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GENETIC MAPPING OF GRASS MONOCULTURE AND GRASS-LEGUME
MIXTURE COMPATIBILITY QTLs IN INTERMEDIATE WHEATGRASS

by

John Mortenson

A thesis submitted in partial fulfillment
of the requirements for the degree

of

MASTERS OF SCIENCE

in

Plant Science

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2019

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ABSTRACT

Genetic Mapping of Grass Monoculture and Grass-Legume Mixture Compatibility QTLs
in Intermediate Wheatgrass

by

John S. Mortenson, Master of Science

Utah State University, 2019

Major Professor: Dr. Earl Creech

Department: Plants, Soil and Climate

Due to increased environmental stewardship and fertilizer prices, there is increased interest in using legume mixes in perennial croplands. The objective of this study was to compare quantitative genetic parameters and quantitative trait loci (QTLs) associated with intermediate wheatgrass (*Thinopyrum intermedium*) when grown in 1) a non-competitive spaced environment, 2) a polyculture with alfalfa (*Medicago sativa*), and 3) a monoculture with crested wheatgrass (*Agropyron desertorum*). Traits evaluated include plant growth characteristics (Zadok's maturity, height, and tiller count), biomass, and forage nutritive value (CP, NDF, ADF, ADL, IVTD, NDFD, NFC, ME, RFQ). A linkage map comprised of 3568 single nucleotide polymorphisms in 21 linkage groups corresponding to 21 homologous chromosome pairs of both parents was used to identify QTLs and QTL x environment interactions (QxE) based on trait averages for each genotype in each environment. Significant genotype x environment interactions were detected for biomass, NDF etc. A total of 26 QTLs were identified, including 6 MASS, 2 TILE, 2 TICR, 1 ZAMA, 1 CP, 3 NDF, 2 ADF, 3 IVTD, and 5 NDFD. A subset of 7

QTLs showed significant QxE interaction. These results indicate that breeders need to evaluate plants in polyculture or swards if these are the intended crop management systems.

PUBLIC ABSTRACT

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John S. Mortenson

Due to increased environmental stewardship and fertilizer prices, there is increased interest in using legume mixes in perennial croplands. The objective of this study was to compare quantitative genetic parameters and quantitative trait loci (QTLs) associated with intermediate wheatgrass (*Thinopyrum intermedium*) when grown in 1) a non-competitive spaced environment, 2) a polyculture with alfalfa (*Medicago sativa*), and 3) a monoculture with crested wheatgrass (*Agropyron desertorum*). Traits evaluated include plant growth characteristics (Zadok's maturity, height, and tiller count), biomass, and forage nutritive value (CP, NDF, ADF, ADL, IVTD, NDFD, NFC, ME, RFQ). A linkage map comprised of 3568 single nucleotide polymorphisms in 21 linkage groups corresponding to 21 homologous chromosome pairs of both parents was used to identify QTLs and QTL x environment interactions (QxE) based on trait averages for each genotype in each environment. Significant genotype x environment interactions were detected for biomass, NDF etc. A total of 26 QTLs were identified, including 6 MASS, 2 TILE, 2 TICR, 1 ZAMA, 1 CP, 3 NDF, 2 ADF, 3 IVTD, and 5 NDFD. A subset of 7 QTLs showed significant QxE interaction. These results indicate that breeders need to evaluate plants in polyculture or swards if these are the intended crop management systems.

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INTRODUCTION AND LITERATURE REVIEW

Benefits of Grass-Legume Polycultures

Crop diversity can positively affect crop productivity, resource use efficiency, and tolerance and resilience to biotic and abiotic stressors, making it a key aspect of agroecosystems (Bybee-Finley, Mirsky, & Ryan, 2016). Intercropping, or growing plants in polyculture, is more common in perennial forage systems where mechanical and biological constraints are less problematic (Bybee-Finley et al., 2016). Systems that emphasize crop diversity, such as grass-legume polycultures, can potentially outperform simplified cropping systems in terms of enhanced supporting and regulating ecosystem services and increased resilience to biotic and abiotic stressors (Bybee-Finley et al., 2016). To maximize benefits of intercropping, one must look at the functional diversity of the species in the polyculture, meaning that the species should occupy different ecological niches that do not overlap each other. These can include nitrogen fixation, rooting depth and plant physiology (Bybee-Finley et al., 2016; Jungers, Wyse, & Sheaffer, 2015; Laidlaw & Teuber, 2001). These niches can develop naturally in nature so that one species does not fight another species for resources (J Hill, 1990). There are two mechanisms that arise in complementary intercropping polycultures, resource partitioning and facilitation of a limited resource like nitrogen (Bybee-Finley et al., 2016). Temperate grasses tend to be less aggressive and are more suitable to be grown in a polyculture with forage legumes than other types of grasses (Laidlaw & Teuber, 2001).

About 37% of non-federal land in the continental United States is either rangeland, pasture, or in the Conservation Reserve Program (Riday & Charles Brummer,

2014). Legumes are often used in pastures and rangelands, and forage legume breeders often consider the benefits of grass-legume mixes (Riday & Charles Brummer, 2014). Cool-season grass-legume pastures are the basis of beef and dairy grazing production systems in warm and warm-temperate regions (Tejera, Speranza, Astigarraga, & Picasso, 2015), where they often improve herbage productivity and animal forage intake (Sanderson, Stout, & Brink, 2016). Furthermore, grass-legume mixtures improves livestock growth performance in comparison to fertilized and unfertilized grass swards, by having improved nutritive value and more consistent distribution of forage throughout the year (Bingham, 2014; Lauriault, Kirksey, & VanLeeuwen, 2005; Mouriño, Albrecht, Schaefer, & Berzaghi, 2003; Wen et al., 2002). The nitrogen supplied by the legume reduces the amount of nitrogen fertilizer needed and it increases the amount of crude protein the grass would produce compared to when it is grown in a non-fertilized monoculture (Bingham, 2014). In a study involving an alfalfa and meadow brome mixture, it was shown that 27 to 32% of the nitrogen used by the meadow brome was provided by the alfalfa (Walley, Tomm, Matus, Slinkard, & van Kessel, 1996). The NDF values in grass-legume polycultures are generally less than in a grass monocultures (Bingham, 2014). Grass-legume polycultures have greater herbage mass compared to non-fertilized grass monocultures, with improved seasonal distribution of herbage production, which increases the ability of a pasture to support livestock grazing throughout the summer (Waldron, Peel, Larson, Mott, & Creech, 2017).

The benefits of a grass-legume mixture are only realized if the grass and the legume are compatible (Sanderson et al., 2016). Furthermore, grasses that are only exposed to monoculture intra-specific competition would not possess the optimal

biological characteristic to thrive in a grass-legume polyculture, as opposed to a grasses specifically developed using the inter-specific competition of polyculture (Waldron et al., 2017; Waldron, Robins, Peel, & Jensen, 2008). This is defined as their ‘ecological combining ability’ or ECA, which is niche differentiation (J. Hill, 1990). Breeding for improved ECA can reduce competitive exclusion between plant species, whereas reciprocal recurrent breeding for ECA between grasses and legumes is predicted to improve performance of grass-legume mixtures (J. Hill, 1990; Waldron et al., 2017; Waldron et al., 2008).

Genotype by Environment Interaction

Phenotypic traits are considered quantitative when they show continuous variation is often affected by more than one gene and can be influenced by the environment, such as biomass and forage nutritive value (Bernardo, 2002). When the environment affects a quantitative trait it in turn affects the expression of the genes (Bernardo, 2002; Falconer, 1989; Lynch & Walsh, 1998). The genotypes of plants that are grown in trials with multiple environments may react differently due to the different climate conditions, soil characteristics, or technical practices. The different responses of genotypes in the various environments are called GxE or genotype by environment interaction (Lacaze & Roumet, 2004). It can also be considered to be the measurement of the relative plasticity of genotypes in terms of the expression of specific phenotypes in the context of variable environmental influences (de Leon, Jannink, Edwards, & Kaeppler, 2016).

Environmental stresses are important constraints that contribute to GxE interaction since they force genotypes to require a regulation on the genetic component in

response to the external factor (Edme' & Glaz, 2012). Traits that are affected by the genotype by environment interaction include protein content, starch quality and yield biomass (Li, Bao, Corke, & Sun, 2017; Liu et al., 2017). These traits have variation in certain environments, but in other environments there is no variation, which demonstrates that the environment has a great influence over agronomic traits (Liu et al., 2017; Nijveen et al., 2017). This means that a species is under different genetic control depending on the environment it is in (Waldron et al., 2017). Environmental factors that can affect genotypes include areas with drought, heat stress, and plant density (Sukumaran, Crossa, Jarquin, Lopes, & Reynolds, 2016).

The GxE affects practically every aspect of the decision making process in plant breeding programs, including the allocation of resources in the program, choosing the testing environment, the germplasm, and breeding strategy (de Leon et al., 2016).

Genotype environment interaction can be used to create prediction models that can help accelerate breeding cycles for complex traits in multi-environmental trials (Sukumaran et al., 2016). One concept of GxE, that is relevant to this study, implies that any given trait evaluated across more than one environment can be analyzed to determine the genetic correlation between environments for that trait (de Leon et al., 2016).

Quantitative Trait Locus (QTL)

A quantitative trait locus (QTL) is a chromosome region that shows statistically significant associations with one or more quantitative phenotypic traits. Genetic mapping and detection of QTLs requires the tracking the inheritance of chromosome regions containing linkage blocks of genes from parents to progeny in families that show

variation for one or more quantitative traits of interest (Ilyas et al., 2014). By mapping the traits associated with specific quantitative trait loci, and using genetic makers we can more effectively pick out alleles that benefit a trait, or know which alleles have a negative effect on a trait, which accelerates the breeding process (Liu et al., 2017; Tanger et al., 2017). Some of the traits affected by QTLs include dehydration tolerance, osmotic adjustment, morphological variation, disease resistance, and chlorophyll content (Chen et al., 2016; Ilyas et al., 2014). Numerous QTLs can affect a trait, but some have a larger effect on the trait than other QTLs in the genome (Chen et al., 2016).

A QTL is significant when progeny with different marker genotypes show a statistically significant difference for a quantitative trait. QTLs that are detected in multiple environments are more stable and more useful (Lacaze & Roumet, 2004) for across environment performance. However, QTL by environment interactions (QxE) are useful in studying the genetic correlations between different environments. The statistical analysis of QxE is similar to that for GxE as demonstrated by (Vargas, van Eeuwijk, Crossa, & Ribaut, 2006) and (van Eeuwijk, Malosetti, Yin, Struik, & Stam, 2005). Within the QTL-mapping population, GxE interactions can be considered on a plant-based scale since each plant in the study is a genotype, whereas, QxE interactions are chromosome based (Vargas et al., 2006). As such, GxE interactions are indicative of which parental genotypes are better adapted to specific environments within the tested environments. Similarly, significant QxE interactions are indicative of which alleles from the parental genotypes have a stronger effect in those specific environments.

Intermediate Wheatgrass

Intermediate wheatgrass (IWG) [*Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey] is utilized as a hay and pasture grass to increase the productivity of marginal land (Kevin B. Jensen et al., 2016) and ranks among the top species in terms of biomass yield potentials in the western U.S. (S. Larson et al., 2017; Robins, 2010) and other temperate regions (Harmony, 2015; Lee, Owens, Boe, & Koo, 2009; Monono, Nyren, Berti, & Pryor, 2013; G. J. Wang et al., 2014). Moreover, IWG is being developed as a dual-purpose perennial forage and grain crop (Cattani Doug, 2017; Cox, Glover, van Tassel, Cox, & DeHaan, 2006; DeHaan et al., 2016; J. M. Jungers, L. R. DeHaan, K. J. Betts, C. C. Sheaffer, & D. L. Wyse, 2017) with major breeding efforts initiated in Canada (Cattani Doug, 2017) and the U.S. (Kevin B. Jensen et al., 2016; X. Zhang et al., 2017a; X. F. Zhang et al., 2016), making it the most genetically studied rangeland grass ever. Recent genetic advancements in IWG include completion of genotype-by-sequencing (GBS) to develop high-density linkage maps (Kantarski et al., 2016), identifying DNA markers associated with functional traits (X. Zhang et al., 2017a), and developing effective models for genomic selection (X. F. Zhang et al., 2016). Moreover, a draft genome sequence of IWG was developed, which has emerged as one of the first fully-annotated cool-season perennial grass genome sequences. These advanced genetic resources make intermediate wheatgrass a useful model for studying GxE in complex genomes often found in forage grasses.

Intermediate wheatgrass is native to the lower mountain belts of southern Europe, through the Middle-East and southern former Soviet Union to western Pakistan (Jensen, Yan, Larson, Wang, & Robins, 2016; R. R. C. Wang et al., 2015). Intermediate wheatgrass was introduced into the United States from the Maikop region of Russia in

1932 (Traci Kantarski et al., 2017), and is a rhizomatous cool-season perennial grass with a large allohexaploid ($2n=6x=42$) genome similar to wheat (Kevin B Jensen et al., 2016; Traci Kantarski et al., 2017). Most intermediate wheatgrass plants require cross-pollination to produce seed, but some plants can be self-pollinated (Traci Kantarski et al., 2017). It is an excellent forage and is great for erosion control in areas with harsh environmental conditions due to its high production, drought and frost tolerance, and non-invasiveness (Traci Kantarski et al., 2017; Mahelka, Kopecký, & Pařtová, 2011; X. Zhang et al., 2017b; X. Zhang, Ohm, Haring, DeHaan, & Anderson, 2015).

Intermediate wheatgrass is resistant to many diseases and pests that affect wheat and other cereal crops (Traci Kantarski et al., 2017). It is viable for interspecific crosses and homology with wheat genomes, which causes it to be extensively used as an alien genetic resource for wheat (Traci Kantarski et al., 2017; Mahelka et al., 2011). The development of genetic and genomic resources for intermediate wheatgrass is used by improving it to become a sustainable source of grain, forage, and/or biofuel (Traci Kantarski et al., 2017). Intermediate Wheatgrass was bred during the 1980's and 1990's as a perennial grain by the Rodale Institute and the USDA plant materials center. During that time, researchers at Rodale chose 14 genets (i.e., genetically identical plants with a common ancestor) for increased grain yield. Nutritionally, intermediate wheatgrass grain is similar to wheat, but with higher protein content and the grains have a lower gluten content (X. Zhang et al., 2015). Current breeding efforts focus on grain size and other domestication traits including reduced seed shattering and selection for free-threshing grain (Traci Kantarski et al., 2017). Besides the economic benefit from the grain of intermediate wheatgrass, the remaining grass creates a substantial forage with high

relative feeding quality when utilized in the spring and fall after grain harvest, which could allow producers to use it as both a grain crop and a forage crop (Jungers et al., 2018).

Ecologically, intermediate wheatgrass enhances the ecosystem with the deeper root systems of perennial crops which improve nutrient use efficiency, and the synchrony of plant demands and nutrient supplies (J.M. Jungers, L.R. DeHaan, K.J. Betts, C.C. Sheaffer, & D.L. Wyse, 2017). The year-round ground cover that intermediate wheatgrass creates reduces soil erosion, sequesters carbon, retains moisture, and cycles nutrients in the soil (Culman, Snapp, Ollenburger, Basso, & DeHaan, 2013; Glover et al., 2010; Jungers et al., 2018). When compared to annual wheat, intermediate wheatgrass reduced N leaching and increased C mineralization in soils (J.M. Jungers et al., 2017). Also, as a perennial crop, intermediate wheatgrass is able to maintain the aforementioned ecosystem functions on marginal landscapes that have limited resources (Glover et al., 2010). Intermediate wheatgrass also has a longer growing season as a perennial, which, when combined with their deeper root system, can sustain greater aboveground production than some annual crops (Glover et al., 2010).

OBJECTIVES

Preliminary research suggests that grass growth response is under different quantitative genetic control in non-competitive spaced-plant situations versus swards, as well as when in a grass monoculture versus a grass-legume polyculture (J. Hill, 1990; Waldron et al., 2017; Waldron et al., 2008). However, there are only a few published studies that have attempted to validate these hypotheses or the grass-legume ECA concepts promoted by J Hill (1990), and neither hypothesis has been evaluated at the DNA level. Therefore, the objective of this study was to compare the classical quantitative genetic parameters, as well as the QTLs associated with intermediate wheatgrass growth when grown in grass-grass monoculture swards (intra-specific competition), grass-legume polyculture swards (inter-specific competition), and as widely-spaced plants (no competition).

MATERIALS AND METHODS

Plant Materials and Evaluations

In 2015, a subset of 192 of the 376 full-sib progeny (genets) from the M26 x M35 intermediate wheatgrass (IWG) mapping population (Kantarski et al. 2017) were established into three experimental environments, based on different systems of management and competition, using clonally replicated spaced-plant field plots. Two of the environments were established as spaced plants in swards using the method of Van Dijk and Winkelhorst (1978), by over-seeding the plots with either grasses or legumes. The plots over-seeded with grasses were considered representative of a grass monoculture sward environment with only intra-specific competition; whereas, plots over-seeded with alfalfa represented a grass-legume mixture sward environment with inter-specific competition. The third environment was a traditional spaced plant nursery, consisting of widely-spaced plants with no intra- or inter-specific competition. Plots were arranged in a split-plot randomized complete block design (RCBD) with three replications. Competition environments were considered whole-plots, whereas the sub-plots were genets. The experimental plots were established at the Utah State University Evans Research Farm, which is approximately 2 km south of Logan, UT (41°45' N, 111°8' W, 1350 m above sea level). The soil type at this site is a Nibley silty clay loam series (fine, mixed, active, mesic Aquic Argixeroll). Climate data at this site for the establishment and data collection years are shown in Figure 1.

The field plots were established on May 12, 2015 by transplanting propagules from a greenhouse started clones to the field in 2-clone plots with 0.5 m between plants and 1.1 m between rows in the monoculture and polyculture sward plots, and 1 m between rows and clones in the widely-spaced no-competition plots. The clones were split in the greenhouse during the winter by separating 18 individual tillers from each genet and then transplanting each tiller into individual cells (Ray Leach Cone-tainer SC-10 Super Cells [21 cm deep, 4 cm diam.], Stuewe and Sons, Corvallis, OR) containing a 3:1 soil/peat mix where they were grown until transplanted to the field. Immediately after transplanting, the area between rows in the simulated sward plots were seeded with a drop-style fertilizer spreader following the methods of Waldron et al. (2017) with either ‘RoadCrest’ turf-type crested wheatgrass (*Agropyron cristatum*) (Asay, Jensen, Horton, Johnson, & Chatterton) at a rate of 11.2 kg pure live seed (PLS) /ha⁻¹ (grass monoculture sward competition), or with ‘Don’ falcata-type alfalfa (*Medicago falcata* L.) (Peel et al., 2009) at a rate of 5.6 kg PLS/ha⁻¹ (grass-legume polyculture sward competition). This resulted in uniform, dense establishment of visibly distinct, short-statured, crested wheatgrass or alfalfa between rows. These competitive swards minimized weed competition, and therefore only minimal hand-weeding was required in the monoculture and polyculture swards throughout the duration of the study. The alfalfa and crested wheatgrass were mowed several times during the summer and the area between the widely-spaced no-competition rows were rototilled each fall. The field plots were irrigated weekly during the establishment year (2015) receiving 3.8 cm of water per wk (approximately 100% season-long ET replacement), and thereafter did not receive

supplemental irrigation. None of the three competition environments received nitrogen fertilizer.

The morphological and agronomic data (Table 1) were obtained in 2016 and 2017 on a plot basis as the average of the two clones. Morphological data included growth stage, plant height, and tiller number. Morphological growth stage was determined using the Zadoks scale on June 20 to the 24 in 2016 and June 19 to the 23 in 2017. In brief, the Zadoks scale is a numerical rating from 0 to 99, where 0-9 represents the germination stages, 10-19 represents the seedling growth stages, 20-29 represents the tillering growth stages, 30-39 represents the stem elongation growth stages, 40-49 represents the booting growth stages, 50-59 represents the inflorescence emergence growth stages, 60-69 represents the anthesis growth stages, 70-79 represent the milk development stages, 80-89 represents the dough development growth stages and 90-99 represents the ripening stages of development (C., T., & F., 1974). Plant height and tiller number were determined when plants were predominately at the inflorescence emergence morphological stage, approaching the anthesis morphological stage, which corresponded to approximately 7 days prior to harvesting the biomass. Height was measured using the average standing tiller height of the clones. The number of tillers in the monoculture and polyculture sward plots were counted by hand. However, tillers in the widely-spaced no-competition plots were too numerous to count by hand, and therefore, the number of tillers was estimated using the following method described. Briefly, the basal area of each clone was determined by measuring the diameter of actively growing tillers and using the diameter to calculate the area (i.e., basal area = $\pi * [\text{diameter}/2]^2$). The number of tillers in a 5-cm cross section of the clone were then counted, converted to tillers/cm² (e.g., area of

cross section = 5 cm multiplied by diameter), and total number of tillers estimated as:

total no. tillers = tillers cm^{-2} x basal area.

Agronomic data consisted of biomass and forage nutritive value. Individual plots were harvested with a sickle-bar mower or hand harvested to an 8-cm stubble height on July 21 to the 22 in 2016 and from July 18 to the 20 in 2017, which corresponded to when most of the plants were at the pre-anthesis stage of plant development. Prior to each harvest, the area between rows was flailed with a mower to remove the biomass from the over-seeded plants, thus the data represents only the biomass of the IWG genets. Biomass subsamples were taken from each plot and dried to a constant weight in a forced-air oven at 60°C and biomass on a dry-matter basis determined. Biomass samples were ground into a powder using a Thomas Wiley Laboratory Model 4 mill (Arthur H Thomas Co, Swedesboro, NJ) to pass through a 1 mm screen, and then were scanned with a Foss XDS near-infrared reflectance spectroscopy instrument (Foss, Eden Prairie, MN). NIRSystem software was used to calibrate existing equations so that they were appropriate for the intermediate wheatgrass samples.

Random samples, from each environment and year, were subjected to wet laboratory analysis and used as independent calibration and validation data sets for crude protein (CP; nitrogen x 6.25), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), in vitro true digestibility (IVTD), Ether Extract (EE), and ash. The *r*-values for validation were 0.88 for ADF, 0.96 for NDF, 0.96 for CP, 0.75 for ADL, 0.90 for IVTD, 0.96 for ASH and 0.81 for EE. Samples used for wet chemistry were analyzed for N using a LECO CHN-2000 and a FP-628 Elemental Analyzer (LECO Corp., St. Joseph, MI). Concentrations of NDF, ADF and IVTD, were determined

following the ANKOM procedures of the Goering and Van Soest (1970) methods (Ankom Technology, 2005 a,b,c,d). Analyses for ADF, ADL, and NDF were made using the ANKOM-200 Fiber Analyzer (ANKOM Technology, Macedon, NY). The first step of the IVTD analysis consisted of a 48-hour in vitro fermentation in the ANKOM Daisy II incubator (ANKOM Technology, Macedon, NY), the second step was performed with the NDF procedure mentioned above. Ash concentrations were determined by ashing at 550°C. Ether extract analysis was done following the AOAC 2003.05 official method by a commercial lab (Dairy One, Ithaca, NY, USA). Metabolizable energy (ME) was calculated as Total digestible nutrients $\times 0.04409 \times 0.82$ (National Research Council, 2000); and Net energy for gain (NEg) was estimated from ME using the equation, $NEg = 1.42ME - 0.17ME^2 + 0.0122ME^3 - 1.65$ (National Research Council, 2000). Total digestible nutrients (TDN) were calculated using the appropriate formula for grass:

$$TDN = (NFC \times 0.98) + (CP \times 0.87) + (FA \times 0.97 \times 2.25) + [NDFn \times (NDFDp \div 100)] - 10; \text{ where non fibrous carbohydrates (NFC) = } 100 - (NDFn + CP + EE + \text{ash}), \text{ fatty acids (FA) = } EE - 1, \text{ nitrogen free NDF (NDFn) = } NDF \times 0.93, \text{ NDF digestibility (NDFD) = 48-h in vitro NDF digestibility, and } NDFDp = 22.7 + 0.664 \times NDFD \text{ (Saha et al., 2013).}$$

Statistical and Genetic Analysis

Morphological and agronomic data were analyzed across years using the MIXED procedure of SAS (SAS Institute Inc., Cary, NC, USA). Competition environment (e.g., widely-spaced, monoculture sward, or polyculture sward) was considered a fixed affect, whereas, year, replication, genet were considered random. Mean comparisons were made

between competition environments using Fisher's protected least significant difference (LSD) test at the $p \leq 0.05$ level of probability. Pearson's correlations among traits were estimated using SAS. Broad-sense heritabilities and standard errors were calculated within each of the three experimental environments based upon full-sibs of a perennial species evaluated at one location over multiple years using SAS REML estimates of variances as described by Holland et al. (2010). Phenotypic and genetic correlations and their standard errors were also estimated among the competition environments using SAS REML estimates as described by Holland (2006).

QTL and QxE analyses were completed using DNA genotypes for 3568 DNA markers. The genetic map with 3568 DNA markers in 21 linkage groups (LGs) corresponds to the 21 chromosomes of intermediate wheatgrass (Kantarski et al., 2016). Morphological and agronomic data were formatted in Excel file and transferred to the data format for the program MapQTL. The LOD thresholds of each trait were determined using a permutation test with 1,000 randomizations to control for genome-wide and chromosome-wide multiple testing with a 5% ($P < 0.05$) error rate. Only the most significant QTL on each linkage group were identified and compared amongst the three environments .

An approach for QTL detection, based on the model for cross-pollinators (MCP) plants, was performed using MapQTL version 6 (Van Ooijen, 2009). All of the map files and locus data used for these QTL analyses were based on the integrated GBS consensus map of M26, M35, and 11 other heterozygous parents (T. Kantarski et al., 2017). All the quantitative trait data were based on LSMEANS trait estimates of progeny, within and among environments, as described above. MCP QTL analysis were performed using the

same single-QTL interval mapping (IM) procedure (Van Ooijen, 2009). The MCP approach for QTL analysis utilized an integrated map containing 21 linkage groups for both parents (T. Kantarski et al., 2017), which was constructed using a model for genetically heterogeneous cross pollinators (Van Ooijen, 2006). The MCP map contained a total 3856 markers, including 1699 markers that were heterozygous in the M26 parent only (with designated genotypes *lm* for M26 and *ll* for M35), 1087 markers that were heterozygous in the M35 parent only (designated genotypes *nn* for M26 and *np* for M35), and 1070 markers that were heterozygous in both parents (with designated genotype *hk* for both parents). In full-sib CP families, one or more QTLs may be heterozygous in one or both parents with up to four possible alleles per QTL. The MCP QTL approach always fits four possible QTL alleles designated *a* and *b* corresponding to marker alleles *l* and *m*, respectively, of the first parent (M26) and QTL alleles *c* and *d* corresponding to marker alleles *n* and *p*, respectively, of the second parent (M35). The more complex MCP QTL analysis (Van Ooijen, 2009) has different theoretical and practical advantages because three possible genotypic effects are fitted including α (difference between *a* and *b* QTL alleles), γ (difference between *c* and *d* QTL alleles) and τ (the intralocus interaction) as deviations from the overall mean (μ) value (Van Ooijen, 2009). If the parents are heterozygous for the same two QTL alleles, *a* and *b*, then τ would represent a dominance deviation term. However, this is never assumed to be the case because MapQTL MCP model always fits separate effects, α and γ , for both parents.

To analyze for significant QTL by environment interactions (Qx \times E), traits were analyzed by each individual statically significant QTL marker using the MIXED procedure of SAS (SAS Institute Inc., Cary, NC, USA) using the type 3 fixed effects test

and considering year (2016 and 2017), environment (Mono, Poly, and Spaced), and QTL allelic combination. (One marker having the highest QTL effect, measured by the Kruskal-Wallis test (Van Ooijen, 2009), was employed as the independent QTL classification variable with *kk*, *hk*, or *hh* genotypes for biparental markers; *lm* or *ll* for M26 markers; and *nn* or *np* for M35 markers. The Kruskal-Wallis test was used as a single-point marker analysis because, in some cases, the IM QTL peak may be located on a marker that has little or no effect if the parents are not heterozygous for the same QTL alleles. For example, an IM QTL peak may be located on a M26 marker even if the QTL came from M35. Thus, for each QTL, one marker having the highest QTL effect, measured by the Kruskal-Wallis test (Van Ooijen, 2009), a single-point marker test, was employed as the independent QTL classification variable to avoid positional inferences made using the IM QTL mapping procedure.. Mean comparisons between years, environments, or QTL allelic combination were made using Fisher's protected least significant difference (LSD) test at the $P \leq 0.05$ level of probability. Fisher's protected LSD comparisons ($P \leq 0.05$) for the QTL allele by Environment interaction means were made following correction to the P -value using the Bonferroni correction; where P -value was divided by the number of significant QTL markers for that corresponding trait. This was needed to counteract the problem of many multiple comparisons. Thus, similar methods were used for GxE and QxE statistical testing.

RESULTS

Phenotypic and Genetic Variation: Relationship Among Environments

Significant Pearson's correlations ($P < 0.05$) were detected for all but one of the 78 possible pairwise comparisons among traits (Table 2). Three relatively strong correlation ($r \geq 0.70$ or $r \leq -0.70$) between biomass (MASS) and tiller length (TILE), MASS and tillers crown (TICR), and TILE AND TICR were observed for the biomass and morphological traits (Table 2). Whereas, there were 10 relatively strong correlations ($r \geq 0.70$ or $r \leq -0.70$) between pairwise comparisons of forage nutritive traits (Table 2). These were comprised of primarily fiber (ADF, NDF, and IVTD) and energy (NDFD, NFC, ME, and RFQ) trait relationships that are well documented in the literature.

Biomass and morphological traits

Year influenced all traits, and the environment by year interaction was highly significant ($P < 0.0001$) for biomass and all morphological traits (Table 3). This was primarily due magnitude differences with greater MASS, and TICR in 2017 than 2016, particularly within the polyculture environment (Table 4). However, the polyculture environment also experienced greater TILE in 2017 compared to 2016, whereas, TILE did not change between years within the spaced and monoculture environments. Phenotypic data are presented as the mean across years herein.

Parents (M26 and M35) and grandparents (C3_3471 and C3_3941) within environment MASS means did not differ ($P > 0.05$) within environments, nor were the across-environment means different ($P > 0.05$) (Table 5). Likewise, there were no

differences ($P>0.05$) between any of the parents or grandparents for TILE or TICR (Table 6). However, grandparent C3_3471 was morphologically more ($P<0.05$) mature (ZAMA) than grandparent C3_3941, and the two parents (M26 and M35) tended to be intermediate in maturity in comparison to the grandparents (Table 5).

In contrast to parent performance, environments differed significantly ($P<0.05$) for mean genet MASS (Table 4), with genets in the widely-spaced environment producing the greatest ($P<0.05$) MASS, followed by the polyculture and then the monoculture environments (Table 4). Average genet TILE and TICR were greatest ($P<0.05$) in the spaced environment, with relatively smaller but still significant differences ($P<0.05$) between the polyculture and monoculture environments (Table 4). In contrast, average genet morphological maturity (ZAMA) did not differ ($P>0.05$) among the three environments (Table 4). Large standard deviations for mean genet MASS were indicative of the wide phenotypic variation observed among genets, especially when growing in the monoculture and polyculture environments (Table 4). Whereas, the lesser standard deviations for TILE suggested less variation among genets in comparison to MASS or TICR.

Moderate to high heritable variation was observed for intermediate wheatgrass biomass and morphological traits within the three environments (H ranged from 0.50 to 0.87; Table 6). The polyculture environment exhibited the lowest heritability for MASS and TICR, but the highest for ZAMA, whereas, the spaced environment had the greatest heritability for MASS, TILE, and TICR (Table 6). Phenotypic correlations between the environments for morphological traits were low to moderate, ranging from 0.10 to 0.58, however, corresponding genetic correlations were much greater, ranging from 0.47 to

0.98 (Table 6). In contrast, both low phenotypic correlations and moderately-low genetic correlations between environments were observed for MASS (Table 6). Spearman's rank correlations were also more consistent with the phenotypic correlations than the genetic correlations, except for TICR between the spaced and polyculture environments where the Spearman's and genetic correlations were similar (Table 6).

Forage nutritive value

The environment by year interactions were also highly significant ($P < 0.0001$) for all forage nutritive traits (Table 3). Again, this was primarily due to overall magnitude differences in the years, as all nutritive value traits except NDFD were more favorable in 2016 than 2017 (Table 3). However, year had the least effect within the monoculture environment, also contributing to the environment by year interaction (Table 4). Forage nutritive value phenotypic data are also presented as the mean across years.

Significant parent/grandparent by environment mean differences were observed for CP, IVTD, and RFQ, however, the differences were inconsistent across environments (Table 5). The two parents (M26 and M35) differed ($P < 0.05$) from each other for CP only in the spaced environment, whereas, the two grandparents (C3_3471 and C3_3941) differed only in the polyculture environment (Table 5). In contrast, the two grandparents differed ($P < 0.05$) from each other for IVTD only in the spaced environment, whereas, the parents differed from each other in the monoculture and polyculture environments (Table 5). The pairs of grandparents and parents differed ($P < 0.05$) from each other for RFQ in both the spaced and polyculture environments, but these differences were not exhibited in the monoculture environment (Table 5). Overall, parent M35 had more favorable

($P < 0.05$) ADF, IVTD, NFD and ME, similar ($P > 0.05$) NDF, ADL and RFQ, but less ($P < 0.05$) CP and NDFD compared to parent M26 (Table 5). In contrast, across environments, grandparent C3_3941 exhibited more favorable ($P < 0.05$) ADL, IVTD, NDFD, ME and RFQ, and similar ($P > 0.05$) CP, NDF, ADF and NFC compared to C3_3471 (Table 5).

Mean genet forage nutritive value varied significantly ($P < 0.05$) amongst the three environments for all measured traits (Table 4). Mean genet CP, NDF, ADF, ME, and RFQ were most favorable ($P < 0.05$) in the polyculture environment, whereas, ADL, IVTD, NDFD, and NFC were most favorable ($P < 0.05$) in the monoculture environment (Table 3). In contrast to biomass and morphological traits, mean genet forage nutritive value was least favorable ($P < 0.05$) in the widely-spaced environment, except for CP, which was intermediate ($P < 0.05$) between polyculture and monoculture environments (Table 4).

With few exceptions, forage nutritive value traits were highly heritable ($H > 0.70$) within all three environments (Table 6). Heritable variation for ADL was moderate ($H = 0.46$ to 0.67), but overall the least heritable in all three environments, relative to the other nutritive traits (Table 6). Crude protein also exhibited moderate, but less than 0.7 heritability in the spaced and monoculture environments (Table 6). Overall, genetic correlations between environments for forage nutritive value traits were very high mostly exceeding $r = 0.8$ (Table 6). The genetic control of forage nutritive value appeared to be least similar between the monoculture and polyculture environments, with correlations of 0.57 , 0.65 , and 0.66 for CP, NDFD, and ADL, respectively. Even so, genetic correlations ranging from 0.80 to 0.94 were exhibited for the remaining nutritive traits between the

monoculture and polyculture environments (Table 6). Like the results for biomass and morphological traits, Spearman's rank correlations were often more similar to the phenotypic correlations than the genetic correlations for forage nutritive traits. However, exceptions included the spaced versus polyculture Spearman's rank correlations for CP, NDF, ADF, ADL, and RFQ being intermediate between the phenotypic and genetic correlations (Table 6).

QTL Analysis

QTL analyses were not performed on NFC, ME or RFQ as they were not directly measured but calculated from the other forage nutritive values. For the MCP QTL analyses, permutation tests were conducted to determine the minimum LOD threshold required to control for 5% genome-wide error rates ($P < 0.05$) for each trait and are shown in table 7. Significant LG-wide QTLs were only reported if they were also significant on a genome-wide basis for at least one environment or the across environment mean. Using these criteria threshold for all 11 traits, there were a total of 26 significant QTLs detected based on three different environments or the average over all three environments (Table 8, Figure 2). Of the 26 total QTLs, 10 were significant within the widely-spaced environment, 15 within the grass monoculture environment, 8 within the grass-legume polyculture environment, and 13 for the across environment mean (Table 8, Figure 2).

Biomass and morphological trait QTLs

Six significant QTLs were identified for MASS (Table 8, Figure 2). Three MASS QTLs, on linkage groups 1, 6, and 15, were only associated with biomass in the monoculture environment (Table 8, Figure 2). Whereas, the other three MASS QTLs, which were also significant in the monoculture environment, were exhibited in other environments; one on linkage group 11 associated with polyculture, one on linkage group 14 shared with spaced and across environments, and one on linkage group 10 significant in all environments (Table 8, Figure 2).

Two significant QTLs were identified for TILE, one each on linkage groups 10, 11, and 21 (Table 9, Figure 2). The TILE QTLs on 10 and 11 were significant across environments and within the spaced, monoculture, and polyculture environments. (Table 8, Figure 2). Two significant QTLs were identified for TICR, one on linkage group 1 associated with the number of tillers in the monoculture environment, and one on linkage group 8 associated with the spaced environment and the across environment mean (Table 8, Figure 2). Only one QTL was identified for ZAMA, which was associated with plant maturity in the spaced environment and across environment mean (Table 8, Figure 2).

Forage nutritive value QTLs

The one significant CP QTL, on linkage group 6, was associated with CP expression in all environments, though only significant on a genome-wide basis for polyculture and across environment mean CP (Table 8, Figure 2). Two QTL's were identified as significant for the concentration of ADF in the plant, one on linkage group 10 associated with ADF in all environments, and one on 16 significant in all environments except polyculture (Table 8, Figure 2). Three QTLs were identified for the concentration of NDF

in the plant, two of which were in the same chromosomal location and followed the same environment-specific pattern as ADF (Table 8, Figure 2). A third QTL for NDF, on linkage group 15, was only associated with NDF expression in the monoculture environment (Table 8, Figure 2). No significant QTLs were identified for ADL.

