

QTL ANALYSES OF YIELD AND YIELD-RELATED TRAITS IN WHEAT USING
A MAPPING POPULATION FROM A TAM 113/GALLAGHER CROSS

A Thesis

by

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ABSTRACT

Understanding genetic architectures of yield and yield components of dryland and irrigated wheat (*Triticum aestivum* L.) is pivotal to developing modern high-yielding germplasm and cultivars, while maintaining end-use quality traits and tolerance to biotic and abiotic stresses. The aim of this study was to construct a genetic map and detect major quantitative trait loci (QTL) linked to yield and yield components using the biparental population developed from the cross ‘TAM 113’/’Gallagher’. Field studies including 191 recombinant inbred lines (RILs) were conducted at McGregor, College Station, and Bushland in Texas during the 2018-2019, 2019-2020, and 2020-2021 growing seasons. A set of 8,261 single nucleotide polymorphisms (SNPs) markers was used to construct a high-density genetic map for all 21 chromosomes using JoinMap 4.0. Genomic regions associated with yield and yield components were detected through linkage analysis and QTL identification using IciMapping. A total of 160 QTL were detected for all traits collected in the study. Among them, 10 QTL were detected at individual environments and 12 cluster QTL regions were identified. One major QTL was located at 34 Mb on chromosome 2D, affecting multiple traits including two consistent QTL for heading date (*Qhd.tamu.2D.34*) and plant height (*Qph.tamu.2D.34*), overlapping with the major photoperiod gene Ppd-1. Another cluster QTL, detected on 2 D at 37 Mb, was very close to a previously identified cluster controlling multiple traits, including yield and kernel area. Other important QTL clusters were located between 52 Mb and 66 Mb on 7D including one consistent QTL for grain yield at 52 Mbp that increased yield up to 24.16 g

m⁻², increased harvest index up to 1 % and increased kernel diameter by 0.03 mm. This study dissects genetic mechanisms associated with yield and its components, thus providing valuable information for wheat improvement.

DEDICATION

This thesis is dedicated to my parents and my sister.

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The mapping population was developed by the Wheat Genetics Program in Amarillo, TX. The population was genotyped using genotyping-by-sequencing by the Texas A&M AgriLife Research Genomics and Bioinformatics Service Center at College Station, TX. All field work and data collection were completed by the wheat genetic and breeding programs from Texas A&M AgriLife Research, and students from West Texas A&M University.

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NOMENCLATURE

| | |
|-------|--------------------------------------|
| AbyE | Additive-By-Environment Interaction |
| ANOVA | Analysis of Variance |
| BC | Backcross |
| BLUE | Best Linear Unbiased Estimators |
| BLUP | Best Linear Unbiased Predictor |
| BMYLD | Biomass Grain Yield |
| CIM | Composite Interval Mapping |
| CTAB | Cetyltrimethylammonium Bromide |
| DH | Double Haploid |
| DNA | Deoxyribonucleic Acid |
| GBS | Genotype-By-Sequencing |
| GEI | Genotype-By-Environment Interaction |
| GS | Genomic Selection |
| HD | Heading Date |
| HI | Harvest Index |
| ICIM | Inclusive Composite Interval Mapping |
| KA | Kernel Area |
| KASP | Kompetitive Allele-Specific |
| KL | Kernel Length |
| KPS | Kernels spike ⁻¹ |

| | |
|------|--|
| KW | Kernel Width |
| LOD | Logarithm of the Odds |
| MAS | Marker-Assisted Selection |
| NIL | Near-Isogenic Lines |
| OAES | Oklahoma Agricultural Experiment Station |
| PCR | Polymerase Chain Reaction |
| PH | Plant Height |
| QTL | Quantitative Trait Loci |
| REML | Residual Maximum Likelihood |
| RILs | Recombinant Inbred Lines |
| SKCS | Single Kernel Characterization System |
| SKW | Single Kernel Weight |
| SPM | Spikes meter ⁻² |
| SNP | Single Nucleotide Polymorphism |
| SRAP | Sequence-Related Amplified Polymorphism |
| SSR | Simple Sequence Repeats |
| STM | Sequence-Tagged Microsatellites |
| TKW | Thousand Kernel Weight |

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1. GENERAL INTRODUCTION

Wheat (*Triticum aestivum* L.) is a widely grown crop, covering about 214 million hectares globally and producing about 734 million metric tons of grain (FAO, 2020). Wheat is an important source of energy for over 30% of the world's population. It also provides essential nutrients such as proteins, vitamins, minerals, phytochemicals, and dietary fiber (Shewry&Hey, 2015). Wheat is mainly utilized for bread, pizza, noodles, biscuit, vital gluten, and fermented beverages for human consumption. Wheat can also be used for animal grazing, cosmetics, and ethanol production (Shewry, 2009).

The current world population is over 7 billion and is estimated to reach 9 billion in the next 30 years (UN, 2019). This population increase creates a gap in food supplies. Expanding the area of production may not be possible due to limited arable land to fill the gap. Therefore, vertical yield increase per area remains the only viable option. The U.S. wheat grain production has increased steadily over the years, while the planted area remained unchanged (USDA, 2019). Increasing wheat production can be achieved using high-yielding varieties and applying best management practices (Bailey-Serres, Parker, Ainsworth, Oldroyd, Schroeder, 2019).

Humans have a long history of selecting desired plant types at basic levels after domestication. After Gregor Mendel discovered the basic principles of heredity, plant breeding became a scientific concept (Smykal et al., 2016). Plant breeding became more sophisticated with the adoption of new technologies and approaches, such as doubled haploidy, marker-assisted selection (MAS), genomic selection (GS), recombinant DNA,

and genome editing (Yan et al., 2017). In general, the use of these technologies in applied plant breeding contributes to time and effort saving in the process, ultimately reducing costs associated with breeding (Ahmar et al., 2020).

Quantitative Trait Loci (QTL) mapping provides the opportunity to associate complex phenotypic traits (quantitative traits) to specific regions in the chromosomes, which can be useful in the application of MAS schemes (Xu, Li, Yang, Xu, 2017). Many studies have been carried out to identify QTL associated with yield and yield-related traits using different DNA markers (Yang et al., 2020). The objectives of this study were twofold:

- 1) To determine the major yield components contributing to grain yield in hard red winter wheat RILs derived from a cross between ‘TAM 113’/’Gallagher’ grown in different Texas environments and to understand the effects of environmental fluctuations on the dynamics of grain yield determination in this population.
- 2) To identify major QTLs associated with grain yield, yield components, and other agronomic traits in RILs grown under different environmental conditions through the single environment and across environment analyses.

2. LITERATURE REVIEW

2.1. Molecular Markers

Molecular markers are handy tools to understand complex traits and have been steppingstones for plant breeding (Jaganathan, Bohra, Thudi, Varshney, 2020). Molecular markers enable identifying variations for specific DNA regions that provide genetic information about individuals (Al-Samarai & Al-Kazaz, 2015). DNA-based markers can be categorized into two groups, Polymerase chain reaction (PCR)-based markers including randomly amplified polymorphic DNA (RAPD), Simple sequence repeats (SSR), amplified fragment length polymorphism (AFLP), single nucleotide polymorphism (SNP), and non-PCR-based marker such as restriction fragment length polymorphism (RFLP) (Agrawal & Shrivastava, 2014).

Single nucleotide polymorphisms have become popular recently, which created a high potential for high throughput genotyping at low costs. Furthermore, abundance in the genome and genetic stability are influential factors in making SNP preferable for plant breeding and genetic studies. Genomic selection, QTL mapping, seed identity testing, and pedigree analysis are brief applications for SNP markers in plant breeding (Smýkal et al., 2016).

2.2. QTL Mapping Studies

Improving grain yield is the primary objective of most wheat breeding programs. Grain yield is a complex trait controlled by many genes or QTL that can be dissected into components such as thousand kernel weight (TKW), single kernel weight (KW), and plant

height (PH) (Ren et al., 2018), among other traits. In the last decades, immense progress has been made in the detection of genes and major stable QTLs associated with yield-related traits in different crops (Li et al., 2010). Additive, dominant, and epistatic gene actions are also essential to understanding the genetic structure, and QTL mapping analysis is an excellent way to decipher genetic information caused by allelic effects (Yang et al., 2018).

QTL mapping studies can be carried out using different mapping populations, such as recombinant inbred lines (RILs), doubled haploids (DH), F2 backcross (BC), and near-isogenic lines (NIL). An F2 segregating population has one cycle of selfing with the lowest cost, but this population is not replicable, and lack of recombination constitutes a significant weakness for mapping (Endelman & Jansky, 2016). RIL populations are considered as the most effective population, but this population requires 5-6 generations to attain an adequate level of homozygosity, and dominance deviation cannot be estimated because most alleles are homozygous (Seymour et al., 2012). Additionally, meiosis occurs at each cycle, increasing the chance of recombination among loci closely linked to each other (Silva, Cruz, Moreira, Barros, 2007). Wheat DH lines are developed from F1 lines using anther culture, microspore culture, or maize pollination, and provide completely homogenous line in a shorter time (Kiviharju, Moisaner, & Tanhuanpaa, 2017; Mochida & Tsujimoto, 2001).

Many statistical methods have been developed to detect QTL and intra-locus genetic effect estimates. One of the most preferred methods is composite interval mapping (CIM), but inclusive composite interval mapping (ICIM) with a two-step mapping strategy

is considered a more efficient statistical method because the algorithm of CIM is not sufficient to complete background control (Meng, Li, Zhang, & Wang, 2015).

Many QTL have been found using linkage maps built by SNP markers for plant height (PH), heading date (HD), total biomass, TKW, and KW in previous studies (Gao et al., 2015; Li et al., 2019; Xin et al., 2020; Dhakal et al., 2021; Yang et al., 2020). It is important to note that the expression of QTL is affected by the environment (Li, Dong, Niu, 2006; Sari et al., 2018; Wang, Vanden Langenberg, Wen, Wehner, & Weng, 2018). The consistency of the QTL is partially attributed to the heritability of the trait involved, and it is generally difficult to detect consistent QTL for low heritable traits (Gahlaut et al., 2017).

2.3. Yield and Yield Components

2.3.1. Grain Yield

Improving grain yield is one of the main goals of modern wheat breeding programs targeting sustainability and food security. Grain yield is quantitatively inherited and strongly affected by the environmental conditions, but it can be dissected into multiple yield components. Therefore, dissecting yield components is essential to develop higher-yielding wheat varieties (Zheng et al., 2010; Liu et al., 2020). During the second half of the twentieth century, the genetic gain has shown a significant increase; however, it has slowed over time. Therefore, to boost genetic gain for grain yield, molecular markers have become indispensable (Ahrends, Eugster, Gaiser, Rueda-Ayala, & Hüging, 2018).

Grain yield in wheat can be defined by three main components, spike m^{-2} (SPM), and kernels spike⁻¹ (KPS), thousand-kernel weight (TKW). Grain yield is considered the

combination of grain number per unit area and grain weight, while grain weight is one of the marketing standards of wheat (Kuchel, Williams, Langridge, Eagles & Jefferies, 2007).

Due to its commercial importance, wheat has been extensively studied to detect genomic regions associated with grain yield. Azadi et al. (2015) mapped twenty-four QTL across ten chromosomes in a RIL population (186 RILs), the majority of these QTL had a minor effect, and the phenotypic variation explained by each QTL was less than 10%. In another study involving 107 DH lines derived from a cross between ‘Fukuho-kumogi’, Japanese wheat cultivar, and ‘Gigas’, an Israeli wheat line, and with the use of different markers (AFLP, RFLP SSR, RAPD) on two morphological traits, a QTL associated with grain yield was detected on chromosome 6A, 6B, and 6D (Heidari, Sayed-Tabatabaei, Saeidi, Kearsy, & Suenaga, 2011).

The expression of QTL for grain yield and its components can be influenced by environmental conditions, including seasonal precipitation, temperature, and soil fertility (Zheng et al., 2010). Several QTL studies showed inconsistent yield QTL detection due to the occurrence of genotype-by-environment interactions (Tura et al., 2020).

2.3.2. Kernel Per Spike

Kernel per spike in wheat is a key trait controlling yield (Shi, Hao, Zhang, Cheng, & Zhang, 2017). According to previous studies, kernel per spike has a significant negative correlation with TKW. Therefore yield increase can be realized either through increase in grain number or TKW (Wurschum, Leiser, Langer, Tucker, & Longin, 2018).

Bindraban et al. (1998) divided wheat development stages into three phases. The second stage, after the passage of anthesis and floret maturation, is critical for the determination of kernel per spike and is often affected by environmental factors like solar radiation and temperature fluctuations. Heat and drought stresses are also considered significant factors affecting kernel per spike by reducing kernel number and kernel size (Sehgal, Sita, Siddique, Kumar, Bhogireddy, 2018). Rustgi, Shafqat, Kumar, Baenziger, & Ali (2013) reported eleven QTL associated with kernel per spike with 3A specific recombinant inbred chromosome lines (3A-RICLs) population using RFLP, SSR, sequence-tagged microsatellites (STM), and diversity array technology (DArT) markers.

2.3.3. Spikes Per Square Meter

Spikes per square meter is a yield component that significantly contributes to grain yield in wheat (Mian, Begum, & Saha, 2020). It is known that there is an association between planting date and the number of spikes per unit area. Early sowing increases tiller number. However, the spikes may not be fertile due to the elongated vegetation period. There is also strong evidence that increases in seeding rate positively contribute to increases in number of spikes per unit area (Shah, Harrison, Boquet, Colyer, & Moore, 1994; Zhu, Chu, Dai, & He, 2019).

Under drought conditions, the number of spikes per square meter negatively impacts kernel number per spike and single kernel weight (Moral, Rharrabti, Villegas, & Royo, 2003). Mengistu, Baenziger, Eskridge, Dweikat, and Wegulo (2012), using SSR and sequence-tagged microsatellites (STM) markers on a DH population, identified one stable QTL, QSsm.neb-3A, associated with spike number on chromosome 3A. In another

instance, Tang et al. (2011), using 184 SSR markers and 34 sequence-related amplified polymorphism markers (SRAP) in a RIL population derived from ‘Chuanmai’, a synthetic hexaploid wheat (SHW), and ‘Chuannong’, a Chinese spring wheat variety, identified nine QTL associated with spikes per square meter across six chromosomes, PVE value ranged from 5.5 to 21%.

2.3.4. Kernel Traits

Kernel traits, including TKW, kernel length (KLEN), kernel width (KWID), kernel area (KE), and perimeter, are key components affecting grain yield in wheat (Liu et al., 2020). TKW is one of the vital yield components that has been progressively improved over time (Wang, Ge, Hao, Dong, & Zhang, 2012). Thousand kernel weight is a highly heritable trait with estimates ranging from 0.59 to 0.8 (Wang, Ge, Hao, Dong, & Zhang, 2012). Thousand kernel weight contributes up to 20% of yield improvement and is considered the main factor for developing superior high-yielding wheat cultivars (Ma et al., 2012). In general, a negative association between TKW and grain number is observed, as increases in kernel number lead to a decrease in kernel weight and size (Tura et al., 2020). Hou, Liu, Hao, Li, and Liu (2020) reported six QTL associated with TKW on chromosomes 2A, 2B, 4A, and 7A in 300 wheat accessions in 2017 and 2018. Kernel width and kernel length are two sub-components of kernel weight, which are positively correlated with kernel weight (Kumar, Mantovani, Seetan, Soltani, & Echeverry-Solarte, 2016).

Kernel morphology can influence market value. Therefore, understanding the genetic basis of kernel weight plays a significant role in developing desired commercial

varieties (Prashant, Kadoo, Desale, Kore, & Dhaliwal, 2012). A large kernel is desired in wheat breeding due to its positive correlation with TKW. Besides, KLEN has shown a positive impact on seedling vigor (Cheng, Kong, Zhang, Xie, & Jia, 2017; Cui, Ding, Li, Zhao, & Li, 2011).

Groos, Robert, Bervas, and Charmet (2003) mapped nine QTL associated with TKW on chromosomes 1D, 2B, 2D, 5B, 6A, 6D, 7A, and 7D in a RIL population derived from a cross between 'Renan' and 'Récital'. Three of these QTL showed significance in all of the environments where these materials were evaluated. The QTL for TKW on chromosome 5B and 7B also control grain protein content and grain yield. In another study, Hai, Guo, Wagner, Xiao, and Friedt. (2008) identified two genomic regions associated with TKW on chromosomes 2B and 7B using 168 SSR markers in a 108-line DH population. The detected QTL explained around 14 % of the phenotypic variation, and one of these QTL was co-localized with kernel per spike.

2.4. Agronomic Traits

2.4.1. Heading Date

Although environmental factors play a significant role in plant growth and development, wheat growth strongly depends on photoperiod, vernalization, their interaction, and earliness *per se* (González, Slafer, & Miralles, 2002). From a breeding perspective, heading date is a selection criterion based on a specific growing area since very early or delayed heading can lead to grain yield losses (Ochagavía, Prieto, Zikhali, Griffiths, & Slafer, 2019). For instance, the grain filling stage is susceptible to temperature. High temperature limits grain filling, which can lead to a drop in grain yield

(Ye et al., 2019). Heading date in small grains is influenced by photoperiod and vernalization genes (Grogan, Brown-Guedira, Haley, McMaster, & Reid, 2016). Vernalization response genes (VRN-1, VRN-2, VRN-3, etc.) regulate the period of exposure to low temperature (Loukoianov, Yan, Blechl, Sanchez, & Dubcovsky, 2005; Whittal, Kaviani, Graf, Humphreys, & Navabi, 2018). Previous studies have shown that several major genes control vernalization and photoperiod response (Guedira et al., 2016; Huang et al., 2018). Photoperiod response genes (Ppd) are another group of genes that control heading date by regulating plant physiology for daylight perception, which is vital for the accumulation of dry matter (Royo, Ammar, Alfaro, Dreisigacker, & del Moral, 2018).

Chen, Sun, Li, Wang, and Shi (2020) reported three additive QTL associated with heading date on chromosomes 1A, 1B, and 2D in introgression line (IL) populations derived from ‘Lumai 14’/ ‘Shaanhan 8675’ evaluated at eight environments for five years.

In another study conducted by Chen, Cheng, Chai, Wang, and Du (2020), five stable QTL were detected on chromosomes 2A, 5B, 6B, 7A, and 7D in a RIL population derived from ‘Yi5029’ and ‘Nongda4332’ varieties. Three QTL regions for HD co-localized with spikelet numbers on chromosomes 2A, 7A, and 7D.

2.4.2. Plant Height

Plant height is a valuable agronomic trait associated with grain yield, biomass, lodging resistance, and disease resistance (Lu et al., 2019). Plant height has a positive relation with spike length and the number of grains per spike. An increase in wheat yield has been attributed to the introduction of reduced height (Rht) genes during the Green

Revolution period (Wurschum, Langer, Longin, Tucker, & Leiser, 2017). Furthermore, semi-dwarf plants are relatively resistant to some diseases and insects, which contributes to yield under high plant density (Liu, Zhang, Feng, & Tian, 2020).

Several dwarfing genes were detected on different chromosomes including Rht-A1 on 4A, Rht-B1 and Rht-11 on 4B, Rht-D1 on 4D Rht8 on 2D, Rht-9 and Rht-3 on 7B, Rht12 on 5A, Rht23 on 5D, and Rht24 on 6A (Chai, Yao, Zhang, Xiao, & Fan, 2021; Daba, Tyagi, Brown-Guedira, & Mohammadi, 2020; Kang, Lin, Song, Yuan, and Zhong, 2012). After integrating reduced height genes into wheat breeding programs, a significant increase in harvest index (HI) has been observed. Harvest index is defined as the ratio between the grain yield and above biomass yield (Dai, Bean, Brown, Bruening, & Edwards, 2016). Gao et al. (2015) identified seven QTL associated with plant height on chromosomes 2BL, 4AL, 4BS, 4DS, 5AS, and 7AL using 246 F8 RILs derived from ‘Zhou 8425B’/‘Chinese Spring’. This study hypothesized that discovering grain yield and yield-related QTL via phenotyping biparental (RILs) populations under different environmental conditions could help to understand and dissect the genetic control of high-yielding modern cultivars.

3. MATERIAL AND METHODS

3.1. Plant Material

A set of 191 Recombinant inbred lines (RIL) derived from a cross between winter wheat varieties 'TAM 113' and 'Gallagher' was developed by single-seed descent method. Gallagher was released by the Oklahoma Agricultural Experiment Station (OAES) in 2012, and the pedigree of Gallagher is OK99711/OK93P656-RMH3299. It is an early maturing variety with good resistance to leaf rust (*Puccinia triticina*), stripe rust (*Puccinia striiformis*), Hessian fly (*Mayetiola destructor*), and soil-borne mosaic virus (Marburger, Silva, Hunger, Edwards, Van der Laan, 2021). TAM 113 was released by Texas A&M AgriLife Research in 2010 and has excellent yield potential and drought tolerance (Rudd et al., 2013). The pedigree of TAM 113 (Rudd, Devkota, Baker, Ibrahim, Worrall, 2013) is TX90V6313/TX94V3724. In the 2018-2019 season, 137 lines were planted, and 191 lines were planted with parents both in 2019-2020 and 2020-2021 growing seasons.

3.2. Field Experimental Design

Field studies were conducted in 2019, 2020, and 2021 at the Texas A&M AgriLife Research stations in College Station (30°32'34.8"N 96°25'47.3"W), Bushland (35°09'35.3"N 102°05'02.9"W), and McGregor (31°22'24.8"N 97°27'05.9"W) (Table 4). At each site the experiment consisted of alpha-lattice experimental design with two replications. The plot size was 4.57 × 1.52 m (15×5ft) and seeded at 50g per plot with standard agronomic practices. Irrigated environment consisted of 2019BSP while other environments dry environment 19CS, 19MCG, 20CS, 20MCG, 20EMN, and 21BD.

Table 1. General information of the trials established in Texas for the evaluation of grain yield and yield component traits using a population derived from a cross between TAM 113 and Gallagher.

| Location | Year of Harvest | Plot Number | Environment Code |
|-----------------|------------------------|--------------------|-------------------------|
| Bushland | 2019 | 274 | 19BSP |
| Bushland | 2020 | 400 | 20EMN |
| Bushland | 2021 | 400 | 21BD |
| College station | 2019 | 274 | 19CS |
| College station | 2020 | 400 | 20CS |
| McGregor | 2019 | 274 | 19MCG |
| McGregor | 2020 | 200 | 20MCG |

BSP= Bushland South Pivot, EMN= Emeny land, MCG= McGregor, CS= College Station, BD= Bushland Dryland

3.3. Phenotypic Data Collection

Days to heading were recorded on a plot mean basis as the number of days from planting to 50% of spikes protrusion from the flag leaf. Plant height was recorded on a plot mean basis and consistent on a measurement from the base of soil to the top of the plant, excluding awns. This trait was collected in all experiments except BSP19. At maturity, whole plots were harvested with a combine harvester for grain yield of each plot from all the trials except the ones at McGregor in 2019. Kernel moistures during harvesting measured by combine harvester ranged from 8.3% (20CS) to (22% 21BD). Yield data were recorded as bushels per acre (Bus/Ac) and converted to gram per square meter (g/m^2). Kernel Characteristics such as kernel hardness index (HARD), kernel diameter (DIAM), moisture content, and single kernel weight (SKW) were collected with a Perten Model Single Kernel Characterization System (SKCS) 4100 (Perten Instruments North America Inc.) based on 300 randomly selected kernels per plot from the study at McGregor in 2020.

Samples from half-meter long inner rows were cut from the ground in each plot at the physical maturity stage, which uniformly represents the whole plot for biomass grain yield (BMYLD), total biomass (BM), TKW, and SPM in three experiments 19BSP, 20EMN, and 21BD (Table 2). All samples were dried in a drying room at 60 °C for three days to reduce moisture before weighing biomass and grain. The harvest index (HI) and KPS were collected according to Yang et al. (2020). Approximately 10 grams of seeds were scanned for each line using an HP 11956A scanner, and Grain Scan software (Whan et al., 2014) was used to determine seed area, perimeter, kernel length, kernel width, and grain number. Thousand kernel weight was calculated by dividing the scanned seed weight by seed number and multiplying by 1000. Lastly, single stem head weight, single head dry weight, and single head grain weight were calculated following the procedure described by Yang et al. (2020).

Table 2. Summary of the phenotypic data collected by environment for three growing seasons.

| Trait | 19BSP | 19MCG | 20EMN | 20MCG | 20CS | 21BD |
|--------|-------|-------|-------|-------|------|------|
| YLD | ✓ | × | ✓ | ✓ | ✓ | ✓ |
| PH | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| HD | ✓ | ✓ | ✓ | × | ✓ | ✓ |
| HeadWt | ✓ | × | ✓ | × | × | ✓ |
| TKW | ✓ | × | ✓ | × | × | ✓ |
| SPM | ✓ | × | ✓ | × | × | ✓ |
| KPS | ✓ | × | ✓ | × | × | ✓ |
| KA | ✓ | × | ✓ | × | × | ✓ |
| PERI | ✓ | × | ✓ | × | × | ✓ |
| KLEN | ✓ | × | ✓ | × | × | ✓ |
| KWID | ✓ | × | ✓ | × | × | ✓ |
| BM | ✓ | × | ✓ | × | × | ✓ |
| BMYLD | ✓ | × | ✓ | × | × | ✓ |
| HI | ✓ | × | ✓ | × | × | ✓ |
| SSHW | ✓ | × | ✓ | × | × | ✓ |
| SHDR | ✓ | × | ✓ | × | × | ✓ |
| SHGW | ✓ | × | ✓ | × | × | ✓ |

YLD: Grain Yield, PH: Plant Height, HD: Heading Date, TKW: Thousand Kernel Weight, SPM: Spikes m⁻², HeadWt: Total Head Weight g m⁻², KPS: Kernels Spike⁻¹, KA: Kernel Area, PERI: Perimeter, KLEN: Kernel Length, KWID: Kernel Width

Only yield was measured from 19CS.

