AP47	2.3	2.2	2.5	2.2	2.6	2	2.5	2.1	2.5	2	2.2	2.4
73	A052×ND270	2.7	2.3	2.5	2.2	2.5	2.2	2.7	2.1	2.6	2.2	2.1	2.4
74	ND274×ND2009	2.7	2.3	1.3	2.2	2.6	2.2	2.7	2.3	2.7	2.1	2.3	2.5
75	A052×ND250	2.6	2.2	2.6	2.1	2.3	2	2.6	2.1	2.5	2	2.2	2.4
76	ND08-53×ND07-226	2.7	2.4	2.6	2.4	2.6	2.2	2.7	2.3	2.7	2.2	2.2	2.6
77	ND07-255×PHJ40	2.6	2.4	2.5	2.4	2.6	2.1	2.6	2.3	2.7	2.2	2.2	2.5
78	ND06-144×ND2006	3.2	2.4	2.4	2.5	2.9	2.3	2.8	2.4	2.7	2.2	2.3	2.6
79	ND291×ND2032	2.6	2.1	2.3	2.1	2.5	2.2	2.9	2.1	2.6	2.1	2.2	2.4
80	ND291×ND07-226	2.1	2.3	2.3	2.2	2.5	2.1	2.8	2.3	2.7	2.1	2.1	2.6
81	ND07-255×NK807	2.5	2.3	2.2	2.2	2.5	2.1	2.6	2.2	2.4	2	2.2	2.4
82	ND06-189×PHJ40	2.9	2.3	2.7	2.3	2.5	2.2	2.9	2.4	2.7	2.2	2.4	2.6
83	ND2014×LP05	2.3	2.3	2.2	2.3	2.5	2.1	2.7	2.1	2.6	2.1	2.1	2.3
84	LB2000×ND270	3.1	2.7	2.8	2.5	2.4	2.3	2.9	2.5	2.9	2.5	2.6	2.7
85	ND274×Il5	2.5	2.1	2.6	2.1	2.4	2.2	2.9	2.2	2.9	2.2	2.4	2.5
86	LB2000×ND2014	2.7	2.6	2.7	2.4	2.6	2.3	2.9	2.4	2.6	2.2	2.3	2.6
87	ND07-212×LP05	2.1	2.4	2.2	2.5	2.4	2	2.7	2.2	2.5	2	2.1	2.3
88	ND2019×AP47	2.5	2.2	2.6	2.2	2.4	1.9	2.6	2.2	2.8	2.1	2.2	2.5
89	LH61×ND270	2	2.5	2.1	2.1	2.4	2.2	2.7	2.2	2.7	2.2	2.3	2.6
90	ND2013×ND2009	2.5	2.2	2.6	2.4	2.7	1.9	2.9	2.2	2.7	2.1	2.2	2.5
91	ND06-189×LP05	2.2	2.3	2.6	2.3	2.3	2.1	2.9	2.1	2.6	2	2.1	2.5
92	ND07-255×LP05	2.5	2.4	2.6	2.3	2.5	2.2	2.6	2.1	2.5	2	2.2	2.4
93	ND2013×Il5	2.4	2.1	2.3	2.1	2.3	2.3	2.8	2.2	2.8	2	2.2	2.4
94	ND2019×Il5	2.6	2.2	2.3	2.2	2.5	2	2.8	2.3	2.8	2.2	2.1	2.4
95	**Thurston 77RM**	2.2	2.3	2.4	2.3	2.6	2.2	2.7	2.2	2.7	2.2	2.3	2.5
96	**Pioneer 79RM**	2.5	2.4	2.2	2.5	2.3	1.9	2.6	2.1	2.5	2	2	2.4
97	**Pioneer 80RM**	2.8	2.3	2.3	2.2	2.3	2.1	2.5	2.1	2.5	2	2.2	2.3
98	**Thurston 82RM**	2.5	2.4	2.4	2.3	2.4	2.1	2.9	2.2	2.9	2.1	2.2	2.3
99	**Syngenta 85RM**	2.5	2.2	2.1	2.1	2.6	1.9	2.7	2	2.6	1.9	1.9	2.2
100	**Monsanto 88RM**	2.2	2	2.4	2	2.2	1.9	2.7	2	2.4	1.9	2	2.2
	Experimental Mean	2.5	2.4	2.5	2.3	2.5	2.1	2.7	2.2	2.7	2.1	2.3	2.5
	CV%	10.8	3.3	10.6	3.4	7.6	5.7	2.8	3.3	2.4	3.2	4.1	3.7
	LSD,0.05	0.5	0.2	0.5	0.2	0.4	0.2	0.1	0.1	0.1	0.1	0.2	0.2
	MSE	0.1	0	0.1	0	0	0	0	0	0	0	0	0

Table A17. Grain Lysine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively.

		2013						2014					
		WS		WW		RDT		WS		WW		RDT	
Entry	Pedigree	NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
1	ND203×ND2001	.	3.3	.	3.1	.	.	3.5	3.0	3.6	3.1	3.2	3.1
2	ND2014×B104	.	3.2	.	3.1	.	.	3.3	2.9	3.3	2.9	3.0	2.8
3	GEM5Derived×ND2001	2.8	3.3	2.7	3.1	.	.	3.3	3.1	3.4	2.9	2.8	3.0
4	ND265×ND2001	2.6	3.2	2.6	3.2	.	.	3.5	3.2	3.5	3.0	3.0	3.0
5	AP49×ND246	2.9	3.2	2.7	3.2	.	.	3.2	3.0	3.5	2.8	2.9	2.8
6	ND274×ND2001	2.9	3.2	2.7	3.2	.	2.8	3.5	3.1	3.3	3.0	3.0	3.1
7	ND290×PHJ40	2.9	3.2	2.5	3.2	3.4	3.1	3.4	3.0	3.4	2.9	2.9	3.1
8	ND203×ND2005	3.0	3.3	2.6	3.1	3.3	3.2	3.2	3.1	3.1	3.0	3.0	3.0
9	AP49×ND290	2.7	3.1	2.5	3.0	3.2	2.8	3.4	2.9	3.1	2.8	3.0	3.0
10	NK779×ND2014	2.7	3.2	2.9	3.2	3.5	2.9	3.6	3.2	3.4	3.2	3.0	3.1
11	ND290×ND2032	3.0	3.2	2.6	3.1	3.3	3.0	3.2	3.0	3.2	3.0	3.0	3.0
12	ND203×ND2002	2.6	3.2	3.0	3.2	3.4	3.0	2.9	2.9	2.9	3.0	3.2	2.9
13	PHG47×ND246	2.9	3.2	2.6	3.1	3.6	3.1	3.5	2.9	3.3	2.9	2.9	2.9
14	AP49×ND06-85	2.8	3.0	2.4	3.0	3.1	2.7	3.2	2.8	3.2	2.8	2.8	3.0
15	ND290×ND07-226	2.7	3.3	2.6	3.2	3.3	2.9	3.2	2.9	3.4	3.0	3.0	3.2
16	NK779×ND2000	3.1	3.1	2.7	3.0	3.5	3.1	3.3	3.1	3.2	3.0	3.1	3.0
17	AP49×ND291	2.8	3.2	2.4	3.1	3.2	2.7	3.2	3.1	3.4	2.9	2.9	2.9
18	ND07-212×B104	3.1	3.4	2.8	3.3	3.2	3.1	3.1	2.9	3.3	2.9	3.0	3.0
19	ND2021×ND2009	2.7	3.6	2.2	3.5	3.4	3.0	3.1	3.2	3.2	3.0	3.0	2.9
20	NP2341×ND07-153	2.9	3.2	2.4	3.1	3.5	3.1	3.3	3.0	3.4	2.8	2.8	2.9
21	ND2013×B104	3.2	3.4	2.2	3.3	3.5	3.2	3.5	3.3	3.7	3.1	3.1	3.1
22	LH61×ND246	2.7	3.2	2.6	3.1	3.5	3.0	3.6	2.9	3.4	2.9	3.1	2.9
23	ND08-343×ND07-153	3.1	3.3	2.7	3.4	3.2	3.0	3.3	3.1	3.4	3.1	2.9	3.2
24	GEM5Derived×ND2002	2.9	3.0	2.6	3.0	3.4	2.7	3.3	2.9	3.3	2.8	2.9	3.0
25	ND06-189×NK807	2.6	3.2	2.8	3.2	3.5	2.9	3.5	3.2	3.4	3.3	3.0	3.2
26	ND2021×ND2005	3.2	3.2	2.8	3.2	3.4	3.2	3.3	3.3	3.2	3.1	3.0	3.0
27	NP2341×ND2000	2.8	3.1	2.7	3.1	3.3	2.8	3.5	3.2	3.4	3.1	3.0	3.0
28	ND06-144×ND2007	2.8	3.3	2.9	3.2	3.0	2.8	3.4	3.1	3.1	2.9	3.1	3.0
29	ND08-343×ND2002	3.1	3.4	2.7	3.4	3.3	3.0	3.2	3.1	3.3	2.9	3.0	3.0
30	NK779×ND2006	3.5	3.2	2.7	3.3	3.8	3.0	3.3	3.1	3.4	3.1	3.4	3.1
31	ND2019×B104	3.1	3.3	3.0	3.3	3.4	2.8	3.4	3.2	3.2	3.2	3.0	3.0
32	ND2021×KMN22	3.1	3.4	2.9	3.3	3.6	3.1	3.4	3.2	3.4	3.2	3.1	3.3
33	ND08-343×ND2007	3.0	3.5	2.4	3.6	3.2	3.1	3.2	3.2	3.2	3.1	2.9	3.1
34	PHG47×ND06-85	2.7	3.0	2.4	2.9	3.5	2.8	3.2	2.7	3.2	2.8	2.6	3.0
35	ND203×ND2004	2.8	3.2	2.7	3.2	3.3	3.0	3.3	3.1	3.1	2.9	3.0	2.9

Table A17. Grain Lysine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

| | | 2013 | | | | | | 2014 | | | | | |
| | | WS | | WW | | RDT | | WS | | WW | | RDT | |
Entry	Pedigree	NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
36	ND06-85×ND2032	3.0	3.0	2.6	2.9	3.2	2.8	3.1	2.9	3.0	2.8	2.9	3.0
37	A052×ND246	3.2	3.1	2.6	3.0	3.4	3.0	3.3	2.8	3.3	3.0	3.1	2.9
38	A052×ND2000	2.8	3.2	2.8	3.1	3.2	2.8	3.2	3.1	3.1	2.9	2.7	3.0
39	NK779×ND250	3.1	3.1	2.7	3.1	3.4	2.8	3.2	2.8	3.3	2.9	2.8	3.0
40	NP2341×ND2006	3.0	3.4	2.6	3.3	3.5	3.0	3.5	3.5	3.5	3.0	2.9	3.1
41	ND2013×KMN22	3.2	3.4	2.9	3.3	3.4	3.2	3.5	3.3	3.6	3.4	3.3	3.2
42	ND07-97×ND07-153	2.8	3.2	2.5	3.4	3.3	3.1	3.4	3.2	3.6	3.2	2.9	3.0
43	ND06-144×ND07-153	3.0	3.2	2.6	3.1	3.1	3.1	3.1	3.1	3.1	2.9	2.8	2.9
44	ND2014×KMN22	3.0	3.1	2.8	3.1	3.6	3.1	3.2	3.2	3.4	3.2	3.0	3.0
45	LB2000×ND2000	2.7	3.3	2.8	3.2	3.6	3.1	3.3	3.2	3.4	3.1	3.0	3.2
46	ND265×ND2005	3.0	3.1	2.6	3.1	3.4	3.0	3.5	3.2	3.5	3.1	2.9	3.0
47	ND274×ND2005	3.0	3.0	2.5	3.0	3.3	3.1	3.3	3.1	3.4	2.9	3.0	3.1
48	ND08-53×NK807	3.0	3.3	2.6	3.2	3.2	3.0	3.1	3.1	3.2	3.0	2.8	3.1
49	ND06-144×ND2002	2.6	3.2	2.4	3.1	3.2	2.7	3.1	3.0	3.1	2.8	2.8	3.0
50	PHG47× D291	2.5	3.0	2.5	3.0	3.2	2.9	3.3	3.1	3.3	3.0	2.8	3.0
51	ND265×ND2009	2.6	3.2	2.4	3.3	3.3	3.0	3.3	3.1	3.4	3.0	2.8	3.0
52	LB2000× ND250	3.0	3.0	2.9	3.0	3.3	2.8	3.3	3.0	3.4	2.9	2.9	2.9
53	ND07-97×ND2007	2.8	3.4	2.7	3.6	3.5	3.2	3.4	3.1	3.4	3.4	3.1	3.1
54	ND2014×AP47	2.7	3.0	2.6	3.0	3.1	2.8	3.1	2.8	3.3	2.7	2.8	2.8
55	ND06-189×AP47	2.8	3.2	2.8	3.2	3.5	3.4	3.3	3.2	3.3	3.2	2.9	3.1
56	NP2341×ND2014	2.9	3.1	2.9	3.1	3.4	3.0	3.5	3.2	3.7	3.0	2.9	3.1
57	ND08-343×ND2004	3.0	3.4	2.7	3.1	3.4	2.9	3.3	3.0	3.4	3.0	3.0	3.0
58	ND265×ND2004	2.9	3.1	2.6	3.3	3.2	3.1	3.4	3.0	3.3	3.0	3.0	2.9
59	ND08-53×PHJ40	3.1	3.4	2.9	3.3	3.3	2.9	3.5	3.0	3.4	3.1	3.1	3.2
60	GEM5Derived×ND2007	3.1	3.3	2.4	3.4	3.3	3.1	3.3	3.2	3.3	3.1	3.0	2.9
61	LH61×ND250	2.4	3.3	2.7	3.1	3.4	2.9	3.2	2.9	3.4	2.9	2.9	2.9
62	ND2019×KMN22	3.0	3.4	2.7	3.3	3.2	3.1	3.5	3.2	3.4	3.3	3.1	3.2
63	LH61×ND06-85	2.6	3.0	2.8	3.0	3.1	2.7	3.1	2.8	3.2	2.7	2.9	3.1
64	GEM 5 Derived×ND2004	3.1	3.3	2.8	3.2	3.3	3.0	3.4	3.1	3.4	3.1	3.0	3.0
65	ND07-97×ND2014	2.7	3.4	2.9	3.3	3.5	3.0	3.5	3.3	3.5	3.3	3.0	3.2
66	ND08-53×ND2032	3.2	3.4	2.7	3.3	3.2	3.1	3.2	3.1	3.3	3.1	3.0	3.1
67	PHG47×ND270	2.9	3.3	2.5	3.1	3.5	3.1	3.6	3.1	3.2	3.3	3.1	3.2
68	ND07-97×ND2006	3.2	3.6	2.8	3.4	3.7	3.0	3.4	3.2	3.5	3.1	3.0	3.2
69	ND07-255×ND07-226	3.1	3.2	2.5	3.1	3.3	2.9	3.2	3.1	3.4	2.9	2.9	3.0
70	ND07-212×NK807	2.9	3.2	2.7	3.1	3.2	3.0	3.2	3.1	3.3	2.9	2.9	3.0

Table A17. Grain Lysine (g kg^{-1} of dry matter) adjusted means of 94 partial diallel crosses with six checks (on bottom) across 12 well-watered (WW), water stressed (WS) and random drought (RDT) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID), Fargo (FAR), and Prosper (PRO), North Dakota respectively (continued).