Three significant QTLs were identified for IVTD (Table 8, Figure 2). Those on linkage groups 10 and 14 were associated with plant digestibility in all environments, whereas, the QTL on linkage group 18 was associated with IVTD in all environments except monoculture (Table 8, Figure 2). In contrast, five QTLs were associated with NDF digestibility (NDFD), but only the one on linkage group 18 was consistently expressed in all environments (Table 8, Figure 2). The NDFD QTL on linkage group 10 was unique to the monoculture environment, whereas, the QTLs on 11, 5, and 9 were expressed in the spaced and polyculture environments, but not in monoculture (Table 8, Figure 2).

QTL x Environment interactions

Twenty-four QTL markers exhibited significant (Bonferroni $P < 0.05$) allele by environment interactions (QxE) and of these, 9 were associated with MASS (Table 9). For all nine MASS QTL markers, the different allelic combinations (i.e., *hh*, *hk*, or *kk*; *ll* or *lm*; and *nn* or *np*) were associated with significant differences ($P < 0.05$) in MASS in the spaced environment but had no effect on MASS in the mono environment (Table 9). Whereas, the different allelic combinations for only four QTL markers were associated with MASS differences ($P < 0.05$) in the polyculture environment (Table 9). Homozygous allelic combinations were associated with greater ($P < 0.05$) MASS in 8 of 9 markers in the spaced environment and 3 of 4 markers in the polyculture environment (Table 9). Six

of the MASS QTL markers were comprised of alleles from both parents (i.e., *h* and *k*), one was comprised of only alleles from the M26 parent (i.e., *l* and *m*), and two were alleles from the M35 parent (i.e., *n* and *p*) (Table 9).

There were two QTL markers with significant QxE effects on the number of tillers produced (TICR), one comprised of alleles from both parents and the other comprised of just the *n* and *p* alleles from the M35 parent (Table 9). The different allelic combinations were associated with differences ($P < 0.05$) in TICR only in the spaced environment, and not in the monoculture or polyculture environments (Table 9). There were no QxE effects observed for TILE or ZAMA.

Eleven QTL markers exhibited significant QxE for various forage nutritive traits, and unlike the biomass and morphological traits, there were not distinct pattern differences between the spaced and monoculture environments (Table 10). There were two QTL markers with significant QxE effects on CP, one comprised of alleles from both parents and one comprised of just the *l* and *m* alleles from the M26 parent (Table 10). The *l* and *m* alleles resulted in differences ($P < 0.05$) only in the spaced environment; whereas, the *h* and *k* alleles were associated with CP differences ($P < 0.05$) in the monoculture and polyculture environments, but not in the spaced environment (Table 10). Three QTL markers exhibited significant QxE effects on NDF, one of which was comprised of the *n* and *p* alleles from the M35 parent and two comprised of alleles from both parents (*h* and *k*) (Table 10). Of note, the heterozygous *np* allelic state resulted in more favorable NDF than the homozygous *nn* alleles in both the spaced and monoculture environments, but not in the polyculture environment (Table 10). Three ADF QTL makers that had significant QxE, and were all comprised of the *h* and *k* alleles from both parents (Table

10). Similar to NDF, the *kk* allelic combination was associated with more favorable ADF than *hh* or *hk* in the spaced and monoculture environments, but not consistently so in the polyculture environment (Table 10). Three QTL markers exhibited significant QxE effects on NDFD, two comprised of the *n* and *p* alleles from the M35 parent and one comprised of alleles from both parents (*h* and *k*) (Table 10). The NDFD QxE interactions were primarily due to magnitude difference among the environments, as the heterozygous *np* state of marker TP196229 and homozygous alleles in TP583925 (*nn*) were consistently associated with greater NDFD in all three environments. In addition, homozygous alleles for T301824 (*hh*) resulted in more favorable NDFD in the spaced and monoculture environments (Table 10).

DISCUSSION

Genetic Control in Spaced-Plants and Swards

Spaced-plant vs sward: biomass and morphological traits

Most forage breeding programs have utilized spaced plant evaluation to select breeding materials. However, the ability of spaced plants to predict sward biomass has been questioned (Casler et al., 1996). Waldron et al. (2008) reported a low genetic correlation of 0.37 between spaced-plant and sward biomass in tall fescue, and concluded that spaced-plant evaluation would be ineffective to improve sward yield. Furthermore, both Waldron et al. (2008) and Hayward and Vivero (1984) surmised that biomass in spaced and sward environments might be under different genetic control. However, this theory had not been evaluated at the DNA level prior to this study. Accordingly, this study presents classical quantitative genetic analysis, as well as QTL and QTL marker by environment analyses to better understand the relationship between these environments.

Similar to Waldron et al. (2008) for biomass, we found low genetic correlations of 0.37 and 0.30 between intermediate wheatgrass spaced-plants and simulated polyculture and monoculture swards, respectively, further suggesting genetic control of biomass is dependent upon the level of inter-plant competition in the environment. Six different QTLs affected biomass production (Table 9). This is the first known report of genetic mapping of biomass in intermediate wheatgrass, but is similar to S. R. Larson, Jensen, Robins, and Waldron (2014) report of eight biomass QTLs in interspecific hybrids between Basin and Creeping wildryes [*Leymus cinereus* (Scribn. & Merr.) Á. Löve] and

[*Leymus triticoides* (Buckley) Pilg.]. Our hypothesis that biomass genetic control is dependent upon the environment was supported by the varying number of QTLs identified for each environment, two for each of the spaced-plant and polyculture environments, and six within the monoculture environment (Table 9). It is noteworthy that both spaced-plant QTLs on linkage groups 10 and 14 were also significant in the monoculture environment, as well as the QTL on linkage group 10 also being significant in the polyculture environment, suggesting the presence of major biomass coding regions at these chromosomal locations.

Nine QTL biomass markers exhibited significant allele by environment interactions, of which five were markers for the two shared biomass QTL on linkage groups 10 and 14 (Table 10). However, within these five markers, no allelic rank changes were exhibited for biomass between environments, rather, the QxE interactions resulted from magnitude differences among environments and the inability to detect allelic differences in the polyculture and monoculture sward environments (Table 10). Therefore, this is further evidence that the QTLs on these linkage groups (10 and 14) contain major biomass coding regions regardless of environment, and supporting the presence of at least some genetic correlation between spaced-plant and sward environments. It is also likely that those QTLs contain the predominant coding regions for spaced-plant biomass, as evidenced by significant differences in biomass associated with the allelic combinations only in the spaced-plant environment. Whereas, the biomass QTLs identified on linkage groups 1, 6, and 15 within the monoculture environment, and a QTL on linkage group 11 identified in both monoculture and polyculture, likely contain additional coding regions that largely contribute to biomass when in a more competitive

environment as opposed to the non-competitive environment of spaced plants. Overall, these data validate the low genetic correlations reported herein and by Waldron et al. (2008), and provide evidence that biomass in spaced-plants and swards is at least partially under different genetic control.

Spaced-plant and sward tiller lengths were genetically correlated ($r_g = 0.91$ and 0.78), and very similar to the genetic correlation of 0.85 between height of tall fescue spaced-plants and swards reported by Waldron et al. (2008). Three QTLs were identified for tiller length (Table 9). Tiller length was highly correlated with biomass (Pearson's $r = 0.73$, Table 3), therefore it was not surprising that a shared across all environments tiller length QTL identified on linkage group 10 corresponded to the same location one of the two major shared biomass QTLs (Table 9). A shared across all environments tiller length QTL was also identified on linkage group 11, but it was not at the same chromosome interval as the biomass QTL on linkage group 11 (Table 9). The third identified QTL was on linkage group 21, but was only significant in the monoculture environment and for the across environment mean (Table 9). In comparison, S. R. Larson et al. (2019) identified eight tiller length QTLs using this same intermediate mapping population, of which only the QTL on linkage group 11 was the same between the two studies. Interestingly in the S. R. Larson et al. (2019) study, this linkage group 11 QTL was not significant in Kansas but was so at the same Utah location as our study, suggesting that this QTL contains gene(s) coding for tiller length when in more arid environments. The high genetic correlation and 66% shared QTLs amongst environments, and lack of QTL markers with significant QxE interaction suggest that tiller length is under similar genetic control whether in a spaced-plant or sward environment. The unique QTL on linkage group 21

identified in the monoculture environment, may explain why the genetic correlation between spaced-plant and monoculture ($r_g=0.78$) was slightly less than that between spaced-plant and polyculture ($r_g=0.91$).

Tillers crown⁻¹ was highly correlated with biomass ($r=0.91$), and as such, spaced-plant and sward environments were only moderately genetically correlated ($r_g=0.59$ and 0.47 , for polyculture and monoculture, respectively). Waldron et al. (2008) reported slightly higher genetic correlation ($r_g=0.67$) between spaced-plants and swards for tiller density in tall fescue but given the different growth habit of these two species (rhizomatous versus non-rhizomatous for IWG and tall fescue, respectively), such slight differences in tiller density and number would be expected. Two QTLs were identified for TICR as compared to four previously identified in this population (S. R. Larson et al., 2019), however, both studies identified a TICR QTL on linkage group 8. S. R. Larson et al. (2019) used spaced-plant evaluation, and likewise the linkage group 8 QTL was only significant for our spaced-plant environment, further validating the importance of this QTL for TICR in non-competitive environments. However, we also identified a TICR QTL on linkage group 1 that was only significant in the monoculture sward, which corresponds to the same interval location as our monoculture-only linkage group 1 MASS QTL (Table 9). Thus, there is QTL evidence for partial but not complete genetic correlation between spaced-plants and swards for TICR. Overall, these data suggest that these morphological traits are partially under the same genetic control between spaced-plant and sward environments, however, genetic control of those traits that are the most correlated with biomass, such as TICR, is more affected by the specific environment.

Spaced-plant vs sward: forage nutritive value

Waldron et al. (2008) reported that spaced-plant evaluation was moderately predictive of sward nutritive fiber and digestibility but not predictive of CP in tall fescue. In comparison, our forage nutritive trait genetic correlations between spaced-plant and sward environments were even higher than that reported by Waldron et al. (2008). And we also found that a spaced-plant environment was only moderately predictive of CP in a grass monoculture (Table 7). Since we did not apply supplemental fertilizer, this discrepancy in CP between the non-competitive spaced-plant and highly competitive monoculture environments was probably mostly due to N availability. This hypothesis is based upon the assumption of some N-transfer between the alfalfa to the grass in the polyculture environment (Carlsson & Huss-Danell, 2003; Heichel & Henjum, 1991), and is consistent with a much greater r_g of 0.80 between spaced-plant and polyculture as compared to 0.53 between the spaced-plant and monoculture environments (Table 7). However, QTL data did not fully support this conclusion since we only identified one CP QTL on linkage group 6 that was shared by both spaced plants and monoculture and polyculture swards (Table 9). Even so, significant QxE interactions for a QTL marker on linkage group 12 showed that specific allelic combinations affected CP in both polyculture and monoculture swards, but not in spaced-plants (Table 11). Whereas, a QTL marker on linkage group 21 also exhibited QxE with alleles affecting CP in spaced-plants but neither monoculture or polyculture swards (Table 11). These QxE results support Waldron et al. (2008) conclusion that CP is under at least partial different control between spaced-plant and sward environments, and suggest that further study is

warranted to examine the role of minor QTLs on linkage groups 12 and 21 on CP synthesis.

Fiber digestibility (NDF and ADF) were highly genetically correlated ($r_{\text{a}} \geq 0.89$) between spaced-plant and sward environments in this study, however, much less so (0.56 and 0.70, for NDF and ADF, respectively) in the Waldron et al. (2008) study. Our QTL data are more in agreement with their study, since only 1 of 3 identified NDF QTL was shared amongst the spaced-plant and monoculture and polyculture sward environments (Table 9). Furthermore, QxE interactions on the two non-shared QTLs on linkage groups 15 and 16 resulted primarily from allelic combinations associated with NDF differences in the monoculture sward and spaced-plant environments (Table 11). It is noteworthy that the two identified ADF QTLs were in the same chromosomal interval as two of the NDF QTLs (linkage groups 10 and 16), providing genetic validation of the relationship between these two highly correlated ($r=0.94$ in this study) fiber traits. Based upon our high genetic correlation and shared IVTD QTLs amongst environments, we agree with Waldron et al. (2008) assumption that whole grass plant digestibility is under similar genetic control in both spaced-plants and swards. In addition, we identified a QTL on linkage group 10 that is significant for both MASS and IVTD, and shared by all environments, suggesting that gene(s) in this chromosomal region may be primarily responsible for the negative correlation between biomass and digestibility in grasses ($r=-0.64$ in this study).

Genetic Control in Grass Monoculture and Grass-Legume Polyculture

Monoculture vs polyculture: biomass and morphological traits

Historically, grass breeders have developed varieties through selection in pure (e.g., monoculture) stands. However, theory suggests that grasses bred in a monoculture environment are only exposed to intra-specific competition, and, thus, not having been exposed to inter-specific competition, will not possess the optimal biological characteristics conducive to coexistence and compatibility in grass-legume mixtures (J. Hill, 1990). This hypothesis is largely unvalidated with only limited genetic studies attempting to investigate the role of genetics in grass-legume mixtures (Annicchiarico, 2003; Waldron et al., 2017). Accordingly, this study presents both classical and DNA-based quantitative genetic analysis to evaluate the genetic control of grasses growing in monoculture or grass-legume polyculture.

We found an intermediate level of genetic correlation ($r_g=0.48$) for biomass between grass monoculture and grass-legume polyculture environments (Table 7). In comparison, Waldron et al. (2017) reported r_g ranging from -0.31 to 0.92, depending upon harvest, between tall fescue biomass in monoculture versus polyculture environments. However, given that we used 1-harvest management strategy, their first harvest results are most comparable to our results. As such, their first harvest biomass, the greatest of the four cuttings comprising 36% of annual biomass, resulted in the same r_g of 0.48 between the two environments (Waldron et al., 2017). Furthermore, in both studies, heritability was consistently greater in the monoculture compared to the polyculture environment.

Six QTLs were identified associated with biomass in monoculture, whereas, only two were associated with biomass in polyculture (Table 9). However, it is important to note that both of these QTLs were shared by the two environments, and included the major QTL on linkage group 10 that was also associated with spaced-plants. Three

biomass QTL markers on linkage group 10 exhibited significant QxE interaction as a result of specific alleles being associated with biomass differences in polyculture (as well as spaced-plants), but not significantly different in the monoculture (Table 10). Thus, these data support the existence of a major biomass QTL on linkage group 10, that is predominant for biomass production in polyculture and non-competitive spaced plants but less so for the highly competitive monoculture environment. The additional biomass QTLs on linkage groups 1, 6, 14, and 15 identified in the monoculture environment, further indicate that biomass in monoculture is under more complex genetic control, possibly due to the increased intra-plant competition for water and nitrogen. Similar patterns of this more complex genetic control in monoculture compared to polyculture were evident for morphological traits. For instance, two QTLs were associated with TILE in polyculture compared to those two plus an additional QTL in monoculture (Table 9). Whereas, no QTL were identified for TICR in the polyculture environment, a linkage group 1 TICR QTL was identified in the monoculture environment corresponding to a monoculture-specific biomass QTL at the same chromosomal position (Table 9).

Overall, the data suggests that genetic control of biomass and morphology of grass grown in a monoculture versus a grass-legume mixture are partially the same, with more complex genetic control within the monoculture as additional genes are expressed possibly due to increased intra-plant competition. Given that we did not apply supplemental N or irrigation during this study, there are possible underlying physiological N-capture and drought-response explanations for these findings. Different rooting depth of intermediate wheatgrass and alfalfa would result in less competition for soil moisture in the polyculture environment compared to monoculture. It is also probable

that there was more N available to the grass in the polyculture due to the legume transfer of atmospheric fixed nitrogen (Carlsson & Huss-Danell, 2003; Heichel & Henjum, 1991). This hypothesis is supported by greater biomass and CP in the polyculture compared to the monoculture (Table 5). Some grass genotypes may also be more efficient in capturing and utilizing this atmospheric-fixed nitrogen and/or are more compatible with the soil biota associated with nitrogen-fixing legumes. Zupping-Dingley, Flynn, Brandl, and Schmid (2015) reported that in several grass species, the grass plants had a changed metabolic fingerprint when grown in grass-legume mixtures versus grass monocultures. They hypothesized that the biochemical composition differences may have been due to rapid co-evolution of the plants with the soil biota, with the primary selection factor being negative plant-soil feedback in the monocultures. This negative feedback may result in differential gene expression between polyculture and monoculture as evidenced by the QTL results herein.

Monoculture vs Polyculture: Forage nutritive value

Intermediate wheatgrass plants in the polyculture environment had more favorable CP, NDF and ADF (measure of cellulose and hemicellulose, respectively), and overall nutritional value (measured as RFQ), but less favorable whole plant digestion (IVTD and NDFD) compared to the monoculture environment (Table 5). This is mostly in agreement with other studies that also reported that forage nutritive value of grasses improves when grown in grass-legume mixtures (Waldron et al., 2019; Zemenchik, Albrecht, & Shaver, 2002). Genetic correlations ranged from 0.57 for CP to 0.90 for IVTD between the polyculture and monoculture environments suggesting mostly similar genetic control

(Table 7). However, only 6 of 14 forage nutritive value QTLs were in common between the two environments (Table 9). Interestingly, the environment in which a nutritive trait had a more favorable value also had less QTLs identified for those traits, except for the CP (Table 9), suggesting that more complex genetic control is associated with decreased nutritive value. Significant QxE interactions for CP, NDF, ADF, and NDFD provide further evidence that nutritive value is at least partially under different genetic control in monoculture and polyculture environments (Table 11). This was especially true for markers of NDF, ADF, and NDFD QTLs that were only identified in the monoculture environment, in which there were greater nutritive value differentiation specific to allelic combinations in monoculture than in polyculture (Table 11). Thus overall, our QTL data only partially corroborate the moderate to high classical genetic correlations we found for forage nutritive value between monoculture and polyculture. We are not aware of other studies comparing forage nutritive value of a grass growing in monoculture versus grass-legume polyculture. Thus, we conclude that forage nutritive value is probably partially to mostly under the same genetic control in monoculture and polyculture environments.

CONCLUSION

The study has revealed that intermediate wheatgrass growth response is primarily under different quantitative genetic control in the three environments as determined by the classical quantitative genetic parameters, as well as the associated QTLs. In comparing spaced-plants versus swards, low genetic correlations and varying number of QTLs indicated that genetic control of biomass is dependent upon the level of intra-plant competition in the environment and largely under different genetic controls within these environments. Shared QTLs between spaced-plants and swards on linkage groups 10 and 14 suggested the presence of general biomass coding regions at these chromosomal locations, whereas, biomass QTLs identified on linkage groups 1, 6, 11, and 15 only within the sward environments likely contain additional coding regions that contribute primarily in more competitive environments. In contrast, moderately high genetic correlations and QTL data indicated that morphological traits were mostly under the same genetic control between spaced-plant and sward environments, however, genetic control of morphological traits highly correlated with biomass, such as tillers crown⁻¹, were also more affected by the environment. The spaced-plant environment was only moderately predictive of sward CP, probably mostly due to N availability. However, based upon high genetic correlation and shared QTLs amongst environments, whole grass plant fiber and digestibility were under similar genetic control in both spaced-plants and swards. In addition, we identified a QTL on linkage group 10 that was significant for both MASS and IVTD, and shared by all environments, suggesting that gene(s) in this chromosomal

region may be primarily responsible for the negative correlation between biomass and digestibility in grasses.

In comparing grass monoculture and grass-legume polyculture environments, we found intermediate levels of genetic correlation, and partially shared QTLs for biomass and morphological traits. These results indicated that the genetic control of biomass and morphology of grass grown in a monoculture versus a grass-legume mixture are partially the same, with more complex genetic control within the monoculture as additional genes are expressed possibly due to increased intra-plant competition. Our QTL data mostly corroborated moderate to high genetic correlations for forage nutritive value between monoculture and polyculture environments, but we found that the environment with more favorable nutritive trait values usually had fewer associated QTLs.

Overall, we conclude that spaced plants, and monoculture and grass-legume polyculture sward environments are not genetically the same, and that intermediate wheatgrass performance is under different genetic control for each environment. Genetic parameters are often population specific, and, thus, research using other populations and species are needed to further elucidate these genetic relationships. In addition, the quantity of QTLs identified were less than previously reported for these traits. However, our QTL findings were based upon the across year mean, and thus, future research should examine genotype by year interactions. Also previous research indicates it may be easier to identify QTLs and QxE using data only after the second year from establishment (Berdahl, Karn, & Hendrickson, 2001). Moreover, we only measured the most significant QTL on a linkage group for each trait, such that there could also be other significant QTLs on the same linkage group for any given trait. In the end, these data suggest that

evaluation of breeding materials in the target environment per se can significantly accelerate the breeding process for creating a variety of intermediate wheatgrass that has been optimized for being grown in a legume polyculture or a grass monoculture.

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Table 1

Trait description, abbreviation, and units of traits measured on the M26 × M35 intermediate wheatgrass mapping population evaluated over two years at Logan, UT, USA in three clonally-replicated competition environments.

Trait description	Trait abbreviation	Units
Biomass	MASS	g plot ⁻¹
Tiller length	TILE	cm
Tillers crown ⁻¹	TICR	no.
Zadok's maturity	ZAMA	0-99
Crude protein	CP	g kg ⁻¹
Neutral detergent fiber	NDF	g kg ⁻¹
Acid detergent fiber	ADF	g kg ⁻¹
Acid detergent lignin	ADL	g kg ⁻¹
In-vitro true digestibility	IVTD	g kg ⁻¹
Neutral detergent fiber digestibility	NDFD	g kg ⁻¹
Nonfibrous carbohydrates	NFC	g kg ⁻¹
Metabolizable energy	ME	Mcal kg ⁻¹
Relative forage quality	RFQ	———

Table 2

Pearson Correlation Coefficient of the 192 full-sib progeny (genets) of the M26 × M35 intermediate wheatgrass mapping population evaluated over two years at Logan, UT, USA in three clonally-replicated competition environments.

Trait	MASS	TILE	TICR	ZAMA	CP	NDF	ADF	ADL	IVTD	NDFD	NFC	ME	RFQ
MASS		***	***	***	***	***	***	***	***	***	***	***	***
TILE	0.73		***	***	***	***	***	***	***	***	***	***	***
TICR	0.91	0.74		***	***	***	***	***	***	***	***	***	***
ZAMA	0.16	0.39	0.18		***	***	***	***	***	***	***	***	***
CP	-0.18	-0.21	-0.19	-0.26		***	***	- - -	***	***	*	***	***
NDF	0.54	0.51	0.61	0.14	-0.58		***	***	***	***	***	***	***
ADF	0.56	0.55	0.61	0.19	-0.65	0.94		***	***	***	***	***	***
ADL	0.26	0.17	0.33	-0.07	-0.01	0.25	0.32		***	*	***	***	***
IVTD	-0.60	-0.66	-0.68	-0.28	0.28	-0.64	-0.62	-0.15		***	***	***	***
NDFD	-0.26	-0.39	-0.29	-0.24	-0.18	0.10	0.08	0.04	0.70		***	***	***
NFC	-0.49	-0.34	-0.56	0.13	-0.03	-0.72	-0.66	-0.57	0.42	-0.12		***	***
ME	-0.59	-0.59	-0.66	-0.18	0.33	-0.68	-0.74	-0.37	0.87	0.49	0.59		***
RFQ	-0.46	-0.47	-0.50	-0.27	0.82	-0.76	-0.84	-0.23	0.69	0.19	0.33	0.81	
*, **, *** Significant at the 0.05, 0.01, and 0.001 probabilities levels, respectively.													

Table 3

ANOVA table of the variables affecting the study

Trait	TRMT	GENET	YR	TRMT*GENET	TRMT*YR	YR*GENET	TRMT*YR*GENET
Morphology and							
Biomass							
MASS	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0456
TILE	<.0001	<.0001	<.0001	0.0081	<.0001	0.2963	0.196
TICR	<.0001	<.0001	<.0001	<.0001	<.0001	0.0342	0.3938
ZAMA	<.0001	<.0001	<.0001	0.0674	<.0001	<.0001	0.0045
Nutritive Value							
CP	<.0001	<.0001	<.0001	<.0001	<.0001	0.0023	0.4681
NDF	<.0001	<.0001	<.0001	0.0001	<.0001	0.0097	0.0027
ADF	<.0001	<.0001	<.0001	0.0001	<.0001	0.1197	0.0797
ADL	<.0001	<.0001	<.0001	0.0423	<.0001	0.3254	0.6777
IVTD	<.0001	<.0001	<.0001	0.0071	<.0001	0.0103	0.0367
NDFD	<.0001	<.0001	<.0001	<.0001	<.0001	0.2662	0.1496
NFC	<.0001	<.0001	<.0001	<.0001	<.0001	0.0359	0.0266
ME	<.0001	<.0001	<.0001	0.001	<.0001	0.0033	0.1734
RFQ	<.0001	<.0001	<.0001	0.0008	<.0001	0.0047	0.1302
Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.							

Table 4

Trait means (\pm SD) and ranges among 192 full-sib progeny (genets) of the M26 \times M35 intermediate wheatgrass mapping population evaluated over two years (2016-2017) at Logan, UT, USA in three clonally-replicated competition environments.

	Widely-spaced			Polyculture			Monoculture			Across Environment Mean		
Trait	2016	2017	AVG	2016	2017	AVG	2016	2017	AVG	2016	2017	AVG
MASS	1275 \pm 455 (67-4578)	1934 \pm 592 (577-5625)	1607 \pm 623 A (67-5625)	123 \pm 94 (1-564)	658 \pm 304 (51-1938)	390 \pm 349 B (1-1937)	70 \pm 79 (1-934)	137 \pm 152 (2-1482)	103 \pm 125 C (1-1482)	489 \pm 589 (1-4578)	905 \pm 807 (2-5625)	697 \pm 736 (1-5625)
TILE	164 \pm 14 (100-210)	160 \pm 17 (40-199)	162 \pm 16 A (40-210)	111 \pm 18 (17-190)	133 \pm 19 (55-187)	122 \pm 22 B (17-190)	116 \pm 19 (48-176)	112 \pm 20 (11-160)	114 \pm 20 C (11-176)	130 \pm 28 (17-210)	135 \pm 24 (11-199)	133 \pm 26 (11-210)
TICR	435 \pm 106 (193-734)	558 \pm 217 (123-1499)	1089 \pm 738 A (123-1499)	30 \pm 29 (1-423)	119 \pm 68 (9-481)	75 \pm 68 B (1-481)	24 \pm 19 (1-123)	30 \pm 26 (1-198)	27 \pm 23 C (1-198)	163 \pm 236 (1-734)	235 \pm 248 (1-1499)	183 \pm 42 (1-1499)
ZAMA	58 \pm 1 (51-61)	56 \pm 2 (47-61)	57 \pm 2 (47-61)	55 \pm 2 (39-59)	56 \pm 3 (47-59)	56 \pm 3 (39-59)	57 \pm 3 (39-59)	56 \pm 3 (47-59)	57 \pm 3 (39-59)	57 \pm 2 (39-61)	56 \pm 2 (47-61)	56 \pm 2 (39-61)
CP	65 \pm 13 (39-122)	47 \pm 8 (25-71)	56 \pm 14 B (25-122)	84 \pm 12 (40-132)	63 \pm 10 (42-106)	73 \pm 15 A (40-132)	50 \pm 11 (28-103)	41 \pm 7 (24-76)	46 \pm 10 C (24-103)	66 \pm 16 (28-132)	51 \pm 11 (24-106)	58 \pm 16 (24-132)
NDF	599 \pm 33 (481-686)	654 \pm 25 (537-726)	627 \pm 40 A (481-726)	545 \pm 33 (421-634)	626 \pm 26 (485-681)	586 \pm 50 C (421-681)	599 \pm 27 (516-686)	595 \pm 33 (473-675)	597 \pm 30 B (473-686)	581 \pm 35 (421-686)	625 \pm 34 (473-726)	603 \pm 41 (421-726)
ADF	394 \pm 19 (328-438)	421 \pm 15 (358-458)	407 \pm 22 A (328-458)	349 \pm 22 (278-407)	399 \pm 17 (320-436)	374 \pm 32 C (278-436)	386 \pm 16 (329-425)	393 \pm 19 (320-438)	390 \pm 18 B (320-438)	376 \pm 24 (278-438)	404 \pm 18 (320-458)	390 \pm 26 (278-458)
ADL	88 \pm 7 (61-110)	95 \pm 6 (73-112)	91 \pm 7 A (61-112)	85 \pm 9 (56-108)	95 \pm 7 (75-112)	90 \pm 9 B (56-112)	79 \pm 11 (48-119)	93 \pm 10 (58-126)	86 \pm 12 C (48-126)	84 \pm 7 (48-119)	94 \pm 5 (58-126)	89 \pm 8 (48-126)
IVTD	694 \pm 28 (621-780)	683 \pm 22 (607-758)	688 \pm 26 C (607-780)	730 \pm 20 (679-798)	713 \pm 23 (650-795)	721 \pm 23 B (650-798)	726 \pm 24 (631-796)	728 \pm 31 (627-821)	727 \pm 28 A (627-821)	717 \pm 25 (621-798)	708 \pm 28 (607-821)	712 \pm 27 (607-821)
NDFD	490 \pm 33 (400-596)	515 \pm 27 (426-621)	502 \pm 33 C (400-621)	503 \pm 37 (385-630)	541 \pm 27 (463-622)	522 \pm 38 B (385-630)	542 \pm 38 (401-660)	543 \pm 40 (401-684)	543 \pm 39 A (401-684)	512 \pm 35 (385-660)	533 \pm 28 (401-684)	523 \pm 33 (385-684)
NFC	267 \pm 29 (193-383)	231 \pm 21 (185-336)	249 \pm 31 C (185-383)	286 \pm 29 (211-394)	232 \pm 18 (198-353)	259 \pm 36 B (198-394)	293 \pm 29 (212-399)	285 \pm 30 (214-422)	289 \pm 30 A (212-422)	282 \pm 25 (193-399)	250 \pm 32 (185-422)	266 \pm 33 (185-422)
ME	2.08 \pm 0.07 (1.84-2.31)	2.04 \pm 0.07 (1.79-2.25)	2.06 \pm 0.07 C (1.79-2.31)	2.21 \pm 0.06 (1.99-2.42)	2.11 \pm 0.06 (1.95-2.34)	2.16 \pm 0.08 A (1.95-2.42)	2.17 \pm 0.08 (1.92-2.39)	2.14 \pm 0.07 (1.93-2.39)	2.15 \pm 0.08 B (1.92-2.39)	2.15 \pm 0.08 (1.84-2.42)	2.10 \pm 0.07 (1.79-2.39)	2.12 \pm 0.08 (1.79-2.42)
RFQ	103 \pm 12 (75-144)	88 \pm 9 (58-120)	96 \pm 13 C (59-144)	127 \pm 10 (94-159)	105 \pm 11 (77-145)	116 \pm 15 A (77-159)	104 \pm 10 (74-146)	95 \pm 10 (72-129)	99 \pm 11 B (72-146)	111 \pm 14 (74-159)	96 \pm 10 (58-145)	104 \pm 14 (58-159)
Average environment values (AVG) within a row followed by a different letter (A,B,C) are significantly different than each other at the 0.05 level of probability.												

Table 5

Trait means among parental genotypes of the M26 × M35 intermediate wheatgrass mapping population (including C3_3471 and C3_3941 grandparents) evaluated over two years at Logan, UT, USA in three clonally-replicated competition environments.

	Widely-spaced					Polyculture					Monoculture					Across Environment Mean			
Trait	C3_3471	C3_3941	M26	M35		C3_3471	C3_3941	M26	M35		C3_3471	C3_3941	M26	M35		C3_3471	C3_3941	M26	M35
MASS	1862.6	2047.1	1594.2	1576		286.9	267.3	461.9	338.9		110.5	24.9	180.4	39.1		753.3	802.8	745.5	649.9
TILE	169.5	172.3	168.2	163.9		116.7	121.5	117.1	134.1		105.5	104.3	122.5	109.8		130.6	132.9	135.7	135.9
TICR	1412.2	1499.9	1022.2	863.7		52.2	61.5	93.1	50.3		31.9	11.1	51.4	11.4		498.8	527.9	388.9	302.1
ZAMA	58.8 A	56.2 C	56.9 BC	58.3 AB		58.7 A	54.3 D	55.9 C	56.9 BC		58.7 A	52.7 D	57.3 ABC	57.1 ABC		58.7 x	54.4 z	56.7 y	57.5 y
CP	59.9 CD	52.5 DE	60.6 BC	42.6 F		68.0 B	78.6 A	68.4 B	67.8 BC		52.4 DE	50.9 DEF	49.6 EF	46.1 EF		60.1 x	60.6 x	59.6 x	52.2 y
NDF	629.2	634	625.3	635		587.6	589	601.5	594.9		595.6	593.7	612.2	585.9		604.1	606	613	605.3
ADF	414	407.5	409.2	407.8		376.4	373.7	388.2	375.4		386.9	387.2	398.1	381.7		392.4 xy	389.3 y	398.5 x	388.3 y
ADL	95.4	85.8	93	89.7		96	93.6	94	92.4		94.9	90.1	83.5	87.4		95.5 x	89.9 y	90.2 y	89.8 y
IVTD	67.627 F	689.9 E	686.2 EF	681.0 EF		708.2 CD	719.3 BC	712.9 CD	729.1 AB		709.4 CD	719.7 BC	702.8 D	738.3 A		698.0 y	709.6 x	700.7 y	716.2 x
NDFD	484.6	509.7	497.6	496.2		502.3	522.1	521.5	543.6		512.5	527.7	514.5	553.6		499.8 z	519.8 xy	511.2 yz	531.1 x
NFC	234.2	259.3	243.2	267.3		263.7	245	246.9	258.4		273.1	284.5	279.8	294.1		257.0 y	262.9 xy	256.6 y	273.3 x
ME	1.98	2.09	2.04	2.07		2.12	2.16	2.13	2.2		2.08	2.14	2.1	2.17		2.06 z	2.13 x	2.09 y	2.15 x
RFQ	89.9 EF	97.2 D	95.8 DE	89.0 F		109.0 BC	119.1 A	110.1 B	118.8 A		96.2 DE	102.0 CD	96.7 D	102.0 D		98.4 z	106.1 x	100.9 yz	103.3 xy
Values within a row followed by a different letter (A,B,C) indicate that the parent × environment means are significantly different than each other at the 0.05 level of probability.																			
Values within a row followed by a different letter (x,y,z) indicate that the across environment means are significantly different than each other at the 0.05 level of probability.																			

Table 6

Broad-sense heritabilities, and phenotypic (rP), genotypic (rG), and spearman (rSP) correlations between three competition environments for 192 clonally-replicated, full-sib progeny (genets) of the M26 × M35 intermediate wheatgrass mapping population evaluated over two years (2016-2017) at Logan, UT, USA.

	Widely-spaced	Polyculture	Monoculture	Across environments		Widely-spaced vs polyculture			Widely-spaced vs monoculture			Monoculture vs polyculture		
Trait	H genet	H genet	H genet	H genet		r _e	r _G	r _{SP}	r _e	r _G	r _{SP}	r _e	r _G	r _{SP}
MASS	0.73±0.03	0.52±0.07	0.61±0.05	0.67±0.04		0.15±0.03	0.37±0.14	0.57***	0.15±0.03	0.30±0.12	0.28***	0.21±0.03	0.48±0.15	0.32***
TILE	0.85±0.02	0.84±0.02	0.79±0.02	0.92±0.01		0.42±0.03	0.91±0.04	0.34***	0.32±0.04	0.78±0.06	0.28***	0.34±0.03	0.85±0.05	0.28***
TICR	0.53±0.07	0.50±0.08	0.64±0.04	0.53±0.05		0.12±0.03	0.59±0.14	0.5***	0.10±0.03	0.47±0.13	0.13***	0.25±0.03	0.62±0.12	0.23***
ZAMA	0.84±0.02	0.87±0.02	0.70±0.03	0.93±0.01		0.58±0.03	0.98±0.02	0.46***	0.50±0.03	0.97±0.03	0.56***	0.41±0.03	0.98±0.04	0.45***
CP	0.66±0.04	0.73±0.04	0.59±0.07	0.80±0.02		0.23±0.03	0.80±0.08	0.6***	0.11±0.03	0.53±0.12	0.44***	0.16±0.03	0.57±0.11	0.42***
NDF	0.82±0.02	0.83±0.03	0.69±0.05	0.90±0.01		0.39±0.03	0.93±0.04	0.74***	0.31±0.04	0.92±0.06	0.16***	0.32±0.03	0.80±0.07	0.12***
ADF	0.81±0.02	0.81±0.02	0.74±0.04	0.89±0.01		0.36±0.36	0.89±0.05	0.67***	0.32±0.03	0.89±0.06	0.34***	0.30±0.03	0.81±0.07	0.3***
ADL	0.62±0.04	0.67±0.04	0.46±0.09	0.77±0.03		0.19±0.03	0.94±0.09	0.42***	0.18±0.03	1.00±0.14	0.39***	0.09±0.03	0.66±0.14	0.44***
IVTD	0.81±0.02	0.78±0.03	0.72±0.04	0.90±0.01		0.42±0.03	1.01±0.04	0.46***	0.24±0.04	0.87±0.06	0.23***	0.36±0.03	0.90±0.05	0.34***
NDFD	0.79±0.02	0.71±0.04	0.75±0.03	0.86±0.02		0.29±0.03	0.94±0.06	0.44***	0.24±0.04	0.82±0.06	0.21***	0.22±0.03	0.65±0.08	0.2***
NFC	0.82±0.02	0.79±0.03	0.82±0.02	0.90±0.01		0.38±0.03	0.87±0.05		0.34±0.04	0.83±0.05		0.26±0.04	0.82±0.06	
ME	0.82±0.03	0.77±0.03	0.78±0.03	0.91±0.01		0.44±0.03	0.97±0.04	0.5***	0.29±0.04	0.84±0.05	0.31***	0.38±0.03	0.94±0.05	0.42***
RFQ	0.77±0.03	0.73±0.04	0.73±0.04	0.88±0.01		0.36±0.03	1.02±0.06	0.64***	0.23±0.04	0.79±0.07	0.4***	0.33±0.03	0.90±0.07	0.48***

*, **, *** Significant at the 0.05, 0.01, and 0.001 probabilities levels, respectively.