3.4. Statistical Analysis

The following linear statistical model was used for the statistical analysis at each environment:

$$Y_{ijk} = \mu + R_i + B_{j(Ri)} + G_k + \varepsilon_{ijk}$$

Where Y_{ijk} = the observation of the k^{th} genotype within the k^{th} block of the i^{th} replicate, μ = overall mean, R_i = the effect of the i^{th} replicate, $B_{j(Ri)}$ = the effect of the j^{th} incomplete block within the i^{th} replicate, G_k = the effect of the k^{th} genotype, and ε_{ijk} = residual error. For the analysis of the combined data across environments, the following linear statistical model was used:

$$Y_{ijkl} = \mu + E_i + R_{j(Ei)} + B_{k(EiRj)} + G_l + GxE_{il} + \varepsilon_{ijkl}$$

Where Y_{ijkl} = the observation of the l^{th} genotype within the k^{th} block of the j^{th} replicate in the i^{th} environment, μ = the overall mean, E_i = the effect of the i^{th} environment, $R_{j(Ei)}$ = the effect of the j^{th} replicate within the i^{th} environment, $B_{k(EiRj)}$ = the effect of the k^{th} incomplete block within the j^{th} replicate in the i^{th} environment, G_l = the genotype effect of the l^{th} genotype, GxE_{il} = the interaction effect of the l^{th} genotype and the i^{th} environment, and ε_{ijkl} was the pooled residual error.

Best linear unbiased predictor (BLUP) values for each individual genotype were estimated using the restricted maximum likelihood (REML) method, assuming a random model in META-R software (Alvarado et al., 2020). BLUP values were used to calculate Pearson's correlation coefficients among the variables included in the study and used for QTL mapping. Besides, broad sense heritability, based on an entry-mean basis within

individual environments and combined across environments, was estimated using the following statistical formulas:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_\epsilon^2}{nRep}}$$

Where H^2 = broad-sense heritability in individual environment, σ_g^2 = the genotypic variance, σ_ϵ^2 = the error variance, and $nRep$ = the number of replications (Alvarado et al., 2020).

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{g\epsilon}^2}{nRep} + \frac{\sigma_\epsilon^2}{(nEnvs \times nRep)}}$$

Where H^2 = broad sense heritability across environments, σ_g^2 = the genotypic variance, $\sigma_{g\epsilon}^2$ = the genotype-by-environment interaction variance, $nEnvs$ = the number of environments and $nRep$ = the number of replications, and σ_ϵ^2 = the error variance.

3.5. Genotypic, Linkage Mapping and QTL Analysis

Genomic DNA was extracted from leaf samples of all RILs using the Cetyltrimethyl Ammonium Bromide (CTAB) method (Doyle, 1991). Following that, DNA concentrations were quantified by comparing the intensity with the known size standards on agarose gel, and DNA was diluted to the correct concentration. Genotyping was performed by the Genomic and Bioinformatics Center at Texas A&M University using the ddRADseq genotyping protocol in Illumina Hiseq400 sequencing system (Peterson, Weber, Kay, Fisher, & Hoekstra, 2012). The SNP's calling was conducted based on the Chinese Spring reference genome from the International Wheat Genome Sequencing

Consortium (IWGSC, 2014) using a web alignment tool at Genomics and Bioinformatics Service of Texas A&M AgriLife Research (Dhakal et al., 2021; Yang, Basnet, Ibrahim, Rudd, & Chen, 2019). After removing redundant SNPs through the BINNING function of Icimapping software and removing more than 20% missing data on Excel spreadsheet, 8,075 out of 99,288 SNP markers were used for constructing linkage map.

Joinmap software 4.0 (Van Ooijen, 2006) and QTL analysis using ICIMapping software version 4.1 (Meng, Li, Zhang, & Wang, 2015) were used for the construction of the linkage map. Detailed procedures for linkage and QTL analyses described in Dhakal et al. (2021) and Yan et al. (2020) were followed. Detected QTL were named as *Qtrait.tamu.chrom.Mbp*, where *Q* was the acronym of QTL, *trait* was the corresponding trait abbreviation, *tamu* was the abbreviation of Texas A&M University, *chrom* indicated chromosome numbers, and *Mbp* was the peak physical location of QTL.

4. RESULTS

4.1. Analysis of Variance and Heritability

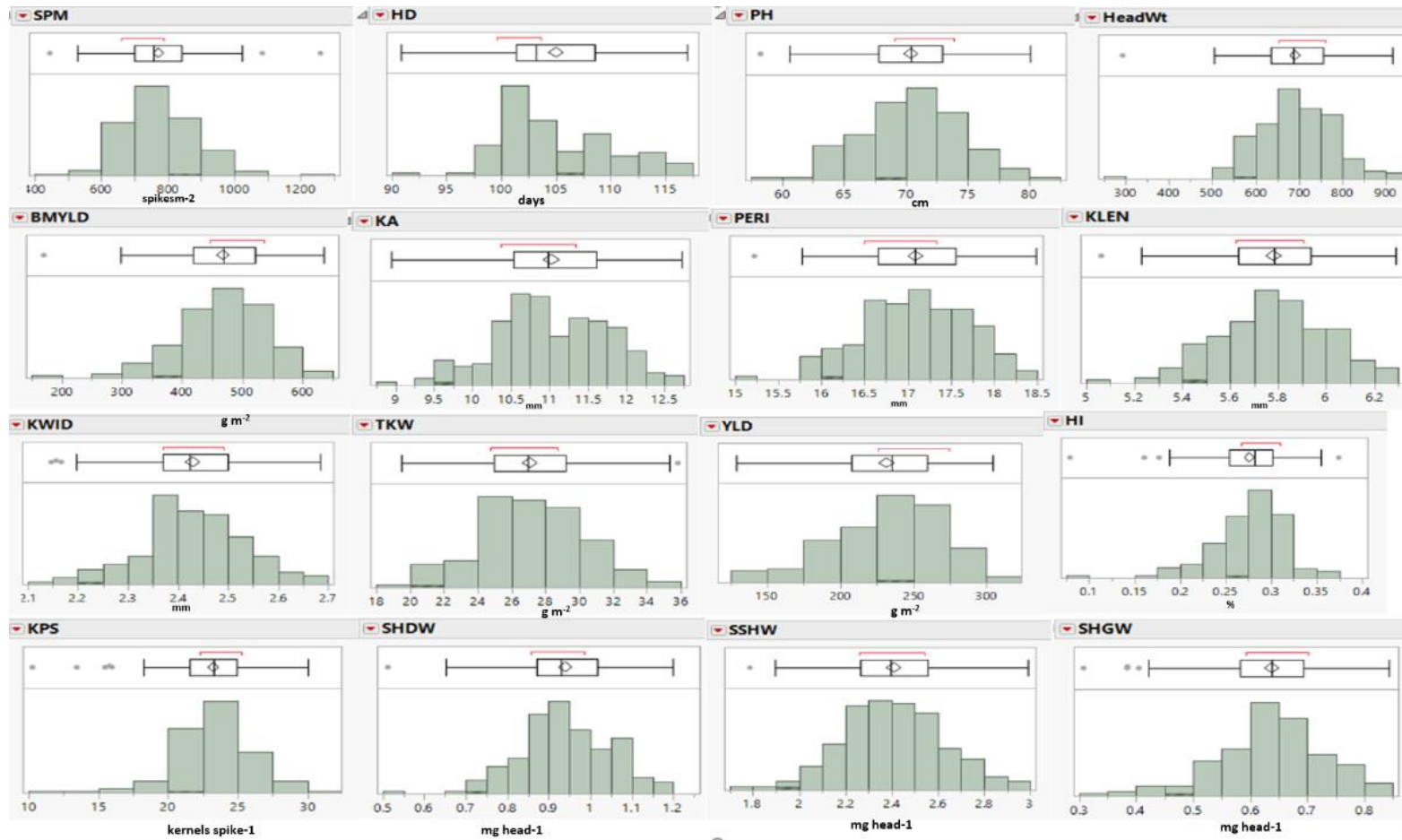
Significant variation among environments, genotypes, and genotype-by-environment interactions for most of the phenotypic traits was observed (Table 3). All traits were highly significant for genotypic effects except BM, HeadWt, and BMYLD. Similarly, GbyE interaction variance is significant for all traits except BM, HI, SPM and HeadWt. For environmental variance, the difference between BM, HD, PH, SPM, HeadWt, TKW, YLD, KPS, SHDW, SSHW, and SHGW were statistically significant but not for HI and seed-related traits (Table 3). Variance components (i.e., genotypic variance, GbyE variance, and Environmental variance) for yield and agronomic traits (i.e., PH and HD) were large due to highly significant effects ($P < 0.001$). Broad-sense heritability (H^2) was classified into three groups: low heritable trait (≤ 0.3), moderate heritable trait (0.4-0.6), and high heritable trait (> 0.6). HD, PH, KA, PERI, KLEN, KWID, TKW, YLD, and SHDW showed higher broad sense heritability ranging from 0.64 - 0.91. Heritability of BM, HeadWt, and BMYLD was low at 0.02, 0.30, and 0.29, respectively. Heritability for SPM, HI, KPS, SSHW, and SHGW were moderate and ranged from 0.49 to 0.56 (Table 3).

Table 3. Analysis of variance and broad-sense heritability assuming source of variations as random, and mean performance corresponding traits across environments.

| Traits ^a | Units | $\sigma^2\text{Gen}^b$ | $\sigma^2\text{G X E}^c$ | $\sigma^2\text{Env}^d$ | $\sigma^2\text{Res}^e$ | H^2^f | Mean \pm SD ^g | LSD ^h | CV ⁱ | Gallagher | TAM113 |
|---------------------|-----------------------------|------------------------|--------------------------|------------------------|------------------------|---------|----------------------------|------------------|-----------------|-----------|---------|
| YLD | g m ² | 1040.7*** | 1668.2*** | 5220.8*** | 683.60 | 0.70 | 231.6 \pm 38.80 | 50.9 | 11.3 | 290.7 | 230.6 |
| TKW | g | 8*** | 1.4*** | 0.5* | 3.20 | 0.80 | 27.1 \pm 3.10 | 3.6 | 6.6 | 28.1 | 29.5 |
| SPM | spikes m ⁻² | 3884.2*** | 926.7ns | 20004.1* | 13832.40 | 0.50 | 772 \pm 107.00 | 132.2 | 15.2 | 715.6 | 840.4 |
| KPS | kernels spike ⁻¹ | 2.7*** | 1.6* | 84.9** | 7.60 | 0.50 | 23.2 \pm 2.70 | 3.5 | 11.9 | 25.5 | 22.7 |
| HI | % | 0.0005** | 0.0002 ns | 0.002 | 0.00 | 0.50 | 0.3 \pm 0.03 | 0.0 | 13.7 | 0.3 | 0.3 |
| HD | days | 20.6*** | 5.6*** | 685*** | 1.80 | 0.90 | 105 \pm 4.90 | 4.8 | 1.3 | 102.7 | 106.6 |
| PH | cm | 12*** | 6.2*** | 276.6*** | 10.70 | 0.80 | 70.4 \pm 3.92 | 4.3 | 4.7 | 70.4 | 72.7 |
| BMYLD | g m ⁻² | 1096.4 ns | 2094.8** | 10868.4** | 6114.00 | 0.30 | 467.4 \pm 71.50 | 80.3 | 16.7 | 511.7 | 532.6 |
| BM | g m ⁻² | 196.01 ns | 5024.17 ns | 492527.5** | 35872.40 | 0.02 | 1728.5 \pm 129.15 | 38.6 | 11.0 | 1,736.1 | 1,831.9 |
| HeadWt | g m ⁻² | 1606.3 ns | 1792.5 ns | 17219.2** | 11263.50 | 0.30 | 691.2 \pm 86.74 | 97.3 | 15.4 | 737.3 | 746.7 |
| KA | mm ² | 0.4*** | 0.05** | 0.03 ns | 0.17 | 0.90 | 11 \pm 0.70 | 0.8 | 3.7 | 11.3 | 11.7 |
| KLEN | mm | 0.04*** | 0.004** | 0.0014 ns | 0.02 | 0.90 | 5.8 \pm 0.20 | 0.2 | 2.1 | 5.8 | 5.9 |
| KWID | mm | 0.01*** | 0.001** | 0.0025 ns | 0.00 | 0.80 | 2.4 \pm 0.10 | 0.1 | 2.2 | 2.5 | 2.5 |
| PERI | mm | 0.3*** | 0.02* | 0 ns | 0.12 | 0.90 | 17.1 \pm 0.60 | 0.6 | 2.0 | 17.3 | 17.5 |
| SHDW | mg ⁻¹ | 0.01*** | 0.002 * | 0.1** | 0.00 | 0.60 | 0.9 \pm 0.10 | 0.2 | 10.6 | 1.0 | 0.9 |
| SSHW | mg ⁻¹ | 0.02*** | 0.01* | 0.1*** | 0.10 | 0.50 | 2.4 \pm 0.21 | 0.3 | 10.0 | 2.5 | 2.4 |
| SHGW | mg ⁻¹ | 0.004*** | 0.003*** | 0.1*** | 0.00 | 0.60 | 0.6 \pm 0.09 | 0.1 | 12.5 | 0.7 | 0.6 |

^aAbbreviations of Traits YLD: Yield from a combine harvester, TKW: Thousand Kernel Weight, SPM: Spikes m⁻², KPS: Kernels Spike⁻¹, HI: Harvest Index, HD: Heading Date, PH: Plant Height, BMYLD; Biomass Grain Yield from 0.5-meter inner row, BM: Biomass, HeadWt: Head Weight, KA; Kernel Area, KLEN: Kernel Length, KWID: Kernel Width, PERI: Perimeter, SHDW: Single Head Dry Weight, SSHW: Single Stem Head Weight, SHGW: Single Head Grain Weight, ^b $\sigma^2\text{Gen}$: Genotypic Variance, ^c $\sigma^2\text{G X E}$: Genotype-by-Environment Variance, ^d $\sigma^2\text{Env}$: Environmental Variance, ^e $\sigma^2\text{Res}$ Pooled Residual Variance, ^f H^2 : Broad Sense Heritability. ^gSD: Standard Deviation, ^hLSD: Least Significant Difference for genotype effect ⁱCV: Coefficient of Variation, ns: non significant *, **, ***, significant at the 0.05, 0.01, and 0.001 probability levels, respectively.

Figure 1. Histogram and Phenotypic distributions of the predicted (BLUP) values for a total of 16 traits of recombinant inbred lines (RIL) across all environments.



4.2. Phenotypic Correlation Among Traits

Pearson's correlation coefficients were calculated to understand the relationships among all traits (Table 4). The correlation coefficient could be categorized into three groups: low (≤ 0.3), moderate (0.4 - 0.6), and high (≥ 0.6). Grain yield had the highest positive correlation with HI ($r = 0.7$, $P < 0.001$), while the correlation between yield and HeadWt, SHDW, SHGW, BMYLD, KPS were moderate ($r = 0.40 - 0.57$, $P < 0.001$). Correlation between HD and all traits except BM, PH, SPM, and KPS was negative. PH was only negatively correlated with SPM, and HeadWt, whereas it was positively correlated with KPS, YLD, HI, KA, PERI, KLEN, TKW, SHDW, SSHW, and SHGW. One of the major yield components, SPM, had significant correlations with all traits except HD and HI.

Seed-related traits showed a higher correlation among each other ($r = 0.81 - 0.96$, $P < 0.001$), except the correlation between KWID and KLEN ($r = 0.37$, $P < 0.001$) and PERI ($r = 0.58$, $P < 0.001$). KWID was highly correlated with TKW ($r = 0.91$, $P < 0.001$). Similarly, head-related traits SHDW, SSHW, and SHGW had high positive correlations among each other ($r = 0.71 - 0.92$, $P < 0.001$). Regarding the phenotypic correlation of all traits from individual environments (Table 8), GYLD had a higher positive correlation with harvest index from 0.56 to 0.65 ($P < 0.001$) at 19BSP, 20 EMN, and 21BD, respectively. PH only significantly correlated with HD ($r = 0.33$, $P < 0.001$), BM ($r = 0.32$, $P < 0.01$), KLEN ($r = 0.17$, $P < 0.05$), and HI ($r = -0.19$, $P < 0.05$) at different significant levels at 19BSP. HD significantly correlated with KPS in 19BPS and 21BD while there was no significant correlation between HD and KPS in overall environment. Additionally,

individual environments showed similar trends for the majority of the traits as overall correlation.

Table 4. Simple Spearman correlation coefficients among traits across environments calculated using best linear unbiased predictor means (BLUPs).

| Traits ^a | HD | PH | HeadWt | BM | KA | PERI | KLEN | KWID | SHDW | SSHW | SHGW | BMYLD | HI | TKW | KPS | SPM |
|---------------------|----------|----------|---------|---------|----------|----------|---------|----------|----------|----------|----------|---------|---------|----------|---------|------|
| PH | 0.10 | | | | | | | | | | | | | | | |
| HeadWt | -0.10 | -0.01 | | | | | | | | | | | | | | |
| BM | 0.08 | 0.13 | 0.79*** | | | | | | | | | | | | | |
| KA | -0.37*** | 0.24*** | 0.30*** | 0.13 | | | | | | | | | | | | |
| PERI | -0.25*** | 0.26*** | 0.29*** | 0.16* | 0.93*** | | | | | | | | | | | |
| KLEN | -0.17* | 0.28*** | 0.25*** | 0.17* | 0.81*** | 0.96*** | | | | | | | | | | |
| KWID | -0.43*** | 0.11 | 0.26*** | 0.05 | 0.84*** | 0.59*** | 0.37*** | | | | | | | | | |
| SHDW | -0.18* | 0.17* | 0.51*** | 0.24*** | 0.57*** | 0.50*** | 0.39*** | 0.53*** | | | | | | | | |
| SSHW | -0.07 | 0.30*** | -0.03 | 0.00 | 0.40*** | 0.35*** | 0.28*** | 0.38*** | 0.75*** | | | | | | | |
| SHGW | -0.27*** | 0.20** | 0.47*** | 0.25*** | 0.59*** | 0.49*** | 0.38*** | 0.59*** | 0.92*** | 0.71*** | | | | | | |
| BMYLD | -0.18* | 0.05 | 0.89*** | 0.72*** | 0.36*** | 0.30*** | 0.26*** | 0.34*** | 0.51*** | 0.05 | 0.64*** | | | | | |
| HI | -0.29*** | 0.04 | 0.67*** | 0.26*** | 0.40*** | 0.30*** | 0.22** | 0.44*** | 0.59*** | 0.09 | 0.68*** | 0.76*** | | | | |
| TKW | -0.45*** | 0.20** | 0.30*** | 0.10 | 0.94*** | 0.79*** | 0.63*** | 0.91*** | 0.60*** | 0.43*** | 0.66*** | 0.40*** | 0.47*** | | | |
| KPS | 0.12 | 0.07 | 0.37*** | 0.27*** | -0.18* | -0.17* | -0.17* | -0.14 | 0.61*** | 0.47*** | 0.59*** | 0.42*** | 0.47*** | -0.15* | | |
| SPM | 0.09 | -0.24*** | 0.46*** | 0.53*** | -0.28*** | -0.24*** | -0.17* | -0.28*** | -0.46*** | -0.70*** | -0.44*** | 0.32*** | 0.06 | -0.30*** | -0.21** | |
| YLD | -0.30*** | 0.14* | 0.40*** | 0.16* | 0.23** | 0.10 | 0.04*** | 0.34*** | 0.41*** | 0.10 | 0.54*** | 0.54*** | 0.70*** | 0.33*** | 0.40*** | 0.00 |

^aAbbreviations of Traits HD: Heading Date, PH: Plant Height, SPM: Spikes m⁻², HeadWt: Head Weight, BMYLD: Biomass Grain Yield from 0.5-meter inner row, KA: Kernel Area, PERI: Perimeter, KLEN: Kernel Length, KWID: Kernel Width, TKW: Thousand Kernel Weight, YLD: Yield from combine harvester, HI: Harvest Index, KPS: Kernels Spike⁻¹, SHDW: Single Head Dry Weight, SSHW: Single Stem Head Weight, SHGW: Single Head Grain Weight, BM: Biomass

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

4.3. Genetic Linkage Map Construction

A set of 8,075 SNP markers were used to construct 25 genetic linkage groups (LGs), covering all 21 wheat chromosomes (Table 5). The length of linkage groups (LGs) ranged from 1D (67.7cM) to 4A (394.4 cM) with an average of 193.8 cM. The total length of the genetic map was 4,844.0 cM with an average of marker interval at 0.6. Besides, the physical length of all groups was 14,753.1Mbp, and the average distance between two SNP markers was 1.8 Mbp. Markers distribution by genome was not equal for all genomes. Genome A (3,106) and genome B (3,206) had more SNPs than genome D (1,763). The total length of A, B, and D genomes were 1,851.4, 1,789.5, and 1,203.1 cM, respectively. SNP per cM for A, B, and D genomes were 0.6, 0.6, and 0.7, while SNP per Mbp were 1.7, 2.2, and 3.8, respectively.

Table 5. Distribution of markers across all genomes and all 21 chromosomes (25 Linkage groups) of the recombinant inbred line (RIL) population

| Chromosome | 25LGs | No. Markers | Genetic Distance | Cumulative Genetic cM Matching | CSS Mb Length Based on Markers with Consistent Genetic and Physical Locations | No. of SNPs/cM | No. of SNPs/Mb |
|------------|-------|-------------|------------------|--------------------------------|---|----------------|----------------|
| 1A | 1 | 514 | 240.7 | 240.7 | 593.2 | 0.5 | 1.2 |
| 1B | 2 | 210 | 104.1 | 344.7 | 688.8 | 0.5 | 3.3 |
| 1D | 3 | 147 | 67.7 | 171.7 | 436.2 | 0.5 | 3.0 |
| 2A | 4 | 426 | 229.1 | 296.7 | 770.1 | 0.5 | 1.8 |
| 2B | 5 | 597 | 284.0 | 513.1 | 799.5 | 0.5 | 1.3 |
| 2D | 6 | 412 | 248.2 | 532.2 | 650.5 | 0.6 | 1.6 |
| 3A | 7 | 403 | 226.1 | 474.3 | 743.5 | 0.6 | 1.8 |
| 3B | 8 | 542 | 342.0 | 568.1 | 808.7 | 0.6 | 1.5 |
| 3D | 9 | 146 | 147.5 | 489.4 | 603.7 | 1.0 | 4.1 |
| 4A | 10 | 596 | 394.4 | 541.8 | 744.4 | 0.7 | 1.2 |
| 4B | 11 | 632 | 376.1 | 770.5 | 673.1 | 0.6 | 1.1 |
| 4D | 12 | 157 | 88.1 | 464.2 | 497.5 | 0.6 | 3.2 |
| 5A | 13 | 204 | 196.9 | 285.0 | 680.7 | 1.0 | 3.3 |
| 5B1 | 14 | 496 | 214.2 | 411.1 | 511.7 | 0.4 | 1.0 |
| 5B2 | 15 | 231 | 137.5 | 351.7 | 713.0 | 0.6 | 3.1 |
| 5D1 | 16 | 29 | 44.9 | 182.4 | 338.0 | 1.5 | 11.7 |
| 5D2 | 17 | 82 | 107.7 | 152.6 | 565.7 | 1.3 | 6.9 |
| 6A1 | 18 | 418 | 236.4 | 344.0 | 600.5 | 0.6 | 1.4 |
| 6A2 | 19 | 18 | 10.3 | 246.7 | 18.7 | 0.6 | 1.0 |
| 6B | 20 | 203 | 149.9 | 160.2 | 719.7 | 0.7 | 3.5 |
| 6D1 | 21 | 205 | 115.3 | 265.1 | 463.8 | 0.6 | 2.3 |
| 6D2 | 22 | 89 | 24.9 | 140.2 | 12.8 | 0.3 | 0.1 |
| 7A | 23 | 527 | 317.6 | 342.5 | 736.7 | 0.6 | 1.4 |
| 7B | 24 | 295 | 181.8 | 499.4 | 744.1 | 0.6 | 2.5 |
| 7D | 25 | 496 | 358.9 | 540.7 | 638.5 | 0.7 | 1.3 |
| Total | | 8,075.0 | 4,844.0 | | 14,753.1 | | |
| Genome A | | 3,106.0 | 1,851.4 | | | | |
| Genome B | | 3,206.0 | 1,789.5 | | | | |
| Genome D | | 1,763.0 | 1,203.0 | | | | |
| Average | | 323.0 | 193.8 | 373.2 | 590.1 | 0.7 | 2.6 |

4.4. QTL Identification

4.4.1. QTL for yield and yield components

A total of 21 QTL were detected for yield based on individual and across environment analyses (Table A2). There were three consistent QTL that appeared in at least two individuals and across six environments (Table 6). The QTL on chromosome 1B at 566.9 Mbp explained total yield variations from 8.4 to 14.7% and increased yield up to 23.7 g m⁻² under high yielding environment 20MCG (Figure A1). Its additive effects explained yield variations by 7.3% with favorable alleles from Gallagher. The QTL on chromosome 2D at 36.8 Mbp explained up to 26.9% of total yield variations and increased yield by 37g m⁻² with the allele from Gallagher under low yielding environment 20CS (Figure A1). The QTL on chromosome 7D at 52.3 Mbp explained up to 12.9% of total yield variations but the additive effect only explained 5.3% of that yield variations. It increased yield by 24.2 g m⁻² with an allele from TAM 113 under medium yielding environment 19CS (Figure A1). Twelve QTL were only identified from single environments or across six environments. Six QTL were identified from one individual environment and across all six environments on chromosomes 1A at 11.3 Mbp, 2B at 64.0 and 571.4 Mbp, on 2D at 34.4 Mbp, and on 4A at 75.9 and 483.8 Mbp. Those QTL with a Gallagher allele increased yield by 37.6 g m⁻² in low yielding environment 20CS while those QTL from TAM 113 alleles increased yield by 17.4 g m⁻² in low yielding environment 20CS (Figure A1).

Only two QTL were mapped for kernels spike⁻¹ from individual or across three environment analyses (Table A2). The QTL on chromosome 5A at 12.8 Mbp increased

kernel spike⁻¹ by 0.88 with Gallagher allele in 20EMN while the QTL on 6A at 582.2 Mbp increased kernel spike⁻¹ by 0.94 with TAM 113 allele in 19BSP.

A total of ten QTL were detected for thousand kernel weight based on individual or across environmental analyses (Table A2). No consistent QTL was identified from more than one individual environment. Six QTL were only identified from a single environment or across the three environments. Among these six QTL, Gallagher allele increased thousand kernel weight by 0.81 g under 20EMN, while TAM 113 allele increased thousand kernel weight by 1.14 g in 19BSP. Four QTL were identified from one environment and across all three environments on chromosome 2D at 34.4 and 37.24 Mbp, on 4D at 18.8 Mbp on 6A at 160.6 Mbp. These QTL with a Gallagher allele increased thousand kernel weight by 1.33 g in 19BSP.