Entry	Pedigree	2013						2014					
		WS		WW		RDT		WS		WW		RDT	
		NV	SID	NV	SID	FAR	PRO	NV	SID	NV	SID	FAR	PRO
71	ND2021×Il5	2.9	3.1	2.6	3.1	3.4	2.9	3.3	3.1	3.2	3.2	2.9	3.0
72	ND07-212×AP47	2.8	3.0	2.5	3.1	3.3	2.8	3.1	2.9	3.0	2.8	2.9	2.9
73	A052×ND270	2.7	3.2	2.6	3.2	3.4	3.1	3.4	3.1	3.2	3.4	3.1	3.0
74	ND274×ND2009	.	3.2	2.3	3.2	3.4	3.0	3.4	3.2	3.5	3.1	2.9	3.2
75	A052×ND250	2.7	3.0	2.5	2.9	3.1	2.8	3.2	3.0	3.0	2.8	2.8	3.0
76	ND08-53×ND07-226	2.9	3.2	2.6	3.2	3.3	3.1	3.2	3.0	3.2	2.9	2.8	3.1
77	ND07-255×PHJ40	3.0	3.3	2.5	3.4	3.3	3.0	3.4	3.1	3.2	3.1	2.9	3.0
78	ND06-144×ND2006	2.9	3.2	2.9	3.1	3.7	3.1	3.3	3.1	3.2	3.1	2.9	3.1
79	ND291×ND2032	2.6	3.2	2.8	3.1	3.3	3.0	3.4	3.0	3.2	3.0	2.9	3.0
80	ND291×ND07-226	3.0	3.1	2.7	3.1	3.2	2.9	3.3	3.2	3.3	3.0	2.9	3.2
81	ND07-255×NK807	3.1	3.2	2.9	3.2	3.3	2.9	3.2	3.1	3.2	2.9	3.0	2.9
82	ND06-189×PHJ40	2.9	3.3	2.8	3.3	3.5	3.0	3.5	3.3	3.5	3.0	3.2	3.4
83	ND2014×LP05	2.8	3.3	2.8	3.2	3.2	3.0	3.2	2.9	3.2	2.9	2.8	2.9
84	LB2000×ND270	.	3.5	3.1	3.3	3.6	3.2	3.4	3.2	3.5	3.3	3.1	3.1
85	ND274×Il5	2.9	3.0	2.5	3.0	3.3	3.0	3.5	3.0	3.6	2.9	2.9	3.1
86	LB2000×ND2014	2.9	3.4	2.9	3.2	3.8	3.2	3.6	3.3	3.4	2.9	3.0	3.2
87	ND07-212×LP05	3.1	3.5	2.6	3.4	3.2	3.0	3.2	3.0	3.3	2.8	2.9	2.9
88	ND2019×AP47	2.5	3.1	2.4	3.1	3.1	2.7	3.0	2.9	3.2	2.9	2.8	3.0
89	LH61×ND270	3.1	3.5	2.5	3.1	3.6	3.0	3.7	2.9	3.6	3.0	3.0	3.1
90	ND2013×ND2009	2.8	3.5	2.6	3.3	3.6	3.4	3.3	3.2	3.3	3.3	3.0	3.0
91	ND06-189×LP05	3.1	3.3	2.7	3.3	3.1	3.0	3.3	3.2	3.3	3.3	3.0	3.3
92	ND07-255×LP05	2.9	3.4	2.6	3.3	3.4	3.2	3.2	3.1	3.1	3.0	2.9	2.8
93	ND2013×Il5	3.0	3.2	3.0	3.1	3.1	2.9	3.6	3.2	3.7	3.2	3.0	3.1
94	ND2019×Il5	2.7	3.1	2.8	3.0	3.1	2.9	3.4	3.1	3.3	3.2	2.9	3.1
95	**Thurston 77RM**	2.9	3.0	2.8	3.1	3.5	3.2	3.7	3.0	3.5	3.0	3.0	3.2
96	**Pioneer 79RM**	2.8	3.2	2.8	3.1	3.3	2.9	3.5	3.2	3.5	3.1	2.9	3.1
97	**Pioneer 80RM**	2.4	3.2	2.7	3.1	3.6	3.0	3.7	3.2	3.7	3.1	3.0	3.2
98	**Thurston 82RM**	2.8	3.2	2.5	3.2	3.2	3.0	3.9	3.2	3.7	3.3	2.9	3.1
99	**Syngenta 85RM**	2.8	3.1	2.7	3.0	3.5	2.8	3.5	3.1	3.6	3.2	3.1	3.1
100	**Monsanto 88RM**	3.1	3.1	2.6	3.3	3.4	2.9	3.5	3.2	3.3	3.1	3.0	3.2
	Experimental Mean	2.9	3.2	2.7	3.2	3.3	3.0	3.3	3.1	3.3	3.0	3.0	3.0
	CV%	7.2	2.9	7.0	2.7	4.8	5.2	3.5	3.1	4.0	3.2	3.6	3.1
	LSD,0.05	0.4	0.2	0.4	0.2	0.3	0.3	0.2	0.2	0.3	0.2	0.2	0.2
	MSE	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Table A18. Visbile brace root spread width (mm) adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
1	ND203×ND2001	.	43.1	.	34.0	25.6	27.7	32.0	32.0
2	ND2014×B104	.	45.2	.	26.0	31.7	25.1	34.0	28.1
3	GEM5Derived×ND2001	19.6	51.7	29.0	34.0	24.6	24.4	37.0	25.8
4	ND265×ND2001	14.8	50.4	20.0	40.0	22.5	21.8	31.0	29.1
5	AP49×ND246	18.4	56.7	31.0	36.0	34.4	22.3	34.0	24.4
6	ND274×ND2001	25.8	51.7	30.0	35.0	32.7	27.0	41.0	36.5
7	ND290×PHJ40	18.8	45.0	27.0	29.0	33.7	32.6	36.0	28.2
8	ND203×ND2005	17.2	50.0	18.0	27.0	18.0	23.1	29.0	22.4
9	AP49×ND290	32.7	52.0	28.0	38.0	48.1	28.3	56.0	39.5
10	NK779×ND2014	25.4	57.1	26.0	35.0	32.3	25.0	36.0	30.9
11	ND290×ND2032	17.6	55.1	26.0	30.0	31.7	19.0	29.0	32.0
12	ND203×ND2002	18.4	53.1	22.0	37.0	21.2	19.1	25.0	20.2
13	PHG47×ND246	20.6	57.3	22.0	29.0	30.2	23.8	30.0	24.1
14	AP49×ND06-85	19.5	53.2	25.0	31.0	35.0	22.8	44.0	28.0
15	ND290×ND07-226	22.5	47.2	22.0	34.0	31.0	20.9	34.0	28.3
16	NK779×ND2000	18.9	54.7	27.0	42.0	39.8	24.8	29.0	33.0
17	AP49×ND291	30.6	56.6	31.0	46.0	44.5	24.1	56.0	36.1
18	ND07-212×B104	16.5	52.1	28.0	27.0	31.0	24.9	35.0	29.5
19	ND2021×ND2009	23.2	51.0	26.0	31.0	35.9	25.1	48.0	27.2
20	NP2341×ND07-153	21.6	51.8	27.0	35.0	38.5	23.7	53.0	36.5
21	ND2013×B104	30.7	46.5	23.0	28.0	43.0	25.7	43.0	40.4
22	LH61×ND246	17.3	68.4	24.0	44.0	46.4	31.6	31.0	26.4
23	ND08-343×ND07-153	22.5	52.0	30.0	25.0	31.8	25.6	49.0	26.6
24	GEM5Derived×ND2002	17.0	47.1	19.0	25.0	22.5	22.3	30.0	24.3
25	ND06-189×NK807	23.4	52.3	28.0	35.0	33.6	23.6	41.0	26.4
26	ND2021×ND2005	26.1	54.4	22.0	26.0	31.9	23.6	41.0	24.0
27	NP2341×ND2000	21.1	46.8	20.0	30.0	28.0	20.4	35.0	22.8
28	ND06-144×ND2007	29.7	65.9	27.0	39.0	30.5	25.7	47.0	37.1
29	ND08-343×ND2002	22.1	50.0	23.0	29.0	24.6	23.0	33.0	18.9
30	NK779×ND2006	28.0	60.1	22.0	40.0	44.9	24.4	46.0	31.1
31	ND2019×B104	23.2	58.1	26.0	50.0	30.7	21.9	38.0	45.1
32	ND2021×KMN22	25.6	42.2	34.0	29.0	32.7	25.1	40.0	32.2
33	ND08-343×ND2007	26.7	59.6	22.0	43.0	29.2	30.6	38.0	36.7
34	PHG47×ND06-85	17.6	45.7	23.0	30.0	29.0	24.2	27.0	23.4
35	ND203×ND2004	17.6	57.3	20.0	31.0	35.6	27.7	31.0	30.6
36	ND06-85×ND2032	21.4	51.4	21.0	35.0	21.9	21.7	34.0	28.6
37	A052×ND246	20.4	54.9	22.0	33.0	40.2	26.8	35.0	28.6
38	A052×ND2000	23.3	54.4	22.0	37.0	31.4	22.8	37.0	24.8
39	NK779×ND250	23.1	47.7	23.0	25.0	29.6	20.7	44.0	28.8
40	NP2341×ND2006	19.6	48.4	28.0	30.0	30.2	25.3	35.0	23.5
41	ND2013×KMN22	30.6	60.9	27.0	34.0	46.8	30.3	49.0	29.7
42	ND07-97×ND07-153	33.3	63.6	32.0	35.0	36.7	29.2	42.0	39.4
43	ND06-144×ND07-153	24.6	52.5	40.0	41.0	28.8	25.6	36.0	34.7
44	ND2014×KMN22	23.8	60.4	28.0	33.0	25.8	26.8	33.0	39.0
45	LB2000×ND2000	25.0	60.5	28.0	32.0	34.5	21.1	32.0	28.6
46	ND265×ND2005	17.5	52.1	23.0	39.0	27.6	22.9	37.0	24.7
47	ND274×ND2005	19.7	46.7	25.0	34.0	26.0	21.2	33.0	26.7
48	ND08-53×NK807	18.8	53.7	28.0	32.0	29.9	19.5	40.0	32.4
49	ND06-144×ND2002	17.5	48.0	25.0	23.0	21.8	21.9	33.0	24.1
50	PHG47× D291	18.8	58.4	28.0	34.0	35.4	25.7	32.0	32.3
51	ND265×ND2009	18.7	60.0	29.0	43.0	43.1	31.9	44.0	43.0
52	LB2000× ND250	19.5	52.9	26.0	33.0	36.8	23.8	42.0	24.7

Table A18. Visbile brace root spread width (mm) adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID) (continued).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
53	ND07-97×ND2007	23.9	55.9	22.0	46.0	43.4	31.0	46.0	41.9
54	ND2014×AP47	27.4	55.2	25.0	33.0	36.3	24.6	42.0	30.9
55	ND06-189×AP47	19.3	59.7	27.0	42.0	28.4	24.2	37.0	31.5
56	NP2341×ND2014	18.1	54.3	24.0	30.0	33.0	25.5	35.0	26.8
57	ND08-343×ND2004	34.0	52.2	23.0	33.0	29.3	28.4	43.0	32.3
58	ND265×ND2004	21.8	67.6	30.0	44.0	37.1	27.5	43.0	31.0
59	ND08-53×PHJ40	19.6	51.2	27.0	36.0	31.7	23.1	41.0	29.2
60	GEM5Derived×ND2007	24.4	51.5	25.0	27.0	37.3	25.6	33.0	32.9
61	LH61×ND250	20.0	54.7	24.0	36.0	27.7	27.6	26.0	31.6
62	ND2019×KMN22	28.8	60.2	27.0	37.0	31.6	25.8	41.0	27.6
63	LH61×ND06-85	21.0	45.2	24.0	32.0	41.6	26.6	39.0	31.0
64	GEM 5 Derived×ND2004	29.1	50.2	20.0	28.0	32.6	25.9	32.0	30.2
65	ND07-97×ND2014	23.7	57.3	22.0	38.0	35.0	29.5	30.0	28.4
66	ND08-53×ND2032	23.8	48.5	21.0	32.0	21.0	19.0	26.0	26.6
67	PHG47×ND270	19.5	53.2	23.0	41.0	29.6	24.7	37.0	28.2
68	ND07-97×ND2006	25.0	53.0	29.0	36.0	31.4	34.6	36.0	34.5
69	ND07-255×ND07-226	24.1	46.2	23.0	24.0	27.7	19.6	38.0	23.8
70	ND07-212×NK807	20.0	51.4	30.0	39.0	29.1	23.3	31.0	35.8
71	ND2021×Il5	22.5	54.8	27.0	37.0	40.5	28.9	38.0	34.7
72	ND07-212×AP47	21.3	55.2	22.0	32.0	36.9	32.9	35.0	31.9
73	A052×ND270	22.3	50.6	29.0	37.0	32.0	21.6	28.0	24.0
74	ND274×ND2009	25.4	54.1	33.0	37.0	40.2	32.5	41.0	36.9
75	A052×ND250	26.5	46.4	22.0	34.0	27.5	23.9	33.0	29.3
76	ND08-53×ND07-226	17.5	42.6	22.0	26.0	23.8	19.3	31.0	28.8
77	ND07-255×PHJ40	21.0	47.5	22.0	25.0	25.9	26.9	36.0	25.1
78	ND06-144×ND2006	15.7	50.2	22.0	28.0	28.4	21.1	32.0	26.6
79	ND291×ND2032	22.3	57.1	21.0	39.0	52.0	20.8	41.0	30.4
80	ND291×ND07-226	20.0	54.0	28.0	35.0	40.4	27.5	35.0	29.2
81	ND07-255×NK807	22.3	51.2	31.0	35.0	28.1	22.8	47.0	26.4
82	ND06-189×PHJ40	16.6	46.1	23.0	28.0	26.0	24.4	31.0	23.9
83	ND2014×LP05	21.2	46.8	29.0	28.0	23.2	27.3	37.0	34.7
84	LB2000×ND270	26.7	52.1	30.0	26.0	22.7	25.3	30.0	25.4
85	ND274×Il5	26.0	55.7	28.0	43.0	41.3	32.1	47.0	40.7
86	LB2000×ND2014	30.1	58.9	27.0	41.0	30.2	25.3	41.0	26.1
87	ND07-212×LP05	24.6	48.8	18.0	27.0	29.6	28.9	38.0	27.9
88	ND2019×AP47	21.6	54.8	25.0	38.0	35.6	31.7	40.0	40.1
89	LH61×ND270	19.8	50.7	25.0	32.0	40.3	31.9	25.0	39.4
90	ND2013×ND2009	30.0	59.6	38.0	39.0	44.7	44.7	46.0	42.0
91	ND06-189×LP05	15.3	55.0	31.0	26.0	22.3	22.8	28.0	34.2
92	ND07-255×LP05	23.1	51.9	29.0	31.0	26.9	24.3	32.0	31.5
93	ND2013×Il5	22.2	51.5	31.0	40.0	38.6	31.8	48.0	34.7
94	ND2019×Il5	18.7	47.9	29.0	36.0	41.1	32.0	47.0	39.8
95	**Thurston 77RM**	19.6	49.8	25.0	31.0	35.9	21.0	49.0	29.1
96	**Pioneer 79RM**	21.8	50.2	28.0	33.0	36.9	20.9	50.0	32.8
97	**Pioneer 80RM**	22.5	54.6	31.0	39.0	56.8	28.7	57.0	40.0
98	**Thurston 82RM**	14.4	49.9	26.0	35.0	37.3	22.6	43.0	36.1
99	**Syngenta 85RM**	27.3	50.8	25.0	41.0	34.2	23.1	50.0	37.1
100	**Monsanto 88RM**	19.5	50.3	26.0	26.0	39.8	25.1	38.0	30.4
	Experimental Mean	22.3	52.8	26.0	34.0	33.1	25.5	38.0	30.7
	CV%	17.6	9.7	14.7	18.3	17.3	14.0	18.3	15.3
	LSD,0.05	7.8	10.2	5.3	8.7	11.3	7.1	9.7	6.6
	MSE	15.4	26.4	14.0	38.0	32.6	12.7	48.0	22.2