Table 7

The LOD Threshold of each trait in each Linkage group and Genome wide set at the 5% significance level.

	MASS	TILE	TICR	ZAMA	CP	NDF	ADF	ADL	IVTD	NDFD
G. W.	4.9	4.9	5	5.2	5	5.2	5.1	4.8	4.9	4.8
1	3.3	3.4	3.4	3.6	3.5	3.5	3.5	3.3	3.3	3.4
2	3.3	3.2	3.4	3.3	3.4	3.2	3.3	3.2	3.2	3.4
3	3.2	3.4	3.3	3.5	3.4	3.4	3.4	3.3	3.3	3.2
4	3.5	3.5	3.5	3.7	3.5	3.5	3.5	3.4	3.5	3.5
5	3.1	3.3	3.3	3.4	3.2	3.4	3.4	3.3	3.3	3.3
6	3.4	3.4	3.5	3.6	3.5	3.6	3.7	3.4	3.3	3.4
7	3.3	3.2	3.3	3.3	3.3	3.2	3.4	3.4	3.4	3.3
8	3.6	3.4	3.5	3.8	3.7	3.7	3.6	3.7	3.6	3.6
9	3.3	3.3	3.5	3.7	3.5	3.7	3.6	3.4	3.6	3.4
10	3.3	3.3	3.2	3.3	3.3	3.3	3.3	3.4	3.5	3.4
11	3.3	3.3	3.3	3.3	3.2	3.3	3.4	3.3	3.3	3.4
12	3.3	3.1	3.1	3.3	3.2	3.3	3.3	3.2	3.2	3.2
13	3.3	3.3	3.4	3.9	3.5	3.6	3.8	3.3	3.5	3.3
14	3.2	3.2	3.2	3.4	3.2	3.3	3.3	3.3	3.3	3.4
15	3.4	3.4	3.5	3.7	3.5	3.4	3.4	3.4	3.3	3.5
16	3.2	3.1	3	3.4	3.3	3.2	3.4	3.2	3.2	3.2
17	3.5	3.4	3.3	3.7	3.4	3.5	3.3	3.4	3.3	3.4
18	3.3	3.3	3.4	3.4	3.3	3.2	3.3	3.4	3.4	3.3
19	3.3	3.3	3.4	3.6	3.4	3.3	3.3	3.3	3.4	3.3
20	3.5	3.5	3.4	3.8	3.6	3.8	3.6	3.4	3.4	3.5
21	3.4	3.2	3.2	3.5	3.4	3.5	3.3	3.3	3.4	3.4

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.

Table 8

The most significant LOD values and genetic position for each trait in each environment that has a QTL with genome-wide significance

Trait	Linkage group	Spaced	Polyculture	Monoculture	Mean	Interval
MASS	1	---	---	5.76 (21.99)**	---	21.99-22.99
MASS	6	---	---	5.11 (99.75)**	---	99.75-101.75
MASS	10	5.04 (86.04)**	3.78 (86.04)*	3.53 (129.41)*	6.45 (86.04)**	62.85-146.27
MASS	11	---	3.97 (7.56)*	5.39 (7.56)**	---	0-12.32
MASS	14	3.27 (72.46)*	---	5.12 (72.46)**	4.33 (72.46)*	63.35-75.46
MASS	15	---	---	5.93 (111.89)**	---	111.89-114.89
TILE	10	5.88 (86.04)**	5.52 (69.07)**	4.59 (73.7)*	5.7 (86.04)**	40.14-120.25
TILE	11	4.42 (133.65)*	4.46 (107.8)*	3.53 (82.99)*	5.19 (82.99)**	76.11-134.64
TICR	1	---	---	5.07 (21.99)**	---	21.97-22.99
TICR	8	5.23 (184.78)**	---	---	4.11 (218.66)*	149.27-272.21
ZAMA	16	5.96 (106.27)**	---	---	4.23 (107.53)*	79.07-129.89
CP	6	3.78 (157.71)*	6.53 (133.95)**	4.1 (133.95)*	5.7 (133.95)**	110.46-165.88
NDF	10	7.79 (114.23)**	6.9 (114.23)**	5.76 (60.85)**	8.05 (114.23)**	41.14-122.72
NDF	15	---	---	5.74 (69.65)**	---	54.96-98.79
NDF	16	4.9 (79.07)*	---	7.77 (107.58)**	5.42 (79.07)**	41.09-157.11
ADF	10	5.79 (114.23)**	6.13 (78.31)**	5.47 (60.85)**	6.87 (48.31)**	34.14-122.72
ADF	16	4.84 (70.47)*	---	7.63 (109.42)**	5.1 (79.07)**	40.09-133.9
IVTD	10	5.41(83.29)**	6.12 (172.33)**	8.72 (78.31)**	7.3 (78.31)**	53.83-121.72
IVTD	14	3.82 (108.63)*	3.54 (90.65)*	5.24 (68.06)**	4.97 (108.63)**	62.35-123.98
IVTD	18	3.96 (172.33)*	6.08 (172.33)**	---	4.96 (172.33)**	147.49-184.83
NDFD	5	4.94 (19.73)**	3.82 (0)*	---	4.06 (0)*	0-53.77
NDFD	9	6.64 (67.87)**	8.32 (79.28)**	---	7.29 (79.28)**	56.76-124.52
NDFD	10	---	---	5.33 (66.52)**	---	51.08-86.72
NDFD	11	5.58 (106.04)**	4.62 (83.06)*	---	4.7 (106.04)*	79.49-113.73
NDFD	18	3.67 (172.33)*	4.88 (177.28)**	3.76 (209.97)*	5.34 (177.28)**	153.73-221.76

* 5% Significance level linkage group wide

** 5% Significance level genome wide

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.

Table 9

The mean comparison trait data for significant QTL markers corresponding with the measured traits, year, allele and linkage group for the biomass and Tillers crown. Only the years and QTL markers with significant GxE are shown. The lm alleles are from parent M26, the np alleles are from parent M35 and the hk alleles are from both parents.

Trait/LG Marker Allele Effect	MASS/10 TP513463 hh, hk, kk			MASS/10 TP301824 hh, hk, kk		MASS/10 TP799882 hh, hk, kk		
	Mean	2016	2017	Mean		Mean	2016	2017
<u>Year</u>								
2016	486.8 (B)			487.7 (B)		487.3 (B)		
2017	900.9 (A)			895.2 (A)		900.1 (A)		
Mean s.e.	15.1			16.1		16		
pval	<.0001			<.0001		<.0001		
<u>Environment</u>								
Spaced	1598.5 (A)	1273 (A)	1923.6 (A)	1597.6 (A)		1599.8 (A)	1274.7 (A)	1924.9 (A)
Poly	383.8 (B)	118.8 (B)	649.5 (B)	379.1 (B)		381.8 (B)	118.3 (B)	645.2 (B)
Mono	99.2 (C)	67.2 (C)	129.9 (C)	97.6 (C)		99.4 (C)	68 (C)	130.9 (C)
Mean s.e.	15.2	17.9	24.7	17.4		17.6	17.3	24.3
pval	<.0001	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001
<u>Allele</u>								
ll, nn, hh	752.7 (A)	525.7 (A)	979.2 (A)	627 (C)		754.2 (A)	527.7 (A)	980.6 (A)
lm, np, hk	707.1 (B)	490.2 (B)	922.7 (B)	706.5 (B)		706.2 (B)	488.4 (B)	924 (B)
kk	621.8 (C)	443.2 (C)	801 (C)	740.8 (A)		620.7 (C)	444.9 (C)	796.4 (C)
Mean s.e.	15.1	17.9	24.6	17.4		17.5	17.3	23.2
pval	<.0001	0.0002	<.0001	<.0001		<.0001	0.0002	<.0001
<u>Env. X Allele</u>								
Spaced x ll, nn, hh	1739.2 (A)	1376.7 (A)	2101.5 (A)	1481.3 (C)		1744.6 (A)	1383.8 (A)	2105.4 (A)
Spaced x lm, np, hk	1604.6 (B)	1269.3 (B)	1939 (B)	1610.2 (B)		1597 (B)	1259.5 (B)	1934.5 (B)
Spaced x kk	1451.6 (C)	1172.9 (C)	1730.3 (C)	1701.3 (A)		1458 (C)	1180.9 (C)	1734.9 (C)
Poly x ll, nn, hh	407.5 (D)	124.6 (DE)	689.9 (D)	330.1 (E)		408.1 (D)	124.4 (DE)	691.6 (D)
Poly x lm, np, hk	406.7 (D)	132.5 (D)	681.7 (D)	399.2 (D)		409.3 (D)	133 (D)	685.4 (D)
Poly x kk	337.4 (E)	99.2 (DE)	577 (E)	408 (D)		328.1 (E)	97.3 (DE)	558.5 (E)
Mono x ll, nn, hh	111.3 (F)	75.6 (E)	146.2 (F)	69.7 (F)		109.9 (F)	74.8 (E)	144.9 (F)
Mono x lm, np, hk	110 (F)	68.7 (E)	147.6 (F)	110.1 (F)		112.4 (F)	72.8 (E)	152.2 (F)
Mono x kk	76.3 (F)	57.4 (E)	95.8 (F)	113.1 (F)		75.9 (F)	56.4 (E)	95.6 (F)
Mean s.e.	18.8	25.2	35.4	23.6		24.1	24.9	35.3
pval	<.0001	0.0004	<.0001	0.0008		<.0001	0.0003	<.0001
pval_Bon	0.0031	0.0031	0.0031	0.0031		0.0031	0.0031	0.0031

Trait/LG Marker Allele Effect	MASS/14 TP524699 nn, np		MASS/14 TP529335 nn, np		MASS/15 TP880985 hh, hk, kk	TICR/8 TP528489 hh, hk, kk
	Mean	2017	Mean	2017	Mean	2016
<u>Year</u>						
2016	490.6 (B)		490.3 (B)		480 (B)	
2017	914.2 (A)		913.8 (A)		897.3 (A)	
Mean s.e.	15.5		15.6		16.8	
pval	<.0001		<.0001		<.0001	
<u>Environment</u>						
Spaced	1609.8 (A)	1942.3 (A)	1610.5 (A)	1943.8 (A)	1581.9 (A)	318.14 (A)
Poly	392.4 (B)	661.4 (B)	390.9 (B)	658.8 (B)	386.2 (B)	30.42 (B)
Mono	105 (C)	139.6 (C)	104.7 (C)	139.7 (C)	97.9 (C)	22.63 (B)
Mean s.e.	16.5	23.4	17.1	24	18.8	6.65
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
<u>Allele</u>						
ll, nn, hh	735.2 (A)	966.7 (A)	735.7 (A)	966.7 (A)	640.2 (B)	114.63 (B)
lm, np, hk	669.6 (B)	862.2 (B)	668.5 (B)	861.5 (B)	709.9 (A)	131.93 (A)
kk	N/A	N/A	N/A	N/A	715.9 (A)	124.64 (AB)
Mean s.e.	15.4	21.1	15.8	21.8	18.6	6.64
pval	<.0001	<.0001	<.0001	<.0001	0.0006	0.004
<u>Env. X Allele</u>						
Spaced x ll, nn, hh	1674.7 (A)	2045.1 (A)	1686.9 (A)	2063 (A)	1461.9 (B)	297.04 (C)
Spaced x lm, np, hk	1544.9 (B)	1839.5 (B)	1534.1 (B)	1824.6 (B)	1617.8 (A)	339.74 (A)
Spaced x kk	N/A	N/A	N/A	N/A	1666.1 (A)	317.65 (B)
Poly x ll, nn, hh	414.4 (C)	696.6 (C)	407.4 (C)	682.9 (C)	368.7 (C)	27.37 (D)
Poly x lm, np, hk	370.4 (D)	626.2 (D)	374.5 (C)	634.8 (C)	399.8 (C)	30.24 (D)
Poly x kk	N/A	N/A	N/A	N/A	390.1 (C)	33.65 (D)
Mono x ll, nn, hh	116.4 (E)	158.3 (E)	112.7 (D)	154.3 (D)	90.1 (D)	19.47 (D)
Mono x lm, np, hk	93.6 (E)	121 (E)	96.8 (D)	125.1 (D)	112.2 (D)	25.8 (D)
Mono x kk	N/A	N/A	N/A	N/A	91.4 (D)	22.62 (D)
Mean s.e.	19.4	29.2	20.6	29.8	26.4	8.56
pval	0.0004	0.0013	<.0001	<.0001	0.0007	0.0092
pval_Bon	0.0031	0.0031	0.0031	0.0031	0.0031	0.0033

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.
 Spaced represents the Spaced environment, Poly represents the polyculture environment, and Mono represents the monoculture environment
 Pval-Bon represents the value from the Bonferroni test.

[illegible]

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA. Spaced represents the Spaced environment, Poly represents the polyculture environment, and Mono represents the monoculture environment. Pval-Bon represents the value from the Bonferroni test.

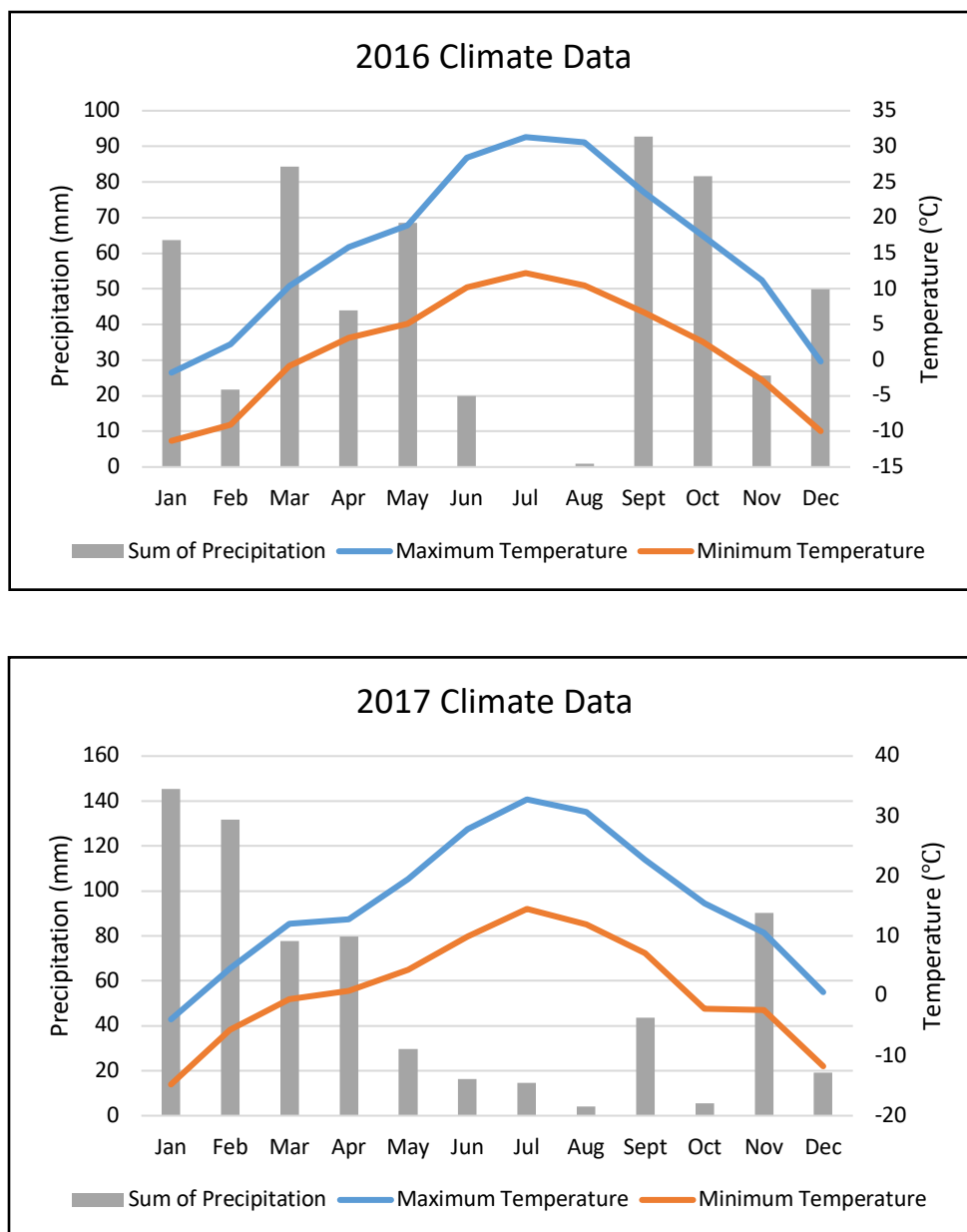


Figure 1

The temperature and precipitation throughout the years the intermediate wheatgrass was growing in the Evans farms.

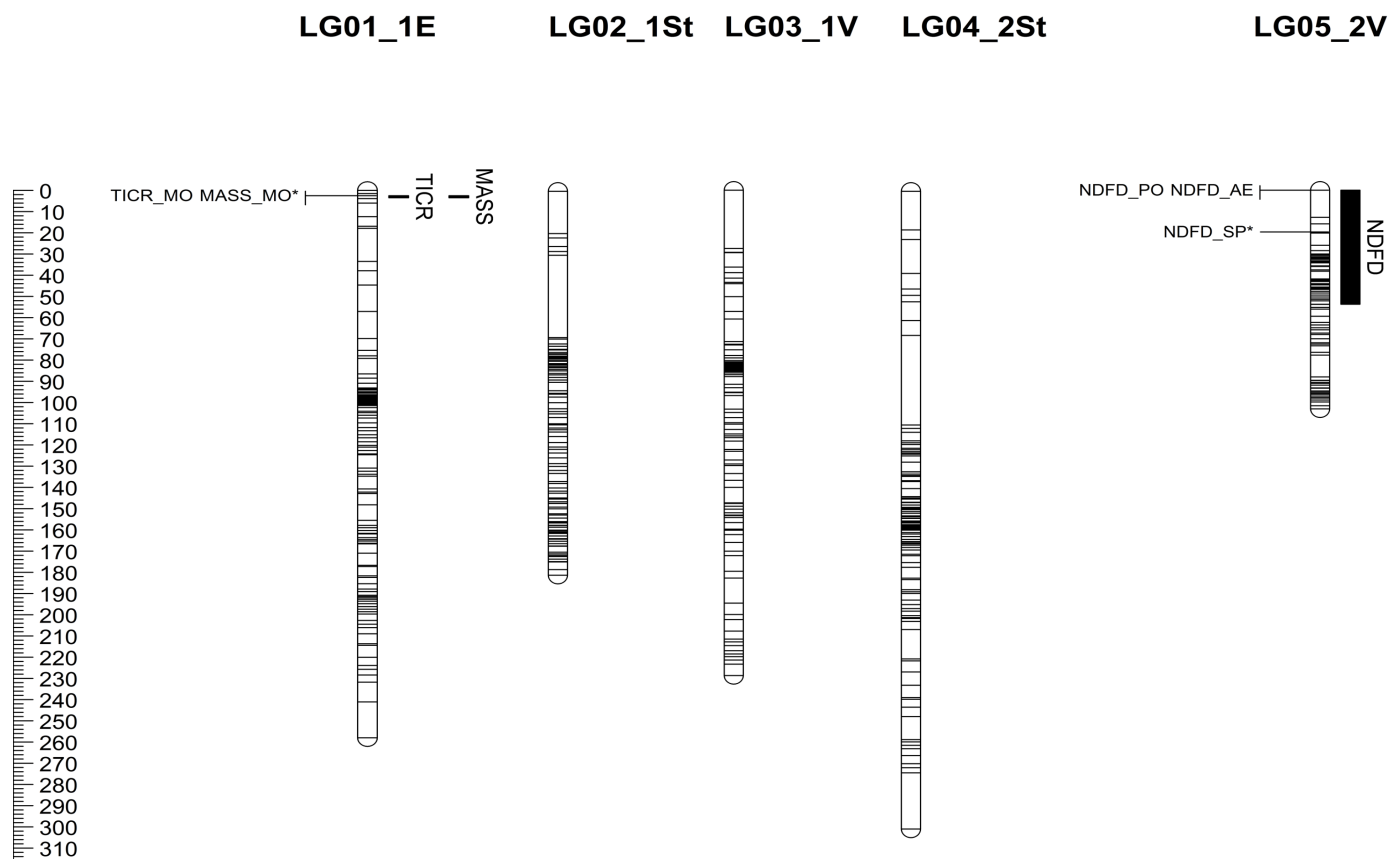


Figure 2

QTL mapping of *Thinopyrum intermedium* in response to the three environmental conditions. The greyed out blocks have one year where the trait has significant GxE interaction. The white blocks have traits that have significant GxE interaction both years. SP represents the spaced environment, PO represents the polyculture environment, MO represents the monoculture environments, and AE represents the mean across the environments.

LG06_2E LG07_3E

LG08_3St

LG09_3V

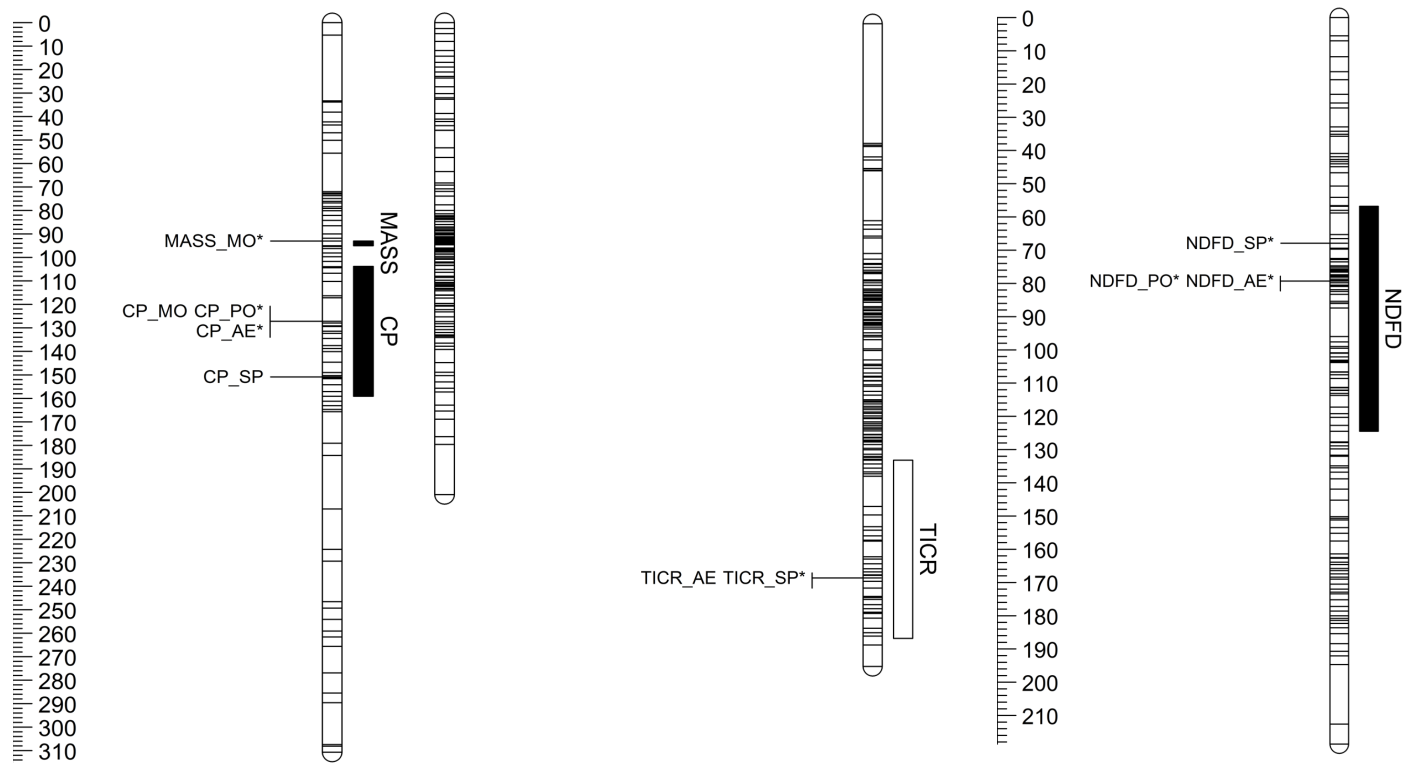
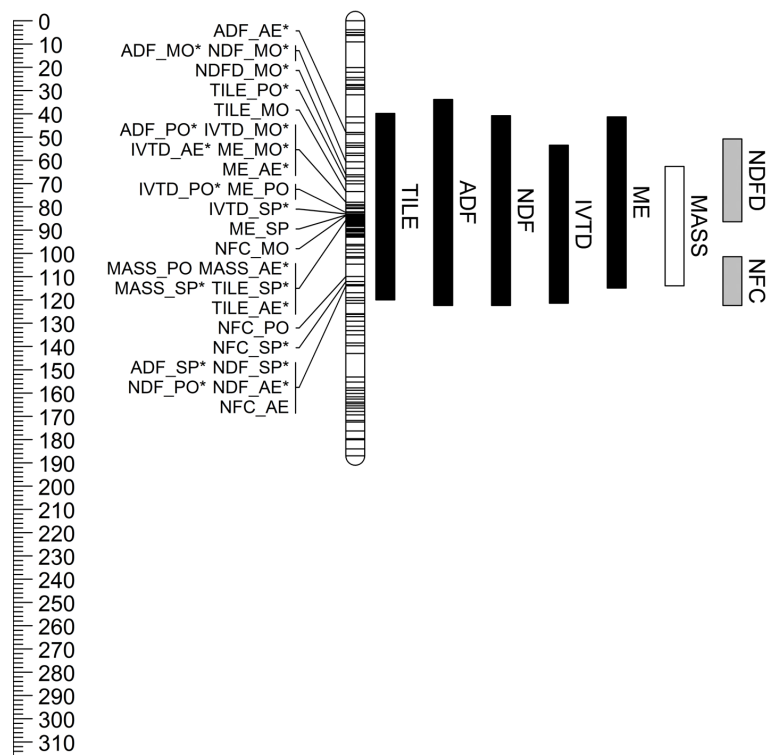
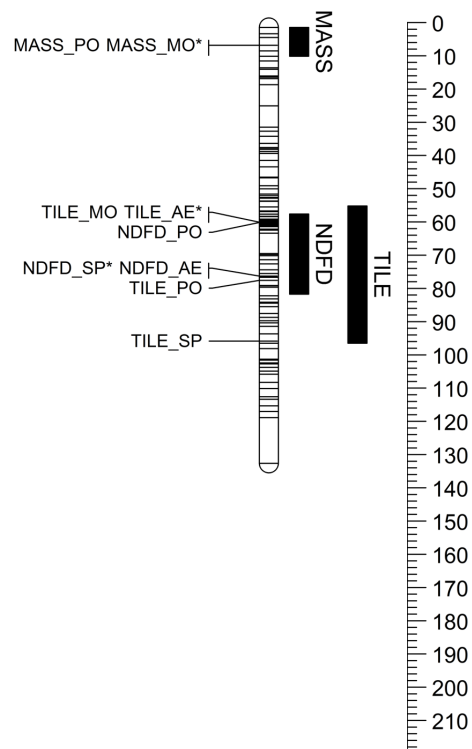


Figure 2 Continued

LG10_4E



LG11_4St



LG12_4V

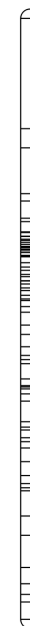


Figure 2 continued

LG13_5St

LG14_5E

LG15_5V

LG16_6V

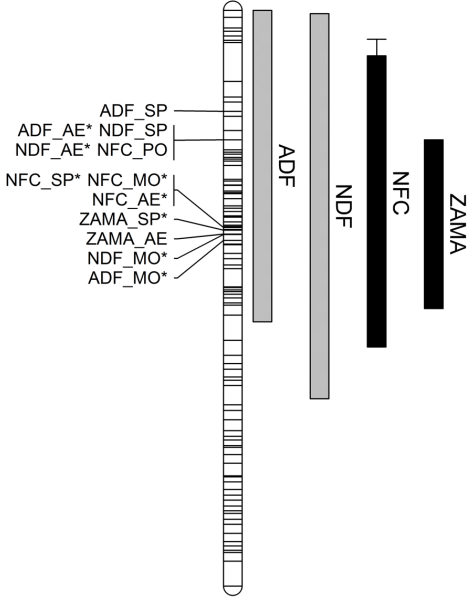
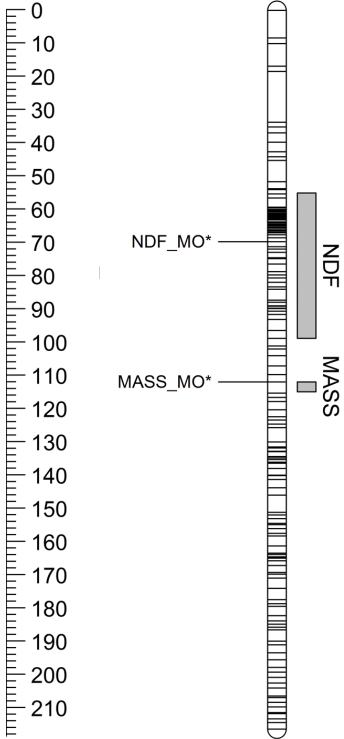
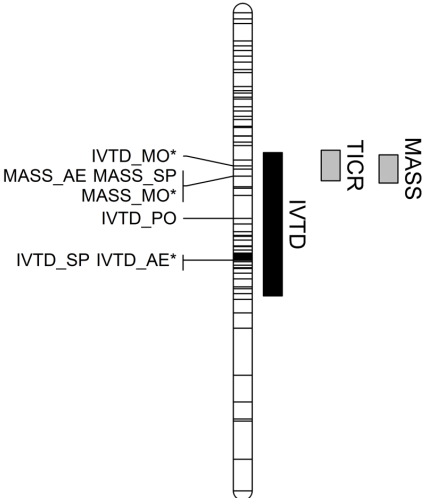
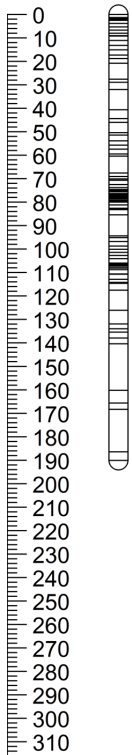


Figure 2 continued

LG17_6St

LG18_6E

LG19_7V

LG20_7E

LG21_7St

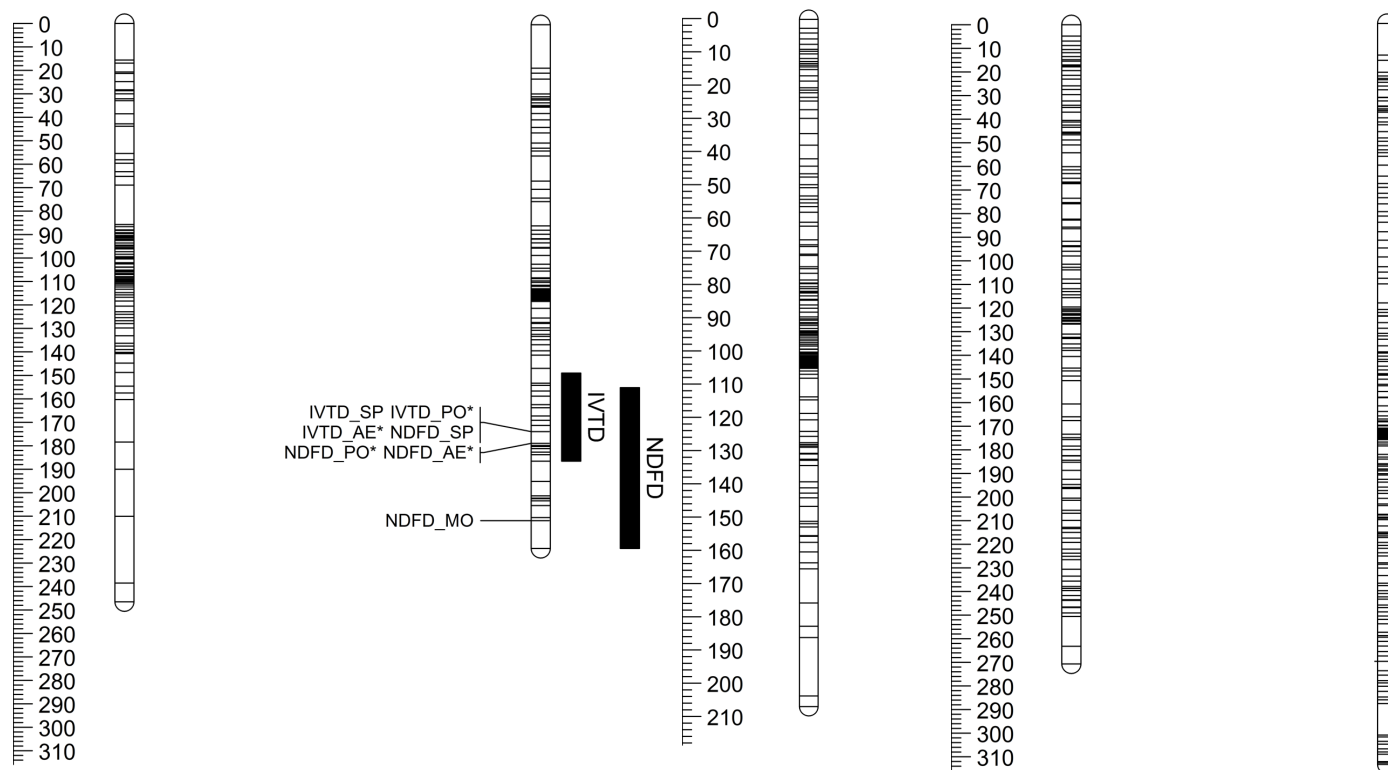


Figure 2 continued

Appendix A. The genotypic correlation (r_G), number of shared QTLs (%Q), and the compared heritabilities between the environments

Trait	Monoculture vs Spaced				Polyculture vs Spaced				Polyculture vs Monoculture			
	r_G	H^2 compared		%Q	r_G	H^2 compared		%Q	r_G	H^2 compared		%Q
		M	S			P	S			P	M	
TILE	0.78 ± 0.06	0.79	0.85	0.67 (2/3)	0.91 ± 0.04	0.84	0.85	1 (2/2)	0.85 ± 0.05	0.84	0.79	0.67 (2/3)
ZAMA	0.97 ± 0.03	0.70	0.84	0 (0/1)	0.98 ± 0.02	0.87	0.84	0 (0/1)	0.98 ± 0.04	0.87	0.70	0 (0/1)
TICR	0.72 ± 0.19	0.64	0.36	0 (0/2)	1.01 ± 0.25	0.50	0.36	0 (0/2)	0.62 ± 0.12	0.50	0.64	0 (0/2)
MASS	0.30 ± 0.12	0.61	0.73	0.33 (2/6)	0.37 ± 0.14	0.52	0.73	0.17 (1/6)	0.48 ± 0.15	0.52	0.61	0.33 (2/6)
ADF	0.89 ± 0.06	0.74	0.81	1 (2/2)	0.89 ± 0.05	0.81	0.81	0.5 (1/2)	0.81 ± 0.07	0.81	0.74	0.5 (1/2)
NDF	0.92 ± 0.06	0.69	0.82	0.67 (2/3)	0.93 ± 0.04	0.83	0.82	0.33 (1/3)	0.80 ± 0.07	0.83	0.69	0.33 (1/3)
NDFD	0.82 ± 0.06	0.75	0.79	0.2 (1/5)	0.94 ± 0.06	0.71	0.79	0.8 (4/5)	0.65 ± 0.08	0.71	0.75	0.2 (1/5)
NFC	0.83 ± 0.05	0.82	0.82	1 (2/2)	0.87 ± 0.05	0.79	0.82	1 (2/2)	0.82 ± 0.06	0.79	0.82	1 (2/2)
CP	0.53 ± 0.12	0.59	0.66	1 (1/1)	0.80 ± 0.08	0.73	0.66	1 (1/1)	0.57 ± 0.11	0.73	0.59	1 (1/1)
IVTD	0.87 ± 0.06	0.72	0.81	0.67 (2/3)	1.01 ± 0.04	0.78	0.81	1 (3/3)	0.90 ± 0.05	0.78	0.72	0.67 (2/3)
ME	0.84 ± 0.05	0.78	0.82	1 (1/1)	0.97 ± 0.04	0.77	0.82	1 (1/1)	0.94 ± 0.05	0.77	0.78	1 (1/1)

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.

In the heritability's compared sections S represents the spaced environment, M represents the monoculture environment, and P represents the polyculture environment.