For harvest index, eight QTL were identified from individual or across environmental analyses (Table A2). There was no consistent QTL detected from more than one individual environment. Four QTL were only detected from single environment or across the three environments, and all QTL were from TAM 113 allele that increased harvest index by 4% in 21BD. The other four QTL were detected from one environment or across all three environments on chromosome 2D at 106.6, 34.42, and 99.2 Mbp, on chromosome 7D at 52.3 Mbp. Those QTL with a Gallagher allele increased harvest index by 10% in 21BD, whereas QTL from TAM 113 alleles increased harvest index up to 8% in 21BD.

4.4.2. QTL of agronomic traits

A total of ten QTL were detected for heading date based on individual and across environment analyses (Table A2). There were three consistent QTL that appeared in more than two or more individual environments out of six environments (Table 6). The first consistent QTL on chromosome 2B at 57.6 Mbp explained total heading date variation from 3.12 to 11.63% and increased heading day by 1.07 days in 20CS. Its additive effect explained heading date variation by 1.85% with Gallagher allele. The second QTL on chromosome 2D colocalized within *Ppd-D1* locus at 34.4 Mbp and explained total heading date variation from 34.5 to 64.45% that increased heading date by 3.1 when analyzed across six environments. Its additive effect explained heading date variation by 54.05% with *Ppd-D1* sensitive allele from TAM 113. The last QTL on chromosome 7D at 70 Mbp explained up to 15.91% heading date variation, but the additive effect only explained 2.24% of heading date variation. It increased the heading date by 0.96 days with Gallagher allele in 20CS. Four QTL were only found from single environments or across environmental analyses. The Gallagher allele increased heading date up to 1.39 days in 19MCG while TAM 113 allele increased heading date by 0.73 days in 21BD (Table A2). Three QTL were detected from one environment and across environments on chromosomes 2B at 63.9 Mbp, on 6B at 3.5 Mbp, and on 7D at 607.8 Mbp. Those QTL from TAM 113 alleles increased heading date by 3.7 days in 20CS while Gallagher allele increased heading date up to 0.72 days in 19BSP (Table A1).

For plant height, a total of 29 QTL were identified from individual and across environment analyses (Table A1). Only one consistent QTL on 2D at 34.4 Mbp was detected from two individual environments, explained plant height variations from 15.46

to 28.79%, and increased plant height by 3.48 cm with TAM 113 allele in 20MCG. Fifteen QTL were only identified from single environments or across environment analyses. Eight QTL with Gallagher allele increased plant height up to 1.8 cm, while seven QTL from TAM 113 allele increased plant height up to 1.75 cm. Thirteen QTL were detected from one environment and across all six environments on chromosome 1A at 349.3 Mbp, on 2D at 68.8 Mbp, and on 4B at 423.5, 484.6, 505.4, 503.9, 614.9, and 645.9 Mbp, on 6A at 102.01, 174.78, 397.3, 318.03, and 86.4 Mbp. Eleven QTL from Gallagher alleles increased plant height by 2.62 cm in 20CS while four QTL from TAM 113 alleles increased plant height up to 1.54 cm in 20CS.

4.4.3. QTL for Kernel-related traits

A set of 35 QTL regions were associated with kernel-related traits (kernel area, length, width, and perimeter) from individual and across environment analyses. A total of five QTL were identified for kernel area from individual environments or across three environments (Table A2). The only consistent QTL, *Qkarea.tamu.2D.37* detected from two single environments and across three environments, explained total kernel area variation from 14.9 to 32.6% and increased kernel area by 0.29 mm² in 20EMN. Its additive effect explained kernel area variation by 18.72% with a favorable allele from Gallagher. Two QTL detected from single environment or across environmental analyses. One of these QTL with Gallagher allele increased kernel area by 0.19 mm² in 20EMN. The other QTL with a favorable allele from TAM 113 increased kernel area by 0.16 mm² in 19BSP. Two QTL were identified for kernel area from one environment and across all three environments. *Qkarea.tamu.6A.572* has Gallagher allele, and it increased kernel area

up to 0.22 mm² in 19BSP while the *Qkarea.tamu.6D.172* from TAM 113 allele increased kernel area by 0.21 mm² in 20EMN.

For kernel length, seven QTL were identified based on single and across three environment analyses (Table A2). The only consistent QTL, *Qklen.tamu.5B.497* identified from two individual environments and across all environments (Table 6), explained total kernel length variations from 4.9 to 12.4%. Its additive effects explained kernel length variation by 10.68% with a favorable allele from TAM 113 and increased kernel length up to 0.06 mm in 19BSP. Two QTL were detected from one single environment or across all environmental analyses. *Qklen.tamu.7A.639* with Gallagher allele increased kernel area by 0.05 mm across environmental analyses while *Qklen.tamu.2D.41* with TAM 113 allele increased kernel area 0.003 mm in 19BSP. Four QTL were identified from one single environment and across all three environments on chromosome 3D at 585.35 Mbp, on chromosome 4A at 29.33 Mbp, and on 6A at 98.33 and 113.23 Mbp, with favorable alleles from Gallagher that increased kernel length by 0.1 mm with *Qklen.tamu.6A.98* in 20EMN.

A total of 18 QTL for kernel width were mapped from single or across environmental analyses. There was no consistent QTL detected from more than one environment. Fifteen QTL appeared at only one single environment or across three environments (Table A2). Eight QTL from Gallagher increased kernel up to 0.04 mm with *Qkwid.tamu.2D.37* in 19BSP while seven QTL from TAM 113 increased kernel width up to 0.03 mm with *Qkwid.tamu.7D.66* in 19BSP. Three QTL were detected from one single environment and across three environmental analyses on chromosome 2D at 34.42 Mbp and 37.24 Mbp and on 3B at 431.27 Mbp. Those QTL from Gallagher increased kernel

width up to 0.03 mm in 21BD and 20 EMN, while the QTL from TAM 113 allele increased kernel width by 0.02 mm in 21BD.

For kernel perimeter, a total of five QTL were identified from single and across all environmental analyses (Table A2). There was only one consistent QTL on chromosome 6A at 98.3 Mbp detected from 19BSP, 20EMN, and across the three environments, and it explained kernel perimeter variations ranging from 11.07 to 19.74%. The additive effect explained 11.8% of perimeter variations and increased kernel perimeter by 0.18 and 0.19 mm with a favorable allele from Gallagher in 19BSP and 20EMN, respectively. Two QTL were identified from an individual environment and two QTL were detected from one single environment and across the three environmental analyses. *Qperi.tamu.2D.33* increased kernel perimeter by 0.16 mm with Gallagher allele under 19BSP. *Qperi.tamu.5B.497* increased kernel perimeter by 0.15 mm with a TAM 113 allele in 20EMN.

Table 6. Consistent QTL associated with yield and yield-related traits detected from individual and across environments.

| QTL name | Chr. | Trait | Peak Pos (Mbp) | Env. | Threshold | LOD | LOD (A) | LOD (AbyE) | Total PVE Ranges | PVE (A) | PVE (AbyE) | Add | Parental alleles | Position (cM) | QTL CI (cM) | LeftMarker | Alleles | Plei. |
|--------------------------|------|-------|----------------|--|------------|----------------|---------|------------|------------------|---------|------------|-------------------|------------------|---------------|---------------|-----------------|---------|-------|
| <i>Qyld.tamu.1B.567</i> | 1B | YLD | 566.9 | AcrossEnv, 19CS, 20CS | 3.5 - 6.4 | 8.6 - 19.47 | 9.55 | 9.16 | 5.78 - 14.68 | 7.37 | 7.31 | (-21.3) - (-8.38) | Gallagher | 9 | 8.5 - 9.5 | chr1B_566956619 | G/A | |
| <i>Qhd.tamu.2B.58</i> | 2B | HD | 57.61 | AcrossEnv, 21BD, 20CS | 3.5 - 5.8 | 4.91 - 16.11 | 7.18 | 8.92 | 2.16 - 11.63 | 1.85 | 1.27 | (-1.07) - (-0.58) | Gallagher | 101 | 100.5 - 101.5 | chr2B_57657606 | T/A | p |
| <i>Qhd.tamu.2D.34</i> | 2D | HD | 34.42 | AcrossEnv, 19BSP, 19MCG, 20CS, 20MCG, 21BD | 3.5 - 5.8 | 22.30 - 157.95 | 103.9 | 54.06 | 34.50 - 64.65 | 54.05 | 10.6 | 3.15 - 4.86 | TAM 113 | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | p |
| <i>Qyld.tamu.2D.37</i> | 2D | YLD | 36.9 | AcrossEnv, 20MCG, 20CS | 3.59 | 9.13-33.40 | 11.37 | 22.03 | 11.70 - 26.90 | 22.3 | 17.6 | (-9.0) - (-37.0) | Gallagher | 63 | 62.5 - 64.5 | chr2D_36584261 | T/G | p |
| <i>Qph.tamu.2D.34</i> | 2D | PH | 34.42 | 19BSP, 20MCG | 3.47 - 5.8 | 11.35 - 19.85 | - | - | 15.46 - 28.79 | - | - | 2.12 - 3.48 | TAM 113 | 61 | 58.5 - 61.5 | chr2D_32901354 | C/T | p |
| <i>Qkarea.tamu.2D.37</i> | 2D | KA | 36.89 | AcrossEnv, 19BSP, 20EMN | 4.85 | 8.67 - 17.81 | 12.42 | 5.38 | 14.90 - 32.60 | 18.72 | 13.95 | (-0.29) - (-0.17) | Gallagher | 63 | 62.5 - 64.5 | chr2D_36584261 | T/G | p |
| <i>Qklen.tamu.5B.497</i> | 5B | KLEN | 496.6 | AcrossEnv, 19BSP, 20EMN | 3.4 - 4.8 | 3.92 - 8.42 | 6.5 | 1.91 | 4.91 - 12.45 | 10.69 | 1.76 | 0.04 - 0.06 | TAM 113 | 211 | 210.5 - 211.5 | chr5B_489969825 | A/G | |
| <i>Qperi.tamu.6A.98</i> | 6A | PERI | 98.33 | AcrossEnv, 19BSP, 20EMN | 3.4 - 4.8 | 5.43 - 12.38 | 7.31 | 5.07 | 11.07 - 19.74 | 11.86 | 7.88 | (-0.19) - (-0.11) | Gallagher | 77 | 76.5 - 77.5 | chr6A_98982341 | C/T | |
| <i>Qyld.tamu.7D.52</i> | 7D | YLD | 52.31 | AcrossEnv, 19BSP, 19CS | 3.4 - 6.4 | 9.69 - 21.59 | 7.26 | 14.32 | 12.13 - 16.87 | 5.28 | 7.59 | 7.08 - 24.16 | TAM 113 | 66 | 65.5 - 66.5 | chr7D_51735477 | A/G | p |
| <i>Qhd.tamu.7D.70</i> | 7D | HD | 70.03 | AcrossEnv, 19BSP, 20CS | 3.4 - 5.8 | 3.78 - 15.91 | 8.79 | 7.19 | 1.73 - 2.42 | 2.24 | 0.18 | (-0.96) - (-0.57) | Gallagher | 94 | 90.5 - 95.5 | chr7D_63208599 | G/A | |

Chr: Chromosome. Abbreviation of traits: YLD: Grain Yield from combine harvester, HD: Heading Date, PH: Plant Height, KA: Kernel Area, KLEN: Kernel Length, PERI: Perimeter, Env: Environment, AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, CI: Confidence Interval, Plei: Pleiotropic, p: affecting more than one trait.

4.4.4. Pleiotropic QTL

A set of 12 QTL regions were identified as pleiotropic QTL affecting more than one trait (Table 7, Figure 2). The first pleiotropic QTL at 57.6 Mbp on 2B was associated with yield and one of the consistent heading date QTL. It increased yield by 16.56 g m⁻² with TAM 113 allele in 20MCG and increased heading date by 1.73 days with Gallagher allele in 20CS. Another QTL at 63.96 Mbp increased heading date 0.29 day with Gallagher allele across environments and increased grain yield by 14.5 g with TAM 113 allele in 21BD. The pleiotropic QTL at 69.34 Mb on 2B increased yield by 37.04 g m⁻² with a TAM 113 allele in 21BD, increased harvest index by 1 %, and single head grain weight by 0.02 mg head⁻¹ with TAM 113 allele across all environments. The QTL at 76.4 Mbp on 2B increased harvest index by 4 % with a TAM 113 allele in 21BD and increased single head grain weight by 0.06 mg head⁻¹ with a TAM 113 allele in 21BD. A QTL detected on chromosome 2B at 84.91 Mbp was associated with yield and kernel width. TAM 113 allele increased yield 12.96 g m⁻² in 19CS and kernel width 0.01 mm across all environments. For the QTL at 31.5 Mbp on 2D, TAM 113 allele increased plant height by 1.01 cm in 21BD, while Gallagher allele increased single stem head weight 0.1 mg head⁻¹ in 21BD. A QTL on chromosome 2D at 34.43 Mbp was associated with yield, heading date, harvest index, kernel width, kernel diameter, plant height, single head grain weight, and thousand kernel weight. The favorable allele from Gallagher increased yield, harvest index, kernel width, kernel diameter, single head grain weight, and thousand kernel weight by up to 30.4 g m⁻², 1 %, 0.02 mm, 0.07 mm, 0.03 mg head⁻¹, and 1.33 g, respectively. In contrast, TAM 113 allele increased heading date, kernel hardness index, plant height by up to 4.86 days,

5.71 %, and 3.48 cm, respectively. Another QTL at 36.9 Mbp on 2D was associated with multiple traits, including kernel area, yield, kernel width, single kernel weight, biomass grain yield, single head dry weight, and thousand kernel weight. A Gallagher allele increased all these traits by up to 0.17mm, 37.6 g m⁻², 0.04 mm, 1.02 mg, 20 g m⁻², 0.09 mg head⁻¹, and 0.38 g, respectively. Biomass, grain yield, and harvest index were linked to QTL on chromosome 4B at 441.13 Mbp. A TAM 113 allele increased biomass grain yield and harvest index by 13.29 g m⁻² and 1%, respectively. A QTL at 171.52 Mbp on 6D was associated with kernel area and single kernel weight. It increased kernel area by 0.21 mm and single kernel weight by 0.86 mg with TAM 113 alleles. A QTL at 52 Mbp on 7D was linked to harvest index and one of consistent heading date QTL. An allele from TAM 113 increased harvest index by 1% and yield by 24.16 g m⁻². A pleiotropic QTL on 7D at 66.02 Mbp increased kernel diameter by 0.03 mm under 19MCG and yield by 22.21 g m⁻² with a TAM 113 allele in 20MCG.

Table 7. Pleiotropic QTL associated with yield and yield-related traits detected from individual and across environment.

| QTL name | Chr. | Trait | Peak Position (Mbp) | Env. | Thr. | LOD | LOD (A) | PVE | PVE (A) | PVE (AbyE) | Add | Parental alleles | Pos (cM) | QTL CI (cM) | Left Marker | All. | Right Marker | All. | Cons. |
|--------------------------|------|-------|---------------------|-----------------------|-----------|--------------|---------|--------------|---------|------------|-------------------|------------------|----------|---------------|----------------|------|----------------|------|-------|
| <i>Qyld.tamu.2B.58</i> | 2B | YLD | 57.6 | 20MCG | 3.59 | 3.68 | - | 4.34 | - | - | 16.52 | TAM 113 | 101 | 99.5 - 101.4 | chr2B_57657606 | T/A | chr2B_57282937 | T/C | |
| <i>Qhd.tamu.2B.58</i> | 2B | HD | 57.6 | AcrossEnv, 21BD, 20CS | 5.85 | 4.91 - 16.11 | 7.18 | 2.16 - 11.63 | 1.85 | 1.27 | (-1.07) - (-0.58) | Gallagher | 101 | 100.5 - 101.5 | chr2B_57657606 | T/A | chr2B_57282937 | T/C | y |
| <i>Qyld.tamu.2B.64</i> | 2B | YLD | 63.96 | AcrossEnv, 21BD | 3.4 - 6.4 | 6.18 - 7.77 | 3.04 | 4.26 - 13.12 | 2.19 | 2.06 | 4.58 - 14.47 | TAM 133 | 105 | 104.5 - 105.5 | chr2B_63428577 | C/T | chr2B_64952887 | G/A | y? |
| <i>Qhd.tamu.2B.64</i> | 2B | HD | 63.96 | AcrossEnv, 19BSP | 3.4 - 5.8 | 9.16 - 10.22 | 1.81 | 1.05 - 8.12 | 0.44 | 0.6 | (-0.29) - (-0.07) | Gallagher | 105 | 104.5 - 105.5 | chr2B_63428577 | C/T | chr2B_64952887 | G/A | y? |
| <i>Qbmyld.tamu.2B.69</i> | 2B | BMYLD | 69.34 | 21BD | 3.4 | 4.24 | 4.50 | 10.34 | - | - | 37.04 | TAM 133 | 108 | 107.5 - 110.5 | chr2B_68426788 | G/A | chr2B_89540772 | C/T | |
| <i>Qhi.tamu.2B.69</i> | 2B | HI | 69.34 | AcrossEnv | 4.9 | 6.19 | 5.40 | 5.19 | 1.97 | 3.21 | 0.01 | TAM 133 | 108 | 107.5 - 110.5 | chr2B_68426788 | G/A | chr2B_89540772 | C/T | |
| <i>Qshgw.tamu.2B.69</i> | 2B | SHGW | 69.34 | AcrossEnv | 4.7 | 5.12 | 4.50 | 12.88 | 5.65 | 7.22 | 0.02 | TAM 133 | 108 | 107.5 - 110.5 | chr2B_68426788 | G/A | chr2B_89540772 | C/T | |
| <i>Qhi.tamu.2B.76</i> | 2B | HI | 76.4 | 21BD | 3.4 | 6.09 | - | 1.80 | - | - | 0.04 | TAM 133 | 109 | 107.5 - 110.5 | chr2B_68426788 | G/A | chr2B_89540772 | C/T | |
| <i>Qshgw.tamu.2B.76</i> | 2B | SHGW | 76.4 | 21BD | 3.5 | 4.86 | - | 10.68 | - | - | 0.06 | TAM 133 | 109 | 107.5 - 110.5 | chr2B_68426788 | G/A | chr2B_89540772 | C/T | |
| <i>Qyld.tamu.2B.85</i> | 2B | YLD | 84.91 | 19CS | 3.6 | 3.67 | - | 3.46 | - | - | 12.96 | TAM 133 | 113 | 112.5 - 114.5 | chr2B_76076511 | #N/A | chr2B_98844071 | T/C | |
| <i>Qkwid.tamu.2B.85</i> | 2B | KWID | 84.91 | AcrossEnv | 4.8 | 4.29 | 3.40 | 3.94 | 2.67 | 1.25 | 0.01 | TAM 133 | 113 | 112.5 - 114.5 | chr2B_76076511 | #N/A | chr2B_98844071 | T/C | |
| <i>Qph.tamu.2D.31</i> | 2D | PH | 31.5 | 21BD | 3.4 | 6.11 | - | 9.52 | - | - | 1.01 | TAM 133 | 58 | 57.5 - 59.5 | chr2D_31103643 | A/G | chr2D_32901354 | C/T | |
| <i>Qsshw.tamu.2D.31</i> | 2D | SSHW | 31.5 | 21BD | 3.5 | 13.84 | 5.14 | 26.43 | - | - | -0.10 | Gallagher | 58 | 57.5 - 59.5 | chr2D_31103643 | A/G | chr2D_32901354 | C/T | |

Chr: Chromosome, Abbreviation of traits: YLD: Grain Yield from combine harvester, HD: Heading Date, BMYLD: Biomass Grain Yield from 0.5-meter inner row, HI: Harvest Index, SHGW: Single Head Grain Weight, KWID: Kernel Width, PH: Plant Height, SSSH: Single Stem Head Weight, DIAM: Kernel Diameter, KHI: Kernel Hardness Index, TKW: Thousand Kernel Weight, KA: Kernel Area, SHDW: Single Head Dry Weight, SKW: Single Kernel weight, Env: Environment, AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, Thr: threshold, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, CI: Confidence Interval, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment.

Table 7. continued

| QTL name | Chr. | Trait | Peak Position (Mbp) | Env. | Thr. | LOD | LOD (A) | PVE | PVE (A) | PVE (AbyE) | Add | Parental alleles | Pos (cM) | QTL CI (cM) | Left Marker | All. | Right Marker | All. | Cons. |
|--------------------------|------|-------|---------------------|--|-----------|---------------|---------|---------------|---------|------------|-------------------|------------------|----------|-------------|----------------|------|----------------|------|-------|
| <i>Qsshw.tamu.2D.31</i> | 2D | SSHW | 31.5 | AcrossEnv | 4.8 | 14.0 | - | 3.04 | 1.31 | 1.72 | -0.04 | Gallagher | 58 | 54.5 - 59.5 | chr2D_31103643 | A/G | chr2D_32901354 | C/T | |
| <i>Qyld.tamu.2D.34</i> | 2D | YLD | 34.43 | AcrossEnv, 19BSP | 3.6 - 6.4 | 17.5 - 21.12 | 9.21 | 17.57 - 21.1 | 6.90 | 10.67 | (-30.4) - (-8.11) | Gallagher | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y? |
| <i>Qhd.tamu.2D.34</i> | 2D | HD | 34.43 | AcrossEnv, 19BSP, 19MCG, 20CS, 20MCG, 21BD | 3.4 - 5.8 | 22.3 - 157.95 | 103.90 | 34.50 - 64.65 | 54.05 | 10.6 | 3.15 - 4.86 | TAM 133 | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y |
| <i>Qhi.tamu.2D.34</i> | 2D | HI | 34.43 | AcrossEnv, 19BSP | 3.4 - 4.9 | 10.96 - 15.78 | 2.19 | 0.80 - 21.81 | 0.78 | 0.02 | 0 | Gallagher | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y? |
| <i>Qkwid.tamu.2D.34</i> | 2D | KWID | 34.43 | AcrossEnv, 21BD | 3.4 - 4.8 | 5.17 - 5.19 | - | 1.78 - 8.62 | 0.68 | 1.09 | (-0.02) - (-0.01) | Gallagher | 61 | 59.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y? |
| <i>Qdiam.tamu.2D.34</i> | 2D | DIAM | 34.43 | 20MCG | 3.5 | 23.51 | - | 35.05 | | | -0.07 | Gallagher | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | |
| <i>Qkhi.tamu.2D.34</i> | 2D | KHI | 34.43 | 20MCG | 3.5 | 23.12 | - | 29.85 | - | - | 5.71 | TAM 133 | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | |
| <i>Qph.tamu.2D.34</i> | 2D | PH | 34.43 | 19BSP, 20MCG | 3.4 | 11.35 - 19.85 | - | 15.46 - 28.79 | - | - | 2.12 - 3.48 | TAM 133 | 61 | 58.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y |
| <i>Qshgw.tamu.2D.34</i> | 2D | SHGW | 34.43 | AcrossEnv, 19BSP | 3.5 - 4.7 | 5.64 - 7.68 | 4.70 | 6.45 - 10.55 | 5.83 | 0.62 | (-0.03) - (-0.02) | Gallagher | 61 | 60.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y? |
| <i>Qtkw.tamu.2D.34</i> | 2D | TKW | 34.43 | AcrossEnv, 19BSP | 3.4 - 4.6 | 12.18 - 13.52 | 5.40 | 9.12 - 17.46 | 7.15 | 10.28 | (-1.33) - (-0.27) | TAM 133 | 61 | 59.5 - 61.5 | chr2D_32901354 | C/T | chr2D_34562299 | T/C | y? |
| <i>Qkarea.tamu.2D.37</i> | 2D | KA | 36.9 | AcrossEnv, 19BSP, 20EMN | 4.8 | 8.67 - 17.81 | 12.42 | 14.90 - 32.60 | 18.72 | 13.95 | (-0.29) - (-0.17) | Gallagher | 63 | 62.5 - 64.5 | chr2D_36584261 | T/G | chr2D_37211804 | A/G | y |
| <i>Qyld.tamu.2D.37</i> | 2D | YLD | 36.9 | AcrossEnv, 20CS | 3.5 - 6.4 | 30.09 - 33.4 | 11.37 | 26.14 - 26.99 | 8.53 | 17.61 | (-37.6) - (-9.00) | Gallagher | 63 | 62.5 - 63.5 | chr2D_36584261 | T/G | chr2D_37211804 | A/G | y? |
| <i>Qkwid.tamu.2D.37</i> | 2D | KWID | 36.9 | 19BSP | 4.7 | 12.48 | - | 17.49 | - | - | -0.04 | Gallagher | 63 | 62.5 - 64.5 | chr2D_36584261 | T/G | chr2D_37211804 | A/G | |

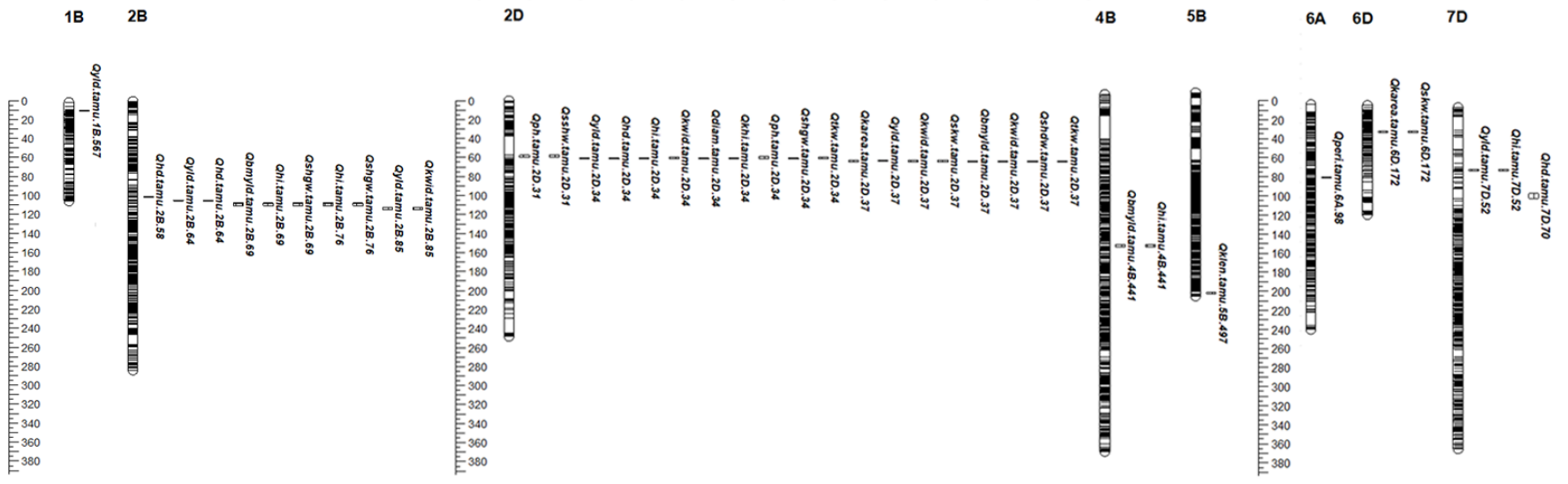
Chr: Chromosome, Abbreviation of traits; YLD: Grain Yield from combine harvester, HD: Heading Date, BMYLD: Biomass Grain Yield from 0.5-meter inner row, HI: Harvest Index, SHGW: Single Head Grain Weight, KWID: Kernel Width, PH: Plant Height, SSHW: Single Stem Head Weight, DIAM: Kernel Diameter, KHI: Kernel Hardness Index, TKW: Thousand Kernel Weight, KA: Kernel Area, SHDW: Single Head Dry Weight, SKW: Single Kernel weight, Env: Environment, AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, Thr: threshold, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, CI: Confidence Interval, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment.