Table A19. Visible braceroot adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
1	ND203×ND2001	.	9.4	.	7.7	9.3	9.6	12.0	15.6
2	ND2014×B104	.	19.5	.	15.0	17.7	15.1	13.0	20.7
3	GEM5Derived×ND2001	10.4	9.2	18.0	10.0	12.7	11.0	12.0	13.9
4	ND265×ND2001	8.7	8.1	14.0	8.7	9.6	8.6	13.0	14.7
5	AP49×ND246	10.3	5.5	13.0	8.9	13.7	12.8	14.0	15.8
6	ND274×ND2001	11.0	8.3	14.0	12.0	13.2	11.6	15.0	15.6
7	ND290×PHJ40	10.6	11.9	15.0	13.0	15.7	14.6	14.0	21.3
8	ND203×ND2005	11.5	4.7	13.0	7.6	8.0	10.6	10.0	10.1
9	AP49×ND290	14.1	13.1	15.0	15.0	19.2	11.8	20.0	26.4
10	NK779×ND2014	13.7	12.9	16.0	11.0	13.4	9.7	12.0	19.7
11	ND290×ND2032	10.3	11.2	14.0	7.7	11.9	9.3	11.0	21.1
12	ND203×ND2002	13.0	5.4	14.0	5.4	12.4	11.6	11.0	17.1
13	PHG47×ND246	9.6	6.3	13.0	11.0	12.3	10.0	13.0	13.1
14	AP49×ND06-85	10.3	9.0	15.0	12.0	15.1	11.2	16.0	15.5
15	ND290×ND07-226	14.4	12.6	14.0	14.0	17.4	13.4	14.0	20.9
16	NK779×ND2000	11.9	12.2	14.0	14.0	12.7	11.2	13.0	15.4
17	AP49×ND291	11.5	10.7	16.0	9.9	17.1	10.7	17.0	17.1
18	ND07-212×B104	11.3	17.6	15.0	18.0	15.4	15.3	14.0	21.1
19	ND2021×ND2009	11.3	16.9	15.0	18.0	15.7	12.9	17.0	15.2
20	NP2341×ND07-153	11.8	14.5	15.0	13.0	18.7	12.1	17.0	15.2
21	ND2013×B104	14.9	16.8	17.0	15.0	18.7	15.8	20.0	28.9
22	LH61×ND246	11.0	5.3	10.0	4.0	12.8	7.7	8.0	12.4
23	ND08-343×ND07-153	15.2	12.6	18.0	15.0	16.4	10.5	14.0	14.9
24	GEM5Derived×ND2002	12.9	10.2	15.0	11.0	11.7	11.4	10.0	14.1
25	ND06-189×NK807	9.1	7.8	16.0	9.0	16.5	10.1	12.0	16.1
26	ND2021×ND2005	13.8	8.2	13.0	8.9	13.9	10.0	10.0	16.0
27	NP2341×ND2000	13.6	8.9	16.0	13.0	12.4	7.7	13.0	14.0
28	ND06-144×ND2007	13.1	7.5	15.0	12.0	14.7	13.0	15.0	17.5
29	ND08-343×ND2002	10.1	8.6	17.0	7.8	15.7	11.2	15.0	13.0
30	NK779×ND2006	11.2	13.4	13.0	11.0	14.0	11.4	13.0	13.5
31	ND2019×B104	13.1	11.5	15.0	11.0	14.3	13.9	15.0	28.5
32	ND2021×KMN22	14.7	12.3	17.0	9.0	15.0	12.1	14.0	17.7
33	ND08-343×ND2007	14.4	12.0	14.0	15.0	13.6	11.7	17.0	18.4
34	PHG47×ND06-85	10.6	9.4	13.0	16.0	11.8	9.7	12.0	13.1
35	ND203×ND2004	9.5	11.1	14.0	11.0	16.8	13.2	11.0	19.1
36	ND06-85×ND2032	10.0	7.5	12.0	11.0	11.9	9.6	11.0	11.1
37	A052×ND246	12.7	13.2	14.0	15.0	13.3	12.4	14.0	12.1
38	A052×ND2000	11.7	13.8	16.0	16.0	16.7	11.2	14.0	16.3
39	NK779×ND250	10.9	13.1	15.0	11.0	12.4	8.5	17.0	15.0
40	NP2341×ND2006	8.1	10.6	16.0	10.0	14.6	9.4	15.0	13.7
41	ND2013×KMN22	14.5	15.0	18.0	9.8	17.2	15.5	17.0	21.3
42	ND07-97×ND07-153	12.6	15.2	15.0	13.0	14.9	11.5	16.0	21.8
43	ND06-144×ND07-153	11.2	10.1	16.0	8.6	12.5	9.6	13.0	19.5
44	ND2014×KMN22	12.6	10.2	16.0	9.7	11.9	13.8	13.0	19.7
45	LB2000×ND2000	13.0	15.5	14.0	13.0	14.2	10.2	13.0	16.5
46	ND265×ND2005	9.7	8.4	14.0	7.5	11.4	10.2	9.7	14.0
47	ND274×ND2005	12.3	10.5	13.0	9.0	13.3	8.9	14.0	13.7
48	ND08-53×NK807	9.0	9.3	14.0	8.6	11.0	9.9	13.0	14.4
49	ND06-144×ND2002	9.3	10.8	14.0	9.4	12.8	14.1	11.0	16.1
50	PHG47× D291	11.0	14.7	14.0	13.0	13.6	11.3	12.0	16.3
51	ND265×ND2009	10.7	10.3	17.0	15.0	16.6	12.3	14.0	18.7
52	LB2000× ND250	12.2	13.9	15.0	13.0	16.4	11.9	9.9	14.2

Table A19. Visible braceroot adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID) (continued).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
53	ND07-97×ND2007	9.3	14.1	12.0	11.0	16.3	15.0	15.0	19.4
54	ND2014×AP47	9.7	12.2	14.0	10.0	15.2	10.4	13.0	17.9
55	ND06-189×AP47	12.1	11.1	13.0	14.0	11.4	13.1	12.0	16.7
56	NP2341×ND2014	10.9	10.5	15.0	9.9	14.7	12.9	13.0	17.3
57	ND08-343×ND2004	13.8	14.9	14.0	8.2	16.5	11.1	18.0	19.4
58	ND265×ND2004	11.4	13.2	14.0	11.0	13.2	11.2	16.0	17.7
59	ND08-53×PHJ40	11.9	11.3	16.0	11.0	13.4	11.1	14.0	11.3
60	GEM5Derived×ND2007	11.2	13.6	14.0	12.0	13.7	11.0	12.0	16.8
61	LH61×ND250	11.8	6.2	13.0	9.3	13.6	9.9	9.3	17.8
62	ND2019×KMN22	15.7	11.2	17.0	10.0	13.5	11.3	13.0	22.5
63	LH61×ND06-85	10.2	6.2	12.0	6.7	12.9	9.3	12.0	11.0
64	GEM 5 Derived×ND2004	14.5	13.4	15.0	14.0	16.5	10.7	13.0	15.3
65	ND07-97×ND2014	11.8	15.1	13.0	14.0	14.4	11.5	11.0	21.1
66	ND08-53×ND2032	11.3	10.2	14.0	8.0	11.2	10.5	8.8	12.2
67	PHG47×ND270	10.7	15.2	12.0	14.0	9.2	8.7	11.0	14.6
68	ND07-97×ND2006	11.4	10.9	13.0	15.0	13.7	8.6	12.0	15.4
69	ND07-255×ND07-226	12.6	12.6	12.0	10.0	16.5	9.3	16.0	17.1
70	ND07-212×NK807	8.0	9.5	16.0	15.0	15.1	13.5	14.0	20.3
71	ND2021×Il5	13.4	8.8	14.0	11.0	17.3	11.3	11.0	17.7
72	ND07-212×AP47	13.7	14.0	14.0	12.0	14.2	12.6	15.0	18.5
73	A052×ND270	13.5	10.5	22.0	11.0	11.9	12.0	13.0	10.0
74	ND274×ND2009	12.6	14.3	17.0	13.0	14.0	13.3	14.0	18.0
75	A052×ND250	14.4	12.1	13.0	11.0	11.1	13.6	14.0	14.9
76	ND08-53×ND07-226	10.4	8.9	12.0	12.0	9.6	7.9	11.0	13.7
77	ND07-255×PHJ40	15.8	10.9	17.0	15.0	17.9	13.1	16.0	18.2
78	ND06-144×ND2006	10.1	12.4	14.0	13.0	14.1	11.0	10.0	16.0
79	ND291×ND2032	10.9	12.0	12.0	10.0	15.6	9.7	14.0	17.6
80	ND291×ND07-226	12.1	13.7	15.0	17.0	16.7	11.8	14.0	17.9
81	ND07-255×NK807	13.0	12.2	16.0	12.0	15.2	8.3	15.0	16.2
82	ND06-189×PHJ40	14.4	17.1	15.0	15.0	13.1	13.3	11.0	16.8
83	ND2014×LP05	12.5	18.8	15.0	16.0	13.7	15.4	15.0	24.5
84	LB2000×ND270	14.4	12.2	14.0	11.0	12.6	9.5	14.0	14.7
85	ND274×Il5	13.5	13.3	15.0	13.0	13.5	9.0	14.0	14.8
86	LB2000×ND2014	12.8	14.4	14.0	16.0	14.1	14.3	13.0	15.9
87	ND07-212×LP05	12.5	12.6	14.0	14.0	14.3	12.9	17.0	21.1
88	ND2019×AP47	10.1	10.4	15.0	10.0	16.7	11.5	15.0	20.8
89	LH61×ND270	9.4	8.5	13.0	5.6	11.3	10.4	11.0	16.1
90	ND2013×ND2009	12.8	20.7	20.0	20.0	19.9	15.4	17.0	22.9
91	ND06-189×LP05	10.4	17.7	16.0	17.0	11.6	14.5	10.0	20.9
92	ND07-255×LP05	14.1	12.7	18.0	12.0	13.7	11.4	14.0	21.3
93	ND2013×Il5	10.7	11.8	11.0	11.0	14.0	7.9	13.0	14.5
94	ND2019×Il5	10.6	8.6	16.0	13.0	13.3	10.4	14.0	19.5
95	**Thurston 77RM**	12.3	9.6	16.0	9.7	13.3	9.3	15.0	15.7
96	**Pioneer 79RM**	11.1	9.1	14.0	8.5	11.9	7.2	16.0	19.0
97	**Pioneer 80RM**	10.7	9.8	14.0	7.5	11.2	5.7	14.0	14.5
98	**Thurston 82RM**	10.1	14.1	17.0	10.0	14.4	10.5	14.0	16.8
99	**Syngenta 85RM**	10.8	11.6	14.0	9.0	11.2	7.3	12.0	16.7
100	**Monsanto 88RM**	11.7	11.8	17.0	18.0	16.2	8.9	13.0	20.0
	Experimental Mean	11.8	11.6	15.0	12.0	14.0	11.2	13.0	17.1
	CV%	14.4	20.4	12.8	23.2	17.4	19.1	15.7	17.2
	LSD,0.05	3.4	4.7	2.6	3.8	4.9	4.2	3.0	4.1
	MSE	2.9	5.6	3.6	7.4	6.0	4.6	4.5	8.6

Table A20. Effective braceroot whorls adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
1	ND203×ND2001	.	1.1	.	1.0	1.0	1.3	1.0	1.3
2	ND2014×B104	.	1.1	.	1.1	1.3	1.6	1.1	1.7
3	GEM5Derived×ND2001	1.0	1.0	1.4	1.2	1.1	1.7	1.3	1.7
4	ND265×ND2001	0.9	1.1	1.0	1.2	1.0	1.5	1.0	1.6
5	AP49×ND246	1.0	1.1	1.0	1.1	1.1	1.3	1.2	1.7
6	ND274×ND2001	1.1	1.0	1.0	1.6	1.4	1.9	1.2	1.8
7	ND290×PHJ40	1.1	1.1	1.0	1.7	1.3	1.5	1.1	1.9
8	ND203×ND2005	0.9	1.0	1.1	1.1	1.0	1.2	1.0	1.4
9	AP49×ND290	1.5	1.3	1.5	1.9	1.6	2.0	1.6	2.0
10	NK779×ND2014	1.1	1.1	1.0	1.6	1.0	1.9	1.1	1.9
11	ND290×ND2032	1.1	1.0	1.1	1.1	1.0	1.3	1.1	1.5
12	ND203×ND2002	1.2	1.0	1.0	1.0	1.0	1.6	1.0	1.5
13	PHG47×ND246	1.1	1.0	1.0	1.2	1.1	1.2	1.1	1.2
14	AP49×ND06-85	1.0	1.1	1.0	1.3	1.2	1.3	1.4	1.7
15	ND290×ND07-226	1.2	1.0	1.0	1.6	1.3	1.4	1.2	1.9
16	NK779×ND2000	1.1	1.1	1.0	1.4	1.3	1.6	1.1	1.6
17	AP49×ND291	1.5	1.3	1.4	1.7	1.6	1.7	1.7	1.9
18	ND07-212×B104	0.9	1.1	1.0	1.0	1.4	1.6	1.1	2.0
19	ND2021×ND2009	1.0	1.1	1.1	1.3	1.0	1.6	1.2	1.6
20	NP2341×ND07-153	1.0	1.4	1.3	1.8	1.8	1.8	2.0	2.2
21	ND2013×B104	1.7	1.1	1.5	1.4	1.3	1.6	1.2	2.1
22	LH61×ND246	1.0	1.1	1.1	1.0	1.3	1.2	1.0	1.0
23	ND08-343×ND07-153	1.4	1.1	1.5	1.4	1.2	1.7	1.4	1.9
24	GEM5Derived×ND2002	1.1	1.0	1.1	1.5	1.2	1.9	1.1	1.5
25	ND06-189×NK807	1.0	1.2	1.2	1.6	1.3	1.5	1.2	1.7
26	ND2021×ND2005	1.3	1.0	1.0	1.3	1.2	1.1	1.1	1.6
27	NP2341×ND2000	1.0	1.0	1.3	1.4	1.1	1.7	1.3	1.4
28	ND06-144×ND2007	1.1	1.1	1.1	1.3	1.2	1.7	1.7	2.0
29	ND08-343×ND2002	1.0	1.4	1.6	1.4	1.1	1.8	1.2	1.3
30	NK779×ND2006	1.2	1.0	1.0	1.1	1.2	1.8	1.0	1.5
31	ND2019×B104	1.0	1.5	1.0	1.0	1.3	1.6	1.2	2.2
32	ND2021×KMN22	1.0	1.1	1.2	1.2	1.5	1.7	1.5	2.2
33	ND08-343×ND2007	1.2	1.4	1.0	1.3	1.2	1.9	1.1	1.9
34	PHG47×ND06-85	1.1	1.1	1.5	1.0	1.2	1.3	1.2	1.5
35	ND203×ND2004	1.0	1.1	1.0	1.0	1.2	1.2	1.1	1.6
36	ND06-85×ND2032	1.0	1.0	1.0	1.0	1.0	1.4	1.0	1.2
37	A052×ND246	1.1	1.0	1.0	1.1	1.2	1.5	1.1	1.5
38	A052×ND2000	1.3	1.1	1.0	1.3	1.0	1.7	1.1	1.9
39	NK779×ND250	1.1	1.1	1.1	1.6	1.1	1.8	1.2	1.7
40	NP2341×ND2006	1.3	1.1	1.2	1.0	1.1	1.8	1.0	1.6
41	ND2013×KMN22	1.6	1.6	1.4	1.8	1.6	2.0	1.4	1.9
42	ND07-97×ND07-153	1.2	1.4	1.5	1.8	1.6	2.0	1.2	1.9
43	ND06-144×ND07-153	1.2	1.2	1.3	1.1	1.3	1.6	1.1	2.0
44	ND2014×KMN22	1.1	1.0	1.0	1.6	1.3	1.9	1.0	2.0
45	LB2000×ND2000	1.1	1.3	1.5	1.6	1.4	2.2	1.1	2.0
46	ND265×ND2005	1.0	1.0	1.0	1.1	1.1	1.1	1.2	1.4
47	ND274×ND2005	1.0	1.1	1.3	1.3	1.3	1.4	1.2	1.7
48	ND08-53×NK807	1.0	1.1	1.0	1.9	1.3	2.0	1.6	1.8
49	ND06-144×ND2002	1.1	1.3	1.1	1.4	1.4	1.4	1.3	1.8
50	PHG47× D291	1.0	1.1	1.0	1.3	1.0	1.7	1.2	1.6
51	ND265×ND2009	1.1	1.6	1.1	1.1	1.1	1.6	1.1	1.8
52	LB2000× ND250	1.3	1.1	1.1	2.0	1.5	1.8	1.3	1.8