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
ADF	PO	10	6.13	78.31	TP271925	36.14-116.23	14.2	TP331941	49.08	16.256
ADF	AE	10	6.87	48.31	TP474398	36.14-121.72	15.7	TP371172	52.83	21.678
ADF	SP	10	5.79	114.23	TP697780	96.31-122.72	13.4	TP510276	119.25	22.719
ADF	MO	10	5.47	60.85	TP714691	34.14-101.71	12.7	TP487284	86.04	20.744
ADF	MO	16	7.63	109.42	TP552520_6H_464	78.26-131.9	17.3	TP444498	107.53	29.786
ADF	AE	16	5.1	79.07	TP661167_6H_11	40.09-133.9	11.9	TP65122	107.58	18.505
ADF*	AE	4	4.21	191.67				TP520706	143.78	8.638
ADF*	MO	4	3.77	22.62				TP801758	22.62	10.127
ADF*	SP	4	3.7	18.07				TP310140	18.07	10.09
ADF*	PO	9	4.02	170.45				TP350053	165.75	12.543
ADF*	AE	12	3.42	64.47				TP209546_4H_466	69.01	16.795
ADF*	PO	12	4.06	64.47				TP677167	68.74	16.312
ADF*	MO	15	4.22	69.65				TP763986	62.39	13.149
ADF*	SP	16	4.84	70.47				TP91004	91.01	16.123
ADF*	AE	19	3.45	203.83				TP299528_7H_577	157.52	6.671
ADL*	AE	8	4.23	272.21				TP824450	272.21	17.563
ADL*	PO	8	4.6	263.13				TP444856	217.62	17.385
ADL*	AE	14	3.81	169.56				TP154488	169.56	13.732
ADL*	PO	18	4.52	193.44				TP571386	179.48	12.306

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
ADL*	SP	18	3.74	116.7				TP43525	115.94	9.792
ADL*	AE	21	3.48	210.38				TP850130	195.5	14.745
ADL*	PO	21	4.24	210.38				TP893276_7H_551	217.62	17.385
CP	AE	6	5.7	133.95	TP44644	110.46-165.88	13.2	TP44644	133.95	25.965
CP	PO	6	6.53	133.95	TP44644	126.97-157.1	15	TP44644	133.95	28.417
CP*	MO	6	4.1	133.95				TP44644	133.95	18.801
CP*	SP	6	3.78	157.71				TP592665	158.4	12.153
CP*	SP	5	3.6	19.73				TP829390	20.17	9.607
CP*	AE	8	3.86	176.68				TP155719	119.75	7.582
CP*	PO	12	4.94	64.47				TP532901	64.47	20.16
CP*	SP	21	3.92	156.94				TP473564	140.52	15.827
IVTD	AE	10	7.3	78.31	TP271925	59.15-87.08	16.6	TP301824	73.7	21.827
IVTD	MO	10	8.72	78.31	TP271925	61.85-83.78	19.5	TP301824	73.7	26.255
IVTD	SP	10	5.41	83.29	TP67572	53.83-121.72	12.6	TP807868	100.02	18.187
IVTD	PO	10	6.12	82.73	TP774095	60.85-87.08	14.1	TP301824	73.7	18.425
IVTD	MO	14	5.24	68.06	TP151207	62.35-97.97	12.2	TP196229	108.63	14.102
IVTD	AE	14	4.97	108.63	TP196229	63.35-123.98	11.6	TP196229	108.63	17.701

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
IVTD	AE	18	4.96	172.33	TP96886	147.49-184.83	11.6	TP44922	169.73	24.126
IVTD	PO	18	6.08	172.33	TP96886	161.92-177.28	14.1	TP44922	169.73	28.737
IVTD*	PO	5	3.54	0				TP647617	0	15.196
IVTD*	MO	7	4.67	41.05				TP583925	43.86	11.14
IVTD*	AE	8	3.68	272.21				TP824450	272.21	13.154
IVTD*	PO	8	3.73	272.21				TP824450	272.21	12.103
IVTD*	AE	9	3.61	66.51				TP84707	66.51	15.911
IVTD*	PO	9	3.74	66.51				TP742242	65.29	15.8
IVTD*	AE	12	3.3	69.84				TP209546_4H_466	69.01	13.653
IVTD*	PO	12	4.07	64.47				TP209546_4H_466	69.01	13.984
IVTD*	SP	12	3.28	69.84				TP209546_4H_466	69.01	16.365
IVTD*	PO	14	3.54	90.65				TP814309	93.14	11.828
IVTD*	SP	14	3.82	108.63				TP196229	108.63	15.085
IVTD*	PO	15	3.49	89.78				TP51697	90.62	11.41
IVTD*	SP	18	3.96	172.33				TP96886	172.33	15.404
IVTD*	MO	17	3.5	111.53				TP392378	106.6	8.962
IVTD*	SP	21	3.41	227.04				TP806301	227.04	14.015
MASS	MO	1	5.76	21.99	TP884376	21.99-22.99	13	TP353941	36.42	7.506
MASS	MO	6	5.11	99.75	TP151810	99.75-101.75	11.6	TP777488	165.88	8.686

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
MASS	SP	10	5.04	86.04	TP456596	73.43-114.23	11.4	TP513463	87.08	18.672
MASS	AE	10	6.45	86.04	TP848673	62.85-91.09	14.4	TP799882_4H_117	86.04	23.314
MASS	MO	11	5.39	7.56	TP903209	0-12.32	12.3	TP491526	158.54	12.483
MASS	MO	14	5.12	72.46	TP256836	63.35-75.46	11.7	TP48221_5H_20	90.65	5.508
MASS	MO	15	5.93	111.89	TP592790	111.89-114.89	13.4	TP880985	61.89	12.434
MASS*	SP	5	4.29	98.1				TP548730	98.1	12.039
MASS*	SP	8	4.59	204.41				TP539	243.76	15.76
MASS*	PO	10	3.78	86.04				TP799882_4H_117	86.04	17.399
MASS*	MO	10	3.53	129.41				TP301824	73.7	13.058
MASS*	PO	11	3.97	7.56				TP557515	117.11	12.397
MASS*	AE	12	3.7	60.18				TP68392	69.84	13.608
MASS*	AE	14	4.33	72.46				TP524699	65.59	11.424
MASS*	SP	14	3.27	72.46				TP529335	72.46	11.448
MASS*	AE	13	4.3	82.11				TP397564	85.57	15.309
MASS*	MO	13	3.42	82.11				TP405091	84.96	11.885
ME	AE	10	5.45	78.31	TP271925	41.56-115.23	12.7	TP774095	82.73	14.722
ME	MO	10	6.58	78.31	TP271925	52.08-87.08	15.1	TP774095	82.73	17.659
ME*	PO	5	3.85	0				TP647617	0	18.203
ME*	PO	7	3.49	14.29				TP310707	123.17	10.789

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
ME*	MO	7	3.45	41.05				TP294131	41.05	11.368
ME*	AE	8	4.7	272.21				TP824450	272.21	16.435
ME*	PO	8	4.62	272.21				TP824450	272.21	14.954
ME*	MO	8	4.45	257.92				TP366872	259.34	13.221
ME*	AE	9	3.79	183.59				TP441695	183.59	11.857
ME*	SP	9	3.58	183.59				TP441695	183.59	13.375
ME*	PO	10	4.48	82.73				TP774095	82.73	11.329
ME*	SP	10	4.22	83.78				TP510276	119.25	13.739
ME*	AE	14	4.44	108.63				TP196229	108.63	14.448
ME*	MO	14	4.95	108.63				TP196229	108.63	15.443
ME*	SP	14	3.98	72.46				TP196229	108.63	10.095
ME*	AE	18	3.9	172.33				TP44922	169.73	21.304
ME*	PO	18	4.78	169.73				TP44922	169.73	24.67
ME*	SP	18	3.32	112.47				TP96886	172.33	13.859
ME*	MO	17	3.5	110.3				TP362609_6H_512	108.19	8.428
ME*	AE	16	3.25	70.47				TP776097	49.81	10.752
ME*	AE	19	3.49	155.74				TP299528_7H_577	157.52	9.55
ME*	PO	19	4.5	155.74				TP299528_7H_577	157.52	13.902
ME*	SP	19	3.72	182.8				TP854268	152.91	11.01
NDF	AE	10	8.05	114.23	TP697780	104.31-121.72	18.1	TP371172	52.83	21.056

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
NDF	PO	10	6.9	114.23	TP697780	103.31-122.72	15.8	TP3711172	52.83	19.69
NDF	SP	10	7.79	114.23	TP697780	104.86-121.72	17.6	TP140334	121.72	25.011
NDF	MO	10	5.76	60.85	TP714691	41.14-115.23	13.4	TP487284	86.04	19.381
NDF	MO	15	5.74	69.65	TP301894	54.96-98.79	13.3	TP763986	62.39	19.591
NDF	MO	16	7.77	107.58	TP109892	79.07-143.52	17.6	TP338072	102.29	27.804
NDF	AE	16	5.42	79.07	TP661167_6H_11	41.09-157.11	12.6	TP444498	107.53	18.936
NDF*	MO	4	3.51	22.62				TP801758	22.62	8.777
NDF*	PO	9	4.05	167.38				TP350053	165.75	10.751
NDF*	AE	12	4.28	64.47				TP156297_4H_420	69.47	20.688
NDF*	PO	12	4.62	64.47				TP209546_4H_466	69.01	18.933
NDF*	SP	12	3.58	71.77				TP186215	74.91	16.792
NDF*	PO	14	3.88	72.46				TP9425	77.07	10.429
NDF*	SP	16	4.9	79.07				TP489803	76.26	16.855
NDF*	AE	19	3.56	203.83				TP530755	146.7	6.123
NDF*	SP	19	3.45	203.83				TP811840	5.91	5.17
NDFD	SP	5	4.94	19.73	TP422451	0-53.77	11.6	TP894003	12.82	19.458
NDFD	AE	9	7.29	79.28	TP421489	56.76-108.6	16.6	TP3486	77.39	24.688

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
NDFD	PO	9	8.32	79.28	TP421489	65.29-124.52	18.7	TP581871	78.68	29.863
NDFD	SP	9	6.64	67.87	TP532204	56.76-103.37	15.2	TP532204	67.87	24.933
NDFD	MO	10	5.33	66.52	TP854818	51.08-86.72	12.4	TP301824	73.7	21.243
NDFD	SP	11	5.58	106.04	TP663746	79.49-113.73	13	TP793636	104.93	18.823
NDFD	AE	18	5.34	177.28	TP111031	153.73-220.97	12.4	TP44922	169.73	21.803
NDFD	PO	18	4.88	177.28	TP111031	162.16-221.76	11.4	TP44922	169.73	18.606
NDFD*	PO	6	3.64	144.34				TP609278	145.56	14.153
NDFD*	AE	5	4.06	0				TP238848	19.73	15.654
NDFD*	PO	5	3.82	0				TP733301	62.38	15.511
NDFD*	MO	7	3.77	43.86				TP583925	43.86	11.96
NDFD*	PO	8	3.76	263.13				TP783591	115.41	11.296
NDFD*	AE	11	4.7	106.04				TP746301	83.06	16.996
NDFD*	PO	11	4.62	83.06				TP746301	83.06	18.193
NDFD*	AE	14	3.98	108.63				TP196229	108.63	13.824
NDFD*	MO	14	4.41	108.63				TP196229	108.63	17.294
NDFD*	SP	14	3.5	108.63				TP196229	108.63	10.648
NDFD*	AE	15	4.33	61.91				TP618775	36.86	15.043
NDFD*	MO	15	3.54	140.08				TP129822	140.08	13.275
NDFD*	SP	15	4.67	89.78				TP618775	36.86	16.858

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
NDFD*	MO	18	3.76	209.97				TP44922	169.73	16.068
NDFD*	SP	18	3.67	172.33				TP44922	169.73	15.556
NDFD*	SP	20	3.77	147.93				TP78757	139.42	7.243
NDFD*	AE	21	3.47	271.89				TP710222	221.17	16.223
NDFD*	SP	21	4.07	271.89				TP697306	271.89	17.21
NFC	SP	10	5.7	112.38	TP735334	101.71-122.72	13.2	TP510276	119.25	16.413
NFC	AE	16	7.53	105.47	TP271474	53.81-126.71	17.1	TP444498	107.53	33.103
NFC	MO	16	6.04	105.47	TP271474	78.26-141.52	14	TP444498	107.53	24.94
NFC	SP	16	6.86	105.47	TP271474	48.8-125.61	15.7	TP527066	102.01	30.502
NFC*	AE	4	3.69	18.07				TP801758	22.62	11.023
NFC*	PO	9	3.7	122.69				TP787056	131.67	18.454
NFC*	AE	10	4.89	114.23				TP440056	86.04	14.237
NFC*	PO	10	4.99	110.15				TP352410	41.56	14.021
NFC*	MO	10	3.74	83.98				TP402360	80.97	16.143
NFC*	AE	12	3.48	69.84				TP66619	60.18	15.03
NFC*	MO	12	3.23	69.84				TP66619	60.18	12.67
NFC*	AE	13	5.01	85.12				TP559503_5H_307	88.03	16.846
NFC*	MO	13	5.27	85.12				TP17432	87.96	22.5
NFC*	AE	15	3.92	62.77				TP830345	62.96	13.719

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
NFC*	MO	15	5.51	62.77				TP763986	62.39	20.304
NFC*	PO	16	5.03	79.07				TP203135	86.76	21.303
NFC*	PO	19	3.52	203.83				TP439989	128.88	8.694
TICR	MO	1	5.07	21.99	TP884376	21.97-22.99	11.8	TP214762	201.85	10.005
TICR	SP	8	5.03	234.7	TP528489	184.78-260.34	11.8	TP528489	234.7	21.363
TICR*	MO	10	3.92	104.86				TP841626	101.71	14.549
TICR*	MO	11	3.57	52.9				TP615362	130.64	8.302
TICR*	PO	12	3.85	104.02				TP157160_4H_502	104.02	14.789
TICR*	MO	14	4.18	72.46				TP48221_5H_20	90.65	8.277
TICR*	MO	15	4.58	178.65				TP880985	61.89	10.791
TICR*	PO	18	4.58	151.76				TP44922	169.73	13.01
TICR*	MO	21	3.51	217.41				TP806301	227.04	10.099
TICR*	MO	19	4.06	54.19				TP708074	34.36	8.494
TICR*	AE	8	4.68	234.7				TP528489	234.7	18.958
TILE	SP	10	5.88	86.04	TP128770	40.14-91.09	13.6	TP799882_4H_117	86.04	17.517
TILE	PO	10	5.52	69.07	TP509238	42.56-115.23	12.8	TP301824	73.7	18.509
TILE	AE	10	5.7	86.04	TP850616	42.56-120.25	13.2	TP301824	73.7	20.005
TILE	AE	11	5.19	82.99	TP400285	76.11-134.64	12.1	TP354685	161.31	10.98

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
TILE	MO	21	5.03	271.89	TP435663	260.53-274.89	11.8	TP293133	267.73	21.621
TILE*	MO	5	4.5	72.04				TP537350	70.07	19.31
TILE*	AE	8	4.73	179.76				TP607583	208.04	12.678
TILE*	PO	8	4.02	179.76				TP607583	208.04	7.763
TILE*	MO	8	4.2	179.76				TP607583	208.04	12.51
TILE*	SP	8	4.56	147.93				TP607583	208.04	10.93
TILE*	AE	9	4.09	79.75				TP659407	54.78	15.19
TILE*	PO	9	3.36	79.75				TP659407	58.78	17.302
TILE*	MO	9	4.52	72.78				TP365106	78.08	7.299
TILE*	MO	10	4.59	73.7				TP301824	73.7	18.832
TILE*	PO	11	4.46	107.8				TP354685	161.31	12.138
TILE*	MO	11	3.53	82.99				TP566324	83.92	8.22
TILE*	SP	11	4.42	133.65				TP354685	161.31	12.596
TILE*	AE	12	3.46	64.47				TP532901	64.47	11.949
TILE*	PO	12	4.16	64.47				TP532901	64.47	14.329
TILE*	AE	14	4.56	68.06				TP151207	68.06	11.519
TILE*	PO	14	3.62	72.46				TP196229	108.63	10.667
TILE*	MO	14	3.38	65.59				TP48221_5H_20	90.65	7.439
TILE*	SP	14	3.51	68.06				TP151207	68.06	12.114
TILE*	PO	18	3.87	135.52				TP44922	169.73	20.246

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
TILE*	AE	21	3.77	156.94				TP217216	214.19	13.114
ZAMA	SP	16	5.96	106.27	TP19381	79.07-129.89	13.8	TP743845	83.43	29.566
ZAMA*	PO	6	4.37	157.1				TP191087	134.72	20.226
ZAMA*	PO	10	3.89	86.19				TP159734	87.08	15.518
ZAMA*	AE	11	4.19	78.49				TP875227_4H_115	81.71	12.953
ZAMA*	MO	11	4.05	81.71				TP875227_4H_115	81.71	14.938
ZAMA*	SP	11	3.98	78.49				TP272027	86.42	12.075
ZAMA*	AE	15	4.52	59.34				TP175699	62.16	12.698
ZAMA*	PO	15	4.46	59.34				TP283477_5H_34	59.34	12.51
ZAMA*	MO	15	4.13	102.04				TP175699	62.16	13.109
ZAMA*	SP	15	3.76	36.86				TP902986	65.49	11.517
ZAMA*	AE	18	3.61	133.37				TP652187	151.76	12.471
ZAMA*	PO	18	4.19	124.21				TP44922	169.73	17.472
ZAMA*	AE	16	4.23	107.53				TP641846	86.76	22.308
ZAMA*	PO	19	3.72	50.72				TP764084_7H_3	15.11	11.322

Appendix B. Quantitative Trait Loci position, range and locus in each Linkage group that significantly affected a trait in at least one of the three environments.

Trait	Environment	Linkage group	LOD	Position	Locus	Interval	r ²	KW_marker	K_position	K_value
ZAMA *	SP	19	3.72	50.72				TP302599	24.57	9.971

* QTL's with only chromosome-wide significance in that environment.

The different environments are represented by SP for spaced environment, MO for monoculture environment, PO for polyculture environment, and AE for across all environments.

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.

Appendix C1. ADF QxE Data

Effect	TP209546 np			TP299528 hk			TP310140 lm		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	37.58 (B)			37.69 (B)			37.66 (B)		
2017	40.37 (A)			40.48 (A)			40.44 (A)		
Mean s.e.	0.11			0.11			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	40.68 (A)	39.33 (A)	42.02 (A)	40.77 (A)	39.44 (A)	42.1 (A)	40.76 (A)	39.44 (A)	42.09 (A)
Poly	37.33 (C)	34.82 (C)	39.86 (B)	37.48 (C)	34.97 (C)	39.99 (B)	37.4 (C)	34.88 (C)	39.92 (B)
Mono	38.91 (B)	38.57 (B)	42.02 (A)	39 (B)	38.65 (B)	39.34 (C)	38.99 (B)	38.66 (B)	42.09 (A)
Mean s.e.	0.13	0.18	0.07	0.12	0.19	0.08	0.13	0.18	0.08
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	39.27 (A)	37.88 (A)	40.66 (A)	39.05 (B)	37.65 (B)	40.44 (B)	38.78 (B)	37.41 (B)	40.16 (B)
lm, np, hk	38.68 (B)	37.27 (B)	40.08 (B)	38.82 (B)	37.42 (C)	40.22 (C)	39.32 (A)	37.9 (A)	40.73 (A)
kk	N/A	N/A	N/A	39.38 (A)	37.98 (A)	40.77 (A)	N/A	N/A	N/A
Mean s.e.	0.11	0.17	0.06	0.12	0.19	0.08	0.12	0.18	0.07
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	40.96 (A)	39.64 (A)	42.28 (A)	40.68 (AB)	39.33 (AB)	42.03 (AB)	40.43 (B)	39.01 (B)	41.85 (B)
Spaced-lm, np, hk	40.39 (B)	39.03 (B)	41.76 (B)	40.57 (B)	39.24 (B)	41.91 (B)	41.1 (A)	39.86 (A)	42.33 (A)
Spaced-kk	N/A	N/A	N/A	41.05 (A)	39.74 (A)	42.36 (A)	N/A	N/A	N/A
Poly-ll, nn, hh	37.7 (E)	35.24 (D)	40.17 (C)	37.43 (E)	34.98 (D)	39.89 (D)	37.21 (E)	34.76 (D)	39.68 (D)
Poly-lm, np, hk	36.97 (F)	34.4 (E)	39.54 (D)	37.06 (E)	34.55 (E)	39.57 (DE)	37.58 (E)	35 (D)	40.16 (C)
Poly-kk	N/A	N/A	N/A	37.95 (D)	35.38 (D)	40.51 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	39.14 (C)	38.75 (B)	39.52 (D)	39.02 (C)	38.64 (C)	39.39 (EF)	38.71 (D)	38.46 (C)	38.94 (E)
Mono-lm, np, hk	38.67 (D)	38.39 (C)	38.93 (E)	38.84 (C)	38.48 (C)	39.18 (F)	39.27 (C)	38.85 (B)	39.68 (D)
Mono-kk	N/A	N/A	N/A	39.14 (C)	38.82 (C)	39.45 (EF)	N/A	N/A	N/A
Mean s.e.	0.15	0.2	0.11	0.17	0.22	0.13	0.16	0.2	0.11
pval	0.5756	0.1419	0.8463	0.2966	0.4459	0.0959	0.5426	0.0456	0.4285
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C1. ADF QxE Data Continued

Effect	TP331941 np			TP350053 hk			TP371172 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	37.59 (B)			37.57 (B)			37.57 (B)		
2017	40.36 (A)			40.38 (A)			40.35 (A)		
Mean s.e.	0.11			0.11			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	40.69 (A)	39.35 (A)	42.03 (A)	40.68 (A)	39.33 (A)	42.04 (A)	40.68 (A)	39.33 (A)	42.02 (A)
Poly	37.35 (C)	34.84 (C)	39.85 (B)	37.32 (C)	34.8 (C)	39.84 (B)	37.33 (C)	34.82 (C)	39.85 (B)
Mono	38.9 (B)	38.58 (B)	39.21 (C)	38.92 (B)	38.58 (B)	39.26 (C)	38.88 (B)	38.56 (B)	39.19 (C)
Mean s.e.	0.12	0.18	0.07	0.12	0.18	0.08	0.12	0.18	0.07
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	38.58 (B)	37.24 (B)	39.93 (B)	38.59 (B)	37.19 (A)	40 (C)	38.55 (B)	37.21 (B)	39.89 (B)
lm, np, hk	39.37 (A)	37.95 (A)	40.8 (A)	39.1 (A)	37.75 (A)	40.45 (B)	39.37 (A)	37.93 (A)	40.82 (A)
kk	N/A	N/A	N/A	39.23 (A)	37.76 (B)	40.69 (A)	N/A	N/A	N/A
Mean s.e.	0.11	0.18	0.06	0.12	0.18	0.07	0.11	0.17	0.06
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	40.34 (B)	38.98 (B)	41.71 (B)	40.35 (B)	38.99 (B)	41.71 (B)	40.32 (B)	38.97 (B)	41.67 (B)
Spaced-lm, np, hk	41.03 (A)	39.72 (A)	42.35 (A)	40.77 (A)	39.5 (A)	42.04 (AB)	41.03 (A)	39.7 (A)	42.36 (A)
Spaced-kk	N/A	N/A	N/A	40.93 (A)	39.51 (A)	42.35 (A)	N/A	N/A	N/A
Poly-ll, nn, hh	36.89 (F)	34.38 (E)	39.4 (E)	36.69 (E)	34.15 (E)	39.24 (DE)	36.87 (F)	34.34 (E)	39.41 (E)
Poly-lm, np, hk	37.8 (E)	35.31 (D)	40.31 (C)	37.55 (D)	35.08 (D)	40.03 (C)	37.79 (E)	35.3 (D)	40.3 (C)
Poly-kk	N/A	N/A	N/A	37.71 (D)	35.16 (D)	40.25 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	38.52 (D)	38.36 (C)	38.68 (F)	38.74 (C)	38.43 (C)	39.05 (E)	38.46 (D)	38.32 (C)	38.59 (F)
Mono-lm, np, hk	39.28 (C)	38.81 (B)	39.74 (D)	38.98 (C)	38.68 (BC)	39.27 (DE)	39.3 (C)	38.81 (B)	39.78 (D)
Mono-kk	N/A	N/A	N/A	39.05 (C)	38.63 (BC)	39.46 (D)	N/A	N/A	N/A
Mean s.e.	0.15	0.2	0.1	0.17	0.22	0.13	0.15	0.2	0.1
pval	0.6114	0.1377	0.107	0.1186	0.1276	0.1685	0.6799	0.1444	0.0453
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C1. ADF QxE Data Continued

Effect	TP444498 hk			TP487284 np			TP510276 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	37.64 (B)			37.57 (B)			37.56 (B)		
2017	40.44 (A)			40.34 (A)			40.34 (A)		
Mean s.e.	0.1			0.1			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	40.73 (A)	39.39 (A)	42.08 (A)	40.66 (A)	39.33 (A)	42 (A)	40.64 (A)	39.3 (A)	41.97 (A)
Poly	37.41 (C)	34.89 (C)	39.93 (B)	37.35 (C)	34.84 (C)	39.86 (B)	37.32 (C)	34.8 (C)	39.85 (B)
Mono	38.98 (B)	38.64 (B)	39.31 (C)	38.86 (B)	38.54 (B)	39.16 (C)	38.9 (B)	38.57 (B)	39.22 (C)
Mean s.e.	0.11	0.18	0.08	0.12	0.17	0.07	0.12	0.19	0.08
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	39.54 (A)	38.15 (A)	40.93 (A)	38.55 (B)	37.23 (B)	39.87 (B)	38.4 (B)	37.05 (B)	39.74 (B)
lm, np, hk	39.03 (B)	37.65 (B)	40.41 (B)	39.36 (A)	37.91 (A)	40.81 (A)	39.21 (A)	37.81 (A)	40.61 (A)
kk	38.55 (C)	37.13 (C)	39.98 (C)	N/A	N/A	N/A	39.24 (A)	37.81 (A)	40.68 (A)
Mean s.e.	0.11	0.18	0.07	0.11	0.16	0.06	0.12	0.19	0.08
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	41.17 (A)	39.81 (A)	42.54 (A)	40.3 (B)	38.97 (B)	41.63 (B)	40 (B)	38.63 (B)	41.37 (B)
Spaced-lm, np, hk	40.75 (B)	39.44 (AB)	42.05 (B)	41.03 (A)	39.68 (A)	42.37 (A)	40.98 (A)	39.64 (A)	42.32 (A)
Spaced-kk	40.28 (C)	38.91 (CD)	41.65 (C)	N/A	N/A	N/A	40.93 (A)	39.63 (A)	42.22 (A)
Poly-ll, nn, hh	37.8 (G)	35.46 (F)	40.15 (D)	36.92 (F)	34.41 (E)	39.45 (E)	36.68 (F)	34.23 (D)	39.14 (D)
Poly-lm, np, hk	37.38 (H)	34.92 (G)	39.85 (D)	37.77 (E)	35.28 (D)	40.28 (C)	37.62 (E)	35.12 (C)	40.12 (C)
Poly-kk	37.04 (H)	34.3 (H)	39.78 (D)	N/A	N/A	N/A	37.66 (E)	35.04 (C)	40.28 (C)
Mono-ll, nn, hh	39.66 (D)	39.19 (BC)	40.12 (D)	38.42 (D)	38.3 (C)	38.53 (F)	38.52 (D)	38.3 (B)	38.72 (E)
Mono-lm, np, hk	38.95 (E)	38.58 (D)	39.32 (E)	39.29 (C)	38.78 (B)	39.79 (D)	39.03 (C)	38.67 (B)	39.39 (D)
Mono-kk	38.34 (F)	38.16 (E)	38.5 (F)	N/A	N/A	N/A	39.15 (C)	38.74 (B)	39.55 (D)
Mean s.e.	0.16	0.22	0.13	0.15	0.19	0.11	0.17	0.23	0.13
pval	0.3739	0.8756	0.0005	0.8571	0.2812	0.0376	0.4378	0.2596	0.5578
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C1. ADF QxE Data Continued

Effect	TP520706 hk			TP65122 hk			TP677167 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	37.57 (B)			37.63 (B)			37.55 (B)		
2017	40.39 (A)			40.43 (A)			40.32 (A)		
Mean s.e.	0.1			0.1			0.1		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	40.65 (A)	39.29 (A)	42.01 (A)	38.95 (B)	38.6 (B)	39.29 (C)	38.85 (B)	38.51 (B)	39.18 (C)
Poly	37.34 (C)	34.82 (C)	39.86 (B)	37.41 (C)	34.89 (C)	39.93 (B)	37.29 (C)	34.81 (C)	39.78 (B)
Mono	38.96 (B)	38.6 (B)	39.3 (C)	40.71 (A)	39.37 (A)	42.06 (A)	40.66 (A)	39.32 (A)	41.99 (A)
Mean s.e.	0.12	0.18	0.08	0.12	0.18	0.08	0.13	0.19	0.08
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	39.22 (A)	37.83 (A)	40.6 (A)	39.54 (A)	38.15 (A)	40.93 (A)	39.26 (A)	37.88 (A)	40.64 (A)
lm, np, hk	39.11 (A)	37.73 (A)	40.48 (A)	39.02 (B)	37.64 (B)	40.41 (B)	38.61 (B)	37.21 (B)	40 (B)
kk	38.62 (B)	37.14 (B)	40.1 (B)	38.52 (C)	37.08 (C)	39.94 (C)	N/A	N/A	N/A
Mean s.e.	0.12	0.18	0.08	0.12	0.18	0.08	0.11	0.18	0.07
pval	<.0001	<.0001	0.0002	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	40.75 (AB)	39.38 (AB)	42.12 (AB)	39.61 (C)	39.14 (BC)	40.07 (DE)	39.11 (C)	38.73 (B)	39.48 (D)
Spaced-lm, np, hk	40.86 (A)	39.56 (A)	42.17 (A)	38.96 (D)	38.6 (D)	39.31 (F)	38.59 (D)	38.28 (C)	38.88 (E)
Spaced-kk	40.34 (B)	38.94 (BC)	41.74 (B)	38.29 (E)	38.07 (E)	38.5 (G)	N/A	N/A	N/A
Poly-ll, nn, hh	37.68 (E)	35.2 (E)	40.16 (C)	37.86 (F)	35.5 (F)	40.23 (D)	37.7 (E)	35.28 (D)	40.14 (C)
Poly-lm, np, hk	37.51 (E)	35.03 (E)	40 (C)	37.33 (G)	34.86 (G)	39.8 (E)	36.88 (F)	34.34 (E)	39.43 (D)
Poly-kk	36.82 (F)	34.22 (F)	39.43 (D)	37.05 (G)	34.33 (H)	39.77 (E)	N/A	N/A	N/A
Mono-ll, nn, hh	39.22 (C)	38.91 (BC)	39.51 (D)	41.15 (A)	39.8 (A)	42.5 (A)	40.96 (A)	39.62 (A)	42.3 (A)
Mono-lm, np, hk	38.94 (CD)	38.61 (CD)	39.26 (D)	40.78 (A)	39.46 (AB)	42.1 (B)	40.35 (B)	39.02 (B)	41.69 (B)
Mono-kk	38.72 (D)	38.27 (D)	39.14 (D)	40.21 (B)	38.85 (CD)	41.57 (C)	N/A	N/A	N/A
Mean s.e.	0.17	0.22	0.14	0.17	0.22	0.13	0.16	0.21	0.12
pval	0.3798	0.2688	0.3505	0.4307	0.8851	0.0025	0.555	0.1626	0.8849
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C1. ADF QxE Data Continued

Effect	TP763986 np			TP801758 lm			TP91004 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	37.64 (B)			37.64 (B)			37.61 (B)		
2017	40.42 (A)			40.42 (A)			40.39 (A)		
Mean s.e.	0.1			0.11			0.1		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	38.97 (B)	38.63 (B)	39.29 (C)	38.96 (B)	38.63 (B)	39.29 (C)	38.93 (B)	38.62 (B)	39.23 (C)
Poly	37.39 (C)	34.89 (C)	39.9 (B)	37.39 (C)	34.87 (C)	39.92 (B)	37.38 (C)	34.86 (C)	39.9 (B)
Mono	40.73 (A)	39.39 (A)	42.07 (A)	40.74 (A)	39.41 (A)	42.07 (A)	40.7 (A)	39.35 (A)	42.04 (A)
Mean s.e.	0.12	0.18	0.07	0.13	0.18	0.08	0.12	0.18	0.08
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	39.22 (A)	37.81 (A)	40.62 (A)	38.75 (B)	37.35 (B)	40.15 (B)	38.48 (C)	37.04 (C)	39.92 (C)
lm, np, hk	38.84 (B)	37.46 (B)	40.22 (B)	39.31 (A)	37.92 (A)	40.7 (A)	39.04 (B)	37.63 (B)	40.45 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	39.49 (A)	38.16 (A)	40.81 (A)
Mean s.e.	0.11	0.17	0.06	0.12	0.17	0.07	0.12	0.18	0.08
pval	0.0002	0.0004	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	39.28 (C)	38.9 (B)	39.64 (C)	38.63 (D)	38.39 (C)	38.86 (E)	38.33 (F)	38.21 (E)	38.44 (F)
Spaced-lm, np, hk	38.65 (D)	38.35 (C)	38.95 (D)	39.3 (C)	38.87 (B)	39.71 (D)	38.97 (E)	38.54 (DE)	39.38 (E)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	39.49 (D)	39.1 (BC)	39.87 (D)
Poly-ll, nn, hh	37.47 (E)	35.01 (D)	39.93 (C)	37.19 (F)	34.66 (E)	39.72 (D)	36.98 (I)	34.21 (H)	39.75 (D)
Poly-lm, np, hk	37.32 (E)	34.77 (D)	39.88 (C)	37.6 (E)	35.08 (D)	40.12 (C)	37.39 (H)	34.9 (G)	39.89 (D)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	37.78 (G)	35.49 (F)	40.07 (D)
Mono-ll, nn, hh	40.9 (A)	39.51 (A)	42.3 (A)	40.43 (B)	39 (B)	41.86 (B)	40.14 (C)	38.7 (CD)	41.57 (C)
Mono-lm, np, hk	40.55 (B)	39.27 (A)	41.84 (B)	41.05 (A)	39.81 (A)	42.28 (A)	40.76 (B)	39.45 (B)	42.07 (B)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	41.19 (A)	39.9 (A)	42.49 (A)
Mean s.e.	0.15	0.2	0.1	0.16	0.2	0.12	0.16	0.22	0.13
pval	0.1513	0.3338	0.007	0.6114	0.2824	0.1006	0.7714	0.5972	0.0034
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C2. Crude Protein QxE Data

Effect	TP155719 lm			AY	TP44644 hk			AY	TP473564 lm		
	AY	2016	2017		AY	2016	2017		AY	2016	2017
Year											
2016	6.64 (A)				6.61 (A)				6.62 (A)		
2017	5.06 (B)				5.03 (B)				5.05 (B)		
Mean s.e.	0.12				0.13				0.11		
pval	<.0001				<.0001				<.0001		
Environment											
Spaced	5.62 (B)	6.51 (B)	4.74 (B)		5.61 (B)	6.49 (B)	4.72 (B)		5.61 (B)	6.49 (B)	4.72 (B)
Poly	7.34 (A)	8.39 (A)	6.3 (A)		7.29 (A)	8.34 (A)	6.25 (A)		7.31 (A)	8.35 (A)	6.27 (A)
Mono	4.59 (C)	5.03 (C)	4.15 (C)		4.56 (C)	5 (C)	4.12 (C)		4.58 (C)	5.02 (C)	4.16 (C)
Mean s.e.	0.13	0.18	0.08		0.13	0.2	0.08		0.12	0.18	0.08
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001
Allele											
ll, nn, hh	5.94 (A)	6.71 (A)	5.16 (A)		5.54 (B)	6.32 (B)	4.76 (B)		5.73 (B)	6.53 (B)	4.93 (B)
lm, np, hk	5.76 (B)	6.57 (B)	4.96 (B)		5.98 (A)	6.78 (A)	5.18 (A)		5.94 (A)	6.72 (A)	5.16 (A)
kk	N/A	N/A	N/A		5.94 (A)	6.73 (A)	5.14 (A)		N/A	N/A	N/A
Mean s.e.	0.12	0.18	0.08		0.13	0.2	0.08		0.12	0.17	0.08
pval	0.0223	0.0192	<.0001		<.0001	<.0001	<.0001		0.0067	0.0022	<.0001
Env. X Allele											
Spaced-ll, nn, hh	5.68 (C)	6.54 (C)	4.81 (C)		5.46 (D)	6.39 (C)	4.54 (D)		5.41 (C)	6.26 (C)	4.57 (D)
Spaced-lm, np, hk	5.57 (C)	6.48 (C)	4.66 (D)		5.71 (C)	6.62 (C)	4.8 (C)		5.8 (B)	6.73 (B)	4.87 (C)
Spaced-kk	N/A	N/A	N/A		5.65 (CD)	6.48 (C)	4.82 (C)		N/A	N/A	N/A
Poly-ll, nn, hh	7.5 (A)	8.53 (A)	6.46 (A)		6.84 (B)	7.86 (B)	5.82 (B)		7.26 (A)	8.34 (A)	6.17 (B)
Poly-lm, np, hk	7.19 (B)	8.25 (B)	6.14 (B)		7.53 (A)	8.56 (A)	6.5 (A)		7.36 (A)	8.36 (A)	6.36 (A)
Poly-kk	N/A	N/A	N/A		7.5 (A)	8.59 (A)	6.42 (A)		N/A	N/A	N/A
Mono-ll, nn, hh	4.64 (D)	5.07 (D)	4.22 (E)		4.32 (F)	4.72 (E)	3.92 (F)		4.52 (D)	4.98 (D)	4.06 (F)
Mono-lm, np, hk	4.54 (D)	5 (D)	4.08 (E)		4.7 (E)	5.16 (D)	4.25 (E)		4.65 (D)	5.06 (D)	4.25 (E)
Mono-kk	N/A	N/A	N/A		4.66 (E)	5.13 (D)	4.19 (E)		N/A	N/A	N/A
Mean s.e.	0.14	0.19	0.09		0.15	0.21	0.1		0.14	0.18	0.09
pval	0.4576	0.2156	0.11		0.0426	0.0313	0.0125		0.2413	0.0042	0.4912
pval_Bon	0.0083	0.0083	0.0083		0.0083	0.0083	0.0083		0.0083	0.0083	0.0083