Table 7. continued

| QTL name | Chr. | Trait | Peak Position (Mbp) | Env. | Thr. | LOD | LOD (A) | PVE | PVE (A) | PVE (AbyE) | Add | Parental alleles | Pos (cM) | QTL CI (cM) | Left Marker | All. | Right Marker | All. | Cons. |
|---------------------------|------|-------|---------------------|------------------------|-----------|---------------|---------|---------------|---------|------------|---------------------|------------------|----------|---------------|-----------------|------|-----------------|------|-------|
| <i>Qskw.tamu.2D.37</i> | 2D | SKW | 36.9 | 20MCG | 3.4 | 8.41 | - | 12.56 | - | - | -1.02 | Gallagher | 63 | 62.5 - 64.5 | chr2D_36584261 | T/G | chr2D_37211804 | A/G | |
| <i>Qbmyld.tamu.2D.37</i> | 2D | BYLD | 37.25 | AcrossEnv, 19BSP | 4.8 | 4.96 - 6.35 | 2.40 | 2.35 - 8.53 | 1.90 | 0.45 | (-20.00) - (-12.43) | Gallagher | 64 | 63.5 - 64.5 | chr2D_37211804 | A/G | chr2D_37257093 | A/G | y? |
| <i>Qkwid.tamu.2D.37</i> | 2D | KWID | 37.25 | AcrossEnv, 20EMN | .35 - 4.8 | 5.30 - 17.37 | 14.00 | 12.68 - 18.20 | 11.69 | 6.5 | (-0.03) - (-0.02) | Gallagher | 64 | 63.5 - 64.5 | chr2D_37211804 | A/G | chr2D_37257093 | A/G | y? |
| <i>Qshdw.tamu.2D.37</i> | 2D | SHDW | 37.25 | AcrossEnv, 21BD | 3.5 - 4.9 | 10.33 - 11.56 | 10.41 | 22.16 - 23.95 | 12.40 | 11.5 | (-0.09) - (-0.04) | Gallagher | 64 | 63.5 - 64.5 | chr2D_37211804 | A/G | chr2D_37257093 | A/G | y? |
| <i>Qtkw.tamu.2D.37</i> | 2D | TKW | 37.25 | AcrossEnv, 20EMN | 3.5 - 4.6 | 5.62 - 6.86 | 3.30 | 8.41 - 12.11 | 4.20 | 4.9 | (-0.96) - 21.43 | Gallagher | 64 | 63.5 - 64.5 | chr2D_37211804 | A/G | chr2D_37257093 | A/G | y? |
| <i>Qbmyld.tamu.4B.441</i> | 4B | BYLD | 441.13 | AcrossEnv | 4.8 | 10.65 | 2.79 | 3.68 | 2.18 | 1.5 | 13.29 | TAM 133 | 160 | 158.5 - 160.5 | chr4B_449765851 | G/A | chr4B_414396615 | G/A | |
| <i>Qhi.tamu.4B.441</i> | 4B | HI | 441.13 | AcrossEnv | 4.9 | 9.75 | 0.80 | 0.46 | 0.31 | 0.15 | 0.01 | TAM 133 | 160 | 158.5 - 160.5 | chr4B_449765851 | G/A | chr4B_414396615 | G/A | |
| <i>Qkarea.tamu.6D.172</i> | 6D | KA | 171.52 | AcrossEnv, 20EMN | 3.5 - 4.8 | 4.71 - 5.27 | 3.77 | 8.24 - 9.97 | 5.46 | 4.5 | 0.09 - 0.21 | TAM 133 | 28 | 27.5 - 28.5 | chr6D_172603833 | C/A | chr6D_170544597 | C/T | y? |
| <i>Qskw.tamu.6D.172</i> | 6D | SKW | 171.52 | 20MCG | 3.4 | 6.14 | - | 8.96 | - | - | 0.86 | TAM 133 | 28 | 27.5 - 28.5 | chr6D_172603833 | C/A | chr6D_170544597 | C/T | |
| <i>Qyld.tamu.7D.52</i> | 7D | YLD | 52.32 | AcrossEnv, 19BSP, 19CS | 3.4 - 6.4 | 9.69 - 21.59 | 7.2 | 12.13 - 16.87 | 5.28 | 7.59 | 7.08 - 24.16 | TAM 133 | 66 | 65.5 - 66.5 | chr7D_51735477 | A/G | chr7D_52399452 | G/A | y |
| <i>Qhi.tamu.7D.52</i> | 7D | HI | 52.32 | AcrossEnv, 19BSP | 3.4 - 4.9 | 4.89 - 6.47 | 2.09 | 0.90 - 9.81 | 0.71 | 0.2 | 0.01 | TAM 133 | 66 | 65.5 - 66.5 | chr7D_51735477 | A/G | chr7D_52399452 | G/A | y? |
| <i>Qdiam.tamu.7D.66</i> | 7D | DIAM | 66.02 | 19MCG | 3.56 | 5.5 | - | 7.60 | - | - | 0.03 | TAM 113 | 89 | 86.5 - 95.5 | chr7D_63208599 | G/A | chr7D_71584239 | A/G | |
| <i>Qyld.tamu.7D.66</i> | 7D | YLD | 66.02 | 20MCG | 3.59 | 5.6 | - | 7.80 | - | - | 22.20 | TAM 113 | 89 | 84.5 - 94.5 | chr7D_63208599 | G/A | chr7D_71584239 | A/G | |

Chr: Chromosome, Abbreviation of traits: YLD: Grain Yield from combine harvester, HD: Heading Date, BMYLD: Biomass Grain Yield from 0.5-meter inner row, HI: Harvest Index, SHGW: Single Head Grain Weight, KWID: Kernel Width, PH: Plant Height, SSHW: Single Stem Head Weight, DIAM: Kernel Diameter, KHI: Kernel Hardness Index, TKW: Thousand Kernel Weight, KA: Kernel Area, SHDW: Single Head Dry Weight, SKW: Single Kernel weight, Env: Environment, AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, Thr: threshold, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, CI: Confidence Interval, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment.

Figure 2. Consistent and pleiotropic QTL detected from single and multi-environment analysis.



4.4.5. Epistasis, epistasis-by-environment, and additive-by-environment interactions

Epistatic interactions with total LOD > 5 were summarized for yield and yield-related traits collected from multiple Texas locations (Table A3). For yield, there were 109 epistatic interactions with overall LOD scores > 5, but none of them had LOD > 10. Four previously identified yield QTL from individual and across environmental additive analyses were also identified across environmental epistasis analysis. The first QTL, *Qyld.tamu.2B.64* had epistatic interaction with *Qyld.tamu.5B.1*. Their epistasis interactions increased yield by 4.56 g m⁻² with favorable alleles from Gallagher and the epistasis-by-environment interaction increased grain yield by 4.59 g m⁻² in 20CS. The QTL *Qyld.tamu.2D.34* interacted with *Qyld.tamu.5B.21*, increased grain yield by 4.17 g m⁻² with favorable alleles from Gallagher, and epistasis-by-environment interaction increased grain yield by 8.59 g m⁻² with favorable alleles from TAM113 in 19BSP. The third major QTL *Qyld.tamu.6D.10* had epistatic interactions with two QTL, *Qyld.tamu.4B.11* and *Qyld.tamu.4B.13*, and increased yield by 5.1 and 3.62 g m⁻² with favorable alleles from TAM 113 and Gallagher, respectively. Epistasis-by-environment interaction of *Qyld.tamu.6D.10* and *Qyld.tamu.4B.11* increased grain yield 8.0 g m⁻² with TAM 113 allele under 19CS while the epistasis-by-environment interaction of *Qyld.tamu.6D.10* and *Qyld.tamu.4B.13* increased grain yield 8.13 g m⁻² with Gallagher allele in 19CS. The fourth major QTL *Qyld.tamu.7D.66* interacting with *Qyld.tamu.6A.596*, had an epistatic interaction that increased grain yield by 6.36 g m⁻² with TAM 113 allele. Their epistasis-by-environment effect increased yield by 4.18 g m⁻² in 19CS.

For plant height, a total of 212 epistatic interactions with total LOD scores > 5 were identified, and only two had overall LOD scores > 10, but none of them had a major effect. There were three plant height QTL associated with epistatic interactions. The first QTL *Qph.tamu.3B.564* interacted with *Qph.tamu.3B.625*. Their epistasis interaction increased plant height by 1.07 cm with the favorable allele from TAM 113 while epistasis-by-environment interaction increased plant height by 1.69 cm with TAM 113 allele in 19CS. The second QTL *Qph.tamu.2D.30* interacted with *Qph.tamu.6A.596*, and their epistasis interactions increased plant height by 0.2 cm with the favorable allele from Gallagher while the epistasis-by-environment interaction increased plant height by 0.78 cm under 19CS. *Qph.tamu.2D.30* also interacted with *Qph.tamu.6D.458*, and its epistasis interaction increased plant height by 0.39 cm with a TAM 113 allele while the epistasis-by-environment interaction increased plant height up to 0.64 cm with a Gallagher allele in 20MCG. The last QTL, *Qph.tamu.4B.646* interacted with *Qph.tam.7D.33*. Their epistatic interaction increased plant height by 0.42 cm with a Gallagher allele, and their epistatic-by-environment interaction increased higher plant height by up to 0.43 cm with a TAM 113 allele in 20EMN.

A total of 251 epistatic interactions were detected with total LOD scores > 5 for heading date, and 22 had total LOD score >10. There were four QTL involved with these interactions. One QTL *Qhd.tamu.1A.566* interacted with *Qhd.tam.4A.714*. Their epistasis increased heading date by 0.46 days with a Gallagher allele, whereas epistasis-by-environment interaction increased heading date by up to 0.71 days with a Gallagher allele in 19CS. *Qhd.tamu.7A.709* interacted with two QTL, *Qhd.tamu.3D.603* and

Qhd.tamu.1B.620. Their epistatic interactions increased heading date by 0.61 and 0.77 days with the Gallagher allele. Epistasis-by-environment interactions increased heading date by 0.34 and 0.38 days with TAM 113 allele in 20EMN and 19CS, respectively. *Qhd.tamu.7D.608* interacted with *Qhd.tamu.6B.660* and their epistasis increased heading date by 0.51 days with a TAM 113 allele while epistasis-by-environment interactions increased heading date by 0.43 days with a Gallagher allele in 21BD. The last QTL, *Qhd.tamu.2D.34* interacted with *Qhd.tamu.2B.106* and their epistasis increased heading date by 0.67 days with a Gallagher allele, while epistasis-by-environment interactions increased heading date up to 0.52 with a TAM 113 allele. No other major QTL showed epistatic interactions for rest of the traits.

Figure 3. Epistatic interactions between QTL associated with yield and yield-related traits at LOD value > 5.0 and LOD value > 10.0.

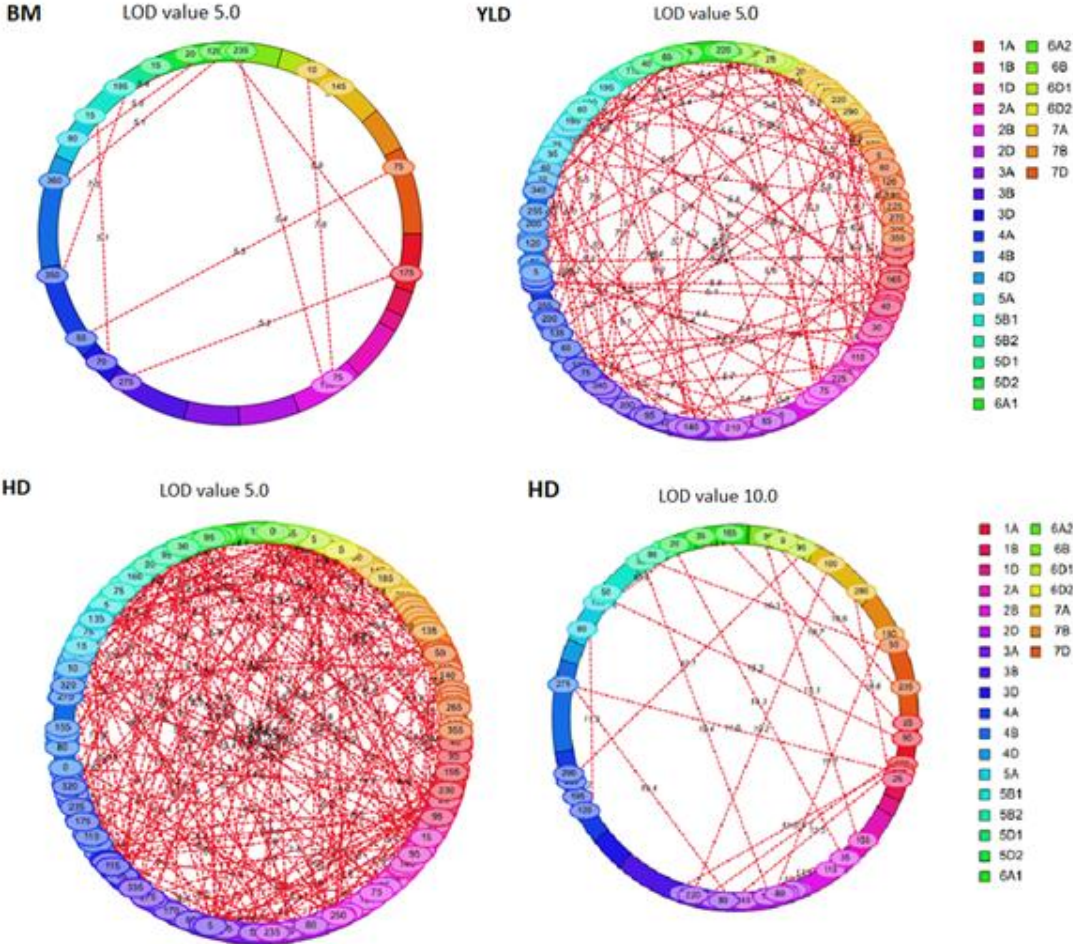
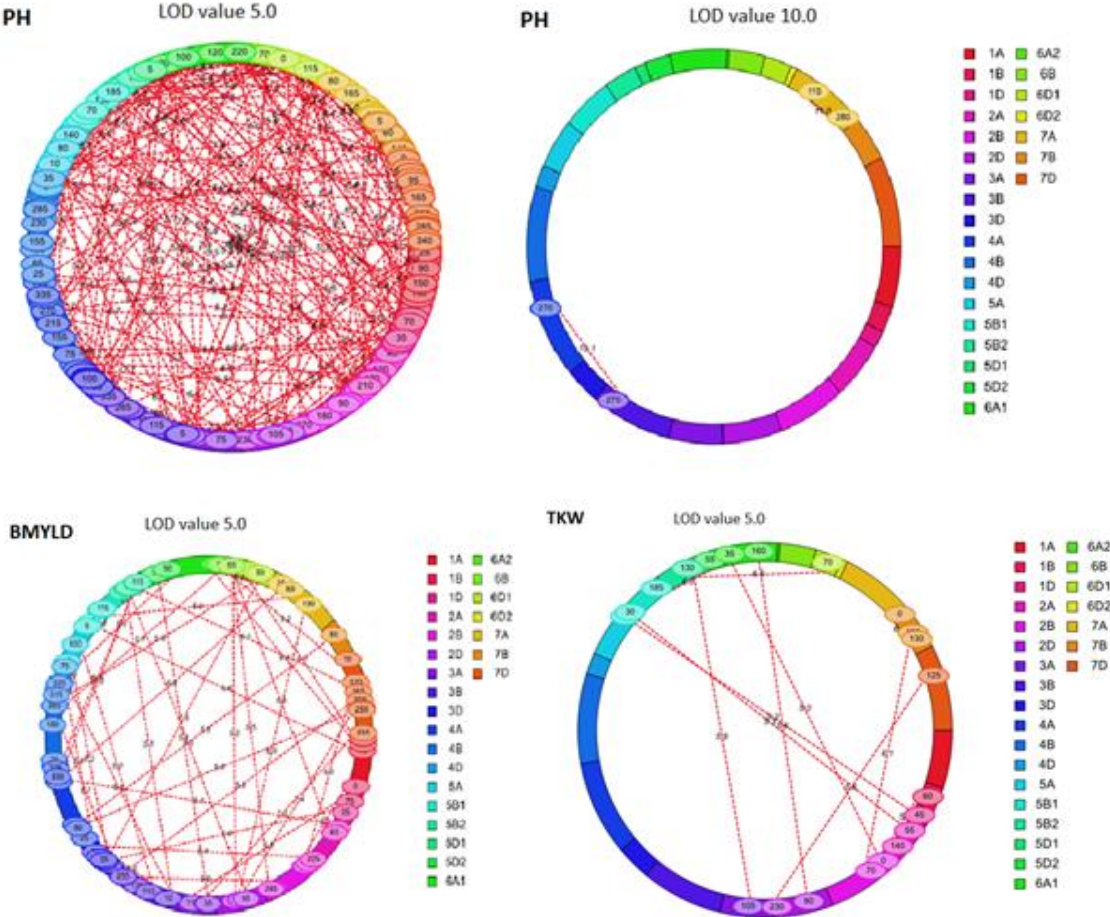


Figure 3. Continued



5. DISCUSSION

Improving yield is the primary objective of all wheat breeding programs. Understanding genetic bases of high yielding ability and components is critical in accelerating genetic gain in wheat improvement.

BLUP values were used to conduct statistical analyses. Combined ANOVA results indicate that the genotypic variation was higher than GbyE and environmental variances for all traits except biomass, grain yield, and head weight. Environmental and genotype-by-environmental interaction were also highly significant for most traits in our study. Genotypic variation and GbyE interaction for seed-related traits were highly significant ($P < 0.001$), but environmental variation was not significant, indicating that the contribution of genetic effect is higher than the environmental effect. Genotypic variation for harvest index was significant ($P < 0.01$), whereas GbyE and environmental variations were not significant for the same traits (Table 3).

Heritability is described as the ratio of genotypic variation over phenotypic variation, and it is a crucial parameter affecting selection response (Piepho & Mohring, 2007). The broad sense heritability (H^2) varied from 0.02 to 0.9 for all traits (Table 3). Heritability values for agronomic and kernel-related traits were over 0.9, indicating that genotypic factors played a significant role in the phenotypic expression of these traits. Xin, Zhu, Wei, Han, and Zhao (2020) also reported high heritability estimates for kernel-related traits. However, broad sense heritability for yield and yield-related traits ranged

from low to high, suggesting that some traits could be affected by environmental factors, as it was reported by Garcia et al. (2019) and Al-Tabbal & Al-Fraihat, (2012).

Simple Pearson correlation coefficients among traits based on best linear unbiased estimates (BLUE) calculated across environments indicated that grain yield showed a negative correlation with heading date, consistent with what has been reported by Ali, Zhang, Rashed, Wang, and Zhang (2020). Gonfa and Tesfaye (2016) have reported different correlations of biomass and grain yield at different irrigation conditions. Similarly, we observed a significant positive correlation between grain yield and biomass under non-irrigated conditions but no correlation under irrigated conditions.

In this research, 156 QTL were mapped on all chromosomes except 1D and 3A (Table A2). Ten QTL were identified in more than two individual environments, and twelve genomic regions affect two or more traits. Several QTL detected for plant height in this study overlapped with previous reports, and some were located near previously identified QTL regions (Semang et al. 2021; Yang et al., 2020; Cao, Xu, Hanif, Xia, & He, 2020; Ma, Zhang, Li, Zou, & Li, 2019). Plant height QTL was found at 614.9 Mbp on chromosome 4B, explained 5.48 to 7.18% of the phenotypic variation. Semang et al. (2021) reported a plant height QTL located at a similar region at 611.1 Mbp on 4B, explaining 16% of the phenotypic variation. Another plant height QTL on chromosome 4B, *Qph.tamu.4B.485*, was also located very close to QTL detected by Semagn et al. (2021) on 4B at 474.9 Mbp.

The yield QTL on 1B at 571.4 Mbp was very close to previously reported QTL on 1B at 573 Mbp (Smith et al., 2021). Additionally, two more yield QTL were detected on

6D at 10.3 Mbp and 7B at 4.2 Mbp. Similarly, Yang et al. (2020) found two yield QTL on 6D and 7B around 10 Mbp away from our results. Recently, Semang et al. (2021) also reported the same yield QTL on 6D at 15.6 Mbp. Rabbi et al. (2021) also reported yield QTL near 7 Mbp at 6D. One consistent yield QTL was identified at 58 Mbp on 2B with 11.6 phenotypic variations. Semagn et al. (2021) found a similar genetic region between 55-62 Mbp on the same chromosome.

Ten genomic regions for heading date were detected on chromosomes 1A, 2B, 2D, 6B, 7A, and 7D. One consistent heading date QTL was mapped at 70 Mbp on 7D. Isham, Wang, Zhao, Wheeler, and Klassen (2021) mapped two heading date QTL at 68 Mbp and 71 Mbp on 7D, and this region could be co-localized with major flowering time gene *FT-D1*. Furthermore, another heading date QTL was detected on 7D in this study (*Qhd.tamu.7D.65*), and this genomic region is a few Mbp away from one major vernalization gene *Vrn3- on chromosome 7D* (Cao, Xu, Hanif, Xia, & He, 2020)

Liu et al. (2020) reported several thousand kernel weight QTL, one of which, (*qTgw.nwipb-6AL*), was mapped at 573 Mbp on 6A, which is also found in our present study. Moreover, another QTL was mapped near 28 Mbp on 2D, 7 Mb far away from our findings.

Multiple QTL were detected for seed related traits, some of them matching with previous reports; For instance, one kernel width QTL was mapped at 34 Mbp on 2D, which is close to a previously reported QTL region at 32 Mbp on the same chromosome (Ma, Zhang, Li, Zou, & Li, 2019). They also mapped kernel length QTL close to 48 Mbp on 2D, and we detected the same QTL 7 Mbp away from his findings. One kernel length QTL on 7A at

638.6 was close to a previously reported QTL region on 7A between 624 and 639 Mb (Cao, Xu, Hanif, Xia, & He, 2020).

Twelve pleiotropic QTL were identified from individual and across environmental analyses. One cluster QTL region was located between 51.2 to 70 Mbp on 7D, affecting multiple yield and yield-related traits. Similarly, Yan et al. (2020) also reported that the physical interval between 64 to 68 Mb was associated with yield and kernel-related traits using the RIL population derived from TAM 112 and TAM 111 hard red winter wheat.

There was two QTL cluster on 2D, one of which was located at 34.4 Mbp on 2D, affecting yield and kernel-related traits. This QTL region was co-localized with one of the photoperiod gene *Ppd-D1* that has pleiotropic effects on heading date, plant height, grain yield, thousand kernel weight, kernel width, and kernel diameter. (Basavaraddi, Savin, Wingen, Bencivenga, & Przewieslik-Allen, 2021; Vitale, Fania, Esposito, Pecorella, & Pecchioni, 2021). Another cluster QTL was located at 37 Mbp on 2D and was associated with thousand kernel weight, kernel width, biomass grain yield, and yield. Those six traits were significantly correlated to each other (Table 4). This suggests that traits with higher correlation could be under similar genotypic controls. Cluster QTL region can be used to design markers for MAS selection to understand the genetic basis of targeted traits (Lv et al., 2016).

Breeding progress is made through accumulating incremental gains for yield and related traits while maintaining quality, adaptation traits, and tolerance to biotic and abiotic stresses. This process utilizes the additive genetic variance for fixing these yield-associated traits.

The ICIM-EPI approach was performed to reveal genotype-by-environment and epistatic interactions between traits. Some QTL were involved with epistatic interactions. For example, four yield QTL (*Qyld.tamu.2B.64*, *Qyld.tamu.2D.34*, *Qyld.tamu.6D.10* and *Qyld.tamu.7D.66*) involved in epistatic interactions and additive-by-additive interactions increased grain yield by 3.79, 6.23, 5.1 and 6.36 g m⁻². In some environments, epistasis-by-environment interaction had higher grain yield increment than epistasis *per se*.

6. CONCLUSION

This research used a population of 191 recombinant inbred lines (RIL) derived from a cross between TAM 113 and Gallagher hard red winter wheat to evaluate yield, yield components, and kernel traits in three different environments in Texas. A set of 8075 SNP markers covering all 21 Chromosomes was used to construct a high-density gene linkage map. We found a total of 156 QTL associated with 20 different traits, of which ten QTL were consistent in at least more than two individual environments, and 12 genomic regions had pleiotropic effect affecting more than one trait. Among those pleiotropic and consistent QTL, four were common at 57.61 on 2B, 34.3 Mb and 36.9 on 2D, 69.9 Mb on 2B, and 52.3 7D.

One QTL region at 2D overlapped with one of the significant photoperiod gene *Ppd-D1*. Another QTL region on 7D could be sharing the same genetic region with flowering time gene *FT-D1*. Among consistent or pleiotropic QTL, three yield, three heading date, two kernel width, one kernel length, one perimeter, one kernel area, one kernel length, one biomass grain yield, one single head grain weight, and one single head dry weight QTL had larger additive than additive-by-environment variation (Table 6, Table 7), that can be used in wheat breeding.