Table A20. Effective braceroot whorls adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID) (continued).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
53	ND07-97×ND2007	1.3	1.1	1.1	1.6	1.3	1.7	1.4	2.1
54	ND2014×AP47	1.0	1.0	1.1	1.3	1.3	1.5	1.1	1.6
55	ND06-189×AP47	1.1	1.2	1.0	1.4	0.9	1.5	1.1	1.9
56	NP2341×ND2014	1.1	1.0	1.2	1.1	1.1	1.8	1.4	1.8
57	ND08-343×ND2004	1.1	1.5	1.4	1.4	1.5	1.9	1.3	2.0
58	ND265×ND2004	1.0	1.2	1.0	1.3	1.4	1.4	1.0	1.9
59	ND08-53×PHJ40	1.0	1.2	1.0	1.6	1.0	1.5	1.4	1.8
60	GEM5Derived×ND2007	1.1	1.3	1.0	1.4	1.3	1.7	1.1	1.9
61	LH61×ND250	1.0	1.2	1.0	1.1	1.3	1.6	1.1	1.8
62	ND2019×KMN22	1.4	1.4	1.4	1.3	1.1	1.5	1.1	1.9
63	LH61×ND06-85	1.1	1.1	1.0	1.3	1.0	1.1	1.3	1.3
64	GEM 5 Derived×ND2004	1.0	1.3	1.1	1.3	1.0	1.6	1.0	1.4
65	ND07-97×ND2014	1.1	1.0	1.1	1.3	1.1	1.7	1.0	1.8
66	ND08-53×ND2032	1.1	1.0	1.0	1.0	1.0	1.2	1.0	1.7
67	PHG47×ND270	1.0	1.1	1.2	1.3	1.1	1.2	1.1	1.7
68	ND07-97×ND2006	1.0	1.1	1.1	1.1	1.0	1.5	1.0	1.8
69	ND07-255×ND07-226	1.2	1.1	1.0	1.3	1.2	1.7	1.3	1.6
70	ND07-212×NK807	1.0	1.0	1.0	1.3	1.2	1.8	1.2	1.9
71	ND2021×Il5	1.3	1.3	1.2	1.6	1.2	1.6	1.0	1.9
72	ND07-212×AP47	1.1	1.2	1.0	1.1	1.4	1.5	1.3	1.8
73	A052×ND270	1.2	1.3	1.4	1.4	1.2	1.6	1.0	1.2
74	ND274×ND2009	1.2	1.3	1.2	1.3	1.4	1.9	1.4	1.9
75	A052×ND250	1.3	1.5	1.1	1.4	1.2	1.2	1.2	1.8
76	ND08-53×ND07-226	1.0	1.0	1.0	1.2	1.0	1.2	1.0	1.3
77	ND07-255×PHJ40	1.1	1.0	1.1	1.3	1.3	1.8	1.2	1.7
78	ND06-144×ND2006	1.0	1.0	1.0	1.1	1.1	1.2	1.1	1.8
79	ND291×ND2032	1.0	1.0	1.0	1.3	1.3	1.4	1.2	1.6
80	ND291×ND07-226	1.3	1.4	1.1	1.4	1.1	1.7	1.4	1.7
81	ND07-255×NK807	1.0	1.4	1.1	1.4	1.6	2.1	1.3	2.2
82	ND06-189×PHJ40	1.0	1.1	1.0	1.4	1.1	1.2	1.2	1.4
83	ND2014×LP05	1.1	1.1	1.0	1.2	1.4	1.9	1.4	2.1
84	LB2000×ND270	1.2	1.1	1.0	1.6	1.1	1.6	1.0	1.7
85	ND274×Il5	1.4	1.3	1.3	1.5	1.1	2.0	1.3	1.9
86	LB2000×ND2014	1.2	1.2	1.3	1.9	1.3	1.6	1.2	1.8
87	ND07-212×LP05	1.2	1.1	1.3	1.4	1.3	1.5	1.2	1.7
88	ND2019×AP47	1.1	1.0	1.0	1.4	1.1	1.7	1.2	1.9
89	LH61×ND270	1.1	1.3	1.0	1.1	1.1	1.3	1.0	1.6
90	ND2013×ND2009	1.3	1.1	1.6	1.4	1.1	1.8	1.2	2.0
91	ND06-189×LP05	1.1	1.0	1.3	1.4	1.0	1.5	1.1	1.7
92	ND07-255×LP05	1.1	1.3	1.3	1.6	1.3	1.9	1.3	2.5
93	ND2013×Il5	1.1	1.3	1.1	1.8	1.2	2.2	1.6	2.1
94	ND2019×Il5	1.0	1.3	1.2	1.3	1.2	2.1	1.0	2.2
95	**Thurston 77RM**	1.1	1.1	0.9	1.4	1.2	1.6	1.4	1.8
96	**Pioneer 79RM**	1.6	1.5	1.0	1.4	1.7	1.8	1.6	2.0
97	**Pioneer 80RM**	1.1	1.4	1.0	1.7	1.4	2.0	1.5	1.9
98	**Thurston 82RM**	1.8	1.3	1.3	1.3	1.5	1.7	1.2	2.0
99	**Syngenta 85RM**	1.1	1.3	1.0	1.4	1.0	1.8	1.2	1.9
100	**Monsanto 88RM**	1.2	1.2	1.2	1.3	1.7	1.9	1.2	1.9
	Experimental Mean	1.1	1.2	1.1	1.3	1.2	1.6	1.2	1.8
	CV%	15.9	15.2	13.0	18.6	16.1	15.1	16.1	12.6
	LSD,0.05	0.4	0.3	0.2	0.3	0.4	0.5	0.3	0.3
	MSE	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.1

Table A21. Root capacitance (nF) adjusted means of 94 partial diallel crosses and six checks (on bottom) across six well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID).

Entry	Pedigree	2013		2014			
		WS	WW	WS		WW	
		NV	NV	NV	SID	NV	SID
1	ND203×ND2001	.	.	63.5	31.5	57.0	47.2
2	ND2014×B104	.	.	74.7	48.5	68.0	50.7
3	GEM5Derived×ND2001	20.0	24.0	56.5	30.4	51.0	43.5
4	ND265×ND2001	46.4	23.0	46.7	30.0	50.0	44.8
5	AP49×ND246	27.9	21.0	44.7	31.6	46.0	42.2
6	ND274×ND2001	39.8	29.0	39.7	30.8	51.0	45.7
7	ND290×PHJ40	32.3	19.0	38.8	33.2	34.0	41.4
8	ND203×ND2005	37.6	23.0	46.6	32.3	40.0	44.7
9	AP49×ND290	24.3	19.0	39.4	27.8	41.0	53.6
10	NK779×ND2014	21.6	26.0	46.7	27.9	51.0	39.8
11	ND290×ND2032	20.6	24.0	37.6	39.1	50.0	41.3
12	ND203×ND2002	22.6	34.0	41.8	33.1	41.0	41.3
13	PHG47×ND246	23.4	27.0	54.0	28.9	46.0	47.4
14	AP49×ND06-85	25.2	20.0	40.3	29.3	38.0	42.6
15	ND290×ND07-226	27.0	25.0	42.3	33.7	57.0	46.4
16	NK779×ND2000	30.8	29.0	55.6	34.2	56.0	42.5
17	AP49×ND291	23.3	24.0	44.1	31.3	43.0	43.9
18	ND07-212×B104	30.1	25.0	77.1	54.0	90.0	72.0
19	ND2021×ND2009	20.6	21.0	38.0	33.5	52.0	45.1
20	NP2341×ND07-153	19.2	21.0	46.4	29.2	52.0	31.5
21	ND2013×B104	26.6	27.0	84.6	56.3	74.0	60.7
22	LH61×ND246	22.1	26.0	47.6	28.8	45.0	45.3
23	ND08-343×ND07-153	24.2	25.0	41.4	34.7	42.0	39.7
24	GEM5Derived×ND2002	25.5	27.0	41.2	42.6	51.0	47.2
25	ND06-189×NK807	24.1	22.0	43.6	32.1	51.0	39.4
26	ND2021×ND2005	35.0	21.0	51.8	30.2	38.0	42.1
27	NP2341×ND2000	25.4	25.0	36.9	23.8	35.0	36.7
28	ND06-144×ND2007	23.1	24.0	42.1	40.4	55.0	59.3
29	ND08-343×ND2002	27.3	24.0	63.5	41.0	54.0	54.8
30	NK779×ND2006	37.6	22.0	38.1	38.6	36.0	34.9
31	ND2019×B104	31.2	24.0	69.1	51.8	61.0	62.9
32	ND2021×KMN22	26.5	29.0	37.5	28.8	55.0	37.8
33	ND08-343×ND2007	23.2	28.0	57.7	51.5	58.0	48.1
34	PHG47×ND06-85	34.8	28.0	43.3	32.9	41.0	38.8
35	ND203×ND2004	23.7	23.0	44.2	35.0	46.0	48.0
36	ND06-85×ND2032	29.3	28.0	42.1	37.7	35.0	38.4
37	A052×ND246	35.6	32.0	36.0	24.5	39.0	45.8
38	A052×ND2000	25.1	22.0	50.3	42.9	45.0	44.4
39	NK779×ND250	30.2	27.0	43.1	35.8	42.0	35.7
40	NP2341×ND2006	17.3	22.0	37.9	40.5	25.0	28.2
41	ND2013×KMN22	26.7	25.0	53.2	37.0	55.0	54.8
42	ND07-97×ND07-153	21.7	23.0	34.9	36.5	43.0	43.5
43	ND06-144×ND07-153	27.0	27.0	39.1	28.8	42.0	43.7
44	ND2014×KMN22	26.9	22.0	51.6	36.8	54.0	53.0
45	LB2000×ND2000	24.9	23.0	45.8	49.1	47.0	46.5
46	ND265×ND2005	20.3	21.0	47.6	27.3	36.0	44.5
47	ND274×ND2005	28.4	35.0	41.5	30.9	37.0	33.9
48	ND08-53×NK807	25.2	24.0	46.0	26.5	40.0	38.9
49	ND06-144×ND2002	25.0	30.0	44.0	32.5	40.0	44.0
50	PHG47× D291	21.4	32.0	64.3	35.8	46.0	46.8
51	ND265×ND2009	19.3	35.0	46.4	29.3	43.0	43.7
52	LB2000× ND250	24.6	24.0	42.3	30.9	38.0	41.8

Table A21. Root capacitance (nF) adjusted means of 94 partial diallel crosses and six checks (on bottom) across six well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID) (continued).