Appendix C2. Crude Protein QxE Data Continued

	TP532901				TP592665				TP829390			
Effect	hk				lm				lm			
	AY	2016	2017		AY	2016	2017		AY	2016	2017	
Year												
2016	6.65 (A)				6.62 (A)				6.65 (A)			
2017	5.07 (B)				5 (B)				5.07 (B)			
Mean s.e.	0.13				0.12				0.12			
pval	<.0001				<.0001				<.0001			
Environment												
Spaced	5.63 (B)	6.52 (B)	4.74 (B)		5.58 (B)	6.48 (B)	4.67 (B)		5.63 (B)	6.52 (B)	4.75 (B)	
Poly	7.36 (A)	8.42 (A)	6.31 (A)		7.28 (A)	8.35 (A)	6.22 (A)		7.35 (A)	8.4 (A)	6.31 (A)	
Mono	4.59 (C)	5.04 (C)	4.14 (C)		4.58 (C)	5.05 (C)	4.12 (C)		4.59 (C)	5.03 (C)	4.15 (C)	
Mean s.e.	0.13	0.19	0.08		0.13	0.18	0.08		0.13	0.18	0.08	
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
Allele												
ll, nn, hh	5.68 (B)	6.52 (B)	4.84 (C)		5.67 (B)	6.51 (B)	4.84 (B)		5.77 (B)	6.58 (B)	4.96 (B)	
lm, np, hk	5.88 (A)	6.66 (AB)	5.11 (B)		5.96 (A)	6.75 (A)	5.17 (A)		5.95 (A)	6.72 (A)	5.17 (A)	
kk	6.02 (A)	6.8 (A)	5.24 (A)		N/A	N/A	N/A		N/A	N/A	N/A	
Mean s.e.	0.13	0.19	0.08		0.12	0.18	0.08		0.12	0.18	0.08	
pval	<.0001	0.0072	<.0001		0.0002	0.0003	<.0001		0.0127	0.0147	<.0001	
Env. X Allele												
Spaced-ll, nn, hh	5.53 (E)	6.42 (D)	4.63 (D)		5.42 (D)	6.31 (D)	4.54 (D)		5.48 (C)	6.37 (D)	4.58 (D)	
Spaced-lm, np, hk	5.65 (E)	6.54 (D)	4.77 (D)		5.74 (C)	6.66 (C)	4.81 (C)		5.79 (B)	6.67 (C)	4.91 (C)	
Spaced-kk	5.71 (E)	6.61 (D)	4.81 (D)		N/A	N/A	N/A		N/A	N/A	N/A	
Poly-ll, nn, hh	7.01 (A)	8.14 (C)	5.9 (C)		7.1 (B)	8.2 (B)	6 (B)		7.23 (A)	8.29 (B)	6.18 (B)	
Poly-lm, np, hk	7.39 (B)	8.42 (B)	6.37 (B)		7.46 (A)	8.5 (A)	6.44 (A)		7.47 (A)	8.51 (A)	6.43 (A)	
Poly-kk	7.68 (C)	8.69 (A)	6.67 (A)		N/A	N/A	N/A		N/A	N/A	N/A	
Mono-ll, nn, hh	4.5 (D)	5.01 (E)	3.99 (F)		4.5 (E)	5.02 (E)	3.98 (F)		4.59 (D)	5.07 (E)	4.12 (E)	
Mono-lm, np, hk	4.61 (D)	5.02 (E)	4.2 (E)		4.67 (E)	5.08 (E)	4.26 (E)		4.58 (D)	4.99 (E)	4.18 (E)	
Mono-kk	4.66 (D)	5.09 (E)	4.24 (E)		N/A	N/A	N/A		N/A	N/A	N/A	
Mean s.e.	0.15	0.2	0.1		0.14	0.19	0.09		0.14	0.19	0.09	
pval	0.0724	0.2124	0.0005		0.5386	0.1758	0.2277		0.1617	0.0276	0.0293	
pval Bon	0.0083	0.0083	0.0083		0.0083	0.0083	0.0083		0.0083	0.0083	0.0083	

Appendix C3. Biomass QxE Data

Effect	TP301824			TP353941			TP397564		
	AY	hk 2016	2017	AY	lm 2016	2017	AY	hk 2016	2017
Year									
2016	487.72 (B)			491.73 (B)			484.4 (B)		
2017	895.15 (A)			913.27 (A)			903.64 (A)		
Mean s.e.	16.12			15.61			15.9		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	1597.61 (A)	1276.64 (A)	1918.53 (A)	1609.75 (A)	1279.12 (A)	1940.38 (A)	1594.44 (A)	1263.98 (A)	1924.64 (A)
Poly	379.07 (B)	118.63 (B)	639.33 (B)	391.6 (B)	123.4 (B)	659.8 (B)	388.64 (B)	121.51 (B)	655.32 (B)
Mono	97.62 (C)	66.93 (C)	128.21 (C)	106.15 (C)	71.37 (C)	140.22 (C)	98.99 (C)	67.13 (C)	131.63 (C)
Mean s.e.	17.4	18.22	24.12	16.18	17	23.61	19.33	17.38	24.03
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	627.01 (C)	452.13 (B)	801.87 (B)	714.82 (A)	503.09 (A)	926.04 (A)	654.78 (B)	453.14 (B)	856.56 (B)
lm, np, hk	706.5 (B)	491.13 (A)	921.75 (A)	690.18 (B)	479.5 (A)	900.89 (A)	730.23 (A)	513.82 (A)	946.83 (A)
kk	740.79 (A)	518.95 (A)	962.45 (A)	N/A	N/A	N/A	697.04 (AB)	485.65 (AB)	908.19 (AB)
Mean s.e.	17.35	18.14	23.98	15.27	15.45	21.26	19.32	17.34	23.97
pval	<.0001	0.0059	<.0001	0.0208	0.0956	0.2202	0.002	0.0013	0.001
Env. X Allele									
Spaced-ll, nn, hh	1481.29 (C)	1203.67 (C)	1758.83 (C)	1633.35 (A)	1301.16 (A)	1965.56 (A)	1509.42 (B)	1182.81 (C)	1836.19 (B)
Spaced-lm, np, hk	1610.24 (B)	1277.62 (B)	1942.83 (B)	1586.15 (B)	1257.07 (A)	1915.2 (A)	1664.72 (A)	1334 (A)	1995.41 (A)
Spaced-kk	1701.31 (A)	1348.65 (A)	2053.93 (A)	N/A	N/A	N/A	1609.17 (A)	1275.12 (B)	1942.32 (A)
Poly-ll, nn, hh	330.05 (E)	98.29 (DE)	561.69 (E)	392.65 (C)	126.44 (B)	658.81 (B)	373.46 (C)	116.39 (DE)	630.48 (C)
Poly-lm, np, hk	399.19 (D)	126.76 (D)	671.54 (D)	390.56 (C)	120.35 (B)	660.78 (B)	404.19 (C)	127.77 (D)	680.67 (C)
Poly-kk	407.97 (D)	130.84 (D)	684.76 (D)	N/A	N/A	N/A	388.27 (C)	120.36 (DE)	654.81 (C)
Mono-ll, nn, hh	69.69 (F)	54.44 (E)	85.09 (F)	118.46 (D)	81.67 (BC)	153.76 (C)	81.47 (D)	60.21 (E)	103.02 (D)
Mono-lm, np, hk	110.08 (F)	68.99 (E)	150.88 (F)	93.85 (D)	61.06 (C)	126.69 (C)	121.79 (D)	79.69 (DE)	164.42 (D)
Mono-kk	113.1 (F)	77.36 (DE)	148.66 (F)	N/A	N/A	N/A	93.69 (D)	61.48 (E)	127.45 (D)
Mean s.e.	23.62	25.99	35.8	18.6	20.93	29.51	29.27	24.74	35.12
pval	0.0008	0.1107	0.0233	0.2109	0.5332	0.5696	0.118	0.0044	0.3624
pval_Bon	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031

Appendix C3. Biomass QxE Data Continued

Effect	TP405091			TP48221			TP491526		
	AY	hk 2016	2017	AY	hk 2016	2017	AY	hk 2016	2017
Year									
2016	486.49 (B)			496.37 (B)			488.96 (B)		
2017	903.06 (A)			927 (A)			908.44 (A)		
Mean s.e.	15.97			16.18			16.82		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	1599.23 (A)	1272.11 (A)	1926.12 (A)	1623.32 (A)	1287.42 (A)	1959.26 (A)	1609.64 (A)	1279.06 (A)	1940.22 (A)
Poly	386.45 (B)	120.2 (B)	652.39 (B)	402.85 (B)	129.07 (B)	676.76 (B)	388.53 (B)	122.36 (B)	654.54 (B)
Mono	98.65 (C)	66.37 (C)	131.5 (C)	108.88 (C)	71.43 (C)	145.52 (C)	97.91 (C)	64.64 (C)	131.26 (C)
Mean s.e.	18.82	18.13	24.96	16.9	18.76	24.75	18.51	19.46	24.84
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
II, nn, hh	692.15 (AB)	488.98 (AB)	895.16 (AB)	707.7 (B)	495.06 (AB)	919.72 (AB)	741.68 (A)	512.83 (A)	970.55 (A)
Im, np, hk	728.19 (A)	512.59 (A)	943.91 (A)	676.05 (C)	470.12 (B)	882.26 (B)	705.12 (B)	500.65 (A)	909.47 (B)
kk	664 (B)	457.12 (B)	870.93 (B)	751.3 (A)	522.74 (A)	979.56 (A)	649.3 (C)	452.58 (B)	846.01 (C)
Mean s.e.	18.79	18.07	24.86	16.81	18.66	24.53	18.47	19.4	24.72
pval	0.005	0.0064	0.0105	<.0001	0.0142	0.0017	<.0001	0.0071	0.0002
Env. X Allele									
Spaced-II, nn, hh	1614.47 (A)	1296.08 (A)	1932.12 (AB)	1597.67 (B)	1279.51 (AB)	1915.9 (B)	1708.36 (A)	1340.04 (A)	2076.83 (A)
Spaced-Im, np, hk	1659.03 (A)	1325.84 (A)	1992.1 (A)	1565.14 (B)	1236.44 (B)	1893.88 (B)	1609.23 (B)	1298.63 (A)	1919.67 (B)
Spaced-kk	1524.19 (B)	1194.41 (B)	1854.15 (B)	1707.16 (A)	1346.31 (A)	2068.01 (A)	1511.35 (C)	1198.5 (B)	1824.17 (C)
Poly-II, nn, hh	370.66 (C)	110.24 (CD)	630.26 (C)	414.33 (C)	129.81 (C)	698.2 (C)	414.79 (D)	132.42 (C)	697.13 (D)
Poly-Im, np, hk	402.56 (C)	131.42 (C)	673.83 (C)	374.36 (C)	114.42 (C)	635.36 (C)	390.99 (D)	125.79 (C)	655.83 (D)
Poly-kk	386.12 (C)	118.94 (CD)	653.08 (C)	419.85 (C)	142.98 (C)	696.72 (C)	359.82 (D)	108.87 (CD)	610.65 (D)
Mono-II, nn, hh	91.31 (D)	60.61 (D)	123.11 (D)	111.1 (D)	75.86 (CD)	145.06 (D)	115.14 (E)	77.52 (CD)	137.68 (E)
Mono-Im, np, hk	122.97 (D)	80.52 (D)	165.81 (D)	88.65 (D)	59.5 (D)	117.55 (D)	101.88 (E)	66.03 (CD)	152.9 (E)
Mono-kk	81.67 (D)	58 (D)	105.57 (D)	126.88 (D)	78.92 (CD)	173.95 (D)	76.72 (E)	50.37 (D)	103.21 (E)
Mean s.e.	27.98	25.86	36.65	22.13	26.58	37.23	25.62	27.24	36.8
pval	0.1211	0.0336	0.4105	0.0157	0.2954	0.2511	0.004	0.0896	0.0321
pval_Bon	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031

Appendix C3. Biomass QxE Data Continued

Effect	TP513463 hk			TP524699 np			TP529335 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	486.82 (B)			490.59 (B)			490.31 (B)		
2017	900.85 (A)			914.21 (A)			913.81 (A)		
Mean s.e.	15.08			15.5			15.63		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	1598.47 (A)	1272.99 (A)	1923.58 (A)	1609.76 (A)	1277.2 (A)	1942.32 (A)	1610.51 (A)	1277.07 (A)	1943.82 (A)
Poly	383.84 (B)	118.8 (B)	649.52 (B)	392.4 (B)	123.31 (B)	661.41 (B)	390.94 (B)	122.88 (B)	658.82 (B)
Mono	99.21 (C)	67.21 (C)	129.85 (C)	105.03 (C)	70.18 (C)	139.64 (C)	104.74 (C)	69.89 (C)	139.67 (C)
Mean s.e.	15.18	17.94	24.67	16.48	17	23.4	17.14	17.18	24.04
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
II, nn, hh	752.66 (A)	525.65 (A)	979.19 (A)	735.16 (A)	503.48 (A)	966.68 (A)	735.66 (A)	504.54 (A)	966.71 (A)
Im, np, hk	707.08 (B)	490.16 (B)	922.74 (B)	669.63 (B)	476.98 (A)	862.23 (B)	668.47 (B)	475.35 (B)	861.5 (B)
kk	621.77 (C)	443.18 (C)	801.01 (C)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	15.13	17.89	24.58	15.4	15.49	21.13	15.8	15.64	21.77
pval	<.0001	0.0002	<.0001	<.0001	0.0589	<.0001	<.0001	0.0403	<.0001
Env. X Allele									
Spaced-II, nn, hh	1739.22 (A)	1376.74 (A)	2101.48 (A)	1674.67 (A)	1304.2 (A)	2045.14 (A)	1686.9 (A)	1310.53 (A)	2063.03 (A)
Spaced-Im, np, hk	1604.58 (B)	1269.3 (B)	1938.97 (B)	1544.85 (B)	1250.2 (B)	1839.5 (B)	1534.12 (B)	1243.6 (B)	1824.61 (B)
Spaced-kk	1451.6 (C)	1172.92 (C)	1730.28 (C)	N/A	N/A	N/A	N/A	N/A	N/A
Poly-II, nn, hh	407.48 (D)	124.61 (DE)	689.86 (D)	414.41 (C)	132.17 (C)	696.59 (C)	407.43 (C)	131.88 (C)	682.85 (C)
Poly-Im, np, hk	406.66 (D)	132.53 (D)	681.7 (D)	370.4 (D)	114.45 (CD)	626.22 (D)	374.45 (C)	113.88 (CD)	634.79 (C)
Poly-kk	337.38 (E)	99.24 (DE)	577 (E)	N/A	N/A	N/A	N/A	N/A	N/A
Mono-II, nn, hh	111.29 (F)	75.6 (E)	146.23 (F)	116.42 (E)	74.08 (DE)	158.3 (E)	112.65 (D)	71.2 (D)	154.26 (D)
Mono-Im, np, hk	110.02 (F)	68.65 (E)	147.56 (F)	93.64 (E)	66.28 (E)	120.97 (E)	96.83 (D)	68.58 (D)	125.09 (D)
Mono-kk	76.33 (F)	57.38 (E)	95.75 (F)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	18.83	25.22	35.42	19.35	20.89	29.16	20.63	21.14	29.81
pval	<.0001	0.0004	<.0001	0.0004	0.3629	0.0013	<.0001	0.1533	<.0001
pval_Bon	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031

Appendix C3. Biomass QxE Data Continued

Effect	TP539 hk			TP548730 hk			TP557515 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	487.82 (B)			502.84 (B)			487.08 (B)		
2017	913.89 (A)			930.39 (A)			905.72 (A)		
Mean s.e.	15.26			15.69			15.18		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	1610.17 (A)	1271.41 (A)	1949.08 (A)	1653.37 (A)	1314.79 (A)	1991.9 (A)	1606.46 (A)	1272.66 (A)	1940.38 (A)
Poly	387.71 (B)	122.14 (B)	653.22 (B)	393.31 (B)	125.86 (B)	660.65 (B)	382.16 (B)	120.12 (B)	644.06 (B)
Mono	104.69 (C)	69.62 (C)	140.46 (C)	103.18 (C)	67.01 (C)	139.1 (C)	100.58 (C)	67.69 (C)	133.78 (C)
Mean s.e.	18.82	18.14	23.87	16.84	18.57	23.71	17.64	17.63	24.22
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
II, nn, hh	648.79 (B)	440.73 (C)	857.23 (B)	710.19 (B)	497.47 (AB)	922.72 (B)	727.78 (A)	504.67 (A)	951.05 (A)
Im, np, hk	689.57 (B)	489.29 (B)	889.93 (B)	674.88 (C)	472.2 (B)	877.31 (B)	711.09 (A)	496.51 (A)	925.75 (A)
kk	764.21 (A)	533.14 (A)	995.61 (A)	764.79 (A)	538 (A)	991.61 (A)	650.34 (B)	459.28 (B)	841.42 (B)
Mean s.e.	18.78	18.07	23.73	16.76	18.47	23.52	17.59	17.55	24.09
pval	<.0001	<.0001	<.0001	<.0001	0.0019	<.0001	0.0004	0.0504	0.0004
Env. X Allele									
Spaced-II, nn, hh	1462.3 (C)	1138.08 (C)	1787.37 (C)	1621.81 (B)	1294.93 (B)	1948.57 (B)	1688.48 (A)	1318.46 (A)	2058.61 (A)
Spaced-Im, np, hk	1584.79 (B)	1273.41 (B)	1895.59 (B)	1533.45 (C)	1224.24 (C)	1842.71 (C)	1608.43 (B)	1284.68 (A)	1932.18 (B)
Spaced-kk	1783.43 (A)	1402.74 (A)	2164.29 (A)	1804.86 (A)	1425.22 (A)	2184.43 (A)	1522.46 (C)	1214.84 (B)	1830.35 (C)
Poly-II, nn, hh	380.14 (D)	117.29 (DE)	643 (D)	409.86 (D)	138.73 (D)	680.84 (D)	389.48 (DE)	122.15 (CD)	656.59 (DE)
Poly-Im, np, hk	382.22 (D)	122.83 (D)	640.99 (D)	390.5 (D)	122.42 (D)	658.59 (D)	412.56 (D)	129.53 (C)	695.24 (D)
Poly-kk	400.78 (D)	126.29 (DE)	675.66 (D)	379.56 (D)	116.44 (DE)	642.51 (D)	344.45 (E)	108.67 (CD)	580.33 (E)
Mono-II, nn, hh	103.93 (E)	66.83 (DE)	141.31 (E)	98.9 (E)	58.74 (E)	138.76 (E)	105.36 (F)	73.41 (CD)	137.95 (F)
Mono-Im, np, hk	101.71 (E)	71.62 (E)	133.2 (E)	100.69 (E)	69.95 (E)	130.64 (E)	112.27 (F)	75.33 (D)	149.84 (F)
Mono-kk	108.43 (E)	70.41 (DE)	146.88 (E)	109.94 (E)	72.33 (DE)	147.89 (E)	84.1 (F)	54.33 (D)	113.57 (F)
Mean s.e.	29.17	26.06	35.97	22.89	26.66	35.66	26.03	25.32	35.64
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0302	0.3856	0.0177
pval_Bon	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031	0.0031

Appendix C3. Biomass QxE Data Continued

		TP68392				TP777488			
Effect		AY		lm		AY		lm	
		2016		2017		2016		2017	
<u>Year</u>									
	2016	490.02 (B)				482.61 (B)			
	2017	911.82 (A)				898.47 (A)			
	Mean s.e.	15.76				12.21			
	pval	<.0001				<.0001			
<u>Environment</u>									
	Spaced	1606.45 (A)	1275.88 (A)	1937.09 (A)		1582.79 (A)	1255.6 (A)	1909.22 (A)	
	Poly	391.88 (B)	123.09 (B)	660.67 (B)		385.83 (B)	121.4 (B)	649.77 (B)	
	Mono	104.42 (C)	69.91 (C)	138.39 (C)		103.01 (C)	70.18 (C)	136.09 (C)	
	Mean s.e.	16.42	16.96	23.62		16.11	15.9	19.4	
	pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
<u>Allele</u>									
	II, nn, hh	741.28 (A)	512.84 (A)	969.7 (A)		711.06 (A)	494.21 (A)	927.91 (A)	
	lm, np, hk	660.56 (B)	466.41 (B)	854.4 (B)		670.02 (B)	470.58 (A)	868.8 (B)	
	kk	N/A	N/A	N/A		N/A	N/A	N/A	
	Mean s.e.	15.5	15.47	21.4		13.55	14.13	16.24	
	pval	<.0001	0.0009	<.0001		0.0186	0.1049	0.0053	
<u>Env. X Allele</u>									
	Spaced-II, nn, hh	1693.14 (A)	1335.15 (A)	2051.25 (A)		1622.37 (A)	1279.07 (A)	1965.59 (A)	
	Spaced-lm, np, hk	1519.77 (B)	1216.62 (B)	1822.93 (B)		1543.2 (B)	1232.13 (A)	1852.85 (B)	
	Spaced-kk	N/A	N/A	N/A		N/A	N/A	N/A	
	Poly-II, nn, hh	418.45 (C)	130.32 (C)	706.7 (C)		401.19 (C)	128.76 (B)	673.25 (C)	
	Poly-lm, np, hk	365.32 (D)	115.85 (CD)	614.65 (D)		370.46 (C)	114.04 (BC)	626.29 (C)	
	Poly-kk	N/A	N/A	N/A		N/A	N/A	N/A	
	Mono-II, nn, hh	112.26 (E)	73.06 (DE)	151.16 (E)		109.61 (D)	74.8 (C)	144.9 (D)	
	Mono-lm, np, hk	96.59 (E)	66.76 (E)	125.62 (E)		96.4 (D)	65.57 (C)	127.28 (D)	
	Mono-kk	N/A	N/A	N/A		N/A	N/A	N/A	
	Mean s.e.	18.89	20.81	29.29		22.06	20.26	26.64	
	pval	<.0001	0.0011	0.0001		0.276	0.5161	0.1695	
	pval_Bon	0.0031	0.0031	0.0031		0.0031	0.0031	0.0031	

Appendix C3. Biomass QxE Data Continued

		TP799882				TP880985			
Effect		hk		2016		hk		2016	
AY		2017		AY		2017		AY	
<u>Year</u>									
	2016	487.32 (B)				480.04 (B)			
	2017	900.06 (A)				897.33 (A)			
	Mean s.e.	16.04				16.79			
	pval	<.0001				<.0001			
<u>Environment</u>									
	Spaced	1599.84 (A)	1274.72 (A)	1924.93 (A)		1581.92 (A)	1252.39 (A)	1911.39 (A)	
	Poly	381.84 (B)	118.25 (B)	645.19 (B)		386.2 (B)	119.19 (B)	652.94 (B)	
	Mono	99.4 (C)	67.99 (C)	130.89 (C)		97.92 (C)	67.34 (C)	128.62 (C)	
	Mean s.e.	17.57	17.33	24.32		18.75	19.12	26.62	
	pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
<u>Allele</u>									
	ll, nn, hh	754.2 (A)	527.68 (A)	980.62 (A)		640.23 (B)	442.01 (B)	838.14 (B)	
	lm, np, hk	706.21 (B)	488.42 (B)	924.03 (B)		709.93 (A)	499.47 (A)	920.5 (A)	
	kk	620.66 (C)	444.86 (C)	796.35 (C)		715.89 (A)	497.43 (A)	934.32 (A)	
	Mean s.e.	17.53	17.26	23.21		18.64	18.94	26.32	
	pval	<.0001	0.0002	<.0001		0.0006	0.0166	0.0088	
<u>Env. X Allele</u>									
	Spaced-ll, nn, hh	1744.61 (A)	1383.76 (A)	2105.4 (A)		1461.85 (B)	1148.61 (B)	1775.18 (B)	
	Spaced-lm, np, hk	1596.95 (B)	1259.49 (B)	1934.5 (B)		1617.8 (A)	1293.48 (A)	1942.06 (A)	
	Spaced-kk	1457.95 (C)	1180.89 (C)	1734.89 (C)		1666.13 (A)	1315.09 (A)	2016.94 (A)	
	Poly-ll, nn, hh	408.09 (D)	124.43 (DE)	691.58 (D)		368.7 (C)	109.67 (CD)	627 (C)	
	Poly-lm, np, hk	409.3 (D)	133.02 (D)	685.43 (D)		399.8 (C)	129.8 (C)	669.69 (C)	
	Poly-kk	328.13 (E)	97.31 (DE)	558.54 (E)		390.1 (C)	118.09 (CD)	662.13 (C)	
	Mono-ll, nn, hh	109.9 (F)	74.84 (E)	144.89 (F)		90.14 (D)	67.76 (CD)	112.25 (D)	
	Mono-lm, np, hk	112.38 (F)	72.76 (E)	152.17 (F)		112.18 (D)	75.15 (D)	149.74 (D)	
	Mono-kk	75.91 (F)	56.37 (E)	95.61 (F)		91.43 (D)	59.11 (D)	123.87 (D)	
	Mean s.e.	24.14	24.86	35.29		26.35	26.99	38.4	
	pval	<.0001	0.0003	<.0001		0.0007	0.0106	0.0321	
	pval_Bon	0.0031	0.0031	0.0031		0.0031	0.0031	0.0031	

Appendix C4. Plant Height QxE Data

Effect	TP151207 np			TP196229 np			TP217216 lm		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	130.01 (B)			129.94 (B)			130.03 (B)		
2017	135.31 (A)			135.18 (A)			135.29 (A)		
Mean s.e.	3.74			3.73			3.75		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	162.12 (A)	163.86 (A)	160.39 (A)	162.02 (A)	163.7 (A)	160.36 (A)	162.14 (A)	163.86 (A)	160.44 (A)
Poly	121.94 (B)	110.65 (C)	133.27 (B)	121.89 (B)	110.74 (C)	133.09 (B)	121.94 (B)	110.74 (C)	133.19 (B)
Mono	113.93 (C)	115.61 (B)	112.2 (C)	113.76 (C)	115.45 (B)	112.03 (C)	113.89 (C)	115.56 (B)	112.15 (C)
Mean s.e.	3.8	2.61	4.94	3.81	2.57	4.96	3.82	2.57	4.99
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	135.29 (A)	132.31 (A)	138.25 (A)	134.21 (A)	131.11 (A)	137.32 (A)	135.74 (A)	132.88 (A)	138.61 (A)
lm, np, hk	130.03 (B)	127.77 (B)	132.32 (B)	130.9 (B)	128.82 (B)	132.99 (B)	129.57 (B)	127.22 (B)	131.92 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	3.77	2.57	4.92	3.76	2.53	4.94	3.78	2.54	4.97
pval	<.0001	<.0001	<.0001	0.0051	0.0085	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	164.78 (A)	166.56 (A)	163 (A)	163.08 (A)	164.88 (A)	161.29 (A)	164.71 (A)	166.52 (A)	162.89 (A)
Spaced-lm, np, hk	159.45 (B)	161.17 (B)	157.77 (B)	160.97 (A)	162.52 (A)	159.43 (A)	159.58 (B)	161.19 (B)	158 (B)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	124.86 (C)	113.2 (D)	136.53 (C)	124.98 (B)	113.51 (B)	136.53 (B)	124.99 (C)	113.18 (D)	136.89 (C)
Poly-lm, np, hk	119.01 (D)	108.09 (E)	130.02 (D)	118.79 (C)	107.98 (C)	129.64 (C)	118.89 (D)	108.3 (E)	129.49 (D)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	116.23 (D)	117.17 (C)	115.22 (E)	114.58 (D)	114.94 (B)	114.16 (D)	117.53 (D)	118.95 (C)	116.04 (E)
Mono-lm, np, hk	111.63 (E)	114.04 (D)	109.18 (F)	112.95 (D)	115.96 (B)	109.9 (E)	110.25 (E)	112.18 (D)	108.26 (F)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	3.91	2.71	4.99	3.94	2.67	5.02	3.95	2.68	5.04
pval	0.8915	0.5085	0.8241	0.2239	0.0107	0.0621	0.7405	0.6489	0.3245
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C4. Plant Height QxE Data Continued

Effect	TP293133			TP301824			TP354685		
	AY	hk 2016	2017	AY	hk 2016	2017	AY	hk 2016	2017
Year									
2016	130.2 (B)			129.22 (B)			130.25 (B)		
2017	135.71 (A)			134.08 (A)			135.72 (A)		
Mean s.e.	3.87			3.82			3.84		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	162.31 (A)	164.16 (A)	160.48 (A)	161.29 (A)	162.97 (A)	159.63 (A)	162.47 (A)	164.09 (A)	160.87 (A)
Poly	122.21 (B)	110.71 (C)	133.78 (B)	120.94 (B)	109.87 (C)	132.08 (B)	122.41 (B)	111.04 (C)	133.86 (B)
Mono	114.35 (C)	115.88 (B)	112.82 (C)	112.72 (C)	114.93 (B)	110.47 (C)	114.06 (C)	115.72 (B)	112.37 (C)
Mean s.e.	3.94	2.63	4.98	3.86	2.64	5.06	3.89	2.62	4.96
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	137.73 (A)	134.81 (A)	140.74 (A)	124.82 (C)	122.93 (C)	126.71 (C)	137.11 (A)	133.92 (A)	140.36 (A)
lm, np, hk	132.27 (B)	129.89 (B)	134.63 (B)	133.54 (B)	130.59 (B)	136.49 (B)	132.78 (B)	130.26 (B)	135.28 (B)
kk	128.87 (C)	126.04 (C)	131.72 (C)	136.6 (A)	134.24 (A)	138.98 (A)	129.05 (C)	126.67 (C)	131.45 (C)
Mean s.e.	3.94	2.63	4.98	3.86	2.64	5.06	3.89	2.62	4.96
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	165.7 (A)	167.7 (A)	163.71 (A)	155.43 (B)	156.35 (B)	154.51 (B)	166.68 (A)	168.33 (A)	165.03 (A)
Spaced-lm, np, hk	162.09 (AB)	163.75 (B)	160.42 (AB)	162.81 (A)	164.81 (A)	160.85 (A)	162.01 (B)	164.08 (B)	159.95 (B)
Spaced-kk	159.13 (B)	161.02 (B)	157.32 (B)	165.64 (A)	167.74 (A)	163.54 (A)	158.73 (B)	159.87 (C)	157.62 (B)
Poly-ll, nn, hh	125.91 (C)	113.94 (DE)	138.11 (C)	113.22 (E)	102.55 (F)	123.96 (D)	127.7 (C)	115.26 (DE)	140.3 (C)
Poly-lm, np, hk	121.79 (CD)	110.99 (E)	132.61 (D)	123.25 (C)	111.75 (E)	134.79 (C)	122.16 (D)	111.01 (F)	133.27 (D)
Poly-kk	118.92 (D)	107.2 (F)	130.63 (D)	126.35 (C)	115.3 (D)	137.5 (C)	117.37 (E)	106.84 (G)	127.99 (E)
Mono-ll, nn, hh	121.57 (CD)	122.81 (C)	120.41 (E)	105.81 (F)	109.89 (E)	101.66 (E)	116.96 (E)	118.15 (D)	115.75 (F)
Mono-lm, np, hk	112.93 (E)	114.94 (D)	110.85 (F)	114.54 (DE)	115.2 (D)	113.83 (E)	114.18 (EF)	115.69 (DE)	112.62 (F)
Mono-kk	108.54 (E)	109.9 (EF)	107.21 (F)	117.8 (D)	119.69 (C)	115.91 (F)	111.05 (F)	113.3 (EF)	108.74 (G)
Mean s.e.	4.16	2.86	5.11	4.03	2.87	5.18	4.08	2.84	5.09
pval	0.2936	0.195	0.1123	0.877	0.6865	0.2612	0.7239	0.764	0.3515
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C4. Plant Height QxE Data Continued

Effect	TP365106			TP44922			TP48221		
	AY	hk 2016	2017	AY	hk 2016	2017	AY	hk 2016	2017
Year									
2016	129.68 (B)			129.56 (B)			131.06 (B)		
2017	134.81 (A)			134.79 (A)			136.04 (A)		
Mean s.e.	3.78			3.73			3.79		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	161.43 (A)	163.05 (A)	159.82 (A)	161.94 (A)	163.61 (A)	160.28 (A)	162.68 (A)	164.57 (A)	160.81 (A)
Poly	121.61 (B)	110.6 (C)	132.67 (B)	121.5 (B)	110.17 (C)	132.87 (B)	123.18 (B)	112.09 (C)	134.3 (B)
Mono	113.7 (C)	115.42 (B)	111.86 (C)	113.09 (C)	115.01 (B)	111.15 (C)	114.79 (C)	116.6 (B)	112.96 (C)
Mean s.e.	3.83	2.57	4.94	3.79	2.57	4.94	3.84	2.58	5.04
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	127.25 (B)	124.16 (C)	130.35 (B)	136.57 (A)	133.62 (A)	139.47 (A)	132.57 (B)	130.71 (B)	134.45 (B)
lm, np, hk	133.71 (A)	130.95 (B)	136.46 (A)	132.36 (B)	129.8 (B)	134.92 (B)	130.98 (B)	128.32 (C)	133.64 (B)
kk	135.77 (A)	133.96 (A)	137.53 (A)	127.6 (C)	125.37 (C)	129.91 (C)	137.1 (A)	134.23 (A)	139.98 (A)
Mean s.e.	3.83	2.57	4.94	3.79	2.57	4.94	3.84	2.58	5.04
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	156.78 (B)	157.77 (B)	155.78 (B)	164.6 (A)	165.77 (A)	163.43 (A)	161.86 (A)	163.5 (AB)	160.22 (A)
Spaced-lm, np, hk	163.94 (A)	165.4 (A)	161.75 (A)	161.9 (AB)	164.03 (AB)	159.79 (B)	161.34 (A)	163.02 (B)	159.7 (A)
Spaced-kk	163.56 (A)	165.98 (A)	161.92 (A)	159.31 (B)	161.03 (B)	157.62 (B)	164.85 (A)	167.2 (A)	162.5 (A)
Poly-ll, nn, hh	116.07 (D)	104.9 (F)	127.34 (D)	127.82 (C)	116.65 (C)	138.97 (C)	121.14 (C)	111.16 (EF)	131.15 (C)
Poly-lm, np, hk	122.91 (C)	111 (E)	134.84 (C)	121.27 (D)	110.09 (D)	132.49 (D)	120.22 (C)	108.86 (F)	131.65 (C)
Poly-kk	125.84 (C)	115.9 (D)	135.84 (C)	115.41 (E)	103.77 (E)	127.16 (E)	128.18 (B)	116.26 (CD)	140.1 (B)
Mono-ll, nn, hh	108.92 (E)	109.81 (E)	107.94 (F)	117.29 (DE)	118.45 (C)	116.01 (F)	114.7 (DE)	117.46 (C)	111.98 (E)
Mono-lm, np, hk	114.26 (D)	115.86 (D)	112.63 (E)	113.91 (E)	115.29 (C)	112.48 (F)	111.38 (E)	113.09 (DE)	109.58 (E)
Mono-kk	117.92 (D)	120.59 (C)	115.01 (E)	108.07 (F)	111.3 (D)	104.96 (G)	118.28 (CD)	119.24 (C)	117.33 (D)
Mean s.e.	4.02	2.79	5.07	4.01	2.82	5.06	4.04	2.84	5.18
pval	0.6676	0.1981	0.7442	0.2837	0.117	0.1984	0.4784	0.5143	0.1746
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C4. Plant Height QxE Data Continued