7. REFERENCES

- Agrawal, P. K., & Shrivastava, R. (2014). Molecular Markers. *In Advances in Biotechnology* (pp. 25-39).
- Ahmar, S., Gill, R. A., Jung, K.-H., Faheem, A., Qasim, M. U., Mubeen, M., & Zhou, W. (2020). Conventional and Molecular Techniques from Simple Breeding to Speed Breeding in Crop Plants: Recent Advances and Future Outlook. *International Journal of Molecular Sciences*, 21(7), 2590.
doi:10.3390/ijms21072590
- Ahrends, H.E., W. Eugster, T. Gaiser, V. Rueda-Ayala, H. Hüging, F. Ewert...S. Siebert. (2018). Genetic yield gains of winter wheat in germany over more than 100 years (1895–2007) under contrasting fertilizer applications. *Environmental Research Letters* 13. doi:10.1088/1748-9326/aade12.
- Al-Samarai, F. R., & Al-Kazaz, A. A. (2015). Molecular Markers: an Introduction and Applications. *European Journal of Molecular Biotechnology*, 9(3), 118-130.
doi:10.13187/ejmb.2015.9.118
- Al-Tabbal, J.A. and Al-Fraihat, A.H. (2012). Genetic variation heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, 4:193-210
- Ali, M., Y. Zhang, A. Rasheed, J. Wang&L. Zhang. (2020). Genomic prediction for grain yield and yield-related traits in chinese winter wheat. *International Journal of Molecular Sciences*, 21. doi:10.3390/ijms21041342.
- Alvarado, G., Rodríguez, F. M., Pacheco, A., Burgueño, J., Crossa, J., Vargas, M., . . . Lopez-Cruz, M. A. (2020). META-R: A software to analyze data from multi-environment plant breeding trials. *The Crop Journal*, 8(5), 745-756.
doi:https://doi.org/10.1016/j.cj.2020.03.010
- Assanga, S.O., M. Fuentealba, G. Zhang, C. Tan, S. Dhakal, J.C. Rudd, . . . S. Liu. (2017). Mapping of quantitative trait loci for grain yield and its components in a us popular winter wheat tam 111 using 90k snps. *PLOS ONE* 12: e0189669.
doi:10.1371/journal.pone.0189669.

- Azadi, A., M. Mardi, E.M. Hervan, S.A. Mohammadi, F. Moradi, M.T. Tabatabaee, . . . G. Mohammadi-Nejad. (2015). Qtl mapping of yield and yield components under normal and salt-stress conditions in bread wheat (*triticum aestivum* l.). *Plant Molecular Biology Reporter* 33: 102-120. doi:10.1007/s11105-014-0726-0.
- Bailey-Serres, J., Parker, J. E., Ainsworth, E. A., Oldroyd, G. E. D., & Schroeder, J. I. (2019). Genetic strategies for improving crop yields. *Nature*, 575(7781), 109-118. doi:10.1038/s41586-019-1679-0
- Basavaraddi, P.A., R. Savin, L.U. Wingen, S. Bencivenga, A.M. Przewieslik-Allen, S. Griffiths...G.A. Slafer. (2021). Interactions between two qtls for time to anthesis on spike development and fertility in wheat. *Scientific Reports*, 11: 2451. doi:10.1038/s41598-021-81857-6.
- Bindraban, P.S., K.D. Sayre&E. Solis-Moya. (1998). Identifying factors that determine kernel number in wheat. *Field Crops Research* 58: 223-234. doi:https://doi.org/10.1016/S0378-4290(98)00097-5.
- Cao, S., D. Xu, M. Hanif, X. Xia&Z. He. (2020). Genetic architecture underpinning yield component traits in wheat. *Theoretical and Applied Genetics*, 133: 1811-1823. doi:10.1007/s00122-020-03562-8.
- Chai, S., Q. Yao, X. Zhang, X. Xiao, X. Fan, J. Zeng, . . . Y. Wang. (2021). The semi-dwarfing gene *rht-dp* from dwarf polish wheat (*triticum polonicum* l.) is the "green revolution" gene *rht-b1b*. *BMC Genomics*, 22: 63. doi:10.1186/s12864-021-07367-x.
- Chen, W., D. Sun, R. Li, S. Wang, Y. Shi, W. Zhang...R. Jing. (2020). Mining the stable quantitative trait loci for agronomic traits in wheat (*triticum aestivum* l.) based on an introgression line population. *BMC Plant Biology*, 20: 275. doi:10.1186/s12870-020-02488-z.
- Chen, Z., X. Cheng, L. Chai, Z. Wang, D. Du, Z. Wang, . . . Z. Ni. (2020). Pleiotropic qtl influencing spikelet number and heading date in common wheat (*triticum aestivum* l.). *Theoretical and Applied Genetics*, 133: 1825-1838. doi:10.1007/s00122-020-03556-6.

- Cheng, R., Z. Kong, L. Zhang, Q. Xie, H. Jia, D. Yu, . . . Z. Ma. (2017). Mapping qtls controlling kernel dimensions in a wheat inter-varietal rIL mapping population. *Theoretical and Applied Genetics*, 130: 1405-1414. doi:10.1007/s00122-017-2896-2.
- Cui, F., A. Ding, J. Li, C. Zhao, X. Li, D. Feng, . . . H. Wang. (2011). Wheat kernel dimensions: How do they contribute to kernel weight at an individual qtl level? *Journal of Genetics*, 90: 409-425. doi:10.1007/s12041-011-0103-9.
- Dai, J., B. Bean, B. Brown, W. Bruening, J.T. Edwards, M. Flowers, . . . J. Wiersma. (2016). Harvest index and straw yield of five classes of wheat. *Biomass & Bioenergy* 85: 223-227.
- Dhakal, S., X. Liu, A. Girard, C. Chu, Y. Yang, S. Wang, . . . S. Liu. (2021). Genetic dissection of end-use quality traits in two widely-adapted wheat cultivars ‘tam 111’ and ‘tam 112’. *Crop Science*, 61: 1944-1959. doi:https://doi.org/10.1002/csc2.20415.
- Dhakal, S., X. Liu, A. Girard, C. Chu, Y. Yang, J. Rudd, . . . S. Liu. (2021). Genome-wide QTL mapping of yield and agronomic traits in two widely adapted winter wheat cultivars from multiple mega-environments. *PeerJ* 9. doi:10.7717/peerj.12350.
- Doyle, J. (1991). DNA Protocols for Plants. In G. M. Hewitt, A. W. B. Johnston, & J. P. W. Young (Eds.), *Molecular Techniques in Taxonomy*, (pp. 283-293). Berlin, Heidelberg: Springer Berlin Heidelberg.
- Endelman, J. B., & Jansky, S. H. (2016). Genetic mapping with an inbred line-derived F2 population in potato. *Theoretical and Applied Genetics*, 129(5), 935-943. doi:10.1007/s00122-016-2673-7
- “FAO,” Food and Agriculture Organization of the United Nations. FAOSTAT Statistical Database., 2020. [Online]. Available: <http://www.fao.org/faostat/en/#home>.
- Gahlaut, V., Jaiswal, V., Tyagi, B. S., Singh, G., Sareen, S., Balyan, H. S., & Gupta, P. K. (2017). QTL mapping for nine drought-responsive agronomic traits in bread

- wheat under irrigated and rain-fed environments. *PLoS ONE*, 12(8), e0182857-e0182857. doi:10.1371/journal.pone.0182857
- Gao, F., Wen, W., Liu, J., Rasheed, A., Yin, G., Xia, X., . . . He, Z. (2015). Genome-Wide Linkage Mapping of QTL for Yield Components, Plant Height and Yield-Related Physiological Traits in the Chinese Wheat Cross Zhou 8425B/Chinese Spring. *Frontiers in Plant Science*, 6(1099). doi:10.3389/fpls.2015.01099
- Garcia, M., P. Eckermann, S. Haefele, S. Satija, B. Sznajder, A. Timmins, . . . D. Fleury. (2019). Genome-wide association mapping of grain yield in a diverse collection of spring wheat (*triticum aestivum* l.) evaluated in southern australia. *PLoS One*, 14: e0211730. doi:10.1371/journal.pone.0211730.
- González, Fernanda & Slafer, Gustavo & Miralles, Daniel. (2002). Vernalization and photoperiod responses in wheat reproductive phases. *Field Crops Research*. 74. 183-195. 10.1016/S0378-4290(01)00210-6.
- Gonfa, A.&K. Tesfaye. (2016). Relationship between grain yield and yield components of the ethiopian durum wheat genotypes at various growth stages. *Tropical and Subtropical Agroecosystems*, 19: 81-91.
- Grogan, S.M., G. Brown-Guedira, S.D. Haley, G.S. McMaster, S.D. Reid, J. Smith...P.F. Byrne. (2016). Allelic variation in developmental genes and effects on winter wheat heading date in the u.S. Great plains. *PLOS ONE*, 11: e0152852. doi:10.1371/journal.pone.0152852.
- Groos, C., N. Robert, E. Bervas&G. Charmet. (2003). Genetic analysis of grain protein-content, grain yield and thousand-kernel weight in bread wheat. *Theoretical and Applied Genetics*, 106: 1032-1040. doi:10.1007/s00122-002-1111-1.
- Guedira, M., Xiong, M., Hao, Y. F., Johnson, J., Harrison, S., Marshall, D., & Brown-Guedira, G. (2016). Heading Date QTL in Winter Wheat (*Triticum aestivum* L.) Coincide with Major Developmental Genes VERNALIZATION1 and PHOTOPERIOD1. *PLoS One*, 11(5), e0154242. doi:10.1371/journal.pone.0154242.

- Hai, L., H. Guo, C. Wagner, S. Xiao & W. Friedt. (2008). Genomic regions for yield and yield parameters in Chinese winter wheat (*Triticum aestivum* L.) genotypes tested under varying environments correspond to QTL in widely different wheat materials. *Plant Sci*, 175: 226-232. doi:10.1016/j.plantsci.2008.03.006.
- Heidari, B., B.E. Sayed-Tabatabaei, G. Saeidi, M. Kearsey & K. Suenaga. (2011). Mapping QTL for grain yield, yield components, and spike features in a doubled haploid population of bread wheat. *Genome*, 54: 517-527. doi:10.1139/g11-017.
- Hou, J., Y. Liu, C. Hao, T. Li, H. Liu...X. Zhang. (2020). Starch metabolism in wheat: Gene variation and association analysis reveal additive effects on kernel weight. *Frontiers in Plant Science*, 11. doi:10.3389/fpls.2020.562008.
- Huang, M., Mheni, N., Brown-Guedira, G., McKendry, A., Griffey, C., Van Sanford, D., . . . Sneller, C. (2018). Genetic analysis of heading date in winter and spring wheat. *Euphytica*, 214(8), 128. doi:10.1007/s10681-018-2199-y
- Isham, K., R. Wang, W. Zhao, J. Wheeler, N. Klassen, E. Akhunov...J. Chen. (2021). QTL mapping for grain yield and three yield components in a population derived from two high-yielding spring wheat cultivars. *Theoretical and Applied Genetics*: 1-17.
- IWGSC, R. Appels, K. Eversole, C. Feuillet, B. Keller, J. Rogers, et al. 2018. Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361:eaar7191. doi:10.1126/science.aar7191
- Jaganathan, D., Bohra, A., Thudi, M., & Varshney, R. K. (2020). Fine mapping and gene cloning in the post-NGS era: advances and prospects. *Theoretical and Applied Genetics*, 133(5), 1791-1810. doi:10.1007/s00122-020-03560-w
- Kang, H.-Y., L.-J. Lin, Z.-J. Song, J.-Y. Yuan, M.-Y. Zhong, H.-Q. Zhang, . . . Y.-H. Zhou. (2012). Identification, fine mapping and characterization of *rht-dp*, a recessive wheat dwarfing (reduced height) gene derived from *Triticum polonicum*. *Genes & Genomics*, 34: 509-515. doi:10.1007/s13258-012-0022-z.

- Kiviharju, E., Moisaner, S., & Tanhuanpaa, P. (2017). Oat Anther Culture and Use of DH-Lines for Genetic Mapping. *Methods Mol Biol*, 1536, 71-93.
doi:10.1007/978-1-4939-6682-0_6
- Kuchel, H., Williams, K. J., Langridge, P., Eagles, H. A., & Jefferies, S. P. (2007). Genetic dissection of grain yield in bread wheat. I. QTL analysis. *Theoretical and Applied Genetics*, 115(8), 1029-1041. doi:10.1007/s00122-007-0629-7
- Kumar, A., E.E. Mantovani, R. Seetan, A. Soltani, M. Echeverry-Solarte, S. Jain, . . . M. Mergoum. (2016). Dissection of genetic factors underlying wheat kernel shape and size in an elite x nonadapted cross using a high density snp linkage map. *Plant Genome*, 9. doi:10.3835/plantgenome2015.09.0081.
- Li, F., Wen, W., Liu, J., Zhang, Y., Cao, S., He, Z., . . . Xia, X. (2019). Genetic architecture of grain yield in bread wheat based on genome-wide association studies. *BMC Plant Biology*, 19(1), 168. doi:10.1186/s12870-019-1781-3
- Li, Y. L., Dong, Y. B., & Niu, S. Z. (2006). QTL analysis of popping fold and the consistency of QTLs under two environments in popcorn. *Yi Chuan Xue Bao*, 33(8), 724-732. doi:10.1016/S0379-4172(06)60105-4
- Liu, H., X. Zhang, Y. Xu, F. Ma, J. Zhang, Y. Cao, . . . D. An. (2020). Identification and validation of quantitative trait loci for kernel traits in common wheat (*triticum aestivum* l.). *BMC Plant Biology* 20: 529. doi:10.1186/s12870-020-02661-4.
- Liu, H., Mullan, D., Zhang, C., Zhao, S., Li, X., Zhang, A., . . . Yan, G. (2020). Major genomic regions responsible for wheat yield and its components as revealed by meta-QTL and genotype–phenotype association analyses. *Planta*, 252(4), 65. doi:10.1007/s00425-020-03466-3
- Liu, S., M. Zhang, F. Feng&Z. Tian. (2020). Toward a "green revolution" for soybean. *Molecular Plant* 13: 688-697. doi:10.1016/j.molp.2020.03.002.
- Liu, T., L. Wu, X. Gan, W. Chen, B. Liu, G. Fedak, . . . B. Zhang. (2020). Mapping quantitative trait loci for 1000-grain weight in a double haploid population of common wheat. *International Journal of Molecular Sciences*, 21. doi:10.3390/ijms21113960.

- Li, Q., Li, L., Yang, X., Warburton, M.L., Bai, G., Dai, J.,... Yan, J.. 2010. Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight. *BMC Plant Biology*. 10:143. doi:10.1186/1471-2229-10-143
- Loukoianov, A., L. Yan, A. Blechl, A. Sanchez&J. Dubcovsky. (2005). Regulation of vrn-1 vernalization genes in normal and transgenic polyploid wheat. *Plant physiology* 138: 2364-2373. doi:10.1104/pp.105.064287.
- Lv, H., Q. Wang, X. Liu, F. Han, Z. Fang, L. Yang, . . . Y. Zhang. (2016). Whole-genome mapping reveals novel qtl clusters associated with main agronomic traits of cabbage (*brassica oleracea* var. *Capitata* l.). *Frontiers in plant science* 7: 989-989. doi:10.3389/fpls.2016.00989.
- Lu, N., Zhou, J., Han, Z., Li, D., Cao, Q., Yao, X., . . . Cheng, T. (2019). Improved estimation of aboveground biomass in wheat from RGB imagery and point cloud data acquired with a low-cost unmanned aerial vehicle system. *Plant Methods*, 15(1), 17. doi:10.1186/s13007-019-0402-3
- Ma, D., Yan, J., He, Z., Wu, L., & Xia, X. (2012). Characterization of a cell wall invertase gene TaCwi-A1 on common wheat chromosome 2A and development of functional markers. *Molecular Breeding*, 29(1), 43-52. doi:10.1007/s11032-010-9524-z
- Ma, J., H. Zhang, S. Li, Y. Zou, T. Li, J. Liu, . . . X. Lan. (2019). Identification of quantitative trait loci for kernel traits in a wheat cultivar chuannong16. *BMC Genetics*, 20: 77. doi:10.1186/s12863-019-0782-4.
- Marburger, D. A., Silva, A. d. O., Hunger, R. M., Edwards, J. T., Van der Laan, L., Blakey, A. M., . . . Carver, B. F. (2021). ‘Gallagher’ and ‘Iba’ hard red winter wheat: Half-sibs inseparable by yield gain, separable by producer preference. *Journal of Plant Registrations*. doi:10.1002/plr2.20116
- Meng, L., Li, H., Zhang, L., & Wang, J. (2015). QTL IciMapping: integrated software for genetic linkage map construction and quantitative trait locus mapping in biparental populations. *The Crop Journal*, 3(3), 269-283.

- Mengistu, N., P.S. Baenziger, K.M. Eskridge, I. Dweikat, S.N. Wegulo, K.S. Gill...A. Mujeeb-Kazi. (2012). Validation of qtl for grain yield-related traits on wheat chromosome 3a using recombinant inbred chromosome lines. *Crop Science*, 52: 1622-1632. doi:10.2135/cropsci2011.12.0677.
- Mian, M.A.K., A.A. Begum&R.R. Saha. (2020). Functional relationship between grain yield and spikes per square meter of wheat as influenced by seed rate under late sown condition. *Bangladesh Agronomy Journal*, 22: 105-113. doi:10.3329/baj.v22i1.44942.
- Mochida, K., & Tsujimoto, H. (2001). Production of Wheat Doubled Haploids by Pollination With Job's Tears (*Coix lachryma-jobi* L.). *Journal of Heredity*, 92(1), 81-83. doi:10.1093/jhered/92.1.81 %J Journal of Heredity
- Moral, L., Y. Rharrabti, D. Villegas&C. Royo. (2003). Evaluation of grain yield and its components in durum wheat under mediterranean conditions: An ontogenic approach. *Agronomy Journal - AGRON J* 95. doi:10.2134/agronj2003.0266.
- Ochagavía, H., Prieto, P., Zikhali, M., Griffiths, S., & Slafer, G. A. (2019). Earliness Per Se by Temperature Interaction on Wheat Development. *Scientific Reports*, 9(1), 2584. doi:10.1038/s41598-019-39201-6
- Peterson, B. K., Weber, J. N., Kay, E. H., Fisher, H. S., & Hoekstra, H. E. (2012). Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species. *PLoS One*, 7(5), e37135. doi:10.1371/journal.pone.0037135
- Piepho, H.P.&J. Mohring. (2007). Computing heritability and selection response from unbalanced plant breeding trials. *Genetics*. 177: 1881-1888. doi:10.1534/genetics.107.074229.
- Prashant, R., N. Kadoo, C. Desale, P. Kore, H.S. Dhaliwal, P. Chhuneja...V. Gupta. (2012). Kernel morphometric traits in hexaploid wheat (*triticum aestivum* l.) are modulated by intricate qtl \times qtl and genotype \times environment interactions. *Journal of Cereal Science* 56: 432-439. doi:10.1016/j.jcs.2012.05.010.

- Rabbi, S., A. Kumar, S. Mohajeri Naraghi, S. Simsek, S. Sapkota, S. Solanki, . . . M. Mergoum. (2021). Genome-wide association mapping for yield and related traits under drought stressed and non-stressed environments in wheat. *Frontiers in Genetics*, 12: 649988. doi:10.3389/fgene.2021.649988.
- Ren, T., Hu, Y., Tang, Y., Li, C., Yan, B., Ren, Z., . . . Li, Z. (2018). Utilization of a Wheat55K SNP Array for Mapping of Major QTL for Temporal Expression of the Tiller Number. *Frontiers in plant science*, 9, 333-333. doi:10.3389/fpls.2018.00333
- Royo, C., K. Ammar, C. Alfaro, S. Dreisigacker, L.F.G. del Moral...D. Villegas. (2018). Effect of ppd-1 photoperiod sensitivity genes on dry matter production and allocation in durum wheat. *Field Crops Research* 221: 358-367. doi:10.1016/j.fcr.2017.06.005.
- Rudd, J. C., Devkota, R. N., Baker, J. A., Ibrahim, A. M., Worrall, D., Lazar, M. D., . . . Graybosch, R. A. (2013). Registration of 'TAM 113' Wheat. *Journal of Plant Registrations*, 7(1), 63-68. doi:10.3198/jpr2011.11.0616crc
- Rustgi, S., M.N. Shafqat, N. Kumar, P.S. Baenziger, M.L. Ali, I. Dweikat, . . . K.S. Gill. (2013). Genetic dissection of yield and its component traits using high-density composite map of wheat chromosome 3a: Bridging gaps between qtls and underlying genes. *PLoS One*, 8: e70526. doi:10.1371/journal.pone.0070526.
- United Nations, Department of Economic and Social Affairs, Population Division (2019). World Population Prospects 2019: Highlights. ST/ESA/SER.A/423.
- USDA, (2019). Small Grains 2019 Summary (September 2019). SSN: 1949-162X
- Sari, E., Berraies, S., Knox, R. E., Singh, A. K., Ruan, Y., Cuthbert, R. D., . . . Fobert, P. R. (2018). High density genetic mapping of Fusarium head blight resistance QTL in tetraploid wheat. *PLoS One*, 13(10), e0204362. doi:10.1371/journal.pone.0204362
- Sehgal, A., K. Sita, K.H.M. Siddique, R. Kumar, S. Bhogireddy, R.K. Varshney, . . . H. Nayyar. (2018). Drought or/and heat-stress effects on seed filling in food crops:

- Impacts on functional biochemistry, seed yields, and nutritional quality. *Front Plant Science*, 9: 1705. doi:10.3389/fpls.2018.01705.
- Semagn, K., M. Iqbal, H. Chen, E. Perez-Lara, D.H. Bemister, R. Xiang, . . . A. N'Diaye. (2021). Physical mapping of qtl associated with agronomic and end-use quality traits in spring wheat under conventional and organic management systems. *Theoretical and Applied Genetics*: 1-21.
- Seymour, D. K., Filiault, D. L., Henry, I. M., Monson-Miller, J., Ravi, M., Pang, A., . . . Maloof, J. N. (2012). Rapid creation of Arabidopsis doubled haploid lines for quantitative trait locus mapping. *Proceedings of the National Academy of Sciences of the United States of America*, 109(11), 4227-4232. doi:10.1073/pnas.1117277109
- Shah, S.A., S.A. Harrison, D.J. Boquet, P.D. Colyer & S.H. Moore. (1994). Management effects on yield and yield components of late-planted wheat. *Crop Science*, 34: crops1994.0011183X003400050029x. doi:https://doi.org/10.2135/cropsci1994.0011183X003400050029x.
- Shewry, P. R. (2009). Wheat. *J Exp Bot*, 60(6), 1537-1553. doi:10.1093/jxb/erp058
- Shewry, P.R. & S.J. Hey. (2015). The contribution of wheat to human diet and health. *Food and Energy Security*, 4: 178-202. doi:10.1002/fes3.64.
- Shi, W., C. Hao, Y. Zhang, J. Cheng, Z. Zhang, J. Liu, . . . J. Guo. (2017). A combined association mapping and linkage analysis of kernel number per spike in common wheat (*triticum aestivum* l.). *Frontiers in Plant Science*, 8. doi:10.3389/fpls.2017.01412.
- Silva, L. d. C. e., Cruz, C. D., Moreira, M. A., & Barros, E. G. d. (2007). Simulation of population size and genome saturation level for genetic mapping of recombinant inbred lines (RILs). *Genetics and Molecular Biology*, 30, 1101-1108. Retrieved from http://www.scielo.br/scielo.php?script=sci_arttext&pid=S1415-47572007000600013&nrm=iso
- Smykal, P., K. Varshney, R., K. Singh, V., Coyne, C. J., Domoney, C., Kejnovský, E., & Warkentin, T. (2016). From Mendel's discovery on pea to today's plant genetics

- and breeding. *Theoretical and Applied Genetics*, 129(12), 2267-2280.
doi:10.1007/s00122-016-2803-2
- Tang, Y.-l., J. Li, Y.-q. Wu, H.-t. Wei, C.-s. Li, W.-y. Yang...F. Chen. (2011). Identification of qtls for yield-related traits in the ecombinant inbred line population derived from the cross between a synthetic hexaploid wheat-derived variety chuanmai 42 and a chinese elite variety chuannong 16. *Agricultural Sciences in China*, 10: 1665-1680. doi:10.1016/s1671-2927(11)60165-x.
- Tura, H., Edwards, J., Gahlaut, V., Garcia, M., Sznajder, B., Baumann, U., . . . Fleury, D. (2020). QTL analysis and fine mapping of a QTL for yield-related traits in wheat grown in dry and hot environments. *Theoretical and Applied Genetics*, 133(1), 239-257. doi:10.1007/s00122-019-03454-6
- Van Ooijen, J. (2006). JoinMap® 4, Software for the calculation of genetic linkage maps in experimental populations. Kyazma BV, Wageningen, 33(10.1371).
- Vitale, P., F. Fania, S. Esposito, I. Pecorella, N. Pecchioni, S. Palombieri, . . . P. De Vita. (2021). Qtl analysis of five morpho-physiological traits in bread wheat using two mapping populations derived from common parents. *Genes (Basel)* 12.
doi:10.3390/genes12040604.
- Wang, L., Ge, H., Hao, C., Dong, Y., & Zhang, X. (2012). Identifying Loci Influencing 1,000-Kernel Weight in Wheat by Microsatellite Screening for Evidence of Selection during Breeding. *PLoS One*, 7(2), e29432.
doi:10.1371/journal.pone.0029432
- Wang, Y., VandenLangenberg, K., Wen, C., Wehner, T. C., & Weng, Y. (2018). QTL mapping of downy and powdery mildew resistances in PI 197088 cucumber with genotyping-by-sequencing in RIL population. *Theoretical and Applied Genetics* s, 131(3), 597-611. doi:10.1007/s00122-017-3022-1
- Whan, A. P., Smith, A. B., Cavanagh, C. R., Ral, J.-P. F., Shaw, L. M., Howitt, C. A., & Bischof, L. (2014). GrainScan: a low cost, fast method for grain size and colour measurements. *Plant Methods*, 10(1), 23. doi:10.1186/1746-4811-10-23

- Whittal, A., M. Kaviani, R. Graf, G. Humphreys & A. Navabi. (2018). Allelic variation of vernalization and photoperiod response genes in a diverse set of north american high latitude winter wheat genotypes. *PLoS One*, 13: e0203068. doi:10.1371/journal.pone.0203068.
- Wurschum, T., S.M. Langer, C.F.H. Longin, M.R. Tucker & W.L. Leiser. (2017). A modern green revolution gene for reduced height in wheat. *Plant Journal*, 92: 892-903. doi:10.1111/tpj.13726.
- Wurschum, T., W.L. Leiser, S.M. Langer, M.R. Tucker & C.F.H. Longin. (2018). Phenotypic and genetic analysis of spike and kernel characteristics in wheat reveals long-term genetic trends of grain yield components. *Theoretical and Applied Genetics*, 131: 2071-2084. doi:10.1007/s00122-018-3133-3.
- Xin, F., Zhu, T., Wei, S., Han, Y., Zhao, Y., Zhang, D., . . . Ding, Q. (2020). QTL Mapping of Kernel Traits and Validation of a Major QTL for Kernel Length-Width Ratio Using SNP and Bulk Segregant Analysis in Wheat. *Scientific Reports*, 10(1), 25. doi:10.1038/s41598-019-56979-7ZD
- Xu, Y., Li, P., Yang, Z., & Xu, C. (2017). Genetic mapping of quantitative trait loci in crops. *The Crop Journal*, 5(2), 175-184. doi:10.1016/j.cj.2016.06.003
- Yan, G., H. Liu, H. Wang, Z. Lu, Y. Wang, D. Mullan, . . . C. Liu. (2017). Accelerated generation of selfed pure line plants for gene identification and crop breeding. *Frontiers in Plant Science*, 8. doi:10.3389/fpls.2017.01786.
- Yang, Y., B. Bashed, A., Ibrahim, J.C. Rudd X., Chen, R., Bowden, . . . S. Liu. (2019). Developing KASP markers on a major stripe rust resistance QTL in a popular wheat TAM 111 using 90K array and genotyping-by-sequencing SNPs. *Crop Science*. doi:10.2135/cropsci2018.05.0349.
- Yang, L., Zhao, D., Meng, Z., Xu, K., Yan, J., Xia, X., . . . Zhang, Y. (2020). QTL mapping for grain yield-related traits in bread wheat via SNP-based selective genotyping. *Theoretical and Applied Genetics*, 133(3), 857-872. doi:10.1007/s00122-019-03511-0

- Yang, Z., Jin, L., Zhu, H., Wang, S., Zhang, G., & Liu, G. (2018). Analysis of Epistasis among QTLs on Heading Date based on Single Segment Substitution Lines in Rice. *Scientific Report*, 8(1), 3059. doi:10.1038/s41598-018-20690-w
- Yang, Y., S. Dhakal, C. Chu, S. Wang, Q. Xue, J.C. Rudd, . . . S. Liu. (2020). Genome wide identification of qtl associated with yield and yield components in two popular wheat cultivars tam 111 and tam 112. *PLOS ONE*, 15. doi:10.1371/journal.pone.0237293.
- Ye, X., Li, J., Cheng, Y., Yao, F., Long, L., Wang, Y., . . . Chen, G. (2019). Genome-wide association study reveals new loci for yield-related traits in Sichuan wheat germplasm under stripe rust stress. *BMC Genomics*, 20(1), 640. doi:10.1186/s12864-019-6005-6
- Zheng, B. S., Le Gouis, J., Leflon, M., Rong, W. Y., Laperche, A., & Brancourt-Hulmel, M. (2010). Using probe genotypes to dissect QTL \times environment interactions for grain yield components in winter wheat. *Theoretical and Applied Genetics*, 121(8), 1501-1517. doi:10.1007/s00122-010-1406-6
- Zhu, Y., J. Chu, X. Dai & M. He. (2019). Delayed sowing increases grain number by enhancing spike competition capacity for assimilates in winter wheat. *European Journal of Agronomy*, 104: 49-62. doi:10.1016/j.eja.2019.01.006.