| Entry | Pedigree | 2013 | | 2014 | | | |
| | | WS | WW | WS | | WW | |
		NV	NV	NV	SID	NV	SID
53	ND07-97×ND2007	25.5	23.0	44.7	38.9	59.0	56.5
54	ND2014×AP47	26.5	24.0	63.3	34.4	59.0	46.8
55	ND06-189×AP47	19.3	21.0	45.4	29.3	44.0	44.1
56	NP2341×ND2014	24.0	16.0	38.1	26.8	38.0	31.1
57	ND08-343×ND2004	29.4	30.0	47.1	33.4	53.0	46.0
58	ND265×ND2004	27.9	21.0	42.3	26.5	35.0	41.9
59	ND08-53×PHJ40	22.6	26.0	37.5	25.3	35.0	35.6
60	GEM5Derived×ND2007	24.7	21.0	44.6	28.2	57.0	46.0
61	LH61×ND250	22.1	25.0	45.7	33.7	47.0	33.5
62	ND2019×KMN22	25.0	34.0	57.5	44.6	61.0	65.4
63	LH61×ND06-85	27.6	23.0	46.4	31.1	48.0	37.9
64	GEM 5 Derived×ND2004	22.5	24.0	40.8	38.7	50.0	43.5
65	ND07-97×ND2014	23.7	26.0	41.0	32.9	43.0	45.0
66	ND08-53×ND2032	23.5	25.0	37.7	34.1	39.0	43.2
67	PHG47×ND270	31.6	22.0	51.7	27.7	33.0	37.3
68	ND07-97×ND2006	22.4	25.0	33.3	32.7	32.0	37.0
69	ND07-255×ND07-226	25.6	31.0	55.1	34.4	62.0	41.4
70	ND07-212×NK807	24.0	24.0	55.2	33.6	59.0	41.8
71	ND2021×Il5	25.0	18.0	50.7	38.6	44.0	44.8
72	ND07-212×AP47	26.8	21.0	48.0	32.5	46.0	41.3
73	A052×ND270	30.4	32.0	36.6	29.5	44.0	38.2
74	ND274×ND2009	30.4	32.0	41.4	35.7	45.0	40.7
75	A052×ND250	23.7	22.0	32.4	25.6	38.0	39.2
76	ND08-53×ND07-226	28.2	27.0	49.6	35.1	46.0	42.1
77	ND07-255×PHJ40	23.3	22.0	42.4	27.7	40.0	36.3
78	ND06-144×ND2006	24.4	25.0	44.6	32.7	37.0	40.3
79	ND291×ND2032	29.2	26.0	46.6	34.7	53.0	47.2
80	ND291×ND07-226	27.6	30.0	58.7	39.0	52.0	49.7
81	ND07-255×NK807	23.2	25.0	54.4	33.3	47.0	39.1
82	ND06-189×PHJ40	21.4	28.0	37.7	28.0	42.0	37.4
83	ND2014×LP05	24.8	29.0	57.6	38.6	62.0	51.7
84	LB2000×ND270	.	24.0	45.2	36.9	43.0	39.5
85	ND274×Il5	24.4	22.0	42.3	30.1	42.0	36.8
86	LB2000×ND2014	26.2	23.0	49.4	32.3	43.0	41.7
87	ND07-212×LP05	28.5	23.0	48.4	30.3	48.0	46.4
88	ND2019×AP47	20.2	24.0	50.5	34.1	57.0	47.4
89	LH61×ND270	25.4	23.0	40.8	32.6	52.0	39.9
90	ND2013×ND2009	26.5	25.0	48.3	44.1	59.0	55.0
91	ND06-189×LP05	22.9	25.0	38.9	28.5	36.0	40.8
92	ND07-255×LP05	25.0	24.0	46.4	36.3	51.0	45.7
93	ND2013×Il5	21.3	32.0	36.8	31.3	43.0	46.5
94	ND2019×Il5	26.6	25.0	55.0	41.6	62.0	46.8
95	**Thurston 77RM**	21.1	26.0	61.0	34.6	52.0	45.8
96	**Pioneer 79RM**	22.5	23.0	40.7	24.1	41.0	37.2
97	**Pioneer 80RM**	22.5	28.0	41.7	25.6	46.0	37.8
98	**Thurston 82RM**	21.0	24.0	46.7	27.0	54.0	40.9
99	**Syngenta 85RM**	24.2	27.0	37.2	25.1	48.0	49.8
100	**Monsanto 88RM**	20.1	29.0	64.8	43.0	63.0	60.7
	Experimental Mean	25.7	25.0	47.1	34.0	47.0	44.1
	CV%	18.7	19.3	14.7	15.7	14.5	10.3
	LSD,0.05	9.5	6.8	13.7	10.6	9.7	6.3
	MSE	23.1	23.0	48.0	28.4	48.0	20.5

Table A22. Stalk diameter (mm) adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
1	ND203×ND2001	.	20.5	.	18.0	23.8	23.0	22.0	20.9
2	ND2014×B104	.	21.1	.	21.0	22.3	22.3	23.0	24.0
3	GEM5Derived×ND2001	15.4	19.8	19.0	20.0	24.1	22.2	21.0	21.4
4	ND265×ND2001	17.9	18.9	16.0	19.0	22.4	20.1	19.0	22.3
5	AP49×ND246	16.2	17.0	16.0	19.0	23.1	22.8	21.0	21.9
6	ND274×ND2001	15.8	18.4	16.0	18.0	19.6	18.6	19.0	17.9
7	ND290×PHJ40	16.9	19.3	16.0	21.0	21.8	23.0	19.0	21.3
8	ND203×ND2005	18.1	18.3	18.0	18.0	21.2	19.6	20.0	21.3
9	AP49×ND290	17.2	19.1	16.0	20.0	19.9	20.8	19.0	21.6
10	NK779×ND2014	14.2	18.6	17.0	20.0	21.1	19.7	21.0	18.2
11	ND290×ND2032	15.6	16.0	16.0	17.0	19.4	19.0	17.0	18.7
12	ND203×ND2002	18.1	22.3	20.0	21.0	24.2	21.2	21.0	21.9
13	PHG47×ND246	16.1	18.9	17.0	20.0	23.2	21.2	20.0	22.1
14	AP49×ND06-85	17.5	19.2	20.0	20.0	21.1	21.2	19.0	24.7
15	ND290×ND07-226	18.3	20.4	18.0	20.0	24.2	19.7	20.0	20.0
16	NK779×ND2000	15.1	19.9	18.0	20.0	21.8	19.1	19.0	19.2
17	AP49×ND291	18.3	22.5	19.0	21.0	22.4	22.1	22.0	22.9
18	ND07-212×B104	19.3	23.3	17.0	21.0	22.9	23.7	22.0	25.9
19	ND2021×ND2009	17.9	19.4	18.0	20.0	22.4	21.9	20.0	23.0
20	NP2341×ND07-153	15.4	17.2	17.0	18.0	20.4	18.2	20.0	19.0
21	ND2013×B104	18.7	19.8	19.0	21.0	23.3	23.0	22.0	24.4
22	LH61×ND246	17.6	19.3	19.0	22.0	23.8	21.4	20.0	22.4
23	ND08-343×ND07-153	16.9	17.7	19.0	21.0	20.5	20.6	20.0	20.6
24	GEM5Derived×ND2002	19.3	21.0	19.0	20.0	23.6	19.5	21.0	22.3
25	ND06-189×NK807	15.8	18.8	16.0	19.0	21.2	18.8	20.0	19.3
26	ND2021×ND2005	20.2	19.1	19.0	19.0	23.2	20.6	22.0	21.2
27	NP2341×ND2000	17.0	18.0	16.0	19.0	22.7	19.7	19.0	19.3
28	ND06-144×ND2007	19.0	19.8	18.0	21.0	21.0	22.6	22.0	23.5
29	ND08-343×ND2002	17.6	22.9	19.0	20.0	23.2	20.2	22.0	23.2
30	NK779×ND2006	16.0	18.5	16.0	19.0	19.3	17.7	19.0	17.9
31	ND2019×B104	18.5	20.0	18.0	20.0	22.9	21.3	21.0	21.1
32	ND2021×KMN22	17.2	19.1	20.0	19.0	22.0	19.5	21.0	20.8
33	ND08-343×ND2007	16.9	20.3	17.0	22.0	23.2	21.2	23.0	24.3
34	PHG47×ND06-85	16.8	18.0	15.0	19.0	20.0	21.0	20.0	18.4
35	ND203×ND2004	15.2	20.8	16.0	19.0	21.8	20.8	21.0	20.3
36	ND06-85×ND2032	17.5	17.6	16.0	19.0	18.7	18.7	18.0	18.6
37	A052×ND246	17.9	18.1	17.0	19.0	21.6	19.9	20.0	21.8
38	A052×ND2000	17.9	18.6	18.0	18.0	21.7	21.2	20.0	22.2
39	NK779×ND250	16.1	17.5	16.0	19.0	22.5	19.2	21.0	19.8
40	NP2341×ND2006	17.0	18.8	15.0	19.0	19.8	19.5	18.0	18.8
41	ND2013×KMN22	16.7	18.5	16.0	20.0	21.2	18.9	19.0	21.9
42	ND07-97×ND07-153	14.1	17.7	16.0	20.0	18.8	20.9	19.0	20.4
43	ND06-144×ND07-153	15.3	19.8	17.0	19.0	20.4	20.4	19.0	19.1
44	ND2014×KMN22	18.4	19.2	18.0	22.0	21.9	20.5	21.0	17.9
45	LB2000×ND2000	17.5	19.6	18.0	20.0	22.2	20.5	21.0	20.3
46	ND265×ND2005	15.2	17.0	16.0	17.0	20.2	18.0	19.0	19.7
47	ND274×ND2005	14.4	18.3	16.0	20.0	19.5	19.1	19.0	19.9
48	ND08-53×NK807	15.6	16.3	16.0	19.0	20.2	19.9	19.0	21.7
49	ND06-144×ND2002	16.6	19.5	18.0	23.0	20.9	19.2	22.0	21.6
50	PHG47× D291	15.3	19.2	16.0	20.0	21.9	20.2	18.0	19.5
51	ND265×ND2009	15.8	18.6	19.0	21.0	21.3	18.8	20.0	21.1
52	LB2000× ND250	16.6	19.8	16.0	20.0	21.9	18.2	20.0	18.6

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Table A22. Stalk diameter (mm) adjusted means of 94 partial diallel crosses and six checks (on bottom) across eight well-watered (WW), water stressed (WS) environments of Nesson Valley, North Dakota (NV), Sidney, Montana (SID) (continued).

Entry	Pedigree	2013				2014			
		WS		WW		WS		WW	
		NV	SID	NV	SID	NV	SID	NV	SID
53	ND07-97×ND2007	16.6	17.9	17.0	23.0	22.3	21.6	21.0	22.4
54	ND2014×AP47	18.1	20.1	17.0	19.0	23.1	22.7	20.0	22.1
55	ND06-189×AP47	17.3	18.5	17.0	18.0	21.9	21.1	20.0	21.6
56	NP2341×ND2014	14.7	18.1	18.0	17.0	20.2	17.6	19.0	20.6
57	ND08-343×ND2004	18.1	20.7	16.0	20.0	19.8	18.1	20.0	20.3
58	ND265×ND2004	16.4	18.1	15.0	19.0	21.2	19.3	19.0	20.7
59	ND08-53×PHJ40	17.3	19.8	19.0	19.0	21.0	19.8	19.0	21.6
60	GEM5Derived×ND2007	17.3	20.3	18.0	20.0	21.4	20.4	21.0	22.2
61	LH61×ND250	16.1	19.4	20.0	19.0	23.1	20.3	21.0	21.0
62	ND2019×KMN22	17.9	22.3	19.0	19.0	21.9	20.8	20.0	22.0
63	LH61×ND06-85	16.9	21.9	20.0	20.0	22.7	22.1	20.0	23.4
64	GEM 5 Derived×ND2004	18.9	18.8	16.0	19.0	21.9	19.2	19.0	18.2
65	ND07-97×ND2014	17.0	18.2	19.0	19.0	23.4	20.8	19.0	19.3
66	ND08-53×ND2032	15.5	17.0	16.0	17.0	19.1	17.8	18.0	17.8
67	PHG47×ND270	16.4	18.4	20.0	19.0	20.1	19.2	16.0	19.6
68	ND07-97×ND2006	15.8	18.1	17.0	17.0	19.7	18.0	18.0	18.9
69	ND07-255×ND07-226	16.8	18.1	19.0	21.0	21.6	18.5	22.0	21.6
70	ND07-212×NK807	15.0	17.5	18.0	18.0	22.4	21.1	21.0	22.3
71	ND2021×Il5	18.3	18.6	18.0	21.0	21.3	21.0	19.0	21.1
72	ND07-212×AP47	19.2	21.1	18.0	20.0	20.8	24.2	21.0	23.5
73	A052×ND270	17.4	17.3	18.0	17.0	21.1	20.3	19.0	20.1
74	ND274×ND2009	13.9	19.8	17.0	19.0	21.0	21.2	19.0	21.0
75	A052×ND250	18.0	18.9	18.0	19.0	20.5	20.1	19.0	22.3
76	ND08-53×ND07-226	19.3	19.3	18.0	18.0	20.7	19.5	20.0	22.2
77	ND07-255×PHJ40	17.4	18.2	18.0	19.0	20.9	20.8	20.0	20.8
78	ND06-144×ND2006	18.2	18.4	18.0	18.0	18.8	16.7	19.0	20.6
79	ND291×ND2032	15.9	18.3	17.0	20.0	20.5	20.1	19.0	22.0
80	ND291×ND07-226	19.0	20.4	18.0	20.0	22.7	22.7	23.0	23.9
81	ND07-255×NK807	16.4	19.3	17.0	18.0	20.9	21.0	18.0	21.7
82	ND06-189×PHJ40	17.2	17.8	17.0	20.0	20.7	20.3	19.0	19.7
83	ND2014×LP05	15.9	19.8	17.0	20.0	22.4	25.8	21.0	23.3
84	LB2000×ND270	19.0	20.5	18.0	18.0	20.7	18.8	18.0	17.7
85	ND274×Il5	14.3	17.4	14.0	18.0	18.3	19.8	16.0	18.7
86	LB2000×ND2014	17.1	19.5	17.0	20.0	20.6	18.4	20.0	19.2
87	ND07-212×LP05	20.1	22.0	17.0	18.0	22.6	21.6	22.0	21.9
88	ND2019×AP47	19.4	19.8	18.0	19.0	22.0	23.4	20.0	23.7
89	LH61×ND270	15.6	18.7	16.0	19.0	21.9	19.3	20.0	19.1
90	ND2013×ND2009	17.3	19.8	19.0	21.0	20.9	22.6	20.0	20.8
91	ND06-189×LP05	17.0	19.4	20.0	20.0	20.8	20.1	20.0	23.4
92	ND07-255×LP05	15.4	19.7	19.0	21.0	21.7	21.8	20.0	21.8
93	ND2013×Il5	16.3	16.3	15.0	17.0	18.4	21.4	18.0	21.2
94	ND2019×Il5	17.0	18.5	17.0	19.0	20.1	21.5	19.0	20.2
95	**Thurston 77RM**	15.6	17.6	17.0	18.0	20.7	19.9	17.0	20.4
96	**Pioneer 79RM**	16.3	17.8	16.0	18.0	19.1	17.4	18.0	19.2
97	**Pioneer 80RM**	14.8	15.7	15.0	17.0	19.4	18.2	18.0	20.9
98	**Thurston 82RM**	14.5	16.1	16.0	17.0	18.4	17.7	18.0	20.6
99	**Syngenta 85RM**	17.0	18.0	16.0	19.0	19.2	19.4	20.0	19.6
100	**Monsanto 88RM**	18.3	21.0	18.0	19.0	20.2	21.6	19.0	21.4
	Experimental Mean	16.9	19.0	17.0	19.0	21.3	20.4	20.0	21.0
	CV%	7.2	6.9	7.9	7.7	5.4	7.0	5.1	7.3
	LSD,0.05	2.4	2.6	1.9	2.1	2.3	2.8	1.4	2.1
	MSE	1.5	1.7	1.9	2.2	1.3	2.0	1.0	2.3

Table A23. Grain moisture and yield adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