Effect	TP532901			TP537350			TP566324		
	AY	hk 2016	2017	AY	hk 2016	2017	AY	lm 2016	2017
Year									
2016	130.14 (B)			130.25 (B)			129.79 (B)		
2017	135.53 (A)			135.21 (A)			134.97 (A)		
Mean s.e.	3.82			3.73			3.77		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	162.52 (A)	164.4 (A)	160.66 (A)	162.13 (A)	163.89 (A)	160.38 (A)	161.96 (A)	163.78 (A)	160.17 (A)
Poly	121.84 (B)	110.49 (C)	133.27 (B)	122.04 (B)	110.97 (C)	133.15 (B)	121.63 (B)	110.4 (C)	132.91 (B)
Mono	114.13 (C)	115.63 (B)	112.59 (C)	114.02 (C)	115.96 (B)	112.02 (C)	113.56 (C)	115.28 (B)	111.77 (C)
Mean s.e.	3.85	2.62	4.94	3.78	2.59	4.98	3.83	2.66	4.95
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	137.11 (A)	134.43 (A)	139.84 (A)	130.61 (B)	128.85 (B)	132.37 (B)	135.05 (A)	132.08 (A)	137.99 (A)
lm, np, hk	130.29 (B)	127.83 (B)	132.73 (B)	130.6 (B)	127.83 (B)	133.37 (B)	129.72 (B)	127.55 (B)	131.9 (B)
kk	131.09 (B)	128.25 (B)	133.94 (B)	136.97 (A)	134.15 (A)	139.81 (A)	N/A	N/A	N/A
Mean s.e.	3.85	2.62	4.94	3.78	2.59	4.98	3.8	2.63	4.93
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	165.66 (A)	167.65 (A)	163.69 (A)	161.6 (A)	163.58 (A)	159.62 (AB)	163.74 (A)	165.25 (A)	162.23 (A)
Spaced-lm, np, hk	159.91 (B)	161.35 (B)	158.48 (B)	160.53 (A)	162.41 (A)	158.65 (B)	160.19 (A)	162.31 (B)	158.1 (B)
Spaced-kk	162.01 (AB)	164.22 (AB)	159.8 (AB)	164.26 (A)	165.69 (A)	162.87 (A)	N/A	N/A	N/A
Poly-ll, nn, hh	127.33 (C)	115.34 (D)	139.43 (C)	120.53 (C)	109.76 (DE)	131.33 (D)	124.82 (B)	112.95 (D)	136.71 (C)
Poly-lm, np, hk	119.58 (D)	108.84 (E)	130.33 (D)	120.07 (C)	108.58 (E)	131.64 (D)	118.44 (C)	107.85 (E)	129.1 (D)
Poly-kk	118.61 (D)	107.29 (E)	130.05 (D)	125.51 (B)	114.57 (C)	136.48 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	118.35 (D)	120.31 (C)	116.41 (E)	109.7 (D)	113.21 (CD)	106.16 (F)	116.59 (C)	118.06 (C)	115.04 (E)
Mono-lm, np, hk	111.39 (E)	113.31 (D)	109.39 (F)	111.21 (D)	112.51 (CD)	109.82 (F)	110.52 (D)	112.5 (D)	108.51 (F)
Mono-kk	112.66 (E)	113.25 (D)	111.97 (F)	121.15 (C)	122.17 (B)	120.08 (E)	N/A	N/A	N/A
Mean s.e.	4.05	2.85	5.07	3.98	2.83	5.12	3.94	2.77	5.01
pval	0.6312	0.5189	0.3246	0.0591	0.1065	0.0083	0.4957	0.4159	0.2472
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C4. Plant Height QxE Data Continued

Effect	TP607583			TP659407			TP799882		
	AY	hk 2016	2017	AY	np 2016	2017	AY	hk 2016	2017
Year									
2016	129.09 (B)			130.51 (B)			129.46 (B)		
2017	134.36 (A)			135.69 (A)			134.29 (A)		
Mean s.e.	3.69			3.68			3.71		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	161.44 (A)	163.23 (A)	159.67 (A)	162.4 (A)	164.22 (A)	160.6 (A)	161.46 (A)	163.14 (A)	159.8 (A)
Poly	121.22 (B)	109.82 (C)	132.7 (B)	122.78 (B)	111.45 (C)	134.13 (B)	121.05 (B)	109.93 (C)	132.22 (B)
Mono	112.52 (C)	114.34 (B)	110.64 (C)	114.13 (C)	115.96 (B)	112.27 (C)	113.11 (C)	115.4 (B)	110.79 (C)
Mean s.e.	3.74	2.56	4.89	3.77	2.53	4.96	3.75	2.62	4.94
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	128.24 (C)	126.56 (B)	129.98 (C)	136.05 (A)	133.38 (A)	138.72 (A)	136.68 (A)	134.68 (A)	138.67 (A)
lm, np, hk	135.13 (A)	132.47 (A)	137.74 (A)	130.15 (B)	127.7 (B)	132.61 (B)	133.26 (B)	130.06 (B)	136.47 (B)
kk	131.81 (B)	128.36 (B)	135.29 (B)	N/A	N/A	N/A	125.68 (C)	123.72 (C)	127.66 (C)
Mean s.e.	3.74	2.56	4.89	3.72	2.5	4.94	3.75	2.62	4.94
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	158.06 (B)	160.32 (B)	155.84 (B)	165.48 (A)	167.37 (A)	163.61 (A)	165.97 (A)	168.52 (A)	163.42 (A)
Spaced-lm, np, hk	163.62 (A)	165.31 (A)	161.92 (A)	159.32 (B)	161.07 (B)	157.58 (B)	162.71 (A)	164.47 (B)	160.98 (A)
Spaced-kk	162.63 (A)	164.04 (AB)	161.24 (A)	N/A	N/A	N/A	155.7 (B)	156.42 (C)	154.98 (B)
Poly-ll, nn, hh	117.69 (DE)	107.44 (F)	128.14 (D)	126.55 (C)	114.89 (CD)	138.24 (C)	126.38 (C)	115.45 (E)	137.33 (C)
Poly-lm, np, hk	124.71 (C)	113.71 (D)	135.66 (C)	119 (D)	108.02 (E)	130.02 (D)	122.87 (C)	111.08 (F)	134.7 (C)
Poly-kk	121.25 (CD)	108.3 (EF)	134.29 (C)	N/A	N/A	N/A	113.9 (D)	103.24 (G)	124.64 (D)
Mono-ll, nn, hh	108.96 (F)	111.91 (DE)	105.96 (G)	116.13 (DE)	117.89 (C)	114.3 (E)	117.68 (D)	120.07 (D)	115.26 (E)
Mono-lm, np, hk	117.06 (E)	118.4 (C)	115.63 (E)	112.12 (E)	114.02 (D)	110.23 (F)	114.21 (D)	114.63 (E)	113.74 (E)
Mono-kk	111.54 (F)	112.73 (D)	110.34 (F)	N/A	N/A	N/A	107.45 (E)	111.5 (EF)	103.37 (F)
Mean s.e.	3.93	2.8	5.02	3.92	2.64	5.02	3.92	2.84	5.06
pval	0.6486	0.4755	0.3939	0.505	0.3462	0.1697	0.9054	0.3791	0.428
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C5. IVTD QxE Data

Effect	TP196229 np			TP209546 np			TP301824 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	71.63 (A)			71.7 (A)			71.77 (A)		
2017	70.75 (B)			70.83 (B)			70.95 (B)		
Mean s.e.	0.16			0.17			0.18		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	68.82 (C)	69.4 (C)	68.25 (C)	68.9 (C)	69.48 (C)	68.33 (C)	68.97 (C)	69.57 (B)	68.37 (C)
Poly	72.08 (B)	72.58 (B)	71.23 (B)	72.17 (B)	73.01 (A)	71.33 (B)	72.19 (B)	72.97 (A)	71.41 (B)
Mono	72.67 (A)	72.92 (A)	72.76 (A)	72.72 (A)	72.61 (B)	72.83 (A)	72.92 (A)	72.77 (A)	73.07 (A)
Mean s.e.	0.17	0.11	0.28	0.17	0.11	0.028	0.19	0.12	0.3
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	70.73 (B)	71.22 (B)	70.24 (B)	70.87 (B)	71.32 (B)	70.42 (B)	72.35 (A)	72.55 (A)	72.15 (A)
lm, np, hk	71.65 (A)	72.05 (A)	71.25 (A)	71.65 (A)	72.07 (A)	71.23 (A)	70.95 (B)	71.48 (B)	70.43 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	70.79 (B)	71.3 (B)	70.27 (B)
Mean s.e.	0.16	0.09	0.27	0.17	0.09	0.27	0.19	0.12	0.3
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	68.36 (E)	68.84 (E)	67.88 (A)	68.45 (E)	68.99 (D)	67.92 (F)	69.91 (E)	70.61 (E)	69.21 (D)
Spaced-lm, np, hk	69.28 (D)	69.95 (D)	68.62 (B)	69.36 (D)	69.97 (C)	68.74 (E)	68.61 (F)	69.2 (F)	68.02 (E)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	68.4 (F)	68.9 (F)	67.89 (E)
Poly-ll, nn, hh	71.7 (C)	72.6 (BC)	70.81 (B)	71.74 (C)	72.56 (B)	70.92 (D)	73.04 (B)	73.59 (A)	72.49 (B)
Poly-lm, np, hk	72.45 (B)	73.25 (A)	71.66 (C)	72.59 (B)	73.46 (A)	71.73 (C)	71.95 (CD)	72.91 (BC)	70.99 (C)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	71.59 (D)	72.42 (CD)	70.77 (C)
Mono-ll, nn, hh	72.13 (B)	72.21 (C)	72.04 (D)	72.43 (B)	72.42 (B)	72.43 (B)	74.1 (A)	73.44 (AB)	74.76 (A)
Mono-lm, np, hk	73.22 (A)	72.96 (AB)	73.48 (E)	73.01 (A)	72.79 (B)	73.22 (A)	72.3 (C)	72.33 (D)	72.28 (B)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	72.37 (C)	72.56 (CD)	72.16 (B)
Mean s.e.	0.19	0.15	0.3	0.19	0.15	0.3	0.23	0.2	0.34
pval	0.4057	0.2685	0.0519	0.2621	0.0894	0.9968	0.2766	0.0963	0.0135
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C5. IVTD QxE Data Continued

Effect	TP392378 hk			TP44922 hk			TP51697 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	71.73 (A)			71.73 (A)			71.75 (A)		
2017	70.87 (B)			70.84 (B)			70.96 (B)		
Mean s.e.	0.17			0.17			0.17		
pval	<.0001						<.0001		
Environment									
Spaced	68.94 (C)	69.51 (B)	68.36 (C)	68.89 (C)	69.45 (B)	68.34 (C)	69.02 (C)	69.57 (C)	68.48 (C)
Poly	72.14 (B)	72.94 (A)	71.35 (B)	72.17 (B)	73.03 (A)	71.31 (B)	72.28 (B)	73.11 (A)	71.46 (B)
Mono	72.82 (A)	72.71 (A)	72.91 (A)	72.8 (A)	72.72 (A)	72.87 (A)	72.76 (A)	72.55 (B)	72.96 (A)
Mean s.e.	0.18	0.12	0.3	0.17	0.12	0.29	0.17	0.12	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	71.17 (B)	71.62 (B)	70.72 (B)	70.52 (C)	71.01 (C)	70.03 (C)	71.77 (A)	72.04 (A)	71.5 (A)
lm, np, hk	70.94 (C)	71.45 (B)	70.43 (B)	71.21 (B)	71.61 (B)	70.81 (B)	70.98 (C)	71.49 (B)	70.47 (C)
kk	71.78 (A)	72.1 (A)	71.47 (A)	72.13 (A)	72.58 (A)	71.68 (A)	71.31 (B)	71.7 (AB)	70.93 (B)
Mean s.e.	0.18	0.12	0.3	0.17	0.11	0.29	0.17	0.12	0.28
pval	<.0001	0.0002	<.0001	<.0001	<.0001	<.0001	<.0001	0.0052	<.0001
Env. X Allele									
Spaced-ll, nn, hh	68.71 (G)	69.19 (D)	68.24 (EF)	68.17 (H)	68.58 (F)	67.76 (G)	69.53 (E)	70.05 (D)	69 (D)
Spaced-lm, np, hk	68.62 (G)	69.23 (D)	68.01 (F)	68.86 (G)	69.47 (E)	68.26 (G)	68.55 (G)	69.16 (E)	67.93 (E)
Spaced-kk	69.49 (F)	70.13 (C)	68.84 (E)	69.64 (F)	70.29 (D)	68.98 (F)	69 (F)	69.5 (DE)	68.5 (D)
Poly-ll, nn, hh	72.04 (DE)	72.94 (A)	71.15 (D)	71.27 (E)	72.18 (C)	70.37 (E)	72.77 (AB)	73.52 (A)	72.03 (B)
Poly-lm, np, hk	71.92 (E)	72.83 (A)	71.01 (D)	72.12 (D)	72.88 (B)	71.36 (D)	71.84 (D)	72.67 (C)	71.01 (C)
Poly-kk	72.47 (BC)	73.06 (A)	71.89 (C)	73.11 (B)	74.03 (A)	72.2 (C)	72.23 (C)	73.15 (AB)	71.32 (C)
Mono-ll, nn, hh	72.76 (B)	72.74 (AB)	72.78 (B)	72.11 (D)	72.26 (C)	71.95 (C)	73.02 (A)	72.55 (BC)	73.46 (A)
Mono-lm, np, hk	72.29 (CD)	72.28 (B)	72.29 (BC)	72.65 (C)	72.47 (C)	72.81 (B)	72.55 (BC)	72.64 (C)	72.46 (B)
Mono-kk	73.4 (A)	73.11 (A)	73.67 (A)	73.64 (A)	73.43 (AB)	73.84 (A)	72.71 (AB)	72.46 (C)	72.96 (A)
Mean s.e.	0.21	0.2	0.34	0.2	0.2	0.33	0.21	0.2	0.33
pval	0.1785	0.1962	0.618	0.5503	0.3501	0.5232	0.396	0.08	0.9607
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C5. IVTD QxE Data Continued

Effect	TP583925 np			TP647617 hk			TP742242 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	71.67 (A)			71.75 (A)			71.59 (A)		
2017	70.81 (B)			70.9 (B)			70.72 (B)		
Mean s.e.	0.17			0.16			0.17		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	68.86 (C)	69.42 (C)	68.3 (C)	68.99 (C)	69.61 (C)	68.37 (C)	68.77 (C)	69.33 (B)	68.21 (C)
Poly	72.74 (A)	72.95 (A)	71.29 (B)	72.22 (B)	73.02 (A)	71.43 (B)	72.03 (B)	72.85 (A)	71.21 (B)
Mono	72.12 (B)	72.63 (B)	72.85 (A)	72.76 (A)	72.63 (B)	72.89 (A)	72.66 (A)	72.58 (A)	72.74 (A)
Mean s.e.	0.18	0.11	0.28	0.17	0.11	0.28	0.18	0.11	0.29
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	71.58 (A)	71.91 (A)	71.25 (A)	71.36 (B)	71.85 (B)	70.87 (B)	70.69 (B)	71.16 (B)	70.22 (B)
lm, np, hk	70.9 (B)	71.42 (B)	70.38 (B)	70.79 (C)	71.19 (C)	70.4 (C)	71.62 (A)	72.02 (A)	71.22 (A)
kk	N/A	N/A	N/A	71.83 (A)	72.22 (A)	71.43 (A)	N/A	N/A	N/A
Mean s.e.	0.17	0.09	0.28	0.17	0.11	0.28	0.17	0.09	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	69.16 (D)	69.72 (C)	68.6 (E)	69.21 (E)	69.94 (E)	68.49 (EF)	68.3 (E)	68.83 (E)	67.77 (F)
Spaced-lm, np, hk	68.56 (E)	69.12 (D)	68 (F)	68.35 (F)	68.73 (F)	67.97 (F)	69.25 (D)	69.83 (D)	68.66 (E)
Spaced-kk	N/A	N/A	N/A	69.41 (E)	70.15 (E)	68.67 (E)	N/A	N/A	N/A
Poly-ll, nn, hh	72.38 (A)	73.13 (A)	71.62 (C)	72.29 (C)	73.06 (AB)	71.52 (C)	71.58 (C)	72.36 (C)	70.8 (D)
Poly-lm, np, hk	71.86 (B)	72.77 (A)	70.96 (D)	71.64 (D)	72.52 (CD)	70.77 (D)	72.48 (B)	73.35 (A)	71.62 (C)
Poly-kk	N/A	N/A	N/A	72.74 (B)	73.48 (A)	72.01 (BC)	N/A	N/A	N/A
Mono-ll, nn, hh	73.21 (B)	72.89 (A)	73.53 (A)	72.57 (BC)	72.53 (BCD)	72.6 (B)	72.2 (B)	72.29 (C)	72.1 (B)
Mono-lm, np, hk	72.27 (C)	72.36 (B)	72.17 (B)	72.39 (BC)	72.32 (D)	72.46 (B)	73.13 (A)	72.88 (B)	73.38 (A)
Mono-kk	N/A	N/A	N/A	73.33 (A)	73.03 (ABC)	73.61 (A)	N/A	N/A	N/A
Mean s.e.	0.2	0.16	0.3	0.21	0.19	0.32	0.2	0.15	0.31
pval	0.1879	0.7256	0.0246	0.1779	0.0673	0.2351	0.9848	0.3054	0.2909
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C5. IVTD QxE Data Continued

Effect	TP806301 hk			TP807868 hk			TP814309 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	71.58 (A)			71.68 (A)			71.63 (A)		
2017	70.72 (B)			70.84 (B)			70.76 (B)		
Mean s.e.	0.17			0.17			0.16		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	68.76 (C)	69.33 (C)	68.18 (C)	68.9 (C)	69.47 (B)	68.33 (C)	68.84 (C)	69.42 (C)	68.27 (C)
Poly	72.06 (B)	72.89 (A)	71.24 (B)	72.12 (B)	72.92 (A)	71.32 (B)	72.07 (B)	72.58 (B)	71.25 (B)
Mono	72.63 (A)	72.53 (B)	72.73 (A)	72.76 (A)	72.64 (A)	72.88 (A)	72.66 (A)	72.9 (A)	72.75 (A)
Mean s.e.	0.18	0.12	0.28	0.18	0.12	0.29	0.17	0.11	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	70.51 (C)	70.96 (B)	70.06 (C)	70.6 (C)	71.06 (C)	70.12 (C)	70.84 (B)	71.34 (B)	70.33 (B)
lm, np, hk	71.31 (B)	71.75 (A)	70.88 (B)	71.16 (B)	71.62 (B)	70.69 (B)	71.55 (A)	71.92 (A)	71.18 (A)
kk	71.63 (A)	72.04 (A)	71.22 (A)	72.03 (A)	72.34 (A)	71.72 (A)	N/A	N/A	N/A
Mean s.e.	0.18	0.12	0.29	0.18	0.11	0.29	0.17	0.09	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	67.95 (F)	68.49 (E)	67.42 (G)	68.14 (G)	68.58 (E)	67.7 (G)	68.55 (E)	69.1 (D)	68 (F)
Spaced-lm, np, hk	69 (E)	69.57 (D)	68.43 (F)	68.77 (F)	69.36 (D)	68.18 (G)	69.13 (D)	69.73 (C)	68.54 (E)
Spaced-kk	69.32 (E)	69.95 (D)	68.69 (F)	69.78 (E)	70.46 (C)	69.1 (F)	N/A	N/A	N/A
Poly-ll, nn, hh	71.59 (D)	72.37 (BC)	70.82 (E)	71.51 (D)	72.32 (B)	70.7 (E)	71.7 (C)	72.54 (B)	70.87 (D)
Poly-lm, np, hk	72.2 (C)	73.05 (A)	71.35 (D)	72.13 (C)	73.05 (A)	71.22 (D)	72.44 (B)	73.25 (A)	71.64 (C)
Poly-kk	72.39 (BC)	73.24 (A)	71.55 (CD)	72.71 (B)	73.38 (A)	72.04 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	71.98 (CD)	72.03 (C)	71.94 (C)	72.13 (C)	72.29 (B)	71.96 (C)	72.25 (B)	72.38 (B)	72.12 (B)
Mono-lm, np, hk	72.74 (B)	72.63 (B)	72.84 (B)	72.56 (B)	72.46 (B)	72.66 (B)	73.07 (A)	72.77 (B)	73.37 (A)
Mono-kk	73.17 (A)	72.93 (AB)	73.4 (A)	73.6 (A)	73.17 (A)	74.02 (A)	N/A	N/A	N/A
Mean s.e.	0.22	0.2	0.33	0.21	0.2	0.33	0.19	0.15	0.3
pval	0.4487	0.6062	0.4843	0.3154	0.0701	0.5046	0.5597	0.5603	0.0652
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C5. IVTD QxE Data Continued

Effect	TP824450 np			TP84707 np			TP96886 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	71.66 (A)			71.57 (A)			71.68 (A)		
2017	70.79 (B)			70.7 (B)			70.8 (B)		
Mean s.e.	0.17			0.16			0.17		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	68.85 (C)	69.43 (C)	68.27 (C)	68.75 (C)	69.32 (C)	68.19 (C)	68.86 (C)	69.42 (C)	68.3 (C)
Poly	72.12 (B)	72.95 (A)	71.3 (B)	72.04 (B)	72.86 (A)	71.22 (B)	72.12 (B)	72.98 (A)	71.26 (B)
Mono	72.7 (A)	72.61 (B)	72.8 (A)	72.62 (A)	72.52 (B)	72.71 (A)	72.73 (A)	72.64 (B)	72.82 (A)
Mean s.e.	0.18	0.11	0.29	0.17	0.11	0.28	0.17	0.12	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	70.82 (B)	71.23 (B)	70.41 (B)	70.67 (B)	71.15 (B)	70.19 (B)	70.56 (C)	71.02 (C)	70.11 (C)
lm, np, hk	71.63 (A)	72.09 (A)	71.17 (A)	71.6 (A)	71.99 (A)	71.21 (A)	71.16 (B)	71.59 (B)	70.73 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	71.99 (A)	72.43 (A)	71.55 (A)
Mean s.e.	0.17	0.09	0.28	0.16	0.09	0.27	0.17	0.11	0.28
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	68.46 (E)	69.02 (D)	67.9 (F)	68.25 (E)	68.8 (E)	67.7 (F)	68.18 (H)	68.57 (F)	67.8 (G)
Spaced-lm, np, hk	69.24 (D)	69.84 (C)	68.65 (E)	69.26 (D)	69.84 (D)	68.67 (E)	68.79 (G)	69.38 (E)	68.2 (G)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	69.6 (F)	70.3 (D)	68.91 (F)
Poly-ll, nn, hh	71.74 (C)	72.53 (B)	70.96 (D)	71.58 (C)	72.39 (BC)	70.77 (D)	71.29 (E)	72.17 (C)	70.42 (E)
Poly-lm, np, hk	72.51 (B)	73.38 (A)	71.64 (C)	72.5 (B)	73.33 (A)	71.67 (C)	72.09 (D)	72.91 (B)	71.28 (D)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	72.97 (B)	73.85 (A)	72.1 (C)
Mono-ll, nn, hh	72.27 (B)	72.15 (B)	72.37 (B)	72.19 (B)	72.26 (C)	72.11 (B)	72.2 (D)	72.31 (C)	72.1 (C)
Mono-lm, np, hk	73.14 (A)	73.06 (A)	73.22 (A)	73.04 (A)	72.78 (B)	73.3 (A)	72.6 (C)	72.49 (C)	72.71 (B)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	73.4 (A)	73.13 (B)	73.64 (A)
Mean s.e.	0.2	0.15	0.31	0.18	0.15	0.3	0.2	0.2	0.33
pval	0.9031	0.9592	0.86	0.8182	0.2008	0.63	0.476	0.2451	0.702
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C6. ME QxE Data

Effect	TP196229 np			TP294131 hk			TP299528 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	2.15 (A)			2.15 (A)			2.15 (A)		
2017	2.09 (B)			2.1 (B)			2.09 (B)		
Mean s.e.	0.01			0.01			0.01		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	2.06 (B)	2.08 (C)	2.03 (C)	2.06 (B)	2.08 (C)	2.03 (C)	2.05 (B)	2.08 (C)	2.03 (C)
Poly	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.2 (A)	2.11 (B)
Mono	2.15 (A)	2.17 (B)	2.14 (A)	2.16 (A)	2.17 (B)	2.14 (A)	2.15 (A)	2.16 (B)	2.14 (A)
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	2.11 (B)	2.14 (B)	2.08 (B)	2.12 (B)	2.15 (A)	2.09 (B)	2.12 (B)	2.15 (B)	2.09 (B)
lm, np, hk	2.13 (A)	2.16 (A)	2.11 (A)	2.12 (C)	2.14 (B)	2.09 (B)	2.13 (A)	2.16 (A)	2.1 (A)
kk	N/A	N/A	N/A	2.13 (A)	2.16 (A)	2.11 (A)	2.11 (C)	2.14 (C)	2.08 (C)
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	0.0018	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	2.05 (E)	2.07 (F)	2.02 (E)	2.06 (E)	2.08 (F)	2.03 (EF)	2.05 (F)	2.08 (E)	2.03 (F)
Spaced-lm, np, hk	2.07 (D)	2.09 (E)	2.04 (D)	2.05 (E)	2.08 (F)	2.03 (F)	2.07 (E)	2.09 (D)	2.05 (E)
Spaced-kk	N/A	N/A	N/A	2.06 (E)	2.08 (F)	2.04 (E)	2.04 (G)	2.06 (F)	2.02 (F)
Poly-ll, nn, hh	2.15 (B)	2.2 (B)	2.1 (C)	2.16 (ABC)	2.21 (AB)	2.11 (CD)	2.16 (BC)	2.2 (AB)	2.11 (C)
Poly-lm, np, hk	2.17 (A)	2.22 (A)	2.12 (B)	2.15 (C)	2.2 (BC)	2.1 (D)	2.17 (A)	2.22 (A)	2.12 (B)
Poly-kk	N/A	N/A	N/A	2.17 (AB)	2.22 (A)	2.12 (BC)	2.14 (D)	2.19 (B)	2.09 (D)
Mono-ll, nn, hh	2.14 (C)	2.15 (D)	2.12 (B)	2.16 (BC)	2.17 (DE)	2.15 (A)	2.15 (CD)	2.16 (C)	2.14 (AB)
Mono-lm, np, hk	2.17 (A)	2.18 (C)	2.15 (A)	2.14 (D)	2.16 (E)	2.13 (B)	2.16 (B)	2.17 (C)	2.15 (A)
Mono-kk	N/A	N/A	N/A	2.17 (A)	2.18 (CD)	2.16 (A)	2.15 (CD)	2.16 (C)	2.13 (B)
Mean s.e.	0.01	<0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
pval	0.1619	0.1914	0.4157	0.1764	0.3432	0.4256	0.1911	0.2395	0.45
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C6. ME QxE Data Continued

Effect	TP310707 lm				TP362609 lm				TP366872 np			
	AY	2016	2017		AY	2016	2017		AY	2016	2017	
Year												
2016	2.15 (A)				2.15 (A)				2.15 (A)			
2017	2.09 (B)				2.09 (B)				2.09 (B)			
Mean s.e.	0.01				0.01				0.01			
pval	<.0001				<.0001				<.0001			
Environment												
Spaced	2.06 (B)	2.08 (C)	2.14 (A)		2.06 (B)	2.21 (A)	2.03 (C)		2.06 (B)	2.08 (C)	2.03 (C)	
Poly	2.16 (A)	2.21 (A)	2.11 (B)		2.16 (A)	2.16 (B)	2.11 (B)		2.16 (A)	2.21 (A)	2.11 (B)	
Mono	2.15 (A)	2.17 (B)	2.03 (C)		2.15 (A)	2.08 (C)	2.14 (A)		2.15 (A)	2.17 (B)	2.14 (A)	
Mean s.e.	0.01	<0.01	0.01		0.01	<0.01	0.01		0.01	<0.01	0.01	
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
Allele												
ll, nn, hh	2.13 (A)	2.16 (A)	2.1 (A)		2.11 (B)	2.14 (B)	2.08 (B)		2.11 (B)	2.14 (B)	2.08 (B)	
lm, np, hk	2.11 (B)	2.14 (B)	2.09 (B)		2.13 (A)	2.16 (A)	2.1 (A)		2.13 (A)	2.16 (A)	2.11 (A)	
kk	N/A	N/A	N/A		N/A	N/A	N/A		N/A	N/A	N/A	
Mean s.e.	0.01	<0.01	0.01		0.01	<0.01	0.01		0.01	<0.01	0.01	
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
Env. X Allele												
Spaced-ll, nn, hh	2.06 (C)	2.09 (E)	2.04 (D)		2.05 (D)	2.07 (F)	2.03 (E)		2.05 (E)	2.07 (F)	2.03 (E)	
Spaced-lm, np, hk	2.05 (D)	2.07 (F)	2.03 (E)		2.07 (C)	2.09 (E)	2.04 (D)		2.07 (D)	2.09 (E)	2.04 (D)	
Spaced-kk	N/A	N/A	N/A		N/A	N/A	N/A		N/A	N/A	N/A	
Poly-ll, nn, hh	2.17 (A)	2.22 (A)	2.12 (B)		2.15 (B)	2.2 (B)	2.1 (C)		2.15 (B)	2.2 (B)	2.1 (C)	
Poly-lm, np, hk	2.15 (B)	2.2 (B)	2.1 (C)		2.16 (A)	2.21 (A)	2.11 (B)		2.17 (A)	2.22 (A)	2.12 (B)	
Poly-kk	N/A	N/A	N/A		N/A	N/A	N/A		N/A	N/A	N/A	
Mono-ll, nn, hh	2.16 (A)	2.17 (C)	2.15 (A)		2.14 (B)	2.15 (D)	2.12 (B)		2.14 (C)	2.15 (D)	2.12 (B)	
Mono-lm, np, hk	2.14 (B)	2.16 (D)	2.13 (B)		2.16 (A)	2.17 (C)	2.15 (A)		2.17 (A)	2.18 (C)	2.15 (A)	
Mono-kk	N/A	N/A	N/A		N/A	N/A	N/A		N/A	N/A	N/A	
Mean s.e.	0.01	<0.01	0.01		0.01	0.01	0.01		0.01	<0.01	0.01	
pval	0.8612	0.7784	0.5364		0.487	0.9912	0.128		0.2091	0.3756	0.135	
pval_Bon	0.0033	0.0033	0.0033		0.0033	0.0033	0.0033		0.0033	0.0033	0.0033	

Appendix C6. ME QxE Data Continued

Effect	TP441695 np			TP44922 hk			TP510276 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	2.16 (A)			2.15 (A)			2.15 (A)		
2017	2.1 (B)			2.1 (B)			2.09 (B)		
Mean s.e.	0.01			0.01			0.01		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	2.16 (A)	2.08 (C)	2.04 (C)	2.06 (B)	2.08 (C)	2.04 (C)	2.06 (B)	2.08 (C)	2.04 (C)
Poly	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.21 (A)	2.11 (B)
Mono	2.06 (B)	2.17 (B)	2.14 (A)	2.16 (A)	2.17 (B)	2.14 (A)	2.15 (A)	2.17 (B)	2.14 (A)
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	2.11 (B)	2.14 (B)	2.08 (B)	2.1 (C)	2.13 (C)	2.07 (C)	2.14 (A)	2.17 (A)	2.11 (A)
lm, np, hk	2.14 (A)	2.17 (A)	2.11 (A)	2.12 (B)	2.15 (B)	2.1 (B)	2.12 (B)	2.15 (B)	2.09 (B)
kk	N/A	N/A	N/A	2.15 (A)	2.18 (A)	2.12 (A)	2.11 (C)	2.14 (C)	2.08 (C)
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	2.05 (D)	2.07 (F)	2.02 (E)	2.04 (F)	2.06 (G)	2.02 (H)	2.08 (D)	2.11 (E)	2.06 (F)
Spaced-lm, np, hk	2.08 (C)	2.1 (E)	2.05 (D)	2.06 (E)	2.08 (F)	2.03 (G)	2.05 (E)	2.07 (F)	2.03 (G)
Spaced-kk	N/A	N/A	N/A	2.08 (D)	2.1 (E)	2.05 (F)	2.04 (E)	2.06 (F)	2.02 (G)
Poly-ll, nn, hh	2.15 (B)	2.2 (B)	2.1 (C)	2.14 (C)	2.19 (C)	2.09 (E)	2.17 (A)	2.22 (A)	2.12 (C)
Poly-lm, np, hk	2.17 (A)	2.22 (A)	2.13 (B)	2.16 (B)	2.2 (B)	2.11 (D)	2.16 (B)	2.21 (AB)	2.11 (DE)
Poly-kk	N/A	N/A	N/A	2.19 (A)	2.24 (A)	2.13 (BC)	2.15 (BC)	2.2 (BC)	2.1 (E)
Mono-ll, nn, hh	2.15 (B)	2.16 (D)	2.13 (B)	2.14 (C)	2.15 (D)	2.12 (CD)	2.17 (A)	2.18 (C)	2.16 (A)
Mono-lm, np, hk	2.17 (A)	2.18 (C)	2.16 (A)	2.15 (B)	2.16 (D)	2.14 (B)	2.15 (B)	2.16 (D)	2.14 (B)
Mono-kk	N/A	N/A	N/A	2.18 (A)	2.19 (BC)	2.16 (A)	2.14 (C)	2.15 (D)	2.12 (CD)
Mean s.e.	0.01	<0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
pval	0.4231	0.1801	0.9567	0.7252	0.4613	0.7727	0.3322	0.4405	0.512
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C6. ME QxE Data Continued

Effect	TP647617 hk			TP774095 np			TP776097 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	2.15 (A)			2.15 (A)			2.15 (A)		
2017	2.1 (B)			2.09 (B)			2.1 (B)		
Mean s.e.	0.01			0.01			0.01		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	2.06 (C)	2.08 (C)	2.04 (C)	2.06 (B)	2.08 (C)	2.03 (C)	2.06 (B)	2.08 (C)	2.04 (C)
Poly	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.21 (A)	2.11 (B)	2.16 (A)	2.21 (A)	2.11 (B)
Mono	2.15 (B)	2.17 (B)	2.14 (A)	2.15 (A)	2.16 (B)	2.14 (A)	2.15 (A)	2.17 (B)	2.14 (A)
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	2.13 (B)	2.15 (B)	2.1 (B)	2.11 (B)	2.14 (B)	2.08 (B)	2.14 (A)	2.17 (A)	2.11 (A)
lm, np, hk	2.11 (C)	2.14 (C)	2.08 (C)	2.13 (A)	2.16 (A)	2.11 (A)	2.11 (B)	2.14 (B)	2.09 (B)
kk	2.14 (A)	2.17 (A)	2.11 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.01	<0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	2.07 (D)	2.09 (D)	2.04 (E)	2.04 (E)	2.07 (F)	2.02 (E)	2.07 (C)	2.1 (E)	2.05 (D)
Spaced-lm, np, hk	2.05 (E)	2.06 (E)	2.03 (F)	2.07 (D)	2.09 (E)	2.05 (D)	2.05 (D)	2.07 (F)	2.03 (E)
Spaced-kk	2.07 (D)	2.1 (D)	2.05 (E)	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	2.16 (B)	2.21 (B)	2.11 (C)	2.15 (B)	2.19 (B)	2.1 (C)	2.17 (A)	2.22 (A)	2.11 (C)
Poly-lm, np, hk	2.15 (C)	2.19 (B)	2.1 (D)	2.17 (A)	2.22 (A)	2.12 (B)	2.15 (B)	2.19 (B)	2.11 (C)
Poly-kk	2.18 (A)	2.23 (A)	2.13 (B)	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	2.15 (BC)	2.17 (C)	2.14 (B)	2.14 (C)	2.15 (D)	2.12 (B)	2.17 (A)	2.18 (C)	2.16 (A)
Mono-lm, np, hk	2.15 (C)	2.16 (C)	2.13 (B)	2.17 (A)	2.18 (C)	2.16 (A)	2.14 (B)	2.15 (D)	2.13 (B)
Mono-kk	2.16 (B)	2.17 (C)	2.15 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.01	0.01	0.01	0.01	<0.01	0.01	0.01	<0.01	0.01
pval	0.2041	0.161	0.355	0.4357	0.866	0.0228	0.6302	0.9641	0.1489
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C6. ME QxE Data Continued

Effect	TP824450 np				TP854268 hk				TP96886 hk			
	AY	2016	2017		AY	2016	2017		AY	2016	2017	
Year												
2016	2.15 (A)				2.15 (A)				2.15 (A)			
2017	2.1 (B)				2.1 (B)				2.09 (B)			
Mean s.e.	0.01				0.01				0.01			
pval	<.0001				<.0001				<.0001			
Environment												
Spaced	2.06 (B)	2.08 (C)	2.03 (C)		2.06 (B)	2.08 (C)	2.04 (C)		2.06 (B)	2.08 (C)	2.04 (C)	
Poly	2.16 (A)	2.21 (A)	2.11 (B)		2.16 (A)	2.21 (A)	2.11 (B)		2.16 (A)	2.21 (A)	2.11 (B)	
Mono	2.15 (A)	2.17 (B)	2.14 (A)		2.15 (A)	2.17 (B)	2.14 (A)		2.15 (A)	2.17 (B)	2.14 (A)	
Mean s.e.	0.01	<0.01	0.01		0.01	<0.01	0.01		0.01	<0.01	0.01	
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
Allele												
ll, nn, hh	2.11 (B)	2.14 (B)	2.08 (B)		2.14 (A)	2.17 (A)	2.11 (A)		2.1 (C)	2.13 (C)	2.08 (C)	
lm, np, hk	2.14 (A)	2.17 (A)	2.11 (A)		2.11 (C)	2.14 (B)	2.09 (C)		2.12 (B)	2.15 (B)	2.09 (B)	
kk	N/A	N/A	N/A		2.12 (B)	2.15 (B)	2.1 (B)		2.14 (A)	2.17 (A)	2.11 (A)	
Mean s.e.	0.01	<0.01	0.01		0.01	<0.01	0.01		0.01	<0.01	0.01	
pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
Env. X Allele												
Spaced-ll, nn, hh	2.05 (D)	2.07 (E)	2.02 (E)		2.08 (D)	2.1 (D)	2.05 (D)		2.04 (F)	2.06 (G)	2.02 (H)	
Spaced-lm, np, hk	2.07 (C)	2.09 (D)	2.04 (D)		2.04 (F)	2.07 (E)	2.02 (E)		2.06 (E)	2.08 (F)	2.03 (G)	
Spaced-kk	N/A	N/A	N/A		2.06 (E)	2.08 (E)	2.04 (D)		2.08 (D)	2.1 (E)	2.05 (F)	
Poly-ll, nn, hh	2.15 (B)	2.2 (B)	2.1 (C)		2.17 (A)	2.22 (A)	2.13 (B)		2.14 (C)	2.19 (C)	2.09 (E)	
Poly-lm, np, hk	2.17 (A)	2.22 (A)	2.12 (B)		2.15 (BC)	2.2 (B)	2.1 (C)		2.16 (B)	2.21 (B)	2.11 (D)	
Poly-kk	N/A	N/A	N/A		2.16 (BC)	2.21 (AB)	2.11 (C)		2.18 (A)	2.23 (A)	2.13 (BC)	
Mono-ll, nn, hh	2.14 (B)	2.15 (C)	2.13 (B)		2.16 (AB)	2.17 (C)	2.15 (A)		2.14 (C)	2.15 (D)	2.12 (CD)	
Mono-lm, np, hk	2.17 (A)	2.18 (B)	2.16 (A)		2.15 (C)	2.16 (C)	2.13 (B)		2.15 (B)	2.16 (D)	2.14 (B)	
Mono-kk	N/A	N/A	N/A		2.15 (BC)	2.17 (C)	2.14 (AB)		2.17 (A)	2.18 (C)	2.16 (A)	
Mean s.e.	0.01	<0.01	0.01		0.01	0.01	0.01		0.01	0.01	0.01	
pval	0.4725	0.5592	0.4148		0.4592	0.253	0.7325		0.8081	0.6579	0.8739	
pval_Bon	0.0033	0.0033	0.0033		0.0033	0.0033	0.0033		0.0033	0.0033	0.0033	