APPENDIX A

Table A1. Simple Spearman correlation coefficients among traits collected in Bushland, TX 2020-2021. Values calculated using predicted means (BLUPs). - 21BD

| TRAIT ^a | HD | PH | BM | SPM | HeadWt | BMGYLD | AREA | PERI | KLEN | KWIDTH | TKW | YLD | HI | KPS | SHW | SSHW |
|--------------------|----------|---------|---------|----------|---------|---------|---------|---------|--------|--------|---------|---------|---------|--------|---------|---------|
| PH | 0.01 | | | | | | | | | | | | | | | |
| BM | 0.05 | 0.35*** | | | | | | | | | | | | | | |
| SPM | 0.29*** | 0.09 | 0.71*** | | | | | | | | | | | | | |
| HeadWt | -0.19** | 0.35*** | 0.84*** | 0.61*** | | | | | | | | | | | | |
| BMGYLD | -0.30*** | 0.34*** | 0.74*** | 0.45*** | 0.93*** | | | | | | | | | | | |
| AREA | -0.07 | 0.20* | 0.17* | -0.11 | 0.08 | 0.05 | | | | | | | | | | |
| PERI | 0.10 | 0.23* | 0.17* | -0.06 | 0.02 | -0.04 | 0.90*** | | | | | | | | | |
| KLEN | 0.09 | 0.20* | 0.16* | -0.03 | 0.02 | -0.04 | 0.79*** | 0.96*** | | | | | | | | |
| KWIDTH | -0.19** | 0.07 | 0.07 | -0.06 | 0.07 | 0.05 | 0.70*** | 0.35*** | 0.18* | | | | | | | |
| TKW | 0.14 | -0.02 | -0.13 | -0.04 | -0.15* | -0.15* | -0.08 | -0.03 | -0.05 | -0.07 | | | | | | |
| YLD | -0.42*** | 0.47*** | 0.40*** | 0.16* | 0.63*** | 0.68*** | -0.02 | -0.12 | -0.11 | 0.00 | -0.14 | | | | | |
| HI | -0.44*** | 0.23** | 0.27** | 0.12 | 0.66*** | 0.82*** | -0.04 | -0.16* | -0.16* | 0.02 | -0.19** | 0.65*** | | | | |
| KPS | 0.14* | -0.02 | -0.14 | -0.04 | -0.15* | -0.16* | -0.09 | -0.04 | -0.06 | -0.08 | 1.00*** | -0.14 | -0.19** | | | |
| SHW | -0.48*** | 0.36*** | 0.43*** | -0.12 | 0.69*** | 0.74*** | 0.22** | 0.10 | 0.08 | 0.16* | -0.18* | 0.65*** | 0.72*** | -0.18* | | |
| SSHW | -0.29*** | 0.32*** | 0.37*** | -0.38*** | 0.28*** | 0.34*** | 0.38*** | 0.31*** | 0.26** | 0.20** | -0.14 | 0.30*** | 0.17* | -0.14* | 0.71*** | |
| SHGW | -0.47*** | 0.34*** | 0.43*** | -0.04 | 0.69*** | 0.85*** | 0.13 | 0.01 | -0.01 | 0.11 | -0.18** | 0.66*** | 0.86*** | -0.18* | 0.91*** | 0.61*** |

^aAbbreviations of Traits HD: Heading Date, BM: Biomass PH: Plant Height, SPM: Spikes m⁻², HeadWt: Head Weight, BMYLD: Biomass Grain Yield from 0.5-meter inner row, KA: Kernel Area, PERI: Perimeter, KLEN: Kernel Length, KWID: Kernel Width, TKW: Thousand Kernel Weight, YLD from combine harvester: Yield, HI: Harvest Index, KPS: Kernels Spike⁻¹, SHDW: Single Head Dry Weight, SSHW: Single Stem Head Weight, SHGW: Single Head Grain Weight
*, **, ***, significant at 0.05, 0.01, and 0.001 probability levels, respectively.

Table A1. Simple Spearman correlation coefficients among traits collected in Bushland, TX 2020-2021. Values calculated using predicted means (BLUPs) – 20EMN

| TRAIT ^a | PH | BM | SPM | HeadWt | BMGYLD | AREA | PERI | KLEN | KWIDTH | TKW | YLD | HI | KPS | SHW | SSHW |
|--------------------|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| BM | 0.16* | | | | | | | | | | | | | | |
| SPM | -0.26*** | 0.60*** | | | | | | | | | | | | | |
| HeadWt | 0.12 | 0.79*** | 0.52** | | | | | | | | | | | | |
| BMGYLD | 0.22** | 0.74*** | 0.39** | 0.84*** | | | | | | | | | | | |
| AREA | 0.42*** | 0.16* | -0.25* | 0.28*** | 0.23** | | | | | | | | | | |
| PERI | 0.36*** | 0.12 | -0.24* | 0.20** | 0.15* | 0.92*** | | | | | | | | | |
| KLEN | 0.30*** | 0.11 | -0.20* | 0.15* | 0.11 | 0.81*** | 0.96*** | | | | | | | | |
| KWIDTH | 0.38*** | 0.17* | -0.19* | 0.30*** | 0.26** | 0.83*** | 0.57*** | 0.35*** | | | | | | | |
| TKW | 0.45*** | 0.19** | -0.26* | 0.30*** | 0.28*** | 0.93*** | 0.77*** | 0.62*** | 0.89*** | | | | | | |
| YLD | 0.46*** | 0.28*** | 0.0 | 0.45*** | 0.55*** | 0.26** | 0.16* | 0.10 | 0.31*** | 0.34*** | | | | | |
| HI | 0.24** | 0.23** | 0.0 | 0.63*** | 0.65*** | 0.28*** | 0.20** | 0.14 | 0.32*** | 0.34*** | 0.68*** | | | | |
| KPS | 0.26** | 0.33*** | -0.15 | 0.50*** | 0.60*** | -0.01 | -0.02 | -0.02 | 0.00 | 0.02 | 0.55*** | 0.72*** | | | |
| SHW | 0.36*** | 0.31*** | -0.33** | 0.63*** | 0.55*** | 0.54*** | 0.45*** | 0.36*** | 0.51*** | 0.57*** | 0.48*** | 0.61*** | 0.68*** | | |
| SSHW | 0.46*** | 0.31*** | -0.56** | 0.18** | 0.28*** | 0.45*** | 0.40*** | 0.36*** | 0.39*** | 0.49*** | 0.24** | 0.11 | 0.50*** | 0.71*** | |
| SHGW | 0.41*** | 0.35*** | -0.29** | 0.51*** | 0.76*** | 0.42*** | 0.34*** | 0.28*** | 0.41*** | 0.48*** | 0.56*** | 0.61*** | 0.73*** | 0.81*** | 0.70*** |

^aAbbreviations of Traits PH: Plant Height, BM: Biomass, SPM: Spikes m⁻², HeadWt: Head Weight, BMYLD: Biomass Grain Yield from 0.5-meter inner row, KA: Kernel Area, PERI: Perimeter, KLEN: Kernel Length, KWID: Kernel Width, TKW: Thousand Kernel Weight, YLD: Yield from combine harvester, HI: Harvest Index, KPS: Kernels Spike⁻¹, SHDW: Single Head Dry Weight, SSHW: Single Stem Head Weight, SHGW: Single Head Grain Weight
*, **, ***, significant at 0.05, 0.01, and 0.001 probability levels, respectively.

Table A1. Simple Spearman correlation coefficients among traits collected in Bushland, TX 2020-2021. Values calculated using predicted means (BLUPs) - 20CS

| TRAIT ^a | HD | PH |
|--------------------|----------|------|
| PH | 0.16* | |
| YLD | -0.58*** | 0.13 |

Table A1. Simple Spearman correlation coefficients among traits collected in Bushland, TX 2020-2021. Values calculated using predicted means (BLUPs) – 19BSP

| TRAIT ^a | HD | PH | BM | SPM | HeadWt | BMGYLD | AREA | PERI | KLEN | KWIDTH | TKW | YLD | HI | KPS | SHW | SSHW |
|--------------------|----------|--------|---------|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| PH | 0.33*** | | | | | | | | | | | | | | | |
| BM | 0.11 | 0.32** | | | | | | | | | | | | | | |
| SPM | 0.06 | 0.06 | 0.67*** | | | | | | | | | | | | | |
| HeadWt | -0.23** | 0.07 | 0.86*** | 0.64*** | | | | | | | | | | | | |
| BMGYLD | -0.41*** | 0.01 | 0.75*** | 0.50*** | 0.91*** | | | | | | | | | | | |
| AREA | -0.58*** | 0.08 | 0.02 | -0.28** | 0.22** | 0.41*** | | | | | | | | | | |
| PERI | -0.45*** | 0.12 | 0.09 | -0.19* | 0.26** | 0.38*** | 0.93*** | | | | | | | | | |
| KLEN | -0.32** | 0.17* | 0.11 | -0.11 | 0.25** | 0.33** | 0.82*** | 0.96*** | | | | | | | | |
| KWIDTH | -0.62*** | -0.05 | -0.07 | -0.34*** | 0.14 | 0.37*** | 0.84*** | 0.61*** | 0.38*** | | | | | | | |
| TKW | -0.65*** | 0.01 | -0.01 | -0.30** | 0.21* | 0.44*** | 0.95*** | 0.82*** | 0.65*** | 0.92*** | | | | | | |
| YLD | -0.36*** | -0.16 | 0.09 | -0.04 | 0.27** | 0.44*** | 0.34*** | 0.24** | 0.18* | 0.38*** | 0.40*** | | | | | |
| HI | -0.65*** | -0.19* | 0.39*** | 0.25** | 0.71*** | 0.89*** | 0.58*** | 0.49*** | 0.39*** | 0.57*** | 0.64*** | 0.56*** | | | | |
| KPS | 0.20* | -0.13 | 0.21* | -0.19* | 0.20* | 0.19* | -0.31** | -0.29** | -0.26** | -0.26** | -0.30** | 0.15 | 0.12 | | | |
| SHW | -0.32** | -0.01 | 0.13 | -0.51*** | 0.32** | 0.40*** | 0.59*** | 0.53*** | 0.43*** | 0.56*** | 0.60*** | 0.36*** | 0.48*** | 0.46*** | | |
| SSHW | -0.01 | 0.13 | -0.20* | -0.85*** | -0.25** | -0.13 | 0.38*** | 0.32** | 0.23** | 0.39*** | 0.39*** | 0.13 | -0.05 | 0.42*** | 0.78*** | |
| SHGW | -0.48*** | -0.05 | 0.14 | -0.43*** | 0.33*** | 0.56*** | 0.69*** | 0.58*** | 0.45*** | 0.70*** | 0.74*** | 0.49*** | 0.68*** | 0.39*** | 0.92*** | 0.68*** |

^aAbbreviations of Traits HD: Heading Date, PH: Plant Height, BM: Biomass, SPM: Spikes m⁻², HeadWt: Head Weight, BMGYLD: Biomass Grain Yield from 0.5-meter inner row, KA: Kernel Area, PERI: Perimeter, KLEN: Kernel Length, KWID: Kernel Width, TKW: Thousand Kernel Weight, YLD: Yield from combine harvester, HI: Harvest Index, KPS: Kernels Spike⁻¹, SHDW: Single Head Dry Weight, SSHW: Single Stem Head Weight, SHGW: Single Head Grain Weight
*, **, ***, significant at 0.05, 0.01, and 0.001 probability levels, respectively.

Table A2. QTL detected for all traits in individual and across environments.

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|--------------------|-----------|--------|------|---------------------|---------------|-----------------|--------|---------|------------|-------|---------|------------|--------|-----------------------|-------|-------|
| BMYLE | Qbmyld.tamu.2B.69 | 21BD | 3.48 | 2B | 69.34 | 108 | chr2B_68426788 | 4.24 | | | 10.34 | | | 37.04 | TAM 113 | | p |
| BMYLE | Qbmyld.tamu.7D.51 | 19BSP | 3.47 | 7D | 51.34 | 64 | chr7D_47632974 | 4.28 | | | 7.28 | | | 18.53 | TAM 113 | | |
| BMYLE | Qbmyld.tamu.2B.19 | 19BSP | 3.47 | 2B | 18.82 | 26 | chr2B_18656478 | 3.76 | | | 6.65 | | | 17.66 | TAM 113 | | |
| BMYLE | Qbmyld.tamu.4B.441 | AcrossEnv | 4.85 | 4B | 441.13 | 160 | chr4B_449765851 | 10.65 | 2.8 | 7.86 | 3.68 | 2.18 | 1.5 | 13.29 | TAM 113 | | p |
| BMYLE | Qbmyld.tamu.4B.551 | AcrossEnv | 4.85 | 4B | 551.23 | 237 | chr4B_541365812 | 18.76 | 2.06 | 16.71 | 6.91 | 1.73 | 5.18 | -11.87 | Gallagher | | |
| BMYLE | Qbmyld.tamu.2D.37 | AcrossEnv | 4.85 | 2D | 37.25 | 64 | chr2D_37211804 | 6.35 | 2.48 | 3.87 | 2.36 | 1.9 | 0.45 | -12.43 | Gallagher | y? | p |
| BMYLE | Qbmyld.tamu.2D.37 | 19BSP | 4.85 | 2D | 37.25 | 64 | chr2D_37211804 | 4.96 | | | 8.53 | | | -20.03 | Gallagher | y? | p |
| DIAM | Qdiam.tamu.7D.66 | 19MCG | 3.56 | 7D | 66.02 | 89 | chr7D_63208599 | 5.55 | | | 7.69 | | | 0.03 | TAM 113 | | p |
| DIAM | Qdiam.tamu.2B.149 | 20MCG | 3.56 | 2B | 149.26 | 120 | chr2B_145617210 | 5.53 | | | 6.69 | | | 0.03 | TAM 113 | | |
| DIAM | Qdiam.tamu.6A.565 | 20MCG | 3.56 | 6A | 564.98 | 179 | chr6A_566172088 | 5.67 | | | 6.83 | | | -0.03 | Gallagher | | |
| DIAM | Qdiam.tamu.2D.34 | 20MCG | 3.56 | 2D | 34.43 | 61 | chr2D_32901354 | 23.51 | | | 35.05 | | | -0.07 | Gallagher | | p |
| HARD | Qhard.tamu.1A.584 | 20MCG | 3.56 | 1A | 583.86 | 235 | chr1A_583256428 | 3.92 | | | 7.22 | | | 2.49 | TAM 113 | | |
| HD | Qhd.tamu.2D.34 | 20MCG | 3.48 | 2D | 34.43 | 61 | chr2D_32901354 | 32.91 | | | 53.52 | | | 4.86 | TAM 113 | y | p |
| HD | Qhd.tamu.2D.34 | 20CS | 3.5 | 2D | 34.43 | 61 | chr2D_32901354 | 48.67 | | | 38.55 | | | 4.55 | TAM 113 | y | p |
| HD | Qhd.tamu.7D.608 | 20CS | 3.5 | 7D | 607.85 | 330 | chr7D_611166154 | 37.22 | | | 25.55 | | | 3.7 | TAM 113 | y? | |
| HD | Qhd.tamu.2D.34 | 19MCG | 3.47 | 2D | 34.43 | 61 | chr2D_32901354 | 22.34 | | | 38.31 | | | 3.21 | TAM 113 | y | p |
| HD | Qhd.tamu.2D.34 | AcrossEnv | 5.85 | 2D | 34.43 | 61 | chr2D_32901354 | 157.96 | 103.9 | 54.06 | 64.66 | 54.05 | 10.6 | 3.15 | TAM 113 | y | p |
| HD | Qhd.tamu.2D.34 | 21BD | 3.48 | 2D | 34.43 | 61 | chr2D_32901354 | 23.43 | | | 34.51 | | | 1.66 | TAM 113 | y | p |
| HD | Qhd.tamu.2D.34 | 19BSP | 3.47 | 2D | 34.43 | 61 | chr2D_32901354 | 30.61 | | | 35.52 | | | 1.51 | TAM 113 | y | p |
| HD | Qhd.tamu.7A.709 | 20MCG | 3.48 | 7A | 709.16 | 285 | chr7A_701123987 | 3.62 | | | 4.4 | | | 1.39 | TAM 113 | | |
| HD | Qhd.tamu.6B.4 | 20CS | 3.5 | 6B | 3.56 | 1 | chr6B_2202189 | 4.18 | | | 1.85 | | | 0.99 | TAM 113 | y? | |
| HD | Qhd.tamu.7D.608 | AcrossEnv | 5.85 | 7D | 607.85 | 330 | chr7D_611166154 | 38.02 | 6.88 | 31.14 | 14.77 | 1.829 | 12.94 | 0.58 | TAM 113 | y? | |

Abbreviation of traits; BMYLE: Biomass Grain Yield from 0.5-meter inner row, HARD: Kernel Hardness, HD: Heading Date, HI: Harvest Index, HeatWt: Head Weight, KA: Kernel Area, KHI: Kernel Hardness Index, KLEN: Kernel Length, KPS: Kernels spike⁻¹, KWID: Kernel Width, PERI: Perimeter, PH: Plant Height, SHDW: Single Head Dry Weight, SHGW: Single Head Grain Weight, SKW: Single Kernel weight, SPM: Spikes m⁻², SSHW: Single Stem Head Weight, TKW: Thousand Kernel Weight, YLD: Grain Yield from combine harvester. Abbreviation of Environments (Env); AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, Plei: Pleiotropic, p: affecting more than one trait, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment

Table A2. QTL detected for all traits in individual and across environments.

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-----------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| HD | Qhd.tamu.1A.566 | AcrossEnv | 4.91 | 1A | 566.29 | 205 | chr1A_565388907 | 5.87 | 4.12 | 1.75 | 1.18 | 1.045 | 0.14 | 0.44 | TAM113 | | |
| HD | Qhd.tamu.6B.4 | AcrossEnv | 5.85 | 6B | 3.56 | 1 | chr6B_2202189 | 7.79 | 6.39 | 1.39 | 2.14 | 1.603 | 0.54 | 0.54 | TAM113 | y? | |
| HD | Qhd.tamu.2B.64 | AcrossEnv | 5.85 | 2B | 63.96 | 105 | chr2B_63428577 | 10.22 | 1.81 | 8.41 | 1.06 | 0.447 | 0.61 | -0.29 | Gallagher | y? | p |
| HD | Qhd.tamu.7D.70 | 19BSP | 3.47 | 7D | 70.03 | 94 | chr7D_63208599 | 5.55 | | | 5.11 | | | -0.57 | Gallagher | y | |
| HD | Qhd.tamu.2B.58 | AcrossEnv | 5.85 | 2B | 57.61 | 101 | chr2B_57657606 | 16.11 | 7.19 | 8.93 | 3.12 | 1.849 | 1.27 | -0.58 | Gallagher | y | p |
| HD | Qhd.tamu.7D.70 | AcrossEnv | 5.85 | 7D | 70.03 | 94 | chr7D_63208599 | 15.92 | 8.8 | 7.12 | 2.42 | 2.238 | 0.18 | -0.64 | Gallagher | y | |
| HD | Qhd.tamu.2B.64 | 19BSP | 3.47 | 2B | 63.96 | 105 | chr2B_63428577 | 9.16 | | | 8.12 | | | -0.72 | Gallagher | y? | p |
| HD | Qhd.tamu.7D.65 | 21BD | 3.48 | 7D | 65.22 | 88 | chr7D_63208599 | 5.28 | | | 6.71 | | | -0.73 | Gallagher | | |
| HD | Qhd.tamu.7D.71 | 20CS | 3.5 | 7D | 70.83 | 95 | chr7D_63208599 | 3.78 | | | 1.73 | | | -0.96 | Gallagher | y | |
| HD | Qhd.tamu.2B.58 | 21BD | 3.48 | 2B | 57.61 | 101 | chr2B_57657606 | 9.48 | | | 11.63 | | | -0.96 | Gallagher | y | p |
| HD | Qhd.tamu.2B.58 | 20CS | 3.5 | 2B | 57.61 | 101 | chr2B_57657606 | 4.91 | | | 2.16 | | | -1.07 | Gallagher | y | p |
| HD | Qhd.tamu.2B.63 | 19MCG | 3.47 | 2B | 63.25 | 104 | chr2B_56732564 | 3.97 | | | 5.49 | | | -1.22 | Gallagher | | |
| HI | Qhi.tamu.2D.99 | 21BD | 3.48 | 2D | 99.25 | 112 | chr2D_96540686 | 23.86 | | | 8.78 | | | 0.08 | TAM113 | y? | |
| HI | Qhi.tamu.2B.76 | 21BD | 3.48 | 2B | 76.4 | 109 | chr2B_68426788 | 6.09 | | | 1.8 | | | 0.04 | TAM113 | | p |
| HI | Qhi.tamu.2D.99 | AcrossEnv | 4.91 | 2D | 99.25 | 112 | chr2D_96540686 | 23.95 | 20.09 | 3.86 | 25.7 | 8.261 | 17.44 | 0.03 | TAM113 | y? | |
| HI | Qhi.tamu.2B.69 | AcrossEnv | 4.91 | 2B | 69.34 | 108 | chr2B_68426788 | 6.19 | 5.45 | 0.74 | 5.19 | 1.975 | 3.22 | 0.01 | TAM113 | | p |
| HI | Qhi.tamu.7D.52 | AcrossEnv | 4.91 | 7D | 52.32 | 66 | chr7D_51735477 | 6.47 | 2.09 | 4.38 | 0.91 | 0.707 | 0.2 | 0.01 | TAM113 | y? | p |
| HI | Qhi.tamu.7D.52 | 19BSP | 3.47 | 7D | 52.32 | 66 | chr7D_51735477 | 4.89 | | | 9.81 | | | 0.01 | TAM113 | y? | p |
| HI | Qhi.tamu.4B.441 | AcrossEnv | 4.91 | 4B | 441.13 | 160 | chr4B_449765851 | 9.75 | 0.83 | 8.91 | 0.46 | 0.308 | 0.15 | 0.01 | TAM113 | | p |
| HI | Qhi.tamu.4B.603 | AcrossEnv | 4.91 | 4B | 603.4 | 258 | chr4B_603463167 | 16.04 | 0.49 | 15.55 | 0.48 | 0.171 | 0.31 | 0 | Gallagher | | |
| HI | Qhi.tamu.2D.34 | AcrossEnv | 4.91 | 2D | 34.43 | 61 | chr2D_32901354 | 15.79 | 2.2 | 13.59 | 0.81 | 0.779 | 0.03 | -0.01 | Gallagher | y? | p |
| HI | Qhi.tamu.2D.34 | 19BSP | 3.47 | 2D | 34.43 | 61 | chr2D_32901354 | 10.96 | | | 21.81 | | | -0.01 | Gallagher | y? | p |

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Table A2. QTL detected for all traits in individual and across environments.