Entry	Pedigree	Grain Moisture (H_2O kg^{-1})				Grain Yield (Mg ha^{-1})			
		2013		2014.0		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	448.9	575.9	329.2	450.3	3.7	3.7	5.3	3.5
2	PHG47	.	185.2	135.3	134.7	2.7	3.5	3.9	1.5
3	LH61	.	534.1	194.8	253.7	0.2	3.3	4.1	2.3
4	ACF052	66.9	345.6	193.2	143.0	3.7	3.8	3.2	2.7
5	ACLB0	165.2	136.7	135.7	118.9	3.0	3.8	4.2	4.4
6	NK779	43.3	89.3	124.6	94.2	2.1	1.5	3.6	1.7
7	NP2341	167.8	171.7	111.3	89.2	8.0	2.7	2.6	3.0
8	ND07-97	58.7	348.9	278.2	314.1	2.7	3.2	2.5	2.0
9	ND06-144	215.3	180.7	115.8	147.2	2.4	4.8	5.3	3.5
10	ND08-343	164.2	413.2	154.7	248.8	3.5	2.2	4.1	3.8
11	GEM5Derived	147.8	164.0	129.3	122.2	4.6	4.7	4.8	4.0
12	ND203	87.8	258.0	129.3	469.7	6.1	2.0	2.3	2.2
13	ND265	.	155.8	104.3	117.6	1.2	2.8	2.5	1.9
14	ND274	52.0	156.9	176.7	137.7	2.2	1.3	2.8	2.4
15	ND2021	64.2	242.8	104.2	192.3	3.9	2.9	3.2	2.6
16	ND2013	131.7	334.6	156.3	81.0	4.7	1.2	1.4	3.7
17	ND2019	103.8	286.3	159.9	172.6	1.5	4.1	5.4	3.5
18	ND2014	139.5	288.2	203.5	182.7	3.5	4.6	2.1	3.1
19	ND07-212	102.7	174.4	121.3	149.8	8.1	4.3	4.4	2.4
20	ND06-189	33.4	131.4	112.2	103.8	2.0	4.7	4.0	2.6
21	ND07-255	60.0	182.3	151.4	222.0	3.7	7.3	5.3	2.5
22	ND08-53	123.8	163.6	148.7	159.5	3.0	3.7	2.8	2.3
23	ND290	113.4	158.3	113.0	72.4	2.0	0.7	1.8	3.5
24	ND291	149.6	381.7	147.9	235.7	2.4	4.0	4.7	4.3
25	ND06-85	71.9	191.7	130.2	190.4	3.0	2.6	1.9	1.9
26	ND246	42.1	180.3	140.8	308.2	1.6	1.6	1.8	3.1
27	ND270	69.8	153.7	113.2	108.4	4.4	2.6	3.6	2.5
28	ND250	69.7	211.9	135.3	227.1	3.3	4.0	3.6	2.6
29	ND2000	71.8	184.9	105.6	160.1	5.2	3.5	4.9	4.2
30	ND2014	107.7	266.0	115.7	181.2	2.5	4.4	5.6	2.2
31	ND2006	225.1	222.8	125.1	165.9	4.1	2.8	3.5	4.2
32	ND07-153	194.3	401.4	225.4	233.9	1.9	0.5	3.3	2.3
33	ND2007	560.7	691.1		.	3.6	2.2	2.5	4.3
34	ND2002	109.4	163.6	103.4	241.3	6.4	3.0	4.4	3.2
35	ND2004	113.5	205.8	119.1	138.8	2.1	4.6	5.8	3.0
36	ND2001	194.0	310.1	260.4	115.4	1.9	3.6	1.1	1.0
37	ND2005	79.5	241.1	115.6	139.9	3.3	3.1	2.8	3.7
38	ND2009	407.5	673.0	470.1	.	3.3	4.3	4.5	4.3
39	Il5	213.8	527.4	260.3	420.4	4.2	3.3	3.9	3.3
40	KMN22	53.9	173.2	130.4	96.5	2.2	1.7	3.5	2.4
41	B104	725.1	.	.	.	0.8	0.9	2.2	2.9
42	ACF47	305.0	631.5	455.5	411.8	4.7	4.9	3.6	2.1
43	LP05	44.2	734.9	492.3	676.1	4.3	3.3	2.9	2.9
44	NK807	127.1	479.9	220.0	296.6	5.1	3.4	4.2	2.9
45	PHJ40	74.7	204.0	103.9	94.4	5.8	4.3	3.9	2.8
46	ND07-226	237.8	320.2	225.8	202.3	5.1	6.0	6.4	3.8
47	ND2032	115.8	486.5	239.4	339.7	4.2	3.6	5.4	3.1
48	**TR3030 89RM**	.	147.5	146.0	141.9	2.7	4.1	6.1	2.7
49	**TR2678 85RM**	118.3	294.3	186.9	169.1	4.9	2.6	4.4	2.5
	Exp. Mean	154.9	294.9	177.7	205.9	3.5	3.3	3.7	2.9
	CV%	60.7	17.0	14.2	17.4	43.6	28.4	19.5	38.5
	LSD,0.05	133.0	70.8	35.8	50.7	2.2	1.3	1.0	1.6
	MSE	8841.9	2508.6	639.2	1283.7	2.3	0.9	0.5	1.3

Table A24. Kernel traits adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

Entry	Pedigree	Grain Test Weight (kg hl^{-1})				Hundred Kernel Weight (g)			
		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	74.2	71.1	49.2	20.8	24.6	22.4	32.1	13.9
2	PHG47	74.1	72.9	67.3	18.6	21.8	17.5	63.4	13.7
3	LH61	.	69.4	64.6	24.0	29.8	27.9	48.9	15.3
4	ACF052	76.1	76.0	60.7	24.2	22.1	21.7	56.0	16.6
5	ACLB0	80.0	80.6	71.1	17.0	19.5	19.2	73.0	17.5
6	NK779	76.9	67.7	69.7	19.8	20.6	17.2	70.3	16.9
7	NP2341	74.4	78.1	68.4	19.4	20.7	20.3	68.2	18.0
8	ND07-97	72.9	74.0	56.2	17.1	19.0	20.1	39.5	11.5
9	ND06-144	77.6	84.6	78.0	22.3	24.0	22.9	71.4	19.0
10	ND08-343	79.6	74.5	70.1	30.3	23.5	28.1	54.1	24.6
11	GEM5Derived	76.4	73.8	68.3	22.5	22.6	23.6	64.0	19.0
12	ND203	77.4	70.3	64.8	14.2	21.6	19.3	39.8	14.4
13	ND265	72.9	75.0	68.8	14.4	22.3	16.9	61.9	14.2
14	ND274	72.6	72.8	67.5	20.6	15.1	21.7	62.5	17.0
15	ND2021	77.4	79.0	74.8	20.8	19.1	20.8	63.7	20.2
16	ND2013	73.8	63.2	68.0	17.9	18.1	22.8	58.8	12.8
17	ND2019	68.7	76.4	68.8	23.6	22.6	23.1	59.4	16.6
18	ND2014	77.8	80.8	67.5	22.7	17.3	20.5	63.0	16.9
19	ND07-212	75.8	77.4	74.4	22.7	21.2	21.4	66.8	18.9
20	ND06-189	63.6	69.4	67.1	18.3	15.6	18.4	60.3	15.2
21	ND07-255	75.3	76.4	71.6	24.2	19.9	22.4	61.4	22.9
22	ND08-53	75.1	77.7	69.0	21.0	19.2	21.3	62.9	17.8
23	ND290	79.8	75.6	71.3	17.8	19.7	17.3	67.5	14.5
24	ND291	77.4	78.9	74.7	20.9	18.4	23.1	60.2	18.1
25	ND06-85	77.9	75.4	64.3	15.8	20.7	19.4	55.6	13.8
26	ND246	70.6	71.0	63.3	16.7	22.3	23.0	47.6	19.9
27	ND270	70.6	75.3	70.8	16.1	18.7	18.5	66.0	13.8
28	ND250	76.8	83.4	74.6	18.7	18.5	19.9	62.2	18.4
29	ND2000	74.4	79.0	76.2	19.1	17.6	21.7	66.6	17.1
30	ND2014	75.5	75.6	74.2	18.7	19.2	19.0	62.4	15.8
31	ND2006	76.3	78.9	70.7	18.6	21.5	22.4	60.7	18.4
32	ND07-153	74.3	66.9	62.8	23.6	25.4	23.9	54.8	17.1
33	ND2007	69.9	67.9	59.4	16.9	22.9	20.4	.	13.1
34	ND2002	74.1	64.9	70.4	16.5	17.2	19.5	54.3	15.8
35	ND2004	78.1	77.1	71.7	18.4	21.9	18.7	61.5	11.2
36	ND2001	74.7	75.2	58.1	20.3	21.2	22.5	.	14.9
37	ND2005	80.7	80.0	75.9	21.5	18.9	23.6	61.0	18.4
38	ND2009	75.5	69.9	41.1	16.8	20.2	20.8	.	12.0
39	Il5	74.0	71.6	59.1	19.5	22.6	21.2	37.2	12.1
40	KMN22	77.3	62.4	71.0	24.4	23.3	23.5	67.2	21.4
41	B104	59.6	68.3	64.7	11.9	27.3	19.3	.	9.5
42	ACF47	73.7	74.4	43.8	26.7	24.7	25.6	37.5	15.9
43	LP05	71.8	67.4	38.6	19.7	18.4	24.1	.	14.9
44	NK807	75.3	75.8	63.4	26.0	25.3	26.9	51.8	20.8
45	PHJ40	77.2	78.8	77.9	24.7	24.2	26.6	63.2	18.7
46	ND07-226	75.9	76.4	63.5	23.4	26.0	24.8	57.1	18.6
47	ND2032	78.4	76.0	62.7	23.5	19.7	21.6	48.7	16.8
48	**TR3030 89RM**	74.6	70.8	67.6	20.6	23.4	16.1	56.5	12.2
49	**TR2678 85RM**	76.1	75.1	65.4	21.1	19.4	24.6	61.4	15.6
	Exp. Mean	74.9	74.1	66.2	20.3	21.2	21.6	58.2	16.4
	CV%	4.1	6.7	4.0	6.7	13.9	6.7	5.6	8.7
	LSD,0.05	4.3	7.0	3.7	1.9	4.2	2.0	4.6	2.0
	MSE	9.4	24.6	6.9	1.8	8.7	2.1	10.5	2.0

Table A25. Lodging adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

Entry	Pedigree	Root Lodging (%)				Stalk Lodging (%)			
		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	43.4	52.4	11.0	5.9	22.6	3.4	5.4	59.6
2	PHG47	2.6	6.0	0.0	0.0	3.2	0.3	0.0	36.5
3	LH61	0.0	46.3	0.0	0.0	0.0	4.7	0.0	31.7
4	ACF052	0.4	7.5	10.8	0.0	1.3	0.2	9.5	31.1
5	ACLB0	17.3	2.2	3.0	0.1	0.1	1.6	0.0	6.4
6	NK779	-0.2	9.7	0.0	0.0	0.3	15.2	0.0	20.7
7	NP2341	9.0	2.8	0.0	0.0	2.8	4.4	0.0	12.5
8	ND07-97	0.0	-1.0	0.0	-0.1	32.8	8.6	4.0	23.1
9	ND06-144	-0.1	0.7	0.0	-0.1	3.8	0.4	1.4	41.1
10	ND08-343	1.5	34.1	4.7	-0.1	3.5	-2.0	1.6	83.7
11	GEM5Derived	1.9	2.6	1.4	-0.2	3.7	-1.5	3.9	30.8
12	ND203	9.3	0.5	6.5	22.9	25.0	72.0	52.1	77.1
13	ND265	24.4	1.2	2.1	-0.1	0.3	65.8	9.6	90.6
14	ND274	0.6	1.2	13.3	-0.1	97.3	74.8	3.3	96.8
15	ND2021	-0.4	1.1	0.0	1.9	2.0	1.0	0.0	47.7
16	ND2013	3.4	7.6	3.6	0.0	28.5	-0.6	1.4	48.3
17	ND2019	-0.4	5.5	0.0	0.0	0.1	-1.1	0.0	60.7
18	ND2014	25.0	23.1	3.1	0.0	26.4	10.8	6.0	36.0
19	ND07-212	8.4	8.7	8.3	0.2	12.7	23.9	16.0	80.5
20	ND06-189	-0.6	0.9	0.0	0.0	0.4	5.0	0.0	52.8
21	ND07-255	7.1	8.1	50.8	0.0	16.5	5.8	1.0	88.5
22	ND08-53	0.2	17.8	16.2	11.5	46.0	72.1	4.2	96.6
23	ND290	0.2	5.8	5.4	-0.1	5.5	20.2	2.7	66.7
24	ND291	0.2	-0.4	0.0	-0.1	0.2	8.9	0.0	44.4
25	ND06-85	7.7	3.3	3.0	-0.1	4.4	90.5	5.0	100.0
26	ND246	19.6	18.6	0.0	10.2	45.2	28.1	88.1	89.9
27	ND270	16.1	3.0	0.0	3.5	9.9	14.2	1.4	16.4
28	ND250	0.9	1.3	0.0	-0.1	76.4	13.0	2.9	42.2
29	ND2000	-0.6	3.3	7.4	0.0	26.8	21.8	5.9	96.3
30	ND2014	-0.7	1.8	0.0	0.0	27.1	29.7	2.6	98.3
31	ND2006	-0.6	7.2	0.0	0.0	2.5	3.8	1.3	32.8
32	ND07-153	-0.2	1.8	0.0	0.0	-1.0	-0.7	0.0	31.5
33	ND2007	25.6	70.4	38.2	4.0	1.8	3.1	0.0	30.8
34	ND2002	-1.1	38.2	15.4	0.0	-0.6	2.8	13.8	91.7
35	ND2004	16.7	0.5	0.0	0.0	0.3	3.5	2.3	46.9
36	ND2001	0.0	16.5	0.0	0.1	5.9	1.5	0.0	35.2
37	ND2005	-0.1	31.2	4.5	0.0	0.4	3.7	0.0	6.3
38	ND2009	1.8	5.2	0.0	0.0	5.9	-0.6	0.0	21.2
39	Il5	0.3	93.0	8.7	3.8	26.0	-0.1	8.4	9.4
40	KMN22	0.0	1.6	0.0	0.2	0.5	1.4	0.0	53.4
41	B104	-0.3	0.9	0.0	0.0	0.7	3.7	0.0	8.6
42	ACF47	0.6	4.6	0.0	0.0	3.7	0.4	4.5	28.0
43	LP05	4.8	21.1	0.0	3.5	0.3	7.8	1.4	28.0
44	NK807	13.4	47.7	1.3	0.0	9.6	3.0	4.2	7.2
45	PHJ40	0.1	7.0	0.0	0.0	2.5	-0.5	0.0	50.0
46	ND07-226	7.4	10.5	0.0	0.0	19.0	8.1	1.6	92.2
47	ND2032	1.8	35.3	23.5	1.7	0.2	7.6	5.8	73.9
48	**TR3030 89RM**	-0.1	4.4	1.5	0.0	21.1	12.6	3.9	43.8
49	**TR2678 85RM**	0.8	4.9	0.0	0.0	0.9	7.9	0.0	0.0
	Exp. Mean	5.4	13.8	5.0	1.4	12.7	13.5	5.6	48.9
	CV%	146.4	78.6	159.3	381.2	133.2	66.2	137.1	51.2
	LSD,0.05	11.3	15.4	11.2	7.5	24.0	12.6	10.9	35.4
	MSE	63.7	118.1	62.8	28.4	287.8	79.7	59.4	627.4