Appendix C7. Number of Tillers QxE Data

Marker Allele Effect	TP157160 hk			TP214762 hk			TP291091 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	126.07 (B)			127.77 (B)			127.37 (B)		
2017	234.65 (A)			235.22 (A)			237.14 (A)		
Mean s.e.	4.35			4.02			4		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	442.21 (A)	325.26 (A)	559.15 (A)	442 (A)	328.57 (A)	555.42 (A)	444.41 (A)	327.48 (A)	561.3 (A)
Poly	73.25 (B)	29.81 (B)	116.7 (B)	74.99 (B)	30.66 (B)	119.36 (B)	75.61 (B)	30.78 (B)	120.49 (B)
Mono	25.62 (C)	23.27 (B)	28.08 (C)	27.49 (C)	24.05 (B)	31.1 (C)	26.74 (C)	23.85 (B)	29.74 (C)
Mean s.e.	5.03	6.4	13.58	4.84	6.74	13.76	4.97	6.64	13.7
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	189.33 (A)	131.39 (A)	247.49 (A)	190.85 (A)	137.44 (A)	244.47 (A)	195.58 (A)	136 (A)	255.29 (A)
lm, np, hk	181.17 (AB)	126.36 (A)	236 (AB)	179.25 (B)	121.82 (B)	236.66 (AB)	176.8 (B)	122.03 (B)	231.66 (B)
kk	170.58 (B)	120.58 (A)	220.44 (B)	174.37 (B)	124.02 (B)	224.74 (B)	174.38 (B)	124.08 (B)	224.59 (B)
Mean s.e.	5.01	6.39	13.57	4.81	6.73	13.75	4.96	6.63	13.69
pval	0.009	0.1961	0.0155	0.0297	0.0082	0.1379	0.0015	0.0186	0.0017
Env. X Allele									
Spaced-ll, nn, hh	461.64 (A)	337.3 (A)	585.98 (A)	460.43 (A)	353.45 (A)	567.41 (A)	469.33 (A)	345.47 (A)	593.19 (A)
Spaced-lm, np, hk	437.39 (B)	324.01 (AB)	550.71 (B)	439.96 (B)	313.89 (B)	565.98 (A)	432.61 (B)	314.28 (B)	550.9 (B)
Spaced-kk	427.62 (B)	314.46 (B)	540.77 (B)	425.63 (B)	318.38 (B)	532.88 (B)	431.3 (B)	322.69 (B)	539.82 (B)
Poly-ll, nn, hh	78.97 (C)	32.12 (C)	125.91 (C)	80.03 (C)	32.35 (C)	127.87 (C)	86.39 (C)	35.55 (C)	137.16 (C)
Poly-lm, np, hk	77.78 (C)	31.33 (C)	124.27 (C)	73.85 (C)	29.55 (C)	118.13 (C)	71.96 (C)	29.04 (C)	115.05 (C)
Poly-kk	62.99 (C)	25.99 (C)	99.92 (C)	71.08 (C)	30.07 (C)	112.07 (C)	68.48 (C)	27.74 (C)	109.25 (C)
Mono-ll, nn, hh	27.4 (D)	24.77 (C)	30.59 (D)	32.1 (D)	26.53 (C)	38.15 (D)	31.01 (D)	26.99 (C)	35.52 (D)
Mono-lm, np, hk	28.33 (D)	23.74 (C)	33.02 (D)	23.95 (D)	22.03 (C)	25.88 (D)	25.83 (D)	22.77 (C)	29.02 (D)
Mono-kk	21.13 (D)	21.3 (C)	20.63 (D)	26.41 (D)	23.6 (C)	29.26 (D)	23.37 (D)	21.8 (C)	24.69 (D)
Mean s.e.	7.52	8.37	16.01	7.63	8.74	16.32	7.95	8.54	16.08
pval	0.2229	0.6731	0.2627	0.3961	0.0202	0.5106	0.2257	0.1996	0.3461
pval_Bon	0.0033333	0.0033333	0.003333	0.003333	0.003333	0.0033333	0.003333	0.003333	0.003333

Appendix C7. Number of Tillers QxE Data Continued

Marker Allele Effect	TP48221 lm			TP484929 hk			TP44922 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	125.92 (B)			125.42 (B)			125.88 (B)		
2017	235.93 (A)			236.93 (A)			235.75 (A)		
Mean s.e.	4.08			4.2			4.13		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	441.13 (A)	323.61 (A)	558.64 (A)	442.62 (A)	322.88 (A)	562.28 (A)	441.76 (A)	323.91 (A)	559.6 (A)
Poly	74.97 (B)	30.5 (B)	119.46 (B)	74.56 (B)	29.98 (B)	119.22 (B)	74.34 (B)	30.26 (B)	118.43 (B)
Mono	26.68 (C)	23.65 (B)	29.85 (C)	26.33 (C)	23.38 (B)	29.44 (C)	26.35 (C)	23.47 (B)	29.37 (C)
Mean s.e.	4.81	6.44	13.42	5.38	6.49	13.59	4.86	6.52	13.58
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	181.01 (A)	125.76 (A)	236.3 (A)	191.18 (A)	130.06 (A)	252.27 (A)	183.83 (A)	128.5 (A)	239.25 (A)
lm, np, hk	180.84 (A)	126.08 (A)	235.66 (A)	180.72 (AB)	128.71 (A)	232.83 (B)	177.8 (A)	123.26 (A)	232.35 (A)
kk	N/A	N/A	N/A	171.61 (B)	117.49 (B)	225.83 (B)	N/A	N/A	N/A
Mean s.e.	4.24	6.08	13.01	5.37	6.48	13.59	4.29	6.17	13.17
pval	0.9701	0.9381	0.9223	0.0251	0.054	0.0111	0.1861	0.2129	0.2945
Env. X Allele									
Spaced-ll, nn, hh	438.49 (A)	321.23 (A)	555.73 (A)	467.76 (A)	334.27 (A)	600.99 (A)	442.74 (A)	328.63 (A)	562.35 (A)
Spaced-lm, np, hk	443.77 (A)	325.98 (A)	561.54 (A)	439.28 (B)	330.32 (A)	548.25 (B)	440.78 (A)	319.19 (A)	556.86 (A)
Spaced-kk	N/A	N/A	N/A	420.82 (B)	304.05 (B)	537.6 (B)	N/A	N/A	N/A
Poly-ll, nn, hh	76.52 (B)	31.64 (B)	121.43 (B)	79.15 (C)	33.04 (C)	125.49 (C)	80.02 (B)	31.85 (B)	128.23 (B)
Poly-lm, np, hk	73.42 (B)	29.35 (B)	117.48 (B)	75.84 (C)	31.77 (C)	120.09 (C)	68.65 (B)	28.67 (B)	108.63 (B)
Poly-kk	N/A	N/A	N/A	68.69 (C)	25.14 (C)	112.08 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	28.02 (C)	24.4 (B)	31.75 (C)	26.62 (D)	22.86 (C)	30.35 (D)	28.73 (C)	25.02 (B)	32.65 (C)
Mono-lm, np, hk	25.33 (C)	22.91 (B)	27.95 (C)	27.06 (D)	24.02 (C)	30.15 (D)	23.97 (C)	21.92 (B)	26.08 (C)
Mono-kk	N/A	N/A	N/A	25.32 (D)	23.27 (C)	27.81 (D)	N/A	N/A	N/A
Mean s.e.	6.23	7.4	14.59	8.68	8.43	15.97	6.26	7.47	14.72
pval	0.6971	0.7516	0.7848	0.0991	0.205	0.03	0.6854	0.7753	0.2926
pval_Bon	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333

Appendix C7. Number of Tillers QxE Data Continued

Marker Allele Effect	TP51697 np			TP528489 hk			TP552520 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	126.04 (B)			123.73 (B)			125.76 (B)		
2017	235.59 (A)			234.29 (A)			235.29 (A)		
Mean s.e.	4.08			4.3			4.13		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	440.56 (A)	323.93 (A)	557.19 (A)	437.69 (A)	318.14 (A)	557.23 (A)	441.47 (A)	323.64 (A)	559.3 (A)
Poly	75.19 (B)	30.4 (B)	119.94 (B)	73.89 (B)	30.42 (B)	117.38 (B)	73.9 (B)	30.19 (B)	117.61 (B)
Mono	26.7 (C)	23.74 (B)	29.78 (C)	25.44 (C)	22.63 (B)	28.31 (C)	26.2 (C)	23.42 (B)	29.09 (C)
Mean s.e.	4.52	6.62	13.49	5.01	6.65	13.74	4.81	6.54	13.59
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
II, nn, hh	173.29 (B)	121.57 (B)	225.04 (B)	166.29 (B)	114.63 (B)	217.88 (B)	184.29 (A)	128.14 (A)	240.53 (A)
Im, np, hk	188.34 (A)	130.48 (A)	246.24 (A)	185.88 (A)	131.93 (A)	239.94 (A)	176.76 (A)	123.36 (A)	230.13 (A)
kk	N/A	N/A	N/A	184.85 (A)	124.64 (AB)	245.11 (A)	N/A	N/A	N/A
Mean s.e.	0.0001	6.27	13.09	5	6.64	13.73	4.26	6.19	13.18
pval	4.07	0.0347	0.0013	0.0011	0.004	0.0078	0.093	0.2604	0.1167
Env. X Allele									
Spaced-II, nn, hh	419.57 (B)	312.23 (B)	526.9 (B)	413.73 (B)	297.04 (C)	530.45 (B)	443.89 (A)	328.14 (A)	559.63 (A)
Spaced-Im, np, hk	461.55 (A)	335.63 (A)	587.49 (A)	451.53 (A)	339.74 (A)	563.29 (A)	439.06 (A)	319.13 (A)	558.97 (A)
Spaced-kk	N/A	N/A	N/A	447.81 (A)	317.65 (B)	577.97 (A)	N/A	N/A	N/A
Poly-II, nn, hh	74.25 (C)	28.83 (C)	119.59 (C)	64.63 (C)	27.37 (D)	101.91 (C)	80.42 (B)	31.59 (B)	129.3 (B)
Poly-Im, np, hk	76.13 (C)	31.97 (C)	120.3 (C)	77.11 (C)	30.24 (D)	124.02 (C)	67.38 (B)	28.8 (B)	105.91 (C)
Poly-kk	N/A	N/A	N/A	79.93 (C)	33.65 (D)	126.22 (C)	N/A	N/A	N/A
Mono-II, nn, hh	26.06 (D)	23.65 (C)	28.62 (D)	20.5 (D)	19.47 (D)	21.28 (D)	28.56 (C)	24.69 (B)	32.67 (D)
Mono-Im, np, hk	27.34 (D)	23.83 (C)	30.94 (D)	28.99 (D)	25.8 (D)	32.51 (D)	23.83 (C)	22.16 (B)	25.52 (D)
Mono-kk	N/A	N/A	N/A	26.81 (D)	22.62 (D)	31.15 (D)	N/A	N/A	N/A
Mean s.e.	5.65	7.55	14.64	7.59	8.56	16.14	6.18	7.5	14.75
pval	<.0001	0.048	0.0001	0.2006	0.0092	0.6033	0.6851	0.7755	0.3496
pval_Bon	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333

Appendix C7. Number of Tillers QxE Data Continued

Marker Allele Effect	TP563504 lm			TP615362 np			TP708074 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	126.09 (B)			125.63 (B)			126.01 (B)		
2017	235.97 (A)			235.36 (A)			236.24 (A)		
Mean s.e.	4.1			4.13			4.14		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	441.7 (A)	324.31 (A)	559.06 (A)	441.41 (A)	323.24 (A)	559.57 (A)	442.24 (A)	324.18 (A)	560.3 (A)
Poly	74.83 (B)	30.37 (B)	119.32 (B)	73.88 (B)	30.22 (B)	117.56 (B)	74.77 (B)	30.42 (B)	119.09 (B)
Mono	26.56 (C)	23.59 (B)	29.65 (C)	26.19 (C)	23.42 (B)	29.07 (C)	26.37 (C)	23.47 (B)	29.44 (C)
Mean s.e.	4.93	6.51	13.57	4.79	6.54	13.6	4.62	6.53	13.62
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	179.65 (A)	125.24 (A)	234.06 (A)	176.79 (A)	122.64 (A)	230.92 (A)	185.63 (A)	125.11 (A)	246.23 (A)
lm, np, hk	182.4 (A)	126.94 (A)	237.97 (A)	184.2 (A)	128.61 (A)	239.88 (A)	176.63 (B)	126.94 (A)	226.32 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	4.32	6.16	13.17	4.25	6.19	13.19	4.16	6.18	13.21
pval	0.5643	0.6855	0.5517	0.096	0.1597	0.1777	0.0258	0.6671	0.0028
Env. X Allele									
Spaced-ll, nn, hh	439.04 (A)	323.74 (A)	554.31 (A)	438.79 (A)	316.69 (A)	560.86 (A)	451.01 (A)	321.29 (A)	580.74 (A)
Spaced-lm, np, hk	444.35 (A)	324.88 (A)	563.82 (A)	444.04 (A)	329.8 (A)	558.27 (A)	433.46 (B)	327.07 (A)	539.85 (B)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	73.82 (B)	29.09 (B)	118.73 (B)	67.7 (B)	29.01 (B)	106.37 (B)	78.96 (C)	31.72 (B)	126.16 (C)
Poly-lm, np, hk	75.83 (B)	31.64 (B)	119.92 (B)	80.07 (B)	31.42 (B)	128.75 (B)	70.57 (C)	29.13 (B)	112.01 (C)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	26.1 (C)	22.89 (B)	29.14 (C)	23.89 (C)	22.21 (B)	25.54 (C)	26.9 (D)	22.32 (B)	31.78 (D)
Mono-lm, np, hk	27.03 (C)	24.29 (B)	30.16 (C)	28.48 (C)	24.63 (B)	32.61 (C)	25.85 (D)	24.62 (B)	27.09 (D)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	6.43	7.45	14.71	6.14	7.5	14.76	5.79	7.5	14.78
pval	0.9261	0.9892	0.8314	0.7308	0.4873	0.2972	0.2471	0.7171	0.0689
pval_Bon	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333

Appendix C7. Number of Tillers QxE Data Continued

Marker Allele Effect	TP774819 np			TP806301 hk			TP880985 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	126.17 (B)			124.82 (B)			125.62 (B)		
2017	236.17 (A)			236.91 (A)			235.38 (A)		
Mean s.e.	4.12			4.16			4.17		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	441.91 (A)	324.42 (A)	559.38 (A)	442.07 (A)	321.13 (A)	563.03 (A)	440.83 (A)	323.44 (A)	558.19 (A)
Poly	74.96 (B)	30.47 (B)	119.47 (B)	74.31 (B)	29.98 (B)	118.69 (B)	74.62 (B)	30.28 (B)	119.05 (B)
Mono	26.63 (C)	23.62 (B)	29.78 (C)	26.22 (C)	23.41 (B)	29.06 (C)	26.06 (C)	23.16 (B)	29.09 (C)
Mean s.e.	4.81	6.52	13.57	5.03	6.68	13.15	5.37	6.29	13.52
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
II, nn, hh	183.23 (A)	127.69 (A)	238.79 (A)	186.16 (A)	127.85 (AB)	244.36 (A)	176.34 (A)	120.13 (B)	232.61 (A)
Im, np, hk	179.1 (A)	124.65 (A)	233.63 (A)	178.08 (A)	130.88 (A)	225.44 (B)	184.67 (A)	131.12 (A)	238.27 (A)
kk	N/A	N/A	N/A	178.36 (A)	115.79 (B)	240.98 (AB)	N/A	N/A	N/A
Mean s.e.	4.26	6.18	13.17	5.01	6.67	13.14	4.6	5.92	13.1
pval	0.3574	0.469	0.432	0.3475	0.0262	0.0465	0.1339	0.0096	0.397
Env. X Allele									
Spaced-II, nn, hh	444.19 (A)	327.64 (A)	560.73 (A)	455.19 (A)	328.07 (A)	582.32 (A)	430.19 (B)	308.71 (B)	551.59 (A)
Spaced-Im, np, hk	439.63 (A)	321.2 (A)	558.03 (A)	437.39 (A)	338.64 (A)	536.18 (B)	451.48 (A)	338.17 (A)	564.79 (A)
Spaced-kk	N/A	N/A	N/A	433.63 (A)	296.67 (B)	570.58 (A)	N/A	N/A	N/A
Poly-II, nn, hh	77.58 (B)	32.47 (B)	122.76 (B)	76.42 (B)	31.83 (C)	121.26 (C)	74.1 (C)	28.93 (C)	119.32 (B)
Poly-Im, np, hk	72.34 (B)	28.47 (B)	116.18 (B)	70.32 (B)	29.47 (C)	111.12 (C)	75.14 (C)	31.62 (C)	118.77 (B)
Poly-kk	N/A	N/A	N/A	76.2 (B)	28.65 (C)	123.68 (C)	N/A	N/A	N/A
Mono-II, nn, hh	27.92 (C)	24.29 (B)	32.88 (C)	26.86 (C)	23.65 (C)	29.5 (D)	24.73 (D)	22.75 (C)	26.93 (C)
Mono-Im, np, hk	25.34 (C)	22.95 (B)	26.69 (C)	26.54 (C)	24.53 (C)	29.01 (D)	27.39 (D)	23.57 (C)	31.26 (C)
Mono-kk	N/A	N/A	N/A	25.24 (C)	22.06 (C)	28.67 (D)	N/A	N/A	N/A
Mean s.e.	6.18	7.46	14.71	7.96	8.84	15.94	7.21	7.28	14.7
pval	0.9692	0.7428	0.9649	0.623	0.0202	0.1809	0.2518	0.008	0.6919
pval_Bon	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333	0.003333

Appendix C8. NDF QxE Data

Effect	TP140334 hk			TP156297 np			TP186215 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	57.96 (B)			58.01 (B)			58.06 (B)		
2017	62.35 (A)			62.43 (A)			62.47 (A)		
Mean s.e.	0.19			0.19			0.19		
pval	<.0001			<.0001					
Environment									
Spaced	62.46 (A)	59.68 (A)	65.23 (A)	62.56 (A)	59.77 (A)	65.36 (A)	62.61 (A)	59.83 (A)	65.39 (A)
Poly	58.4 (C)	54.33 (B)	62.46 (B)	58.46 (C)	54.39 (B)	62.53 (B)	58.5 (C)	54.43 (B)	62.56 (B)
Mono	59.61 (B)	59.84 (A)	59.35 (C)	59.64 (B)	59.85 (A)	59.4 (C)	59.68 (B)	59.88 (A)	59.45 (C)
Mean s.e.	0.23	0.26	0.21	0.25	0.26	0.21	0.25	0.26	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	59.05 (B)	56.95 (B)	61.13 (B)	59.69 (B)	57.44 (B)	61.92 (B)	60.77 (A)	58.59 (A)	62.95 (A)
lm, np, hk	60.65 (A)	58.42 (A)	62.87 (A)	60.75 (A)	58.57 (A)	62.93 (A)	59.75 (B)	57.5 (B)	61.98 (B)
kk	60.76 (A)	58.47 (A)	63.05 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.23	0.26	0.21	0.22	0.25	0.19	0.22	0.25	0.19
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	61.2 (B)	58.35 (C)	64.05 (B)	62.01 (B)	59.11 (B)	64.9 (B)	63.15 (A)	60.44 (A)	65.87 (A)
Spaced-lm, np, hk	63.05 (A)	60.35 (A)	65.76 (A)	63.12 (A)	60.44 (A)	65.81 (A)	62.07 (B)	59.22 (C)	64.91 (B)
Spaced-kk	63.12 (A)	60.34 (A)	65.89 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	57.16 (E)	53.13 (E)	61.19 (D)	57.86 (E)	53.68 (D)	62.05 (D)	59.11 (D)	55.18 (D)	63.04 (C)
Poly-lm, np, hk	58.92 (D)	54.89 (D)	62.95 (C)	59.05 (D)	55.1 (C)	63 (C)	57.88 (E)	53.69 (E)	62.08 (D)
Poly-kk	59.11 (D)	54.97 (D)	63.25 (C)	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	58.79 (D)	59.38 (B)	58.14 (F)	59.19 (D)	59.52 (B)	58.81 (F)	60.06 (C)	60.15 (AB)	59.94 (E)
Mono-lm, np, hk	59.91 (C)	60.02 (AB)	59.78 (E)	60.09 (C)	60.18 (A)	59.99 (E)	59.31 (CD)	59.6 (BC)	58.96 (F)
Mono-kk	60.12 (C)	60.11 (AB)	60.12 (E)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.33	0.33	0.27	0.32	0.3	0.24	0.32	0.3	0.24
pval	0.6553	0.0517	0.763	0.8754	0.1103	0.694	0.6966	0.0474	0.9975
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C8. NDF QxE Data Continued

Effect	TP209546 np			TP338072 hk			TP350053 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	58.02 (B)			58.14 (B)			58.06 (B)		
2017	62.43 (A)			62.57 (A)			62.48 (A)		
Mean s.e.	0.19			0.18			0.19		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	62.57 (A)	59.79 (A)	65.36 (A)	62.69 (A)	59.91 (A)	65.47 (A)	62.63 (A)	59.85 (A)	65.42 (A)
Poly	58.46 (C)	54.39 (B)	62.53 (B)	58.6 (C)	54.54 (B)	62.67 (B)	58.47 (C)	54.4 (B)	62.53 (B)
Mono	59.65 (B)	59.86 (A)	59.4 (C)	59.78 (B)	59.96 (A)	59.57 (C)	59.72 (B)	59.91 (A)	59.5 (C)
Mean s.e.	0.25	0.26	0.21	0.22	0.26	0.21	0.23	0.26	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	60.76 (A)	58.57 (A)	62.94 (A)	61.24 (A)	59.03 (A)	63.44 (A)	59.74 (C)	57.59 (B)	61.89 (C)
lm, np, hk	59.69 (B)	57.45 (B)	61.92 (B)	60.32 (B)	58.14 (B)	62.48 (B)	60.3 (B)	58.15 (A)	62.45 (B)
kk	N/A	N/A	N/A	59.51 (C)	57.23 (C)	61.78 (C)	60.77 (A)	58.42 (A)	63.11 (A)
Mean s.e.	0.22	0.25	0.19	0.22	0.26	0.2	0.23	0.26	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0005	<.0001
Env. X Allele									
Spaced-ll, nn, hh	63.12 (A)	60.42 (A)	65.82 (A)	63.5 (A)	60.71 (A)	66.29 (A)	62.16 (B)	59.39 (B)	64.93 (B)
Spaced-lm, np, hk	62.02 (B)	59.15 (B)	64.9 (B)	62.71 (A)	59.97 (B)	65.44 (B)	62.6 (AB)	59.88 (AB)	65.32 (B)
Spaced-kk	N/A	N/A	N/A	61.85 (B)	59.03 (C)	64.67 (C)	63.14 (A)	60.29 (A)	66 (A)
Poly-ll, nn, hh	59.07 (D)	55.12 (C)	63.02 (C)	59.27 (DE)	55.39 (D)	63.16 (D)	57.55 (E)	53.48 (D)	61.62 (E)
Poly-lm, np, hk	57.85 (E)	53.66 (D)	62.04 (D)	58.45 (EF)	54.49 (E)	62.42 (E)	58.67 (D)	54.68 (C)	62.66 (D)
Poly-kk	N/A	N/A	N/A	58.08 (F)	53.74 (F)	62.42 (E)	59.18 (CD)	55.05 (C)	63.31 (C)
Mono-ll, nn, hh	60.09 (C)	60.16 (A)	59.99 (E)	60.95 (C)	60.98 (A)	60.87 (F)	59.51 (C)	59.89 (AB)	59.11 (G)
Mono-lm, np, hk	59.21 (D)	59.55 (B)	58.81 (F)	59.79 (D)	59.97 (B)	59.59 (G)	59.65 (C)	59.9 (AB)	59.37 (G)
Mono-kk	N/A	N/A	N/A	58.6 (EF)	58.93 (C)	58.25 (H)	59.99 (C)	59.94 (AB)	60.02 (F)
Mean s.e.	0.32	0.3	0.24	0.33	0.33	0.27	0.33	0.33	0.27
pval	0.838	0.0782	0.7221	0.4248	0.9221	0.001	0.3536	0.0605	0.3541
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C8. NDF QxE Data Continued

Effect	TP371172 np			TP444498 hk			TP487284 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	58.02 (B)			58.13 (B)			58.02 (B)		
2017	62.41 (A)			62.56 (A)			62.41 (A)		
Mean s.e.	0.2			0.18			0.18		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	62.58 (A)	59.8 (A)	65.36 (A)	62.68 (A)	59.9 (A)	65.46 (A)	62.56 (A)	59.79 (A)	65.34 (A)
Poly	58.46 (C)	54.4 (B)	62.52 (B)	58.6 (C)	54.54 (B)	62.66 (B)	58.49 (C)	54.43 (B)	62.55 (B)
Mono	59.62 (B)	59.85 (A)	59.36 (C)	59.76 (B)	59.94 (A)	59.55 (C)	59.58 (B)	59.81 (A)	59.33 (C)
Mean s.e.	0.25	0.26	0.21	0.22	0.26	0.21	0.24	0.24	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	59.54 (B)	57.41 (B)	61.66 (B)	61.22 (A)	58.99 (A)	63.44 (A)	59.51 (B)	57.41 (B)	61.6 (B)
lm, np, hk	60.9 (A)	58.62 (A)	63.17 (A)	60.34 (B)	58.15 (B)	62.51 (B)	60.91 (A)	58.61 (A)	63.21 (A)
kk	N/A	N/A	N/A	59.48 (C)	57.23 (C)	61.72 (C)	N/A	N/A	N/A
Mean s.e.	0.22	0.24	0.2	0.22	0.26	0.21	0.21	0.23	0.2
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	61.99 (B)	59.17 (B)	64.8 (B)	63.52 (A)	60.75 (A)	66.29 (A)	61.93 (B)	59.15 (B)	64.7 (B)
Spaced-lm, np, hk	63.18 (A)	60.43 (A)	65.93 (A)	62.72 (B)	59.97 (B)	65.47 (B)	63.2 (A)	60.43 (A)	65.98 (A)
Spaced-kk	N/A	N/A	N/A	61.81 (C)	59 (C)	64.62 (C)	N/A	N/A	N/A
Poly-ll, nn, hh	57.71 (E)	53.62 (D)	61.79 (D)	59.27 (EF)	55.38 (D)	63.16 (D)	57.77 (E)	53.7 (D)	61.83 (D)
Poly-lm, np, hk	59.21 (D)	55.18 (C)	63.26 (C)	58.49 (FG)	54.51 (E)	62.48 (E)	59.2 (D)	55.15 (C)	63.26 (C)
Poly-kk	N/A	N/A	N/A	58.03 (G)	53.72 (F)	62.33 (E)	N/A	N/A	N/A
Mono-ll, nn, hh	58.94 (D)	59.44 (B)	58.4 (F)	60.87 (D)	60.84 (A)	60.87 (F)	58.84 (D)	59.38 (B)	58.27 (F)
Mono-lm, np, hk	60.3 (C)	60.25 (A)	60.32 (E)	59.8 (E)	59.99 (B)	59.59 (G)	60.33 (C)	60.24 (A)	60.38 (E)
Mono-kk	N/A	N/A	N/A	58.61 (FG)	58.98 (C)	58.21 (H)	N/A	N/A	N/A
Mean s.e.	0.32	0.29	0.24	0.33	0.33	0.27	0.32	0.28	0.24
pval	0.8536	0.1594	0.0582	0.5241	0.9891	0.002	0.9346	0.3329	0.0383
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C8. NDF QxE Data Continued

Effect	TP489803 hk			TP530755 hk			TP763986 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	58.05 (B)			58.01 (B)			58.13 (B)		
2017	62.44 (A)			62.37 (A)			62.53 (A)		
Mean s.e.	0.19			0.2			0.19		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	62.62 (A)	59.86 (A)	65.38 (A)	62.57 (A)	59.81 (A)	65.33 (A)	62.68 (A)	59.9 (A)	65.45 (A)
Poly	58.5 (C)	54.44 (B)	62.57 (B)	58.41 (C)	54.36 (B)	62.47 (B)	58.56 (C)	54.51 (B)	62.61 (B)
Mono	59.62 (B)	59.84 (A)	59.38 (C)	59.6 (B)	59.83 (A)	59.33 (C)	59.76 (B)	59.96 (A)	59.54 (C)
Mean s.e.	0.23	0.26	0.21	0.24	0.27	0.21	0.25	0.26	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	61.09 (A)	58.98 (A)	63.2 (A)	59.96 (B)	57.89 (B)	62.01 (B)	60.75 (A)	58.51 (A)	62.97 (A)
lm, np, hk	60.32 (B)	58.07 (B)	62.56 (B)	60.6 (A)	58.35 (A)	62.84 (A)	59.92 (B)	57.74 (B)	62.09 (B)
kk	59.33 (C)	57.09 (C)	61.57 (C)	60.02 (B)	57.76 (B)	62.27 (B)	N/A	N/A	N/A
Mean s.e.	0.23	0.26	0.21	0.24	0.27	0.22	0.22	0.25	0.19
pval	<.0001	<.0001	<.0001	0.0125	0.0036	<.0001	0.0004	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	63.55 (A)	61 (A)	66.11 (A)	62.37 (A)	59.71 (AB)	65.03 (B)	63.1 (A)	60.28 (A)	65.92 (A)
Spaced-lm, np, hk	62.61 (B)	59.8 (C)	65.43 (B)	62.89 (A)	60.07 (A)	65.7 (A)	62.26 (B)	59.52 (B)	64.99 (B)
Spaced-kk	61.69 (C)	58.77 (D)	64.62 (C)	62.45 (A)	59.65 (AB)	65.25 (AB)	N/A	N/A	N/A
Poly-ll, nn, hh	59.2 (EF)	55.4 (E)	63 (D)	57.99 (E)	53.92 (D)	62.06 (D)	58.71 (D)	54.72 (C)	62.7 (C)
Poly-lm, np, hk	58.55 (F)	54.48 (F)	62.63 (DE)	58.93 (CD)	54.86 (C)	63 (C)	58.41 (D)	54.31 (C)	62.52 (C)
Poly-kk	57.75 (G)	53.43 (G)	62.08 (E)	58.32 (DE)	54.3 (CD)	62.34 (D)	N/A	N/A	N/A
Mono-ll, nn, hh	60.52 (D)	60.53 (AB)	60.5 (F)	59.51 (BC)	60.03 (AB)	58.94 (F)	60.44 (C)	60.54 (A)	60.3 (D)
Mono-lm, np, hk	59.78 (DE)	59.92 (BC)	59.6 (G)	59.99 (B)	60.13 (A)	59.83 (E)	59.09 (D)	59.37 (B)	58.77 (E)
Mono-kk	58.56 (FG)	59.08 (D)	58.03 (H)	59.29 (BC)	59.33 (B)	59.22 (F)	N/A	N/A	N/A
Mean s.e.	0.33	0.33	0.27	0.35	0.34	0.28	0.32	0.29	0.24
pval	0.8893	0.6479	0.0264	0.8946	0.3499	0.9713	0.1852	0.1626	0.0003
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C8. NDF QxE Data Continued

Effect	TP801758 lm			TP811840 hk			TP9425 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	58.09 (B)			58.05 (B)			58.25 (B)		
2017	62.5 (A)			62.43 (A)			62.61 (A)		
Mean s.e.	0.2			0.2			0.19		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	62.66 (A)	59.91 (A)	65.4 (A)	62.6 (A)	59.83 (A)	65.36 (A)	62.78 (A)	60.03 (A)	65.53 (A)
Poly	58.51 (C)	54.45 (B)	62.57 (B)	58.4 (C)	54.38 (B)	62.43 (B)	58.7 (C)	54.7 (B)	62.7 (B)
Mono	59.72 (B)	59.89 (A)	59.53 (C)	59.72 (B)	59.9 (A)	59.5 (C)	59.82 (B)	59.99 (A)	59.61 (C)
Mean s.e.	0.27	0.27	0.21	0.24	0.26	0.22	0.23	0.27	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	59.84 (B)	57.62 (B)	62.04 (B)	60.27 (AB)	58.25 (A)	62.29 (B)	60.72 (A)	58.54 (A)	62.9 (A)
lm, np, hk	60.75 (A)	58.54 (A)	62.96 (A)	60.54 (A)	58.33 (A)	62.74 (A)	60.02 (B)	57.78 (B)	62.26 (B)
kk	N/A	N/A	N/A	59.91 (B)	57.54 (B)	62.27 (B)	60.56 (A)	58.41 (A)	62.69 (A)
Mean s.e.	0.23	0.25	0.19	0.24	0.26	0.21	0.23	0.27	0.21
pval	0.0004	<.0001	<.0001	0.0324	<.0001	0.0045	0.0058	<.0001	0.0005
Env. X Allele									
Spaced-ll, nn, hh	62.15 (B)	60.62 (A)	65.09 (B)	62.66 (A)	59.94 (AB)	65.37 (AB)	63.16 (A)	60.36 (A)	65.96 (A)
Spaced-lm, np, hk	63.17 (A)	59.2 (B)	65.71 (A)	62.89 (A)	60.07 (AB)	65.7 (A)	62.37 (B)	59.56 (B)	65.18 (B)
Spaced-kk	N/A	N/A	N/A	62.25 (A)	59.49 (B)	65.02 (B)	62.81 (AB)	60.17 (AB)	65.45 (AB)
Poly-ll, nn, hh	58.16 (E)	54.11 (D)	62.21 (D)	58.29 (DE)	54.53 (C)	62.04 (D)	58.92 (EF)	54.94 (C)	62.9 (C)
Poly-lm, np, hk	58.85 (DE)	54.79 (C)	62.93 (C)	59.01 (CD)	54.95 (C)	63.07 (C)	58.15 (F)	53.99 (D)	62.33 (C)
Poly-kk	N/A	N/A	N/A	57.92 (E)	53.64 (D)	62.19 (D)	59.02 (DE)	55.18 (C)	62.86 (C)
Mono-ll, nn, hh	59.2 (D)	59.56 (B)	58.81 (F)	59.87 (B)	60.26 (A)	59.47 (E)	60.09 (C)	60.3 (A)	59.83 (D)
Mono-lm, np, hk	60.24 (C)	60.22 (A)	60.24 (E)	59.71 (BC)	59.96 (AB)	59.44 (E)	59.54 (CDE)	59.79 (AB)	59.27 (D)
Mono-kk	N/A	N/A	N/A	59.57 (BC)	59.5 (AB)	59.6 (E)	59.84 (CD)	59.89 (AB)	59.74 (D)
Mean s.e.	0.35	0.31	0.25	0.34	0.33	0.28	0.33	0.34	0.28
pval	0.832	0.1296	0.0705	0.5057	0.2895	0.0302	0.8664	0.2693	0.8883
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C9. NDFD QxE Data

Effect	TP129822 hk			TP196229 np			TP238848 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	50.95 (B)			51.11 (B)			51.3 (B)		
2017	53.12 (A)			53.29 (A)			53.42 (A)		
Mean s.e.	0.15			0.13			0.13		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	50.12 (C)	48.82 (C)	51.41 (B)	50.19 (C)	48.9 (C)	51.48 (B)	50.39 (C)	49.15 (C)	51.63 (B)
Poly	52.03 (B)	50.09 (B)	53.97 (A)	52.15 (B)	50.22 (B)	54.08 (A)	52.33 (B)	50.39 (B)	54.27 (A)
Mono	53.96 (A)	53.92 (A)	53.99 (A)	54.27 (A)	54.21 (A)	54.31 (A)	54.36 (A)	54.34 (A)	54.36 (A)
Mean s.e.	0.16	0.24	0.32	0.15	0.24	0.32	0.15	0.24	0.32
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	51.62 (B)	50.58 (B)	52.65 (B)	51.66 (B)	50.61 (B)	52.7 (B)	52.13 (B)	51.1 (B)	53.16 (B)
lm, np, hk	52.66 (A)	51.58 (A)	53.74 (A)	52.74 (A)	51.6 (A)	53.88 (A)	51.78 (C)	50.59 (C)	52.97 (B)
kk	51.82 (B)	50.66 (B)	52.98 (B)	N/A	N/A	N/A	53.16 (A)	52.19 (A)	54.12 (A)
Mean s.e.	0.16	0.24	0.32	0.14	0.22	0.31	0.15	0.24	0.33
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	49.94 (F)	48.58 (E)	51.29 (D)	49.7 (F)	48.26 (E)	51.13 (E)	50.27 (F)	49.13 (E)	51.41 (D)
Spaced-lm, np, hk	50.5 (E)	49.26 (DE)	51.73 (D)	50.68 (E)	49.53 (D)	51.82 (D)	49.65 (G)	48.13 (F)	51.17 (D)
Spaced-kk	49.91 (F)	48.6 (E)	51.22 (D)	N/A	N/A	N/A	51.24 (E)	50.19 (D)	52.3 (C)
Poly-ll, nn, hh	51.58 (D)	49.66 (D)	53.49 (C)	51.84 (D)	50.01 (CD)	53.66 (C)	52.14 (D)	50.21 (D)	54.07 (B)
Poly-lm, np, hk	52.56 (C)	50.59 (C)	54.52 (AB)	52.46 (C)	50.43 (C)	54.49 (B)	51.77 (DE)	49.87 (D)	53.67 (B)
Poly-kk	51.96 (D)	50.02 (CD)	53.9 (BC)	N/A	N/A	N/A	53.09 (C)	51.1 (C)	55.07 (A)
Mono-ll, nn, hh	53.35 (B)	53.51 (B)	53.18 (C)	53.44 (B)	53.57 (B)	53.29 (C)	53.99 (B)	53.96 (B)	54.01 (B)
Mono-lm, np, hk	54.93 (A)	54.88 (A)	54.97 (A)	55.1 (A)	54.84 (A)	55.33 (A)	53.92 (B)	53.75 (B)	54.07 (B)
Mono-kk	53.59 (B)	53.36 (B)	53.82 (C)	N/A	N/A	N/A	55.16 (A)	55.3 (A)	55 (A)
Mean s.e.	0.21	0.34	0.38	0.19	0.28	0.34	0.22	0.33	0.38
pval	0.0047	0.4096	0.0613	0.0086	0.084	0.0004	0.6627	0.4018	0.8183
pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