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|--------|--------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|--------|-----------------------|-------|-------|
| HI | Qhi.tamu.2D.107 | AcrossEnv | 4.91 | 2D | 106.64 | 114 | chr2D_104650607 | 33.36 | 30.84 | 2.51 | 41.3 | 14.28 | 27.02 | -0.03 | Gallagher | y? | |
| HI | Qhi.tamu.2D.107 | 21BD | 3.48 | 2D | 106.64 | 114 | chr2D_104650607 | 33.2 | | | 14.28 | | | -0.1 | Gallagher | y? | |
| HeadWt | Qhw.tamu.1A.10 | 21BD | 3.48 | 1A | 10.02 | 5 | chr1A_9877409 | 3.73 | | | 6.2 | | | -52.53 | Gallagher | | |
| KA | Qkarea.tamu.6D.172 | AcrossEnv | 3.52 | 6D | 171.52 | 28 | chr6D_172603833 | 4.71 | | | 8.24 | | | 0.21 | TAM113 | y? | p |
| KA | Qkarea.tamu.6D.351 | 19BSP | 3.47 | 6D | 350.82 | 43 | chr6D_362479513 | 3.73 | | | 6.05 | | | 0.16 | TAM113 | | p |
| KA | Qkarea.tamu.6D.172 | AcrossEnv | 4.85 | 6D | 171.52 | 28 | chr6D_172603833 | 5.28 | 3.77 | 1.51 | 9.97 | 5.456 | 4.52 | 0.09 | TAM113 | y? | p |
| KA | Qkarea.tamu.6A.572 | AcrossEnv | 4.85 | 6A | 572.4 | 188 | chr6A_571690944 | 6.19 | 2.05 | 4.14 | 9.08 | 2.855 | 6.23 | -0.07 | Gallagher | y? | |
| KA | Qkarea.tamu.2D.37 | AcrossEnv | 4.85 | 2D | 36.9 | 63 | chr2D_36584261 | 17.81 | 12.42 | 5.39 | 32.68 | 18.72 | 13.95 | -0.17 | Gallagher | y | p |
| KA | Qkarea.tamu.6A.562 | 20EMN | 3.52 | 6A | 562.27 | 174 | chr6A_562265727 | 4.29 | | | 7.44 | | | -0.2 | Gallagher | | p |
| KA | Qkarea.tamu.6A.572 | 19BSP | 3.47 | 6A | 572.4 | 188 | chr6A_571690944 | 6.1 | | | 10.77 | | | -0.22 | Gallagher | y? | |
| KA | Qkarea.tamu.2D.37 | 19BSP | 4.85 | 2D | 36.9 | 63 | chr2D_36584261 | 8.67 | | | 14.9 | | | -0.25 | Gallagher | y | p |
| KA | Qkarea.tamu.2D.37 | 20EMN | 4.85 | 2D | 36.9 | 63 | chr2D_36584261 | 8.85 | | | 16.23 | | | -0.29 | Gallagher | y | p |
| KHI | Qkhi.tamu.2D.34 | 20MCG | 3.56 | 2D | 34.43 | 61 | chr2D_32901354 | 23.12 | | | 29.85 | | | 5.71 | TAM113 | | p |
| KHI | Qkhi.tamu.4B.665 | 20MCG | 3.56 | 4B | 664.95 | 361 | chr4B_664910777 | 4.73 | | | 4.81 | | | -2.28 | Gallagher | | |
| KHI | Qkhi.tamu.5D.8 | 20MCG | 3.56 | 5D | 7.77 | 2 | chr5D_6333523 | 4.78 | | | 4.87 | | | -2.31 | Gallagher | | |
| KHI | Qkhi.tamu.2B.65 | 20MCG | 3.56 | 2B | 65.44 | 106 | chr2B_64954626 | 8.28 | | | 8.84 | | | -3.11 | Gallagher | | |
| KLEN | Qklen.tamu.5B.497 | 19BSP | 3.47 | 5B | 496.62 | 211 | chr5B_489969825 | 3.92 | | | 7.71 | | | 0.06 | TAM113 | y | p |
| KLEN | Qklen.tamu.5B.497 | 20EMN | 3.52 | 5B | 496.62 | 211 | chr5B_489969825 | 4.17 | | | 4.91 | | | 0.05 | TAM113 | y | p |
| KLEN | Qklen.tamu.5B.497 | AcrossEnv | 4.85 | 5B | 496.62 | 211 | chr5B_489969825 | 8.42 | 6.5 | 1.92 | 12.45 | 10.69 | 1.77 | 0.04 | TAM113 | y | p |
| KLEN | Qklen.tamu.2D.41 | AcrossEnv | 4.85 | 2D | 41.12 | 70 | chr2D_38687722 | 5.93 | 0.02 | 5.91 | 10.89 | 0.037 | 10.86 | 0 | TAM113 | | p |
| KLEN | Qklen.tamu.3D.585 | AcrossEnv | 4.85 | 3D | 585.36 | 126 | chr3D_585018045 | 6.4 | 1.33 | 5.07 | 9.2 | 2.062 | 7.14 | -0.02 | Gallagher | y? | |
| KLEN | Qklen.tamu.6A.113 | AcrossEnv | 4.85 | 6A | 113.23 | 129 | chr6A_105002720 | 5.91 | 1.38 | 4.53 | 9.74 | 2.2 | 7.54 | -0.02 | Gallagher | y? | |

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Table A2. QTL detected for all traits in individual and across environments.

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| KLEN | Qklen.tamu.4A.29 | AcrossEnv | 4.85 | 4A | 29.34 | 20 | chr4A_29303359 | 5.32 | 2.84 | 2.48 | 7.12 | 4.477 | 2.64 | -0.03 | Gallagher | y? | |
| KLEN | Qklen.tamu.6A.98 | AcrossEnv | 4.85 | 6A | 98.34 | 77 | chr6A_98982341 | 14.28 | 3.98 | 10.3 | 20.8 | 6.461 | 14.34 | -0.03 | Gallagher | y? | p |
| KLEN | Qklen.tamu.3D.585 | 20EMN | 3.52 | 3D | 585.36 | 126 | chr3D_585018045 | 3.87 | | | 4.54 | | | -0.05 | Gallagher | y? | |
| KLEN | Qklen.tamu.4A.29 | 20EMN | 3.52 | 4A | 29.34 | 20 | chr4A_29303359 | 4.26 | | | 5.11 | | | -0.05 | Gallagher | y? | |
| KLEN | Qklen.tamu.7A.639 | 19BSP | 3.47 | 7A | 638.67 | 214 | chr7A_639295826 | 3.63 | | | 6.93 | | | -0.05 | Gallagher | | |
| KLEN | Qklen.tamu.6A.113 | 19BSP | 3.47 | 6A | 113.23 | 129 | chr6A_105002720 | 5.82 | | | 11.49 | | | -0.07 | Gallagher | y? | |
| KLEN | Qklen.tamu.6A.98 | 20EMN | 3.52 | 6A | 98.34 | 77 | chr6A_98982341 | 14.23 | | | 18.91 | | | -0.1 | Gallagher | y? | p |
| KPS | Qkps.tamu.6A.586 | 19BSP | 3.47 | 6A | 586.24 | 200 | chr6A_586202172 | 6.71 | | | 16.17 | | | 0.95 | TAM113 | | |
| KPS | Qkps.tamu.5A.13 | 20EMN | 3.52 | 5A | 12.83 | 29 | chr5A_12691384 | 4.71 | | | 10.03 | | | -0.88 | Gallagher | | |
| KWID | Qkwid.tamu.7D.66 | 19BSP | 3.47 | 7D | 66.02 | 89 | chr7D_63208599 | 8.3 | | | 12.64 | | | 0.04 | TAM113 | y? | p |
| KWID | Qkwid.tamu.7D.67 | AcrossEnv | 4.85 | 7D | 66.83 | 90 | chr7D_63208599 | 11.59 | 9.17 | 2.43 | 8.2 | 6.6 | 1.6 | 0.02 | TAM113 | y? | p |
| KWID | Qkwid.tamu.2B.703 | 21BD | 3.48 | 2B | 703.26 | 212 | chr2B_696048977 | 5.21 | | | 8.87 | | | 0.02 | TAM113 | | |
| KWID | Qkwid.tamu.3B.431 | 21BD | 3.48 | 3B | 431.27 | 69 | chr3B_427070695 | 4.75 | | | 8.07 | | | 0.02 | TAM113 | y? | |
| KWID | Qkwid.tamu.6D.351 | AcrossEnv | 4.85 | 6D | 350.82 | 43 | chr6D_362479513 | 5.75 | 5.42 | 0.33 | 5.26 | 4.282 | 0.98 | 0.02 | TAM113 | | p |
| KWID | Qkwid.tamu.2B.85 | AcrossEnv | 4.85 | 2B | 84.91 | 113 | chr2B_76076511 | 4.29 | 3.46 | 0.83 | 3.94 | 2.679 | 1.26 | 0.01 | TAM113 | | p |
| KWID | Qkwid.tamu.3B.431 | AcrossEnv | 4.85 | 3B | 431.27 | 69 | chr3B_427070695 | 5.39 | 2.22 | 3.17 | 2.15 | 1.732 | 0.42 | 0.01 | TAM113 | y? | |
| KWID | Qkwid.tamu.2B.698 | AcrossEnv | 4.85 | 2B | 697.55 | 211 | chr2B_696048977 | 5.56 | 1.9 | 3.65 | 2.13 | 1.47 | 0.66 | 0.01 | TAM113 | | |
| KWID | Qkwid.tamu.3B.26 | AcrossEnv | 4.85 | 3B | 26 | 35 | chr3B_25733703 | 2.85 | 1.52 | 1.33 | 2.45 | 1.181 | 1.26 | 0.01 | TAM113 | | |
| KWID | Qkwid.tamu.2D.34 | AcrossEnv | 4.85 | 2D | 34.43 | 61 | chr2D_32901354 | 5.2 | 0.86 | 4.34 | 1.78 | 0.681 | 1.1 | -0.01 | Gallagher | y? | p |
| KWID | Qkwid.tamu.6D.463 | AcrossEnv | 4.85 | 6D | 462.71 | 111 | chr6D_462634429 | 2.62 | 1.4 | 1.22 | 1.79 | 1.083 | 0.7 | -0.01 | Gallagher | | |
| KWID | Qkwid.tamu.1A.336 | AcrossEnv | 4.85 | 1A | 335.94 | 83 | chr1A_301162467 | 2.83 | 2.52 | 0.31 | 2.63 | 1.947 | 0.69 | -0.01 | Gallagher | | |
| KWID | Qkwid.tamu.1A.406 | AcrossEnv | 4.85 | 1A | 405.71 | 131 | chr1A_46276720 | 3.19 | 2.68 | 0.51 | 3.06 | 2.034 | 1.02 | -0.01 | Gallagher | | |

Abbreviation of traits; BMYLD: Biomass Grain Yield from 0.5-meter inner row, HARD: Kernel Hardness, HD: Heading Date, HI: Harvest Index, HeatWt: Head Weight, KA: Kernel Area, KHI: Kernel Hardness Index, KLEN: Kernel Length, KPS: Kernels spike⁻¹, KWID: Kernel Width, PERI: Perimeter, PH: Plant Height, SHDW: Single Head Dry Weight, SHGW: Single Head Grain Weight, SKW: Single Kernel weight, SPM: Spikes m⁻², SSHW: Single Stem Head Weight, TKW: Thousand Kernel Weight, YLD: Grain Yield from combine harvester. Abbreviation of Environments (Env); AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emery Land 2020, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, Plei: Pleiotropic, p: affecting more than one trait, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment

Table A2. QTL detected for all traits in individual and across environments.

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| KWID | Qkwid.tamu.1A.406 | AcrossEnv | 4.85 | 1A | 405.92 | 116 | chr1A_399489700 | 3.16 | 2.84 | 0.32 | 2.97 | 2.204 | 0.76 | -0.01 | Gallagher | | |
| KWID | Qkwid.tamu.1A.480 | AcrossEnv | 4.85 | 1A | 480.28 | 111 | chr1A_485182245 | 3.2 | 3.06 | 0.15 | 3.13 | 2.369 | 0.76 | -0.01 | Gallagher | | |
| KWID | Qkwid.tamu.6A.562 | AcrossEnv | 4.85 | 6A | 562.27 | 174 | chr6A_562265727 | 3.98 | 3.27 | 0.71 | 3.64 | 2.591 | 1.05 | -0.01 | Gallagher | | p |
| KWID | Qkwid.tamu.1B.620 | AcrossEnv | 4.85 | 1B | 619.99 | 25 | chr1B_619535304 | 4.48 | 3.76 | 0.72 | 4.81 | 2.965 | 1.85 | -0.01 | Gallagher | | |
| KWID | Qkwid.tamu.2D.34 | 21BD | 3.48 | 2D | 34.43 | 61 | chr2D_32901354 | 5.17 | | | 8.62 | | | -0.02 | Gallagher | y? | p |
| KWID | Qkwid.tamu.2D.37 | AcrossEnv | 4.85 | 2D | 37.25 | 64 | chr2D_37211804 | 17.38 | 14 | 3.38 | 18.2 | 11.69 | 6.52 | -0.02 | Gallagher | y? | p |
| KWID | Qkwid.tamu.2D.37 | 20EMN | 3.52 | 2D | 37.25 | 64 | chr2D_37211804 | 5.3 | | | 12.68 | | | -0.03 | Gallagher | y? | p |
| KWID | Qkwid.tamu.2D.37 | 19BSP | 3.47 | 2D | 36.9 | 63 | chr2D_36584261 | 12.48 | | | 17.49 | | | -0.04 | Gallagher | | p |
| PERI | Qperi.tamu.5B.497 | 20EMN | 3.52 | 5B | 496.62 | 211 | chr5B_489969825 | 3.76 | | | 7.64 | | | 0.15 | TAM113 | y? | p |
| PERI | Qperi.tamu.2D.41 | 21BD | 3.48 | 2D | 41.12 | 70 | chr2D_38687722 | 3.91 | | | 9.7 | | | 0.15 | TAM113 | | p |
| PERI | Qperi.tamu.5B.497 | AcrossEnv | 4.83 | 5B | 496.62 | 211 | chr5B_489969825 | 5.87 | 5.06 | 0.81 | 9.89 | 8.251 | 1.64 | 0.1 | TAM113 | y? | p |
| PERI | Qperi.tamu.2D.33 | AcrossEnv | 4.83 | 2D | 33.14 | 60 | chr2D_32901354 | 5.22 | 1.29 | 3.93 | 6.75 | 1.904 | 4.84 | -0.05 | Gallagher | y? | |
| PERI | Qperi.tamu.6A.98 | AcrossEnv | 4.83 | 6A | 98.34 | 77 | chr6A_98982341 | 12.38 | 7.31 | 5.07 | 19.75 | 11.86 | 7.89 | -0.11 | Gallagher | y | p |
| PERI | Qperi.tamu.2D.33 | 19BSP | 3.47 | 2D | 33.14 | 60 | chr2D_32901354 | 5.23 | | | 9.04 | | | -0.16 | Gallagher | y? | |
| PERI | Qperi.tamu.2D.37 | 20EMN | 3.52 | 2D | 36.9 | 63 | chr2D_36584261 | 4.45 | | | 8.81 | | | -0.17 | Gallagher | | p |
| PERI | Qperi.tamu.6A.98 | 19BSP | 3.47 | 6A | 98.34 | 77 | chr6A_98982341 | 6.91 | | | 11.55 | | | -0.18 | Gallagher | y | p |
| PERI | Qperi.tamu.6A.98 | 20EMN | 3.52 | 6A | 98.34 | 77 | chr6A_98982341 | 5.43 | | | 11.07 | | | -0.19 | Gallagher | y | p |
| PH | Qph.tamu.2D.34 | 20MCG | 3.48 | 2D | 34.43 | 61 | chr2D_32901354 | 19.85 | | | 28.79 | | | 3.48 | TAM113 | y | p |
| PH | Qph.tamu.4B.424 | 19MCG | 3.47 | 4B | 423.5 | 105 | chr4B_430792975 | 16.32 | | | 10.36 | | | 2.5 | TAM113 | y? | |
| PH | Qph.tamu.2D.34 | 19BSP | 3.47 | 2D | 34.43 | 61 | chr2D_32901354 | 11.36 | | | 15.46 | | | 2.12 | TAM113 | y | p |
| PH | Qph.tamu.2D.28 | 20CS | 3.5 | 2D | 28.26 | 51 | chr2D_22290058 | 6.95 | | | 10.09 | | | 1.75 | TAM113 | | |
| PH | Qph.tamu.5B.490 | 20CS | 3.5 | 5B | 490.39 | 208 | chr5B_489384278 | 7.21 | | | 7.79 | | | 1.55 | TAM113 | | |

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Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-----------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| PH | Qph.tamu.2D.69 | 19MCG | 3.47 | 2D | 68.81 | 93 | chr2D_68797075 | 5.78 | | | 3.19 | | | 1.38 | TAM113 | y? | |
| PH | Qph.tamu.2D.32 | AcrossEnv | 6.51 | 2D | 32.27 | 59 | chr2D_31103643 | 43.91 | 34.77 | 9.14 | 36.3 | 20.82 | 15.49 | 1.36 | TAM113 | | |
| PH | Qph.tamu.2B.646 | 19BSP | 3.47 | 2B | 645.72 | 175 | chr2B_645610956 | 3.7 | | | 4.62 | | | 1.16 | TAM113 | | |
| PH | Qph.tamu.2D.31 | 21BD | 3.48 | 2D | 31.5 | 58 | chr2D_31103643 | 6.11 | | | 9.52 | | | 1.01 | TAM113 | | p |
| PH | Qph.tamu.3B.564 | 21BD | 3.48 | 3B | 563.95 | 110 | chr3B_563291707 | 3.65 | | | 5.51 | | | 0.77 | TAM113 | | |
| PH | Qph.tamu.5B.489 | AcrossEnv | 3.52 | 5B | 488.95 | 207 | chr5B_488397473 | 9.29 | 3.77 | 5.51 | 5.37 | 2.13 | 3.24 | 0.43 | TAM113 | | |
| PH | Qph.tamu.2D.69 | AcrossEnv | 6.51 | 2D | 68.81 | 93 | chr2D_68797075 | 6.99 | 3.14 | 3.85 | 4.29 | 1.789 | 2.5 | 0.4 | TAM113 | y? | |
| PH | Qph.tamu.4B.424 | AcrossEnv | 6.51 | 4B | 423.5 | 105 | chr4B_430792975 | 17.6 | 2.65 | 14.95 | 12.19 | 1.503 | 10.69 | 0.36 | TAM113 | y? | |
| PH | Qph.tamu.6A.318 | AcrossEnv | 6.51 | 6A | 318.04 | 100 | chr6A_383955363 | 8.57 | 1.04 | 7.53 | 3.72 | 0.552 | 3.16 | -0.22 | Gallagher | y? | |
| PH | Qph.tamu.6A.89 | AcrossEnv | 6.51 | 6A | 88.63 | 67 | chr6A_100368136 | 9.67 | 1.5 | 8.17 | 6.34 | 0.86 | 5.48 | -0.28 | Gallagher | | |
| PH | Qph.tamu.6A.397 | AcrossEnv | 6.51 | 6A | 397.39 | 88 | chr6A_369369749 | 12.1 | 1.5 | 10.59 | 4.11 | 0.87 | 3.24 | -0.28 | Gallagher | y? | |
| PH | Qph.tamu.6A.102 | AcrossEnv | 6.51 | 6A | 102.01 | 82 | chr6A_102090552 | 6.93 | 2.14 | 4.79 | 6.69 | 1.219 | 5.47 | -0.33 | Gallagher | y? | |
| PH | Qph.tamu.4B.615 | AcrossEnv | 6.51 | 4B | 614.94 | 265 | chr4B_612610190 | 7.19 | 2.26 | 4.93 | 3.12 | 1.267 | 1.86 | -0.33 | Gallagher | y? | |
| PH | Qph.tamu.6A.175 | AcrossEnv | 6.51 | 6A | 174.79 | 123 | chr6A_184344892 | 9.5 | 2.88 | 6.62 | 6.91 | 1.622 | 5.29 | -0.38 | Gallagher | y? | |
| PH | Qph.tamu.4B.50 | AcrossEnv | 6.51 | 4B | 50.4 | 91 | chr4B_56298857 | 7.52 | 3.06 | 4.46 | 4.33 | 1.74 | 2.59 | -0.39 | Gallagher | y? | |
| PH | Qph.tamu.1A.349 | AcrossEnv | 4.84 | 1A | 349.34 | 97 | chr1A_265556603 | 6.67 | 3.25 | 3.42 | 4.14 | 1.83 | 2.31 | -0.4 | Gallagher | y? | |
| PH | Qph.tamu.6A.86 | AcrossEnv | 6.51 | 6A | 86.43 | 70 | chr6A_86557461 | 17.97 | 3.54 | 14.43 | 12.77 | 2.021 | 10.74 | -0.42 | Gallagher | y? | |
| PH | Qph.tamu.1A.85 | AcrossEnv | 6.51 | 1A | 84.79 | 81 | chr1A_62276029 | 9.59 | 3.61 | 5.98 | 4.5 | 2.044 | 2.46 | -0.42 | Gallagher | | |
| PH | Qph.tamu.4B.505 | AcrossEnv | 6.51 | 4B | 505.5 | 66 | chr4B_508667019 | 7.19 | 3.96 | 3.23 | 4.35 | 2.207 | 2.14 | -0.44 | Gallagher | y? | |
| PH | Qph.tamu.4A.36 | AcrossEnv | 6.51 | 4A | 35.68 | 24 | chr4A_35060935 | 6.72 | 5.77 | 0.95 | 4.92 | 3.254 | 1.66 | -0.54 | Gallagher | | |
| PH | Qph.tamu.4B.646 | AcrossEnv | 6.51 | 4B | 645.96 | 285 | chr4B_645618725 | 8.5 | 6.34 | 2.16 | 6.89 | 3.609 | 3.28 | -0.56 | Gallagher | y? | |
| PH | Qph.tamu.4B.485 | AcrossEnv | 6.51 | 4B | 484.67 | 188 | chr4B_475417745 | 25.54 | 8.67 | 16.87 | 19.6 | 4.915 | 14.68 | -0.66 | Gallagher | y? | |

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Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| PH | Qph.tamu.1A.392 | 21BD | 3.48 | 1A | 391.69 | 101 | chr1A_385940529 | 3.85 | | | 5.74 | | | -0.78 | Gallagher | | |
| PH | Qph.tamu.3D.558 | 20CS | 3.5 | 3D | 558.14 | 90 | chr3D_558034362 | 3.53 | | | 3.72 | | | -1.06 | Gallagher | | |
| PH | Qph.tamu.4B.615 | 20EMN | 3.52 | 4B | 614.94 | 265 | chr4B_612610190 | 5.48 | | | 8.29 | | | -1.11 | Gallagher | y? | |
| PH | Qph.tamu.2A.385 | 19BSP | 3.47 | 2A | 384.67 | 125 | chr2A_271026277 | 4.43 | | | 5.57 | | | -1.27 | Gallagher | | |
| PH | Qph.tamu.1A.349 | 20CS | 3.5 | 1A | 349.34 | 97 | chr1A_265556603 | 5.43 | | | 5.94 | | | -1.35 | Gallagher | y? | |
| PH | Qph.tamu.4B.505 | 19BSP | 3.47 | 4B | 505.5 | 66 | chr4B_508667019 | 4.99 | | | 6.52 | | | -1.37 | Gallagher | y? | |
| PH | Qph.tamu.1A.60 | 20EMN | 3.52 | 1A | 59.87 | 80 | chr1A_45627022 | 8.42 | | | 13.33 | | | -1.41 | Gallagher | | |
| PH | Qph.tamu.4B.50 | 20CS | 3.5 | 4B | 50.4 | 91 | chr4B_56298857 | 6.08 | | | 6.49 | | | -1.41 | Gallagher | y? | |
| PH | Qph.tamu.6A.318 | 20EMN | 3.52 | 6A | 318.04 | 100 | chr6A_383955363 | 8.4 | | | 13.92 | | | -1.44 | Gallagher | y? | |
| PH | Qph.tamu.6A.397 | 21BD | 3.48 | 6A | 397.39 | 88 | chr6A_369369749 | 11.82 | | | 19.43 | | | -1.45 | Gallagher | y? | |
| PH | Qph.tamu.4B.646 | 20MCG | 3.48 | 4B | 645.96 | 285 | chr4B_645618725 | 5.77 | | | 7.17 | | | -1.74 | Gallagher | y? | |
| PH | Qph.tamu.6A.89 | 19MCG | 3.47 | 6A | 88.63 | 67 | chr6A_100368136 | 9.62 | | | 5.65 | | | -1.85 | Gallagher | | |
| PH | Qph.tamu.6A.102 | 20MCG | 3.48 | 6A | 102.01 | 82 | chr6A_102090552 | 6.66 | | | 8.44 | | | -1.88 | Gallagher | y? | |
| PH | Qph.tamu.6A.175 | 19BSP | 3.47 | 6A | 174.79 | 123 | chr6A_184344892 | 9.25 | | | 12.9 | | | -1.93 | Gallagher | y? | |
| PH | Qph.tamu.6A.86 | 20CS | 3.5 | 6A | 86.43 | 70 | chr6A_86557461 | 17.95 | | | 22.36 | | | -2.62 | Gallagher | y? | |
| PH | Qph.tamu.4B.485 | 19MCG | 3.47 | 4B | 484.67 | 188 | chr4B_475417745 | 24.05 | | | 17.25 | | | -3.22 | Gallagher | y? | |
| SHDW | Qshdw.tamu.2A.747 | 19BSP | 3.51 | 2A | 746.93 | 36 | chr2A_746960172 | 5.04 | | | 10.43 | | | 0.03 | TAM113 | y? | p |
| SHDW | Qshdw.tamu.2A.747 | AcrossEnv | 4.9 | 2A | 746.93 | 36 | chr2A_746960172 | 5.92 | 3 | 2.93 | 4.09 | 3.418 | 0.67 | 0.02 | TAM113 | y? | p |
| SHDW | Qshdw.tamu.1A.74 | AcrossEnv | 4.9 | 1A | 74.22 | 118 | chr1A_74644136 | 6.15 | 4.55 | 1.6 | 5.22 | 5.164 | 0.06 | -0.02 | Gallagher | y? | p |
| SHDW | Qshdw.tamu.1A.74 | 19BSP | 3.51 | 1A | 74.22 | 118 | chr1A_74644136 | 3.72 | | | 7.58 | | | -0.03 | Gallagher | y? | p |
| SHDW | Qshdw.tamu.2D.264 | 19BSP | 3.51 | 2D | 263.59 | 129 | chr2D_267421652 | 3.83 | | | 7.78 | | | -0.03 | Gallagher | | |
| SHDW | Qshdw.tamu.2D.37 | AcrossEnv | 4.9 | 2D | 37.25 | 64 | chr2D_37211804 | 11.56 | 10.41 | 1.15 | 23.96 | 12.4 | 11.56 | -0.04 | Gallagher | y? | p |