Table A26. Height Traits adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

Entry	Pedigree	Ear Height (cm)				Plant Height (cm)			
		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	110.0	100.3	101.9	136.8	237.9	221.0	217.7	236.0
2	PHG47	47.8	52.7	27.8	46.7	192.2	183.6	151.0	131.5
3	LH61	67.3	60.2	48.9	77.2	198.1	179.0	162.0	163.6
4	ACF052	61.3	81.9	52.8	88.7	179.4	181.0	158.8	174.8
5	ACLB0	48.8	65.9	53.8	76.5	197.9	170.7	171.7	180.8
6	NK779	54.8	40.7	40.7	46.8	178.5	158.9	149.8	140.8
7	NP2341	79.5	64.7	32.0	75.8	204.0	148.1	137.3	150.8
8	ND07-97	61.5	59.6	46.8	65.1	178.6	177.5	161.5	153.7
9	ND06-144	80.5	66.5	57.4	78.2	210.7	185.1	172.4	170.0
10	ND08-343	77.5	72.0	61.0	78.8	202.1	220.5	199.8	201.2
11	GEM5Derived	76.8	61.0	48.7	65.5	187.4	178.3	164.3	162.0
12	ND203	78.3	63.2	59.7	74.0	196.9	190.7	179.8	182.6
13	ND265	48.3	63.8	45.3	67.3	153.7	168.7	144.9	147.8
14	ND274	59.8	49.0	30.1	54.0	154.0	152.4	136.9	136.8
15	ND2021	67.0	63.9	51.4	74.1	200.3	202.1	170.3	196.5
16	ND2013	80.3	74.5	58.2	93.5	212.1	217.4	205.0	200.0
17	ND2019	69.8	70.5	59.3	96.3	190.0	217.6	199.9	206.7
18	ND2014	85.8	73.2	55.5	94.0	195.3	181.9	170.4	179.0
19	ND07-212	86.7	70.7	57.3	77.2	203.7	190.3	177.4	171.6
20	ND06-189	65.0	61.1	48.1	67.5	168.0	172.3	156.7	154.0
21	ND07-255	80.5	78.0	58.7	82.0	182.9	214.5	168.0	176.8
22	ND08-53	59.0	50.9	34.0	59.5	178.5	170.2	134.7	138.3
23	ND290	59.8	37.4	30.6	51.2	192.8	143.8	129.1	123.3
24	ND291	53.3	51.6	35.0	65.7	182.3	189.7	179.8	169.2
25	ND06-85	67.3	64.1	44.5	65.7	184.5	157.7	137.8	123.3
26	ND246	72.7	65.0	47.7	76.4	200.7	185.9	160.0	184.6
27	ND270	52.8	33.4	30.0	42.7	163.4	140.6	142.9	114.1
28	ND250	64.5	51.1	52.6	60.2	168.6	161.6	153.4	140.8
29	ND2000	74.8	64.0	53.5	68.8	199.1	177.6	168.1	152.8
30	ND2014	72.0	78.4	64.2	89.7	211.9	189.4	181.8	166.6
31	ND2006	47.3	51.2	46.3	76.5	166.3	177.4	162.7	171.7
32	ND07-153	80.8	75.4	68.4	94.9	224.3	210.4	204.3	196.4
33	ND2007	79.8	88.1	71.2	121.2	231.0	224.8	221.5	222.9
34	ND2002	73.7	44.4	37.5	42.5	223.7	145.5	129.6	128.8
35	ND2004	55.3	66.2	50.1	80.5	177.0	193.0	178.6	189.4
36	ND2001	78.5	79.7	58.9	88.8	180.9	181.4	168.4	176.9
37	ND2005	70.8	69.1	46.3	74.5	187.7	187.0	167.3	178.9
38	ND2009	74.3	77.3	69.1	101.5	217.3	223.2	227.0	211.5
39	Il5	74.0	64.8	65.5	103.7	181.9	200.2	193.8	196.7
40	KMN22	59.8	49.0	40.3	65.5	206.1	200.6	204.5	204.7
41	B104	68.0	60.1	58.9	78.0	184.0	172.8	165.8	174.1
42	ACF47	87.0	85.6	53.5	100.0	210.9	201.3	190.3	193.7
43	LP05	77.0	66.0	49.8	86.6	184.7	182.6	170.8	181.2
44	NK807	70.8	64.6	61.2	82.5	207.0	188.6	183.2	186.7
45	PHJ40	83.3	72.4	60.8	90.3	176.2	181.3	171.2	176.9
46	ND07-226	75.5	60.1	46.4	74.0	203.5	199.8	170.0	168.3
47	ND2032	67.0	49.1	47.2	66.3	199.2	199.3	209.4	196.6
48	**TR3030 89RM**	57.3	75.2	65.6	85.3	163.1	179.7	188.3	177.0
49	**TR 2678 85RM**	62.0	49.6	37.6	63.1	192.3	184.2	169.5	178.3
	Exp. Mean	69.5	64.0	51.5	77.0	192.3	184.9	171.8	172.3
	CV%	12.7	6.0	8.8	9.2	9.0	3.6	3.2	3.4
	LSD,0.05	12.5	5.4	6.4	10.0	24.5	9.4	7.9	8.3
	MSE	78.2	14.7	20.7	50.2	300.9	43.9	30.9	34.2

Table A27. Flowering traits adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

| | | Days of Anthesis | | | | Days of Silking | | | | Anthesis Silking Interval | | | |
| | | 2013.0 | | 2014.0 | | 2013.0 | | 2014.0 | | 2013.0 | | 2014.0 | |
Entry	Pedigree	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	77.8	69.8	80.2	76.7	75.9	70.9	79.8	76.7	1.5	-1.0	0.5	0.0
2	PHG47	70.8	75.8	73.4	73.6	70.0	76.7	75.7	73.3	0.0	-1.3	-2.5	0.5
3	LH61	62.8	74.3	75.2	73.2	63.5	75.5	77.8	74.8	-1.0	-1.1	-3.0	-2.0
4	ACF052	62.8	73.0	73.8	73.2	61.0	72.9	75.7	74.5	1.0	0.7	-2.0	-1.5
5	ACLB0	61.3	73.3	67.6	65.8	61.2	74.0	67.7	65.8	-0.5	-0.9	-0.5	0.0
6	NK779	60.4	73.3	64.1	65.3	60.5	74.7	65.5	66.1	-0.5	-2.1	-1.5	-1.0
7	NP2341	64.8	75.7	65.6	69.6	66.5	77.0	65.4	69.8	-2.0	-1.5	0.0	-0.5
8	ND07-97	59.7	69.3	70.6	70.2	61.4	71.2	74.5	72.6	-1.0	-1.6	-3.5	-2.5
9	ND06-144	64.2	72.8	65.7	68.6	65.6	73.0	65.4	68.2	-1.0	-0.4	0.5	0.5
10	ND08-343	61.1	69.8	65.1	67.7	62.5	70.7	66.5	67.6	-1.0	-0.7	-1.5	-0.5
11	GEM5Derived	65.7	74.5	63.7	67.2	67.6	77.2	64.9	67.3	-1.5	-1.9	-1.0	-0.5
12	ND203	63.0	71.3	62.9	66.3	64.0	72.3	62.9	65.6	-1.0	-1.0	0.0	0.5
13	ND265	69.1	67.3	64.4	67.8	69.5	67.5	64.7	67.4	0.0	-0.7	0.0	0.0
14	ND274	60.2	73.1	67.4	67.6	62.1	73.8	67.6	68.1	-1.0	-0.6	0.0	-1.0
15	ND2021	62.1	70.1	65.4	68.5	64.3	73.5	68.9	69.5	-2.0	-3.0	-3.0	-1.0
16	ND2013	64.5	81.6	75.5	74.4	67.0	83.3	81.7	75.6	-2.5	-1.8	-6.0	-1.0
17	ND2019	68.0	71.7	73.9	74.5	70.4	73.0	74.8	75.0	-2.5	-1.1	-1.0	-1.0
18	ND2014	68.6	72.9	72.0	73.9	69.0	74.0	76.7	73.2	-0.5	-0.3	-4.5	0.5
19	ND07-212	59.1	74.2	67.2	70.1	60.4	79.1	69.8	71.5	-1.0	-4.9	-2.5	-1.5
20	ND06-189	62.1	75.2	67.7	69.1	63.4	72.8	68.1	69.3	-1.0	1.9	0.0	-0.5
21	ND07-255	65.6	77.0	62.7	66.4	66.0	79.0	65.0	68.0	0.0	-2.0	-2.0	-2.0
22	ND08-53	63.2	74.8	68.7	67.7	65.1	77.2	71.0	68.6	-1.5	-1.9	-2.0	-0.5
23	ND290	61.1	77.3	64.3	66.7	64.8	78.6	67.4	68.6	-3.5	-1.1	-3.0	-1.5
24	ND291	62.0	73.3	66.7	68.7	65.3	76.3	68.5	69.5	-3.0	-2.4	-2.0	-1.0
25	ND06-85	60.6	74.5	67.3	66.7	61.3	77.2	67.4	67.7	-0.5	-1.7	0.0	-1.0
26	ND246	63.3	73.8	62.5	67.3	61.0	78.8	61.4	68.5	3.0	-4.7	1.0	-1.0
27	ND270	63.2	72.3	60.5	65.3	63.3	72.5	63.2	65.8	0.5	-0.5	-2.5	-0.5
28	ND250	60.2	78.2	59.0	64.6	61.8	78.8	59.2	65.1	-1.0	-0.4	0.0	-0.5
29	ND2000	63.0	72.5	63.9	67.5	64.6	73.2	66.2	68.3	-1.5	-0.8	-2.0	-0.5
30	ND2014	65.5	74.0	65.6	69.4	66.7	72.6	69.5	71.4	-1.5	0.9	-4.0	-1.5
31	ND2006	57.9	80.0	63.0	66.5	58.2	79.8	63.6	66.3	-0.5	0.1	-1.0	0.0
32	ND07-153	64.5	74.2	69.1	69.0	64.7	73.2	72.5	71.0	-0.5	1.4	-3.5	-2.0
33	ND2007	74.5	73.5	80.3	77.1	79.4	73.8	87.1	78.8	-5.0	-0.7	-7.0	-2.0
34	ND2002	69.0	74.0	68.8	72.6	69.9	74.5	68.9	70.6	-1.0	-1.4	0.0	2.0

Table A27. Flowering traits adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND (continued).

Entry	Pedigree	Days of Anthesis				Days of Silking				Anthesis Silking Interval			
		2013		2014		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
35	ND2004	67	72.4	71.8	73.4	69.7	73.8	74.8	73.9	-2.5	-1.8	-3.0	-0.5
36	ND2001	70	69.4	78.7	74.2	70.7	71.5	81	75.8	-0.5	-1.7	-2.0	-1.0
37	ND2005	63	71.4	70.9	73.1	64.8	72.3	73.8	75.8	-2.0	-1.0	-3.0	-2.0
38	ND2009	75.4	75.9	79.3	75.8	76.8	75.5	83	76.7	-1.5	0.7	-4.0	0.0
39	Il5	73	68.6	79.3	76.2	73.3	71.5	79.9	76.9	-0.5	-2.0	-0.5	-0.5
40	KMN22	64.5	71.4	73.6	69.8	65.5	73.1	75.9	73.2	-1	-1.6	-2.5	-3.0
41	B104	77.1	76.4	86.1	.	87.3	78.8	90.7	.	-10	-2.8	-4.5	.
42	ACF47	72.6	76.2	75.1	76.6	74.3	77.6	76.1	77.3	-1.5	-1.2	-1.0	-0.5
43	LP05	68.8	74.9	80.1	75.7	69.4	77.1	84.2	76.4	-1.0	-2.4	-4.0	-0.5
44	NK807	65.3	72.9	72.3	73.7	66.1	73	72.6	72.9	-1.5	-0.6	-0.5	1.0
45	PHJ40	62.7	71.9	68.2	69.8	63.1	74.2	68.7	70.9	-1.0	-2.4	-1.0	-1.5
46	ND07-226	66.3	71.6	69.2	71.2	66.1	73.2	71.1	72.1	-0.5	-1.2	-2.0	-1.0
47	ND2032	63.3	74.4	69	70.8	62.8	74.7	69.1	71.4	0.0	-0.7	-0.5	-0.5
48	**TR3030 89RM**	63.9	73.4	71.5	74.4	64.1	74	71.9	73.7	-0.5	-1.5	-0.5	0.5
49	**TR2678 85RM**	66.9	74.7	73	71.6	69.1	74.7	74.8	71.9	-2.5	-0.4	-2.0	-0.5
	Exp. Mean	65.3	73.6	69.8	70.5	66.6	74.8	71.7	71.2	-1.2	-1.2	-1.8	-0.7
	CV%	5.5	5.2	1.8	1.2	4.9	5.9	2.1	1.3	-99.6	-152.7	-55.4	-137.7
	LSD,0.05	5.1	5.4	1.8	1.2	4.6	6.2	2.1	1.3	1.7	2.6	1.4	1.4
	MSE	12.8	14.8	1.6	0.7	10.5	19.1	2.3	0.9	1.5	3.4	1.0	1.0

Table A28. Amino acids compositions adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

		Methionine g kg⁻¹ of dry matter				Cysteine g kg⁻¹ of dry matter				Lysine g kg⁻¹ of dry matter			
		2013		2014		2013		2014		2013		2014	
Entry	Pedigree	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	2.6	2.3	2.4	2.9	2.4	2.2	2.4	2.7	3.2	3.0	3.3	3.8
2	PHG47	3.2	2.0	2.5	3.0	2.8	2.1	2.5	3.2	3.6	2.9	3.2	3.4
3	LH61	2.1	2.2	2.4	2.8	2.2	2.2	2.4	2.9	3.0	3.1	3.1	3.4
4	ACF052	2.6	2.6	2.0	2.5	2.4	2.5	2.2	2.7	3.4	3.2	3.0	3.6
5	ACLB0	2.9	2.1	2.6	3.0	2.6	2.1	2.7	3.0	3.3	3.0	3.2	3.3
6	NK779	3.4	2.4	2.6	3.0	2.9	2.4	2.7	2.9	3.5	3.1	3.2	3.3
7	NP2341	2.5	2.3	2.6	2.5	2.4	2.2	2.6	2.8	3.1	3.0	3.2	3.1
8	ND07-97	3.1	2.3	2.6	2.9	2.7	2.3	2.7	2.9	3.6	3.1	3.2	3.5
9	ND06-144	3.3	2.2	2.2	2.3	2.9	2.2	2.3	2.6	3.6	2.9	3.0	3.0
10	ND08-343	2.9	2.5	3.1	3.1	2.6	2.3	2.8	3.1	3.4	3.2	3.5	3.4
11	GEM5Derived	2.6	2.4	2.0	2.6	2.4	2.3	2.3	2.8	3.3	3.0	2.9	3.3
12	ND203	.	2.0	2.5	2.6	.	2.1	2.7	2.8	.	2.9	3.3	3.1
13	ND265	3.5	2.2	2.8	2.8	3.0	2.2	2.9	3.0	4.0	2.9	3.4	3.5
14	ND274	3.3	2.0	2.6	3.3	3.0	2.0	2.8	3.4	3.6	2.8	3.2	3.5
15	ND2021	3.5	2.2	2.8	3.2	3.0	2.2	2.9	3.2	3.7	2.9	3.3	3.2
16	ND2013	2.9	2.4	3.2	3.2	2.7	2.2	2.9	3.2	3.5	3.1	3.5	3.5
17	ND2019	2.8	2.0	2.5	2.7	2.6	2.0	2.4	2.9	3.5	3.1	3.2	3.1
18	ND2014	3.0	2.0	2.6	2.8	2.8	2.0	2.6	2.9	3.4	2.9	3.2	3.2
19	ND07-212	2.7	2.3	2.4	2.5	2.6	2.3	2.5	2.7	3.4	3.2	3.1	3.2
20	ND06-189	3.7	2.2	2.6	3.5	3.1	2.2	2.6	3.2	4.0	3.0	3.4	3.6
21	ND07-255	2.8	2.1	2.4	2.4	2.5	2.1	2.5	2.7	3.5	3.3	3.1	3.0
22	ND08-53	3.0	2.0	2.7	2.9	2.7	2.1	2.7	3.0	3.6	2.9	3.2	3.4
23	ND290	3.2	2.3	2.5	3.1	2.8	2.3	2.7	3.1	3.4	3.1	3.2	3.3
24	ND291	3.2	2.0	2.4	2.6	2.9	2.1	2.4	2.9	3.6	2.9	3.2	3.3
25	ND06-85	2.7	2.4	2.5	2.3	2.6	2.3	2.6	2.6	3.2	3.2	3.3	3.2
26	ND246	3.4	2.6	3.0	2.9	2.9	2.4	2.9	2.9	3.8	3.3	3.4	3.3
27	ND270	3.0	2.3	2.4	2.9	2.6	2.2	2.6	3.1	3.7	3.2	3.3	3.4
28	ND250	2.6	2.3	2.5	2.6	2.5	2.3	2.7	2.9	3.2	3.1	3.1	3.0
29	ND2000	2.8	2.2	2.3	2.5	2.6	2.1	2.4	2.8	3.4	3.1	3.1	2.9
30	ND2014	3.1	2.7	2.4	2.7	2.7	2.5	2.5	2.9	3.8	3.1	3.2	3.2
31	ND2006	2.6	2.2	2.9	3.0	2.6	2.1	2.9	3.1	3.3	3.2	3.3	3.2
32	ND07-153	2.9	2.6	2.4	2.6	2.7	2.4	2.6	2.9	3.5	3.2	3.2	3.2
33	ND2007	2.8	2.5	2.8	2.8	2.8	2.3	3.0	2.7	3.8	3.2	4.2	.
34	ND2002	2.4	1.9	1.9	2.2	2.3	2.0	2.2	2.5	3.0	2.7	2.9	3.2

Table A28. Amino acids compositions adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND (continued).