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Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|--------|-----------------------|-------|-------|
| SHDW | Qshdw.tamu.2D.37 | 21BD | 3.51 | 2D | 37.25 | 64 | chr2D_37211804 | 10.33 | | | 22.16 | | | -0.09 | Gallagher | y? | p |
| SHGW | Qshgw.tamu.2B.76 | 21BD | 3.51 | 2B | 76.4 | 109 | chr2B_68426788 | 4.86 | | | 10.68 | | | 0.06 | TAM113 | | p |
| SHGW | Qshgw.tamu.7D.55 | 21BD | 3.51 | 7D | 55.4 | 71 | chr7D_54833302 | 4.57 | | | 10.23 | | | 0.06 | TAM113 | | |
| SHGW | Qshgw.tamu.2A.747 | 19BSP | 3.51 | 2A | 746.93 | 36 | chr2A_746960172 | 5.43 | | | 10.08 | | | 0.03 | TAM113 | y? | p |
| SHGW | Qshgw.tamu.7D.55 | AcrossEnv | 4.76 | 7D | 55.4 | 71 | chr7D_54833302 | 6.17 | 6.13 | 0.04 | 12.4 | 7.478 | 4.92 | 0.03 | TAM113 | | |
| SHGW | Qshgw.tamu.2B.69 | AcrossEnv | 4.76 | 2B | 69.34 | 108 | chr2B_68426788 | 5.12 | 4.51 | 0.61 | 12.88 | 5.652 | 7.22 | 0.02 | TAM113 | | p |
| SHGW | Qshgw.tamu.7D.68 | AcrossEnv | 4.76 | 7D | 68.43 | 92 | chr7D_63208599 | 5.07 | 2.53 | 2.54 | 3.15 | 3.009 | 0.14 | 0.02 | TAM113 | | |
| SHGW | Qshgw.tamu.2A.747 | AcrossEnv | 4.76 | 2A | 746.93 | 36 | chr2A_746960172 | 5.64 | 1.19 | 4.45 | 2.93 | 1.472 | 1.46 | 0.01 | TAM113 | y? | p |
| SHGW | Qshgw.tamu.2D.34 | AcrossEnv | 4.76 | 2D | 34.43 | 61 | chr2D_32901354 | 7.69 | 4.78 | 2.91 | 6.46 | 5.83 | 0.63 | -0.02 | Gallagher | y? | p |
| SHGW | Qshgw.tamu.2D.34 | 19BSP | 3.51 | 2D | 34.43 | 61 | chr2D_32901354 | 5.65 | | | 10.55 | | | -0.03 | Gallagher | y? | p |
| SKW | Qskw.tamu.6D.172 | 20MCG | 3.48 | 6D | 171.52 | 28 | chr6D_172603833 | 6.14 | | | 8.96 | | | 0.86 | TAM113 | | p |
| SKW | Qskw.tamu.5A.606 | 20MCG | 3.48 | 5A | 606.28 | 142 | chr5A_604579136 | 3.99 | | | 5.64 | | | 0.68 | TAM113 | | |
| SKW | Qskw.tamu.2D.37 | 20MCG | 3.48 | 2D | 36.9 | 63 | chr2D_36584261 | 8.41 | | | 12.56 | | | -1.02 | Gallagher | | p |
| SKW | Qskw.tamu.6A.573 | 20MCG | 3.48 | 6A | 573.08 | 189 | chr6A_571690944 | 8.37 | | | 12.93 | | | -1.03 | Gallagher | | |
| SPM | Qspm.tamu.5A.637 | AcrossEnv | 4.81 | 5A | 637.08 | 159 | chr5A_636992509 | 5.31 | 4.15 | 1.16 | 6.17 | 4.758 | 1.41 | -20.88 | Gallagher | y? | |
| SPM | Qspm.tamu.5A.637 | 20EMN | 3.52 | 5A | 637.08 | 159 | chr5A_636992509 | 4.1 | | | 10.67 | | | -36.3 | Gallagher | y? | |
| SSHW | Qsshw.tamu.2B.28 | 20EMN | 3.51 | 2B | 28.1 | 56 | chr2B_28097658 | 60.92 | | | 18.59 | | | 0.24 | TAM113 | y? | |
| SSHW | Qsshw.tamu.4A.447 | 19BSP | 3.51 | 4A | 447.31 | 139 | chr4A_335786182 | 25.89 | | | 8.85 | | | 0.23 | TAM113 | y? | |
| SSHW | Qsshw.tamu.4B.224 | 20EMN | 3.51 | 4B | 223.89 | 116 | chr4B_210535748 | 19.85 | | | 3.49 | | | 0.1 | TAM113 | y? | |
| SSHW | Qsshw.tamu.4A.447 | AcrossEnv | 4.8 | 4A | 447.31 | 139 | chr4A_335786182 | 26.44 | 20.39 | 6.05 | 16.57 | 5.868 | 10.7 | 0.08 | TAM113 | y? | |
| SSHW | Qsshw.tamu.2B.28 | AcrossEnv | 4.8 | 2B | 28.1 | 56 | chr2B_28097658 | 61.19 | 16.42 | 44.76 | 17.03 | 4.602 | 12.43 | 0.07 | TAM113 | y? | |
| SSHW | Qsshw.tamu.5A.628 | 20EMN | 3.51 | 5A | 628.13 | 153 | chr5A_626143346 | 5.49 | | | 0.8 | | | 0.05 | TAM113 | | |

Abbreviation of traits; BMYLD: Biomass Grain Yield from 0.5-meter inner row, HARD: Kernel Hardness, HD: Heading Date, HI: Harvest Index, HeatWt: Head Weight, KA: Kernel Area, KHI: Kernel Hardness Index, KLEN: Kernel Length, KPS: Kernels spike⁻¹, KWID: Kernel Width, PERI: Perimeter, PH: Plant Height, SHDW: Single Head Dry Weight, SHGW: Single Head Grain Weight, SKW: Single Kernel weight, SPM: Spikes m⁻², SSHW: Single Stem Head Weight, TKW: Thousand Kernel Weight, YLD: Grain Yield from combine harvester. Abbreviation of Environments (Env); AcrossEnv: Across Environments, 19CS: College Station 2019, 20CS: College Station 2020, 21BD: Bushland Dryland 2021, 19BSP: Bushland South Pivot 2019, 19MCG: McGregor 2019, 20MCG: McGregor 2020, 20EMN: Emeny Land 2020, LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AbyE: Additive by Environment Effect, Add: Additive Effect, cM: centimorgan, Plei: Pleiotropic, p: affecting more than one trait, Cons: Consistent, y: identified at least two single environment, y?: identified one individual and across environment

Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|-------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| SSHW | Qsshw.tamu.4B.224 | AcrossEnv | 4.8 | 4B | 223.89 | 116 | chr4B_210535748 | 19.91 | 4.51 | 15.4 | 3.15 | 1.242 | 1.91 | 0.04 | TAM113 | y? | |
| SSHW | Qsshw.tamu.5A.627 | AcrossEnv | 4.8 | 5A | 626.72 | 152 | chr5A_626143346 | 7.2 | 4.7 | 2.51 | 1.46 | 1.15 | 0.31 | 0.04 | TAM113 | | |
| SSHW | Qsshw.tamu.2D.31 | AcrossEnv | 4.8 | 2D | 31.5 | 58 | chr2D_31103643 | 14 | 5.14 | 8.86 | 3.04 | 1.312 | 1.73 | -0.04 | Gallagher | | p |
| SSHW | Qsshw.tamu.4B.238 | AcrossEnv | 4.8 | 4B | 237.93 | 131 | chr4B_214009418 | 28.34 | 6.13 | 22.21 | 4.98 | 1.651 | 3.32 | -0.04 | Gallagher | y? | |
| SSHW | Qsshw.tamu.4D.489 | 21BD | 3.51 | 4D | 488.73 | 84 | chr4D_488578794 | 3.52 | | | 5.85 | | | -0.05 | Gallagher | | |
| SSHW | Qsshw.tamu.1A.293 | AcrossEnv | 4.8 | 1A | 293.1 | 117 | chr1A_332686690 | 10.48 | 8.06 | 2.42 | 2.62 | 2.149 | 0.47 | -0.05 | Gallagher | y? | |
| SSHW | Qsshw.tamu.1A.293 | 20EMN | 3.51 | 1A | 293.1 | 117 | chr1A_332686690 | 6.39 | | | 0.93 | | | -0.05 | Gallagher | y? | |
| SSHW | Qsshw.tamu.1A.74 | 19BSP | 3.51 | 1A | 74.22 | 118 | chr1A_74644136 | 3.77 | | | 0.96 | | | -0.08 | Gallagher | | p |
| SSHW | Qsshw.tamu.4B.17 | 19BSP | 3.51 | 4B | 16.56 | 22 | chr4B_16480364 | 4.23 | | | 1.11 | | | -0.08 | Gallagher | | |
| SSHW | Qsshw.tamu.4A.409 | AcrossEnv | 4.8 | 4A | 409.3 | 150 | chr4A_493726644 | 35.55 | 27.67 | 7.88 | 25.63 | 8.397 | 17.24 | -0.1 | Gallagher | y? | |
| SSHW | Qsshw.tamu.2D.31 | 21BD | 3.51 | 2D | 31.5 | 58 | chr2D_31103643 | 13.84 | | | 26.43 | | | -0.1 | Gallagher | | p |
| SSHW | Qsshw.tamu.4B.238 | 20EMN | 3.51 | 4B | 237.93 | 131 | chr4B_214009418 | 28.26 | | | 5.57 | | | -0.13 | Gallagher | y? | |
| SSHW | Qsshw.tamu.4A.409 | 19BSP | 3.51 | 4A | 409.3 | 150 | chr4A_493726644 | 35.2 | | | 13.82 | | | -0.29 | Gallagher | y? | |
| TKW | Qtkw.tamu.7D.65 | 19BSP | 3.47 | 7D | 65.22 | 88 | chr7D_63208599 | 8.44 | | | 12.89 | | | 1.14 | TAM113 | | |
| TKW | Qtkw.tamu.7D.62 | AcrossEnv | 4.94 | 7D | 62.01 | 85 | chr7D_61665314 | 9.96 | 7.7 | 2.26 | 13.33 | 10.02 | 3.31 | 0.58 | TAM113 | | |
| TKW | Qtkw.tamu.6A.161 | AcrossEnv | 4.6 | 6A | 160.62 | 116 | chr6A_162293239 | 7.33 | 2.21 | 5.13 | 9.78 | 2.847 | 6.94 | -0.31 | Gallagher | y? | |
| TKW | Qtkw.tamu.4D.19 | AcrossEnv | 4.94 | 4D | 18.87 | 28 | chr4D_9929888 | 5.29 | 2.76 | 2.53 | 6.41 | 3.556 | 2.86 | -0.35 | Gallagher | y? | |
| TKW | Qtkw.tamu.1B.620 | AcrossEnv | 4.6 | 1B | 619.6 | 24 | chr1B_619535304 | 5.02 | 2.9 | 2.12 | 7.25 | 3.725 | 3.53 | -0.36 | Gallagher | | |
| TKW | Qtkw.tamu.2D.37 | AcrossEnv | 4.6 | 2D | 37.25 | 64 | chr2D_37211804 | 5.87 | 3.33 | 2.54 | 9.2 | 4.292 | 4.9 | -0.38 | Gallagher | y? | p |
| TKW | Qtkw.tamu.2D.34 | AcrossEnv | 4.6 | 2D | 34.43 | 61 | chr2D_32901354 | 12.41 | 5.48 | 6.93 | 17.44 | 7.157 | 10.29 | -0.49 | Gallagher | y? | p |
| TKW | Qtkw.tamu.7A.640 | 19BSP | 3.47 | 7A | 639.97 | 215 | chr7A_638247862 | 3.53 | | | 4.57 | | | -0.68 | Gallagher | | |
| TKW | Qtkw.tamu.6A.573 | 21BD | 3.53 | 6A | 573.37 | 190 | chr6A_573274893 | 4.12 | | | 8.9 | | | -0.73 | Gallagher | | |

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Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|-------|-----------------------|-------|-------|
| TKW | Qtkw.tamu.4D.19 | 21BD | 3.53 | 4D | 18.87 | 28 | chr4D_9929888 | 4.98 | | | 10.48 | | | -0.79 | Gallagher | y? | |
| TKW | Qtkw.tamu.6A.572 | 20EMN | 3.52 | 6A | 572.01 | 185 | chr6A_572104165 | 4.06 | | | 8.68 | | | -0.81 | Gallagher | | |
| TKW | Qtkw.tamu.2D.37 | 20EMN | 3.52 | 2D | 37.25 | 64 | chr2D_37211804 | 5.62 | | | 12.11 | | | -0.96 | Gallagher | y? | p |
| TKW | Qtkw.tamu.6A.161 | 19BSP | 3.47 | 6A | 160.62 | 116 | chr6A_162293239 | 7.15 | | | 9.66 | | | -0.99 | Gallagher | y? | |
| TKW | Qtkw.tamu.2D.34 | 19BSP | 3.47 | 2D | 34.43 | 61 | chr2D_32901354 | 12.18 | | | 17.46 | | | -1.33 | Gallagher | y? | p |
| YLD | Qyld.tamu.7D.52 | 19CS | 3.63 | 7D | 52.32 | 66 | chr7D_51735477 | 11.61 | | | 12.13 | | | 24.16 | TAM113 | y | p |
| YLD | Qyld.tamu.7D.66 | 20MCG | 3.59 | 7D | 66.02 | 89 | chr7D_63208599 | 5.62 | | | 7.83 | | | 22.21 | TAM113 | | p |
| YLD | Qyld.tamu.4A.76 | 20CS | 3.5 | 4A | 75.9 | 40 | chr4A_69708392 | 8.54 | | | 5.82 | | | 17.44 | TAM113 | y? | |
| YLD | Qyld.tamu.2B.58 | 20MCG | 3.59 | 2B | 57.61 | 101 | chr2B_57657606 | 3.68 | | | 4.34 | | | 16.56 | TAM113 | | p |
| YLD | Qyld.tamu.2B.571 | 21BD | 3.48 | 2B | 571.41 | 156 | chr2B_572204779 | 7.68 | | | 16.6 | | | 16.26 | TAM113 | y? | |
| YLD | Qyld.tamu.4A.710 | 19CS | 3.63 | 4A | 710.33 | 352 | chr4A_709865490 | 4.94 | | | 4.68 | | | 14.99 | TAM113 | | |
| YLD | Qyld.tamu.2B.64 | 21BD | 3.48 | 2B | 63.96 | 105 | chr2B_63428577 | 6.18 | | | 13.12 | | | 14.47 | TAM113 | y? | p |
| YLD | Qyld.tamu.7D.52 | 19BSP | 3.47 | 7D | 52.32 | 66 | chr7D_51735477 | 9.69 | | | 16.87 | | | 13.17 | TAM113 | y | p |
| YLD | Qyld.tamu.7B.4 | 19CS | 3.63 | 7B | 4.22 | 12 | chr7B_4035451 | 3.8 | | | 3.58 | | | 13.1 | TAM113 | | |
| YLD | Qyld.tamu.6D.10 | 20CS | 3.5 | 6D | 10.33 | 20 | chr6D_10311612 | 4.94 | | | 3.21 | | | 12.99 | TAM113 | | |
| YLD | Qyld.tamu.2B.85 | 19CS | 3.63 | 2B | 84.91 | 113 | chr2B_76076511 | 3.67 | | | 3.46 | | | 12.96 | TAM113 | | p |
| YLD | Qyld.tamu.7D.52 | AcrossEnv | 6.4 | 7D | 52.32 | 66 | chr7D_51735477 | 21.59 | 7.27 | 14.32 | 12.88 | 5.282 | 7.59 | 7.08 | TAM113 | y | p |
| YLD | Qyld.tamu.2B.64 | AcrossEnv | 6.4 | 2B | 63.96 | 105 | chr2B_63428577 | 7.77 | 3.05 | 4.72 | 4.26 | 2.198 | 2.07 | 4.58 | TAM113 | y? | p |
| YLD | Qyld.tamu.2B.571 | AcrossEnv | 6.4 | 2B | 571.41 | 156 | chr2B_572204779 | 8.09 | 2.11 | 5.98 | 4.83 | 1.531 | 3.3 | 3.82 | TAM113 | y? | |
| YLD | Qyld.tamu.4A.76 | AcrossEnv | 6.4 | 4A | 75.9 | 40 | chr4A_69708392 | 9.62 | 0.54 | 9.09 | 5.87 | 0.391 | 5.48 | 1.92 | TAM113 | y? | |
| YLD | Qyld.tamu.1A.11 | AcrossEnv | 6.4 | 1A | 11.28 | 8 | chr1A_11207721 | 7.55 | 0.11 | 7.44 | 4.87 | 0.083 | 4.79 | -0.89 | Gallagher | y? | |
| YLD | Qyld.tamu.4A.484 | AcrossEnv | 6.4 | 4A | 483.81 | 91 | chr4A_486382996 | 18.4 | 4.86 | 13.55 | 12.49 | 3.552 | 8.94 | -5.8 | Gallagher | y? | |

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Table A2. Continued

| Trait | QTL name | Env. | Thres. | Chr. | Peak position (Mbp) | Position (cM) | LeftMarker | LOD | LOD (A) | LOD (AbyE) | PVE | PVE (A) | PVE (AbyE) | Add | Allele Increase Trait | Cons. | Plei. |
|-------|------------------|-----------|--------|------|---------------------|---------------|-----------------|-------|---------|------------|-------|---------|------------|--------|-----------------------|-------|-------|
| YLD | Qyld.tamu.7B.728 | 19BSP | 3.47 | 7B | 728.09 | 162 | chr7B_728700316 | 3.93 | | | 6.32 | | | -8.05 | Gallagher | | |
| YLD | Qyld.tamu.2D.34 | AcrossEnv | 6.4 | 2D | 34.43 | 61 | chr2D_32901354 | 21.12 | 9.22 | 11.9 | 17.58 | 6.903 | 10.67 | -8.11 | Gallagher | y? | p |
| YLD | Qyld.tamu.1B.567 | AcrossEnv | 6.4 | 1B | 566.97 | 9 | chr1B_566956619 | 19.47 | 9.96 | 9.52 | 14.68 | 7.368 | 7.32 | -8.38 | Gallagher | y | |
| YLD | Qyld.tamu.2D.37 | AcrossEnv | 6.4 | 2D | 36.9 | 63 | chr2D_36584261 | 33.4 | 11.37 | 22.03 | 26.15 | 8.528 | 17.62 | -9 | Gallagher | y | p |
| YLD | Qyld.tamu.1A.564 | 20CS | 3.5 | 1A | 563.99 | 200 | chr1A_563051268 | 3.59 | | | 2.31 | | | -11.02 | Gallagher | | |
| YLD | Qyld.tamu.7B.717 | 20CS | 3.5 | 7B | 717.42 | 153 | chr7B_716454686 | 3.91 | | | 2.54 | | | -11.53 | Gallagher | | |
| YLD | Qyld.tamu.4B.623 | 20CS | 3.52 | 4B | 623.17 | 268 | chr4B_623071554 | 4.16 | | | 2.66 | | | -11.79 | Gallagher | | |
| YLD | Qyld.tamu.1A.11 | 20CS | 3.5 | 1A | 11.28 | 8 | chr1A_11207721 | 6.97 | | | 4.7 | | | -15.7 | Gallagher | y? | |
| YLD | Qyld.tamu.1B.567 | 20CS | 3.5 | 1B | 566.97 | 9 | chr1B_566956619 | 8.6 | | | 5.78 | | | -17.46 | Gallagher | y | |
| YLD | Qyld.tamu.1B.567 | 19CS | 3.63 | 1B | 566.97 | 9 | chr1B_566956619 | 9.59 | | | 9.38 | | | -21.3 | Gallagher | y | |
| YLD | Qyld.tamu.7D.275 | 20MCG | 3.59 | 7D | 275.08 | 174 | chr7D_274379353 | 6.27 | | | 7.63 | | | -21.97 | Gallagher | | |
| YLD | Qyld.tamu.1B.567 | 20MCG | 3.59 | 1B | 566.97 | 9 | chr1B_566956619 | 7.27 | | | 8.9 | | | -23.75 | Gallagher | Y | |
| YLD | Qyld.tamu.4A.484 | 20CS | 3.5 | 4A | 483.81 | 91 | chr4A_486382996 | 17.3 | | | 12.87 | | | -25.96 | Gallagher | y? | |
| YLD | Qyld.tamu.2D.37 | 20MCG | 3.59 | 2D | 36.9 | 63 | chr2D_36584261 | 9.14 | | | 11.73 | | | -27.2 | Gallagher | y | p |
| YLD | Qyld.tamu.7B.731 | 20MCG | 3.59 | 7B | 731.14 | 171 | chr7B_732628699 | 9.37 | | | 12.19 | | | -27.69 | Gallagher | | |
| YLD | Qyld.tamu.2D.34 | 19CS | 3.63 | 2D | 34.43 | 61 | chr2D_32901354 | 17.57 | | | 19.14 | | | -30.42 | Gallagher | y? | p |
| YLD | Qyld.tamu.2D.37 | 20CS | 3.5 | 2D | 36.9 | 63 | chr2D_36584261 | 30.09 | | | 26.99 | | | -37.64 | Gallagher | y | p |

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Table A3. Epistatic interactions involved with major QTL

| Trait | Loci 1 | Position (cM) 1 | peak Mbp | LeftMarker1 | Loci 2 | Position (cM) 2 | Peak (Mbp) 2 | LeftMarker2 | LOD | LOD (AA) | LOD (AAbyE) | PVE | PVE (AA) | PVE (AAbyE) | Add1 | Add2 | AddbyAdd |
|-------|-----------------|-----------------|----------|-----------------|-----------------|-----------------|--------------|-----------------|------|----------|-------------|-----|----------|-------------|------|------|----------|
| YLD | Qyld.tamu.4B.11 | 5 | 10.6 | chr4B_10393064 | Qyld.tamu.6D.10 | 20 | 10.3 | chr6D_10311612 | 6.0 | 4.0 | 2.0 | 1.2 | 0.8 | 0.4 | -2.0 | 1.4 | 5.2 |
| YLD | Qyld.tamu.4B.13 | 15 | 12.8 | chr4B_12369792 | Qyld.tamu.6D.10 | 20 | 10.3 | chr6D_10311612 | 5.4 | 2.0 | 3.4 | 1.0 | 0.4 | 0.6 | 0.8 | 2.0 | -3.6 |
| YLD | Qyld.tamu.2B.64 | 105 | 64.0 | chr2B_63428577 | Qyld.tamu.5B.1 | 0 | 1.0 | chr5B_978437 | 5.8 | 3.6 | 2.2 | 0.9 | 0.6 | 0.3 | 0.8 | -2.5 | -4.6 |
| YLD | Qyld.tamu.2D.34 | 60 | 33.1 | chr2D_32901354 | Qyld.tamu.5B.21 | 40 | 21.1 | chr5B_20696411 | 6.0 | 2.7 | 3.3 | 1.1 | 0.5 | 0.6 | -3.5 | -3.3 | -4.2 |
| HD | Qhd.tamu.1A.566 | 205 | 566.3 | chr1A_565388907 | Qhd.tamu.4A.714 | 380 | 713.7 | chr4A_708146969 | 7.8 | 4.9 | 2.9 | 1.3 | 0.8 | 0.5 | 0.5 | 0.1 | -0.5 |
| HD | Qhd.tamu.2B.106 | 115 | 106.1 | chr2B_101775233 | Qhd.tamu.2D.33 | 60 | 33.1 | chr2D_32901354 | 13.5 | 9.4 | 4.1 | 1.6 | 1.6 | 0.1 | -0.1 | 3.0 | -0.7 |
| HD | Qhd.tamu.3D.603 | 145 | 602.6 | chr3D_602632145 | Qhd.tamu.7A.709 | 270 | 702.6 | chr7A_701123987 | 5.5 | 3.8 | 1.7 | 0.8 | 0.6 | 0.2 | -0.1 | 0.2 | -0.4 |
| HD | Qhd.tamu.1B.620 | 25 | 620.0 | chr1B_619535304 | Qhd.tamu.7A.709 | 280 | 707.0 | chr7A_701123987 | 10.6 | 8.3 | 2.3 | 1.4 | 1.2 | 0.2 | 0.1 | 0.2 | 0.6 |
| HD | Qhd.tamu.6B.660 | 65 | 660.2 | chr6B_656922280 | Qhd.tamu.7D.608 | 330 | 607.8 | chr7D_611166154 | 8.2 | 4.8 | 3.4 | 1.2 | 0.7 | 0.5 | 0.1 | 0.6 | 0.5 |
| PH | Qph.tamu.3B.564 | 110 | 563.9 | chr3B_563291707 | Qph.tamu.3B.625 | 160 | 625.5 | chr3B_625827886 | 6.5 | 2.4 | 4.1 | 0.1 | 0.1 | 0.0 | -1.1 | 1.3 | 1.1 |
| PH | Qph.tamu.2D.30 | 55 | 30.0 | chr2D_22290058 | Qph.tamu.6A.596 | 220 | 595.5 | chr6A_595061983 | 7.1 | 0.8 | 6.3 | 1.0 | 0.1 | 0.8 | 0.5 | 0.2 | -0.2 |
| PH | Qph.tamu.2D.30 | 55 | 30.0 | chr2D_22290058 | Qph.tamu.6D.458 | 100 | 457.6 | chr6D_457987070 | 6.3 | 3.5 | 2.8 | 0.9 | 0.5 | 0.4 | 0.5 | -0.1 | 0.4 |
| PH | Qph.tamu.4B.646 | 285 | 646.0 | chr4B_645618725 | Qph.tamu.7D.33 | 40 | 33.4 | chr7D_28855364 | 6.1 | 4.1 | 2.0 | 0.8 | 0.6 | 0.2 | -0.5 | -0.1 | -0.4 |

Abbreviation of traits; HD: Heading Date, PH: Plant Height, YLD: Grain Yield from combine harvester. LOD: Logarithm of the Odds, PVE: Phenotypic Variation Explained, AA: additive by additive (Epistasis), AAbyE; Epistasis by environment interaction, AddbyAdd: Additive by Additive, Add: Additive Effect, cM: centimorgan.

Figure A1: Phenotypic distribution of grain yield across six environments in Texas.