Entry	Pedigree	Methionine g kg^{-1} of dry matter				Cysteine g kg^{-1} of dry matter				Lysine g kg^{-1} of dry matter			
		2013		2014		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
35	ND2004	3.1	2.2	2.2	2.4	2.7	2.2	2.3	2.8	3.5	3.1	2.9	3
36	ND2001	2.7	2	3.1	3.1	2.6	2	3	3.2	3.4	2.9	3.4	3.5
37	ND2005	3	2	2.8	3.2	2.7	2	2.8	3.2	3.4	2.8	3.4	3.2
38	ND2009	3.1	2.2	2	2.8	2.8	2.1	2.4	3	3.5	3.1	3.3	3.5
39	Il5	2.4	2.1	2.4	2.8	2.3	2.1	2.3	2.9	3.1	2.8	3.1	3.1
40	KMN22	3.2	3.1	3	3.3	2.8	2.7	2.7	3	3.5	3.5	3.4	3.4
41	B104	2.8	2.3	2.9	3.1	2.8	2.2	2.9	2.8	3.7	3.3	4.1	.
42	ACF47	2.5	2.3	1.9	2.3	2.5	2.3	2.2	2.6	3.1	3.2	2.8	3
43	LP05	2.8	2.4	2.2	2.6	2.5	2.3	2.6	2.7	3.5	3.1	3.4	4.3
44	NK807	2.6	2.6	2.2	2.4	2.5	2.4	2.4	2.7	3.3	3.2	3.2	3.2
45	PHJ40	3	2.7	2.2	2.8	2.6	2.4	2.4	2.9	3.4	3.2	3.1	3.2
46	ND07-226	2.5	2.5	2.2	2.5	2.3	2.4	2.4	2.8	3.3	3.2	3.2	3.2
47	ND2032	3.4	2.4	2.3	2.5	2.9	2.3	2.4	2.8	3.7	3.1	3.1	3.2
48	**TR3030 89RM**	3	2.4	1.8	2.4	2.7	2.3	2.1	2.6	3.6	3.1	3	3.2
49	**TR2678 85RM**	2.8	2.3	2.3	2.6	2.5	2.2	2.3	2.8	3.3	3	3.2	3.3
	Exp. Mean	2.9	2.3	2.5	2.8	2.7	2.2	2.6	2.9	3.5	3.1	3.2	3.3
	CV%	11.9	5.4	8.2	3.9	8.4	4.4	5.1	2.7	6.5	2.9	4.3	4.3
	LSD,0.05	0.5	0.2	0.3	0.2	0.3	0.1	0.2	0.1	0.3	0.1	0.2	0.2
	MSE	0.1	0	0	0	0	0	0	0	0	0	0	0

Table A29. Grain oil and protein compositions adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

Entry	Pedigree	Grain Protein g kg⁻¹ of dry matter				Grain Oil g kg⁻¹ of dry matter			
		2013		2014		2013		2014	
		FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	114.4	109.4	87.8	112.5	31.2	40.0	32.9	33.1
2	PHG47	158.3	99.8	108.4	133.7	42.8	40.9	49.1	43.2
3	LH61	107.4	111.0	92.3	119.4	36.8	40.9	42.8	36.8
4	ACF052	127.4	125.0	75.7	108.4	38.7	36.2	38.3	37.9
5	ACLB0	134.0	94.5	104.3	125.0	41.3	38.3	44.7	46.3
6	NK779	159.7	116.3	112.2	126.8	42.5	40.6	42.9	47.3
7	NP2341	119.0	105.8	107.9	108.7	38.8	38.3	43.4	42.4
8	ND07-97	148.9	113.2	111.9	129.0	36.5	47.4	37.8	36.0
9	ND06-144	155.8	105.0	76.4	89.5	42.7	36.8	48.1	41.7
10	ND08-343	140.2	113.8	129.1	139.3	44.2	43.4	49.6	47.2
11	GEM5Derived	128.1	113.2	83.2	114.7	39.2	39.0	38.0	37.7
12	ND203	.	97.3	105.4	108.4	.	42.0	31.2	28.0
13	ND265	165.3	105.6	125.3	120.8	31.2	47.3	30.1	32.3
14	ND274	158.1	91.7	109.2	146.0	36.1	39.6	40.5	33.1
15	ND2021	165.2	104.5	123.8	140.9	36.5	43.1	43.0	43.1
16	ND2013	141.0	114.8	128.4	132.6	40.0	43.0	48.5	35.0
17	ND2019	129.9	100.0	99.1	112.7	35.3	36.8	45.1	41.4
18	ND2014	145.8	97.0	109.6	118.8	35.5	43.4	44.1	43.1
19	ND07-212	132.0	115.5	98.0	106.3	41.2	41.4	46.6	42.4
20	ND06-189	179.1	107.9	115.9	147.6	45.8	46.2	49.1	43.9
21	ND07-255	130.0	100.2	95.2	106.8	40.8	41.0	43.0	43.2
22	ND08-53	148.1	98.4	109.9	125.9	36.4	39.9	43.9	34.6
23	ND290	150.2	120.6	107.4	131.6	38.0	47.0	42.8	37.7
24	ND291	150.5	100.5	101.6	115.0	35.1	38.6	39.5	33.9
25	ND06-85	129.8	118.5	98.8	92.1	40.0	44.1	41.5	37.2
26	ND246	154.9	127.3	122.6	120.6	32.5	41.6	33.6	33.4
27	ND270	148.0	114.8	108.0	131.3	46.6	39.6	47.0	44.9
28	ND250	129.1	112.8	114.6	123.9	42.9	47.0	50.6	51.3
29	ND2000	134.4	110.0	90.2	103.5	41.8	42.2	41.3	41.6
30	ND2014	140.4	131.9	88.1	116.3	37.2	39.1	44.3	44.6
31	ND2006	131.4	102.9	130.3	134.5	38.3	40.3	34.3	34.0
32	ND07-153	148.7	128.7	110.5	127.8	37.0	38.3	44.0	46.1
33	ND2007	145.6	122.6	138.2	132.2	37.7	47.4	50.5	49.7
34	ND2002	111.8	92.1	74.2	94.7	39.1	42.1	38.8	34.7
35	ND2004	146.0	101.7	76.5	97.3	35.0	41.9	34.3	29.3
36	ND2001	130.0	90.1	135.6	140.4	32.6	40.1	35.1	38.3
37	ND2005	138.7	93.1	116.1	141.2	44.4	45.3	47.9	53.1
38	ND2009	150.2	103.7	77.7	134.5	34.7	43.2	49.6	52.4
39	Il5	114.0	105.5	91.7	117.4	35.3	45.6	41.9	42.7
40	KMN22	149.9	146.6	121.5	144.7	34.7	41.6	38.6	42.2
41	B104	131.4	113.8	113.3	125.8	26.2	42.0	35.0	36.1
42	ACF47	117.1	122.9	72.7	107.2	29.2	44.8	36.1	40.0
43	LP05	129.6	117.4	94.1	125.4	35.5	46.8	40.5	44.9
44	NK807	127.0	125.7	90.8	103.0	38.2	39.4	41.0	39.0
45	PHJ40	135.5	128.5	88.8	113.7	37.8	45.0	41.2	37.2
46	ND07-226	120.5	126.6	83.3	110.1	39.9	39.7	42.7	42.6
47	ND2032	161.0	119.2	84.4	100.2	40.2	46.8	40.5	34.1
48	**TR3030 89RM**	147.0	114.7	66.5	103.0	42.4	44.3	44.9	45.7
49	**TR2678 85RM**	129.6	110.8	85.4	110.4	37.2	39.4	37.7	32.4
	Exp. Mean	139.4	111.1	101.9	119.8	38.0	42.0	41.8	40.2
	CV%	11.5	5.2	10.3	3.8	9.8	4.5	5.2	6.1
	LSD,0.05	22.8	8.2	14.9	6.4	5.3	2.7	3.1	3.5
	MSE	258.9	33.4	111.1	20.6	14.0	3.5	4.7	6.1

Table A30. Grain starch compositions adjusted means of 47 inbred parents and two checks (on bottom) across eight environments of Fargo (FAR) and Prosper (PRO), ND.

		Extractable Starch, g kg⁻¹ of dry matter				Total Starch, g kg⁻¹ of dry matter			
		2013		2014		2013		2014	
Entry	Pedigree	FAR	PRO	FAR	PRO	FAR	PRO	FAR	PRO
1	ACF49	607.5	617.0	626.0	605.0	708.4	703.5	721.2	687.1
2	PHG47	554.5	643.2	604.5	601.5	655.8	710.9	690.8	671.4
3	LH61	.	627.2	605.0	597.5	707.3	700.2	709.0	686.1
4	ACF052	594.5	606.1	646.5	619.0	688.2	692.8	727.2	699.3
5	ACLB0	568.0	640.4	608.5	572.5	679.9	716.6	697.4	675.6
6	NK779	531.0	618.6	612.5	570.0	655.5	695.0	692.8	674.0
7	NP2341	601.0	628.3	606.5	592.0	694.9	708.5	695.9	690.5
8	ND07-97	567.5	610.4	610.0	583.5	670.3	692.3	698.5	680.3
9	ND06-144	552.5	631.5	631.5	628.0	657.2	712.1	720.7	712.2
10	ND08-343	563.5	600.0	582.5	578.0	672.5	696.2	672.4	662.9
11	GEM5Derived	582.0	605.3	668.5	614.0	687.3	702.8	726.7	698.3
12	ND203	.	632.0	616.5	619.5	.	712.2	706.1	705.1
13	ND265	515.0	626.0	585.5	604.0	661.9	700.3	692.0	692.6
14	ND274	539.5	647.4	623.5	562.5	657.5	721.8	694.2	662.2
15	ND2021	541.5	625.7	597.0	582.0	658.0	706.5	685.7	668.2
16	ND2013	568.0	601.9	556.5	566.0	675.9	696.5	668.9	670.7
17	ND2019	574.0	645.1	635.0	613.5	686.3	715.3	703.6	692.3
18	ND2014	578.0	651.6	620.5	597.0	678.3	710.9	697.0	687.2
19	ND07-212	593.0	617.7	651.0	616.0	681.8	697.0	705.9	701.5
20	ND06-189	498.0	625.3	586.0	524.5	629.9	699.0	682.8	655.2
21	ND07-255	584.0	628.3	649.5	629.5	684.2	706.6	711.7	698.5
22	ND08-53	569.5	626.5	614.0	581.5	671.6	712.5	692.8	685.3
23	ND290	550.5	603.0	615.0	599.0	669.2	687.3	695.8	680.1
24	ND291	558.5	635.4	633.5	635.5	670.3	714.8	709.0	699.8
25	ND06-85	606.5	594.7	631.0	647.0	687.1	689.4	707.2	717.7
26	ND246	553.0	590.9	599.5	587.5	667.4	686.7	690.3	692.3
27	ND270	562.0	616.1	616.5	565.0	658.5	700.8	693.0	669.1
28	ND250	601.5	598.1	627.5	614.0	683.9	691.4	687.2	677.7
29	ND2000	580.5	617.7	646.0	620.0	679.4	702.2	717.1	703.3
30	ND2014	561.5	578.8	614.0	580.0	675.5	686.1	713.5	687.9
31	ND2006	576.5	631.6	610.0	591.0	684.3	707.2	687.8	681.2
32	ND07-153	581.5	593.8	630.5	624.0	670.6	689.2	693.3	672.7
33	ND2007	581.0	583.8	561.0	.	667.2	682.9	653.5	666.7
34	ND2002	603.0	633.2	650.0	630.5	700.9	717.4	729.3	716.3
35	ND2004	553.0	619.5	647.0	606.0	675.6	707.5	730.5	714.3
36	ND2001	583.5	630.8	590.0	579.5	688.8	722.1	678.9	666.6
37	ND2005	571.5	633.9	594.0	554.0	671.2	710.2	681.9	648.7
38	ND2009	579.5	627.5	638.5	.	671.3	704.5	708.8	653.9
39	Il5	620.0	613.1	644.5	617.5	704.7	703.4	712.4	684.8
40	KMN22	563.5	566.6	583.0	558.0	673.4	669.6	690.5	665.1
41	B104	590.0	597.1	533.5	.	690.9	695.8	686.8	.
42	ACF47	639.5	612.4	681.5	664.0	708.3	686.0	737.1	696.4
43	LP05	589.0	599.8	613.5	584.0	686.1	690.0	699.4	.
44	NK807	595.0	596.8	633.5	625.5	689.4	691.5	713.3	698.1
45	PHJ40	581.0	582.1	641.0	607.0	682.0	682.8	716.3	695.7
46	ND07-226	613.0	589.8	629.5	620.5	694.0	687.9	720.2	696.2
47	ND2032	549.0	605.9	632.5	600.5	656.1	686.2	721.1	707.3
48	**TR3030 89RM**	557.5	598.5	662.5	605.0	663.4	693.8	727.8	692.4
49	**TR2678 85RM**	582.5	607.6	625.5	615.0	687.7	706.0	718.7	698.8
	Exp. Mean	573.7	614.6	618.8	599.7	677.5	700.0	702.3	685.9
	CV%	4.6	1.3	2.7	1.9	2.3	0.7	1.5	0.7
	LSD,0.05	37.4	11.1	23.4	16.1	21.9	6.6	14.5	6.3
	MSE	699.7	61.2	273.1	130.1	239.0	21.9	105.1	20.0