Effect	TP301824 hk			TP3486 np			TP44922 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	51.3 (B)			51.11 (B)			51.23 (B)		
2017	53.48 (A)			53.29 (A)			53.42 (A)		
Mean s.e.	0.16			0.14			0.13		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	50.37 (C)	49.14 (C)	51.59 (B)	50.21 (C)	48.9 (C)	51.51 (B)	50.31 (C)	49.03 (C)	51.6 (B)
Poly	52.22 (B)	50.2 (B)	54.23 (A)	52.18 (B)	50.24 (B)	54.11 (A)	52.22 (B)	50.25 (B)	54.19 (A)
Mono	54.59 (A)	54.54 (A)	54.63 (A)	54.21 (A)	54.16 (A)	54.26 (A)	54.43 (A)	54.39 (A)	54.46 (A)
Mean s.e.	0.17	0.25	0.34	0.14	0.24	0.32	0.14	0.23	0.33
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	53.25 (A)	52.01 (A)	54.5 (A)	51.47 (B)	50.41 (B)	52.52 (B)	51.38 (C)	50.28 (C)	52.47 (C)
lm, np, hk	51.9 (B)	50.88 (B)	52.91 (B)	52.93 (A)	51.79 (A)	54.06 (A)	52.19 (B)	51.1 (B)	53.28 (B)
kk	52.02 (B)	50.98 (B)	53.05 (B)	N/A	N/A	N/A	53.39 (A)	52.28 (A)	54.5 (A)
Mean s.e.	0.17	0.25	0.34	0.14	0.23	0.31	0.14	0.23	0.33
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	51.23 (F)	50.21 (C)	52.26 (D)	49.46 (F)	48.12 (E)	50.79 (D)	49.45 (G)	47.99 (G)	50.91 (E)
Spaced-lm, np, hk	49.94 (G)	48.62 (D)	51.26 (E)	50.96 (E)	49.69 (D)	52.23 (C)	50.21 (F)	48.94 (F)	51.46 (E)
Spaced-kk	49.92 (G)	48.59 (D)	51.26 (E)	N/A	N/A	N/A	51.28 (E)	50.14 (DE)	52.43 (D)
Poly-ll, nn, hh	52.64 (D)	50.34 (C)	54.93 (B)	51.38 (D)	49.37 (D)	53.38 (B)	51.25 (E)	49.24 (EF)	53.27 (C)
Poly-lm, np, hk	52.09 (E)	50.33 (C)	53.84 (C)	52.98 (C)	51.11 (C)	54.85 (A)	52.23 (D)	50.31 (D)	54.15 (B)
Poly-kk	51.93 (E)	49.94 (C)	53.92 (C)	N/A	N/A	N/A	53.18 (C)	51.19 (C)	55.17 (A)
Mono-ll, nn, hh	55.9 (A)	55.49 (A)	56.3 (A)	53.58 (B)	53.75 (B)	53.4 (B)	53.43 (C)	53.62 (B)	53.23 (C)
Mono-lm, np, hk	53.67 (C)	53.7 (B)	53.64 (C)	54.85 (A)	54.57 (A)	55.11 (A)	54.14 (B)	54.06 (B)	54.23 (B)
Mono-kk	54.2 (B)	54.42 (B)	53.96 (C)	N/A	N/A	N/A	55.72 (A)	55.5 (A)	55.91 (A)
Mean s.e.	0.22	0.35	0.4	0.16	0.29	0.34	0.2	0.33	0.39
pval	0.0003	0.01	0.0078	0.3442	0.1047	0.7136	0.4454	0.7323	0.3193
pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

Effect	TP532204			TP581871			TP583925		
	AY	np 2016	2017	AY	np 2016	2017	AY	np 2016	2017
Year									
2016	51.1 (B)			51.08 (B)			51.17 (B)		
2017	53.26 (A)			53.26 (A)			53.36 (A)		
Mean s.e.	0.14			0.13			0.14		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	50.16 (C)	48.87 (C)	51.44 (B)	50.16 (C)	48.89 (C)	51.43 (B)	50.25 (C)	48.96 (C)	51.54 (B)
Poly	52.14 (B)	50.2 (B)	54.09 (A)	52.13 (B)	50.19 (B)	54.07 (A)	52.19 (B)	50.23 (B)	54.15 (A)
Mono	54.23 (A)	54.2 (A)	54.25 (A)	54.22 (A)	54.15 (A)	54.28 (A)	54.35 (A)	54.3 (A)	54.39 (A)
Mean s.e.	0.14	0.23	0.32	0.14	0.21	0.31	0.16	0.22	0.32
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	51.5 (B)	50.47 (B)	52.53 (B)	51.47 (B)	50.4 (B)	52.53 (B)	52.62 (A)	51.42 (A)	53.81 (A)
lm, np, hk	52.85 (A)	51.71 (A)	53.99 (A)	52.87 (A)	51.75 (A)	53.99 (A)	51.91 (B)	50.91 (B)	52.91 (B)
kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.13	0.21	0.31	0.13	0.19	0.3	0.14	0.2	0.31
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0054	<.0001
Env. X Allele									
Spaced-ll, nn, hh	49.37 (F)	48 (D)	50.74 (D)	49.42 (F)	48.07 (E)	50.76 (D)	50.54 (D)	49.27 (D)	51.81 (D)
Spaced-lm, np, hk	50.95 (E)	49.74 (C)	52.15 (C)	50.91 (E)	49.71 (D)	52.1 (C)	49.97 (E)	48.66 (E)	51.27 (E)
Spaced-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	51.39 (D)	49.41 (C)	53.36 (B)	51.32 (D)	49.32 (D)	53.31 (B)	52.23 (C)	50.13 (C)	54.34 (B)
Poly-lm, np, hk	52.9 (C)	50.99 (B)	54.81 (A)	52.95 (C)	51.06 (C)	54.83 (A)	52.15 (C)	50.34 (C)	53.96 (BC)
Poly-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	53.75 (B)	54 (A)	53.5 (B)	53.67 (B)	53.82 (B)	53.51 (B)	55.09 (A)	54.88 (A)	55.28 (A)
Mono-lm, np, hk	54.71 (A)	54.41 (A)	54.99 (A)	54.77 (A)	54.49 (A)	55.05 (A)	53.62 (B)	53.73 (B)	53.5 (C)
Mono-kk	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.17	0.28	0.35	0.17	0.26	0.34	0.19	0.27	0.35
pval	0.0226	0.0053	0.9785	0.0996	0.0317	0.8513	<.0001	0.0109	0.0004
pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

Effect	TP609278 hk			TP618775 hk			TP697306 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	51.17 (B)			51.18 (B)			51.13 (B)		
2017	53.29 (A)			53.38 (A)			53.28 (A)		
Mean s.e.	0.15			0.14			0.14		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	50.27 (C)	48.99 (C)	51.55 (B)	50.29 (C)	49 (C)	51.57 (B)	50.19 (C)	48.94 (C)	51.44 (B)
Poly	52.08 (B)	50.16 (B)	54.01 (A)	52.29 (B)	50.39 (B)	54.18 (A)	52.19 (B)	50.23 (B)	54.15 (A)
Mono	54.33 (A)	54.34 (A)	54.31 (A)	54.27 (A)	54.12 (A)	54.4 (A)	54.23 (A)	54.2 (A)	54.26 (A)
Mean s.e.	0.17	0.27	0.33	0.16	0.24	0.33	0.15	0.23	0.33
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	51.47 (B)	50.4 (B)	52.54 (B)	51.43 (C)	50.42 (C)	52.44 (C)	51.33 (C)	50.39 (B)	52.27 (C)
lm, np, hk	52.61 (A)	51.44 (A)	53.78 (A)	52.27 (B)	51.2 (B)	53.33 (B)	52.36 (B)	51.28 (A)	53.43 (B)
kk	52.6 (A)	51.65 (A)	53.55 (A)	53.15 (A)	51.89 (A)	54.39 (A)	52.93 (A)	51.7 (A)	54.15 (A)
Mean s.e.	0.17	0.27	0.33	0.16	0.24	0.33	0.15	0.23	0.33
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	49.59 (E)	48.28 (D)	50.9 (D)	49.36 (G)	48.06 (F)	50.65 (E)	49.19 (F)	48.1 (F)	50.29 (G)
Spaced-lm, np, hk	50.67 (D)	49.32 (C)	52.02 (C)	50.25 (F)	48.96 (E)	51.54 (D)	50.34 (E)	49.01 (E)	51.66 (F)
Spaced-kk	50.55 (D)	49.37 (C)	51.72 (CD)	51.26 (E)	49.98 (D)	52.54 (C)	51.05 (D)	49.72 (DE)	52.38 (E)
Poly-ll, nn, hh	51.09 (D)	48.86 (CD)	53.33 (B)	51.64 (DE)	49.95 (D)	53.33 (C)	51.49 (D)	49.6 (E)	53.39 (D)
Poly-lm, np, hk	52.67 (C)	50.72 (B)	54.62 (A)	52.12 (D)	50.12 (D)	54.13 (B)	52.26 (C)	50.37 (CD)	54.15 (C)
Poly-kk	52.48 (C)	50.9 (B)	54.07 (AB)	53.1 (C)	51.11 (C)	55.1 (A)	52.82 (B)	50.72 (C)	54.92 (AB)
Mono-ll, nn, hh	53.72 (B)	54.05 (A)	53.38 (B)	53.29 (C)	53.26 (B)	53.33 (C)	53.31 (B)	53.49 (B)	53.13 (DE)
Mono-lm, np, hk	54.5 (A)	54.28 (A)	54.69 (A)	54.44 (B)	54.53 (A)	54.33 (B)	54.48 (A)	54.45 (A)	54.5 (BC)
Mono-kk	54.78 (A)	54.68 (A)	54.87 (A)	55.08 (A)	54.58 (A)	55.54 (A)	54.91 (A)	54.67 (A)	55.15 (A)
Mean s.e.	0.26	0.38	0.4	0.23	0.35	0.39	0.2	0.33	0.39
pval	0.4235	0.1334	0.6655	0.4044	0.1777	0.9657	0.5595	0.8935	0.6639
pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

Effect	TP710222 hk			TP733301 hk			TP746301 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	51.16 (B)			51.23 (B)			51.22 (B)		
2017	53.32 (A)			53.31 (A)			53.35 (A)		
Mean s.e.	0.13			0.12			0.14		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	50.21 (C)	48.94 (C)	51.48 (B)	50.28 (C)	49.02 (C)	51.53 (B)	50.33 (C)	49.07 (C)	51.59 (B)
Poly	52.22 (B)	50.28 (B)	54.17 (A)	52.27 (B)	50.39 (B)	54.16 (A)	52.29 (B)	50.35 (B)	54.22 (A)
Mono	54.28 (A)	54.23 (A)	54.33 (A)	54.25 (A)	54.25 (A)	54.24 (A)	54.24 (A)	54.23 (A)	54.25 (A)
Mean s.e.	0.14	0.24	0.32	0.14	0.24	0.31	0.15	0.23	0.32
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	53.06 (A)	51.95 (A)	54.16 (A)	51.59 (C)	50.6 (B)	52.58 (C)	53.17 (A)	52.07 (A)	54.26 (A)
lm, np, hk	52.15 (B)	51.06 (B)	53.23 (B)	52.18 (B)	50.97 (B)	53.39 (B)	52.01 (B)	50.87 (B)	53.14 (B)
kk	51.51 (C)	50.43 (C)	52.59 (C)	53.03 (A)	52.08 (A)	53.96 (A)	51.68 (C)	50.71 (B)	52.65 (C)
Mean s.e.	0.14	0.24	0.32	0.14	0.24	0.3	0.15	0.23	0.32
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	51.08 (F)	49.83 (D)	52.32 (C)	49.75 (E)	48.57 (E)	50.93 (F)	51.37 (E)	50.12 (C)	52.62 (E)
Spaced-lm, np, hk	50.2 (G)	48.88 (E)	51.53 (D)	50.06 (E)	48.53 (E)	51.59 (E)	49.89 (F)	48.54 (D)	51.24 (F)
Spaced-kk	49.36 (H)	48.12 (F)	50.59 (E)	51.02 (D)	49.96 (D)	52.08 (E)	49.73 (F)	48.56 (D)	50.89 (F)
Poly-ll, nn, hh	52.99 (D)	51.15 (C)	54.84 (A)	51.52 (CD)	49.55 (D)	53.49 (CD)	53.33 (C)	51.43 (B)	55.24 (A)
Poly-lm, np, hk	52.11 (E)	50.2 (D)	54.02 (B)	52.03 (C)	50.04 (D)	54.03 (BC)	51.91 (D)	49.98 (C)	53.84 (CD)
Poly-kk	51.58 (F)	49.49 (DE)	53.66 (B)	53.27 (B)	51.58 (C)	54.95 (A)	51.62 (DE)	49.64 (C)	53.59 (D)
Mono-ll, nn, hh	55.11 (A)	54.89 (A)	55.32 (A)	53.51 (B)	53.69 (B)	53.32 (D)	54.81 (A)	54.66 (A)	54.93 (AB)
Mono-lm, np, hk	54.13 (B)	54.12 (AB)	54.15 (B)	54.45 (A)	54.34 (AB)	54.55 (AB)	54.22 (B)	54.1 (A)	54.34 (BC)
Mono-kk	53.6 (C)	53.68 (B)	53.52 (B)	54.79 (A)	54.71 (A)	54.86 (A)	53.7 (C)	53.94 (A)	53.46 (D)
Mean s.e.	0.2	0.34	0.38	0.22	0.34	0.37	0.21	0.33	0.38
pval	0.8577	0.9501	0.6583	0.1531	0.1868	0.4733	0.0879	0.2955	0.301
pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

		TP783591			TP78757		
		lm			hk		
Effect		AY	2016	2017	AY	2016	2017
<u>Year</u>							
	2016	51.09 (B)			51.14 (B)		
	2017	53.26 (A)			53.29 (A)		
	Mean s.e.	0.13			0.15		
	pval	<.0001			<.0001		
<u>Environment</u>							
	Spaced	50.19 (C)	48.92 (C)	51.47 (B)	50.23 (C)	48.98 (C)	51.49 (B)
	Poly	52.16 (B)	50.2 (B)	54.12 (A)	52.21 (B)	50.28 (B)	54.14 (A)
	Mono	54.17 (A)	54.13 (A)	54.21 (A)	54.2 (A)	54.14 (A)	54.25 (A)
	Mean s.e.	0.14	0.23	0.31	0.16	0.25	0.34
	pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
<u>Allele</u>							
	ll, nn, hh	51.78 (B)	50.56 (B)	53.01 (B)	51.85 (B)	50.86 (B)	52.83 (B)
	lm, np, hk	52.57 (A)	51.6 (A)	53.52 (A)	52.08 (B)	50.99 (B)	53.17 (B)
	kk	N/A	N/A	N/A	52.71 (A)	51.55 (A)	53.87 (A)
	Mean s.e.	0.13	0.21	0.3	0.16	0.24	0.34
	pval	<.0001	<.0001	0.0013	<.0001	0.0136	<.0001
<u>Env. X Allele</u>							
	Spaced-ll, nn, hh	49.88 (F)	48.53 (E)	51.22 (C)	49.8 (E)	48.64 (C)	50.96 (E)
	Spaced-lm, np, hk	50.51 (E)	49.3 (D)	51.71 (C)	49.99 (E)	48.62 (C)	51.36 (E)
	Spaced-kk	N/A	N/A	N/A	50.91 (D)	49.69 (B)	52.13 (D)
	Poly-ll, nn, hh	51.69 (D)	49.47 (D)	53.92 (B)	52.06 (C)	50.18 (B)	53.95 (BC)
	Poly-lm, np, hk	52.62 (C)	50.92 (C)	54.32 (AB)	52.09 (C)	50.16 (B)	54.02 (BC)
	Poly-kk	N/A	N/A	N/A	52.46 (C)	50.49 (B)	54.44 (AB)
	Mono-ll, nn, hh	53.77 (B)	53.67 (B)	53.87 (B)	53.68 (B)	53.76 (A)	53.59 (C)
	Mono-lm, np, hk	54.57 (A)	54.59 (A)	54.54 (A)	54.15 (B)	54.18 (A)	54.12 (BC)
	Mono-kk	N/A	N/A	N/A	54.77 (A)	54.48 (A)	55.05 (A)
	Mean s.e.	0.17	0.28	0.34	0.22	0.35	0.4
	pval	0.559	0.2814	0.797	0.2598	0.4926	0.5756
	pval_Bon	0.0026	0.0026	0.0026	0.0026	0.0026	0.0026

Appendix C9. NDFD QxE Data Continued

		TP793636				TP894003			
Effect		hk				hk			
		AY	2016	2017		AY	2016	2017	
<u>Year</u>									
	2016	51.27 (B)				51.31 (B)			
	2017	53.39 (A)				53.49 (A)			
	Mean s.e.	0.14				0.14			
	pval	<.0001				<.0001			
<u>Environment</u>									
	Spaced	50.37 (C)	49.12 (C)	51.61 (B)		50.44 (C)	49.21 (C)	51.68 (B)	
	Poly	52.31 (B)	50.36 (B)	54.26 (A)		52.35 (B)	50.39 (B)	54.32 (A)	
	Mono	54.32 (A)	54.31 (A)	54.33 (A)		54.41 (A)	54.32 (A)	54.48 (A)	
	Mean s.e.	0.15	0.23	0.33		0.16	0.25	0.32	
	pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
<u>Allele</u>									
	ll, nn, hh	53.17 (A)	52.09 (A)	54.24 (A)		53.18 (A)	52.22 (A)	54.13 (A)	
	lm, np, hk	51.87 (B)	50.73 (B)	53.02 (B)		51.77 (C)	50.56 (C)	52.98 (C)	
	kk	51.95 (B)	50.97 (B)	52.93 (B)		52.25 (B)	51.13 (B)	53.36 (B)	
	Mean s.e.	0.15	0.23	0.33		0.16	0.25	0.32	
	pval	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	
<u>Env. X Allele</u>									
	Spaced-ll, nn, hh	51.42 (D)	50.25 (D)	52.59 (C)		51.3 (E)	50.28 (D)	52.32 (D)	
	Spaced-lm, np, hk	49.73 (E)	48.35 (E)	51.11 (D)		49.58 (G)	48.02 (F)	51.13 (E)	
	Spaced-kk	49.95 (E)	48.76 (E)	51.13 (D)		50.45 (F)	49.32 (E)	51.58 (DE)	
	Poly-ll, nn, hh	53.25 (C)	51.28 (C)	55.21 (A)		53.17 (C)	51.24 (C)	55.11 (A)	
	Poly-lm, np, hk	51.84 (D)	49.92 (D)	53.75 (B)		51.79 (DE)	49.91 (DE)	53.69 (C)	
	Poly-kk	51.83 (D)	49.87 (D)	53.8 (B)		52.09 (D)	50.03 (DE)	54.16 (BC)	
	Mono-ll, nn, hh	54.85 (A)	54.74 (A)	54.93 (A)		55.07 (A)	55.15 (A)	54.97 (A)	
	Mono-lm, np, hk	54.05 (B)	53.9 (B)	54.19 (B)		53.94 (B)	53.76 (B)	54.11 (BC)	
	Mono-kk	54.07 (B)	54.28 (AB)	53.87 (B)		54.22 (B)	54.06 (B)	54.36 (AB)	
	Mean s.e.	0.2	0.32	0.38		0.24	0.34	0.38	
	pval	0.0789	0.2585	0.4797		0.5004	0.1434	0.8478	
	pval_Bon	0.0026	0.0026	0.0026		0.0026	0.0026	0.0026	

Appendix C10. NFC QxE Data

Effect	TP17432 lm			TP203135 hk			TP352410 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	28.24 (A)			28.2 (A)			28.23 (A)		
2017	25 (B)			24.95 (B)			25 (B)		
Mean s.e.	0.11			0.1			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	24.98 (C)	26.79 (C)	23.18 (B)	24.94 (C)	26.73 (C)	23.14 (B)	24.96 (C)	26.75 (C)	23.16 (B)
Poly	25.93 (B)	28.61 (B)	23.23 (B)	25.89 (B)	28.57 (B)	23.2 (B)	25.92 (B)	28.61 (B)	23.22 (B)
Mono	28.95 (A)	29.31 (A)	28.6 (A)	28.89 (A)	29.28 (A)	28.51 (A)	28.96 (A)	29.32 (A)	28.61 (A)
Mean s.e.	0.18	0.17	0.13	0.15	0.17	0.13	0.18	0.16	0.12
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	27.11 (A)	28.7 (A)	25.52 (A)	25.69 (C)	27.22 (C)	24.15 (C)	27.09 (A)	28.7 (A)	25.47 (A)
lm, np, hk	26.13 (B)	27.77 (B)	24.48 (B)	26.56 (B)	28.18 (B)	24.93 (B)	26.14 (B)	27.75 (B)	24.52 (B)
kk	N/A	N/A	N/A	27.47 (A)	29.18 (A)	25.77 (A)	N/A	N/A	N/A
Mean s.e.	0.15	0.15	0.11	0.15	0.17	0.13	0.14	0.15	0.11
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	25.47 (D)	27.29 (D)	23.66 (C)	23.98 (G)	25.66 (F)	22.31 (G)	25.32 (D)	27.08 (D)	23.55 (C)
Spaced-lm, np, hk	24.49 (E)	26.29 (E)	22.7 (D)	24.92 (F)	26.73 (E)	23.11 (EF)	24.6 (E)	26.42 (E)	22.78 (D)
Spaced-kk	N/A	N/A	N/A	25.9 (E)	27.81 (D)	24 (D)	N/A	N/A	N/A
Poly-ll, nn, hh	26.26 (C)	28.93 (B)	23.56 (C)	25.08 (F)	27.47 (D)	22.68 (FG)	26.44 (C)	29.29 (AB)	23.58 (C)
Poly-lm, np, hk	25.6 (CD)	28.3 (C)	22.9 (D)	25.87 (E)	28.55 (C)	23.17 (E)	25.4 (D)	27.93 (C)	22.85 (D)
Poly-kk	N/A	N/A	N/A	26.73 (D)	29.69 (AB)	23.75 (D)	N/A	N/A	N/A
Mono-ll, nn, hh	29.6 (A)	29.89 (A)	29.33 (A)	27.99 (C)	28.52 (C)	27.47 (C)	29.5 (A)	29.73 (A)	29.29 (A)
Mono-lm, np, hk	28.29 (B)	28.73 (BC)	27.86 (B)	28.89 (B)	29.26 (B)	28.52 (B)	28.42 (B)	28.91 (B)	27.93 (B)
Mono-kk	N/A	N/A	N/A	29.79 (A)	30.04 (A)	29.55 (A)	N/A	N/A	N/A
Mean s.e.	0.25	0.21	0.16	0.26	0.25	0.19	0.25	0.21	0.16
pval	0.4321	0.3125	0.0134	0.9908	0.6799	0.1475	0.7267	0.1167	0.0438
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C10. NFC QxE Data Continued

Effect	TP402360			TP439989			TP440056		
	AY	np 2016	2017	AY	hk 2016	2017	AY	np 2016	2017
Year									
2016	28.15 (A)			28.29 (A)			28.21 (A)		
2017	24.91 (B)			25.03 (B)			24.97 (B)		
Mean s.e.	0.11			0.1			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	24.89 (C)	26.7 (C)	23.08 (B)	25 (C)	26.79 (C)	23.21 (B)	24.94 (C)	26.73 (C)	23.14 (B)
Poly	25.88 (B)	28.57 (B)	23.18 (B)	25.98 (B)	28.68 (B)	23.26 (B)	25.9 (B)	28.59 (B)	23.2 (B)
Mono	28.82 (A)	29.16 (A)	28.48 (A)	29.01 (A)	29.39 (A)	28.63 (A)	28.93 (A)	29.3 (A)	28.57 (A)
Mean s.e.	0.18	0.17	0.14	0.15	0.17	0.14	0.18	0.16	0.12
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	26.04 (B)	27.68 (B)	24.4 (B)	27.17 (A)	28.92 (A)	25.42 (A)	26.09 (B)	27.73 (B)	24.44 (B)
lm, np, hk	27.02 (A)	28.61 (A)	25.42 (A)	26.35 (B)	27.97 (B)	24.73 (B)	27.09 (A)	28.69 (A)	25.5 (A)
kk	N/A	N/A	N/A	26.46 (B)	27.97 (B)	24.96 (B)	N/A	N/A	N/A
Mean s.e.	0.15	0.15	0.12	0.15	0.17	0.13	0.15	0.15	0.11
pval	<.0001	<.0001	<.0001	0.0002	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	24.49 (E)	26.31 (E)	22.66 (D)	25.48 (DE)	27.41 (D)	23.55 (C)	24.5 (E)	26.31 (E)	22.7 (D)
Spaced-lm, np, hk	25.29 (D)	27.09 (D)	23.49 (C)	24.72 (F)	26.53 (E)	22.9 (D)	25.37 (D)	27.15 (D)	23.58 (C)
Spaced-kk	N/A	N/A	N/A	24.8 (EF)	26.42 (E)	23.18 (CD)	N/A	N/A	N/A
Poly-ll, nn, hh	25.47 (D)	28.04 (C)	22.87 (D)	26.52 (C)	29.45 (AB)	23.6 (C)	25.41 (D)	28 (C)	22.81 (D)
Poly-lm, np, hk	26.29 (C)	29.09 (B)	23.48 (C)	25.68 (D)	28.34 (C)	23 (D)	26.4 (C)	29.18 (B)	23.59 (C)
Poly-kk	N/A	N/A	N/A	25.73 (D)	28.26 (C)	23.17 (CD)	N/A	N/A	N/A
Mono-ll, nn, hh	28.17 (B)	28.69 (B)	27.66 (B)	29.5 (A)	29.91 (A)	29.1 (A)	28.34 (B)	28.87 (B)	27.81 (B)
Mono-lm, np, hk	29.46 (A)	29.64 (A)	29.3 (A)	28.65 (B)	29.03 (B)	28.27 (B)	29.51 (A)	29.72 (A)	29.32 (A)
Mono-kk	N/A	N/A	N/A	28.87 (AB)	29.24 (AB)	28.52 (AB)	N/A	N/A	N/A
Mean s.e.	0.25	0.21	0.17	0.26	0.26	0.2	0.25	0.21	0.16
pval	0.5601	0.7551	0.001	0.9968	0.8842	0.9656	0.8299	0.5451	0.0209
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C10. NFC QxE Data Continued

Effect	TP444498 hk			TP510276 hk			TP527066 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	28.11 (A)			28.31 (A)			28.1 (A)		
2017	24.89 (B)			25.04 (B)			24.88 (B)		
Mean s.e.	0.1			0.1			0.1		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	24.86 (C)	26.64 (C)	23.08 (B)	25.06 (C)	26.87 (C)	23.25 (B)	24.84 (C)	26.62 (C)	23.05 (B)
Poly	25.82 (B)	28.47 (B)	23.15 (B)	25.98 (B)	28.69 (B)	23.26 (B)	25.81 (B)	28.46 (B)	23.15 (B)
Mono	28.82 (A)	29.22 (A)	28.44 (A)	28.99 (A)	29.36 (A)	28.62 (A)	28.81 (A)	29.2 (A)	28.43 (A)
Mean s.e.	0.15	0.17	0.13	0.15	0.18	0.13	0.15	0.17	0.13
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	25.49 (C)	27.04 (C)	23.94 (C)	27.49 (A)	29.15 (A)	25.82 (A)	25.49 (C)	27.02 (C)	23.96 (C)
lm, np, hk	26.66 (B)	28.3 (B)	25.01 (B)	26.32 (B)	27.93 (B)	24.71 (B)	26.67 (B)	28.33 (B)	25.02 (B)
kk	27.36 (A)	28.99 (A)	25.72 (A)	26.22 (B)	27.84 (B)	24.6 (B)	27.29 (A)	28.93 (A)	25.65 (A)
Mean s.e.	0.15	0.17	0.13	0.15	0.18	0.13	0.15	0.17	0.13
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	23.82 (F)	25.46 (H)	22.18 (G)	25.99 (D)	27.83 (D)	24.15 (C)	23.77 (F)	25.42 (G)	22.12 (F)
Spaced-lm, np, hk	24.99 (E)	26.83 (G)	23.15 (F)	24.57 (E)	26.39 (E)	22.76 (D)	25.03 (E)	26.86 (F)	23.19 (E)
Spaced-kk	25.76 (D)	27.63 (EF)	23.9 (D)	24.62 (E)	26.38 (E)	22.86 (D)	25.71 (DE)	27.58 (E)	23.85 (D)
Poly-ll, nn, hh	24.96 (E)	27.35 (FG)	22.56 (G)	26.75 (C)	29.6 (AB)	23.88 (C)	24.99 (E)	27.38 (EF)	22.59 (F)
Poly-lm, np, hk	26.03 (D)	28.77 (CD)	23.27 (EF)	25.64 (D)	28.25 (D)	23 (D)	26.03 (D)	28.79 (CD)	23.26 (E)
Poly-kk	26.46 (D)	29.3 (BC)	23.6 (DE)	25.55 (D)	28.22 (CD)	22.87 (D)	26.41 (D)	29.21 (BC)	23.59 (DE)
Mono-ll, nn, hh	27.69 (C)	28.31 (DE)	27.08 (C)	29.73 (A)	30.03 (A)	29.44 (A)	27.72 (C)	28.27 (D)	27.18 (C)
Mono-lm, np, hk	28.94 (B)	29.28 (B)	28.59 (B)	28.74 (B)	29.14 (B)	28.36 (B)	28.97 (B)	29.32 (B)	28.61 (B)
Mono-kk	29.85 (A)	30.06 (A)	29.65 (A)	28.49 (B)	28.92 (BC)	28.06 (B)	29.75 (A)	30.01 (A)	29.49 (A)
Mean s.e.	0.26	0.25	0.19	0.25	0.26	0.2	0.26	0.25	0.19
pval	0.7896	0.8049	0.0031	0.9266	0.7992	0.5392	0.8145	0.8146	0.0213
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C10. NFC QxE Data Continued

Effect	TP559503 lm			TP66619 hk			TP763986 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	28.22 (A)			28.34 (A)			28.17 (A)		
2017	24.98 (B)			25.04 (B)			24.93 (B)		
Mean s.e.	0.11			0.11			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	24.96 (C)	26.77 (C)	23.16 (B)	25.06 (C)	26.9 (C)	23.21 (B)	24.91 (C)	26.71 (C)	23.11 (B)
Poly	25.91 (B)	28.59 (B)	23.22 (B)	26 (B)	28.7 (B)	23.29 (B)	25.88 (B)	28.55 (B)	23.19 (B)
Mono	28.93 (A)	29.3 (A)	28.57 (A)	29.02 (A)	29.42 (A)	28.63 (A)	28.86 (A)	29.22 (A)	28.5 (A)
Mean s.e.	0.18	0.16	0.13	0.16	0.17	0.13	0.17	0.17	0.13
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	27.09 (A)	28.69 (A)	25.49 (A)	26.27 (B)	27.88 (B)	24.66 (B)	26.15 (B)	27.76 (B)	24.52 (B)
lm, np, hk	26.11 (B)	27.74 (B)	24.47 (B)	26.4 (B)	27.98 (B)	24.83 (B)	26.95 (A)	28.56 (A)	25.34 (A)
kk	N/A	N/A	N/A	27.4 (A)	29.16 (A)	25.64 (A)	N/A	N/A	N/A
Mean s.e.	0.15	0.15	0.11	0.16	0.17	0.13	0.14	0.15	0.11
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	25.45 (D)	27.27 (D)	23.62 (C)	24.62 (E)	26.49 (F)	22.76 (D)	24.62 (E)	26.46 (E)	22.78 (E)
Spaced-lm, np, hk	24.48 (E)	26.26 (E)	22.69 (D)	24.73 (E)	26.45 (F)	23.02 (D)	25.21 (DE)	26.97 (D)	23.44 (C)
Spaced-kk	N/A	N/A	N/A	25.81 (CD)	27.77 (E)	23.86 (C)	N/A	N/A	N/A
Poly-ll, nn, hh	26.25 (C)	28.92 (B)	23.54 (C)	25.63 (D)	28.18 (DE)	23.08 (D)	25.64 (CD)	28.23 (C)	23.04 (DE)
Poly-lm, np, hk	25.58 (CD)	28.26 (C)	22.89 (D)	25.75 (D)	28.44 (CD)	23.04 (D)	26.12 (C)	28.88 (B)	23.33 (CD)
Poly-kk	N/A	N/A	N/A	26.62 (C)	29.48 (AB)	23.74 (C)	N/A	N/A	N/A
Mono-ll, nn, hh	29.59 (A)	29.88 (A)	29.31 (A)	28.56 (B)	28.98 (BC)	28.16 (B)	28.18 (B)	28.61 (BC)	27.75 (B)
Mono-lm, np, hk	28.27 (B)	28.71 (BC)	27.83 (B)	28.73 (B)	29.04 (B)	28.42 (B)	29.53 (A)	29.83 (A)	29.25 (A)
Mono-kk	N/A	N/A	N/A	29.78 (A)	30.24 (A)	29.31 (A)	N/A	N/A	N/A
Mean s.e.	0.25	0.21	0.16	0.28	0.26	0.2	0.25	0.25	0.16
pval	0.4358	0.3546	0.0112	0.9936	0.9546	0.7754	0.1495	0.1198	<.0001
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C10. NFC QxE Data Continued

Effect	TP787056 hk			TP801758 lm			TP830345 np		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	28.22 (A)			28.2 (A)			28.12 (A)		
2017	24.94 (B)			24.92 (B)			24.87 (B)		
Mean s.e.	0.1			0.11			0.11		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	24.97 (C)	26.79 (C)	23.14 (B)	24.9 (C)	26.71 (C)	23.09 (B)	24.84 (C)	26.65 (C)	23.03 (B)
Poly	25.88 (B)	28.58 (B)	23.17 (B)	25.88 (B)	28.56 (B)	23.18 (B)	25.82 (B)	28.49 (B)	23.14 (B)
Mono	28.88 (A)	29.27 (A)	28.49 (A)	28.92 (A)	29.32 (A)	28.52 (A)	28.84 (A)	29.22 (A)	28.46 (A)
Mean s.e.	0.15	0.17	0.13	0.18	0.17	0.14	0.18	0.17	0.13
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	26.07 (B)	27.65 (C)	24.49 (B)	26.98 (A)	28.61 (A)	25.35 (A)	26.08 (B)	27.72 (B)	24.43 (B)
lm, np, hk	26.62 (A)	28.18 (B)	25.06 (A)	26.15 (B)	27.79 (B)	24.5 (B)	26.92 (A)	28.52 (A)	25.32 (A)
kk	27.04 (A)	28.81 (A)	25.26 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.15	0.17	0.13	0.14	0.14	0.12	0.14	0.15	0.12
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	24.53 (E)	26.34 (D)	22.73 (DE)	25.27 (D)	27.06 (C)	23.48 (C)	24.54 (E)	26.45 (D)	22.64 (E)
Spaced-lm, np, hk	24.85 (DE)	26.56 (D)	23.14 (CD)	24.53 (E)	26.36 (D)	22.69 (D)	25.13 (DE)	26.85 (D)	23.41 (C)
Spaced-kk	25.52 (CD)	27.49 (C)	23.55 (C)	N/A	N/A	N/A	N/A	N/A	N/A
Poly-ll, nn, hh	25.16 (DE)	27.64 (C)	22.66 (E)	26.32 (A)	29.16 (A)	23.47 (C)	25.52 (CD)	28.08 (C)	22.95 (DE)
Poly-lm, np, hk	26 (BC)	28.66 (B)	23.33 (C)	25.43 (B)	27.97 (B)	22.89 (D)	26.12 (C)	28.9 (B)	23.33 (CD)
Poly-kk	26.49 (B)	29.43 (A)	23.54 (C)	N/A	N/A	N/A	N/A	N/A	N/A
Mono-ll, nn, hh	28.53 (A)	28.97 (AB)	28.09 (B)	29.35 (C)	29.6 (A)	29.11 (A)	28.17 (B)	28.65 (B)	27.7 (B)
Mono-lm, np, hk	29.02 (A)	29.33 (A)	28.68 (A)	28.48 (D)	29.04 (A)	27.92 (B)	29.5 (A)	29.79 (A)	29.23 (A)
Mono-kk	29.1 (A)	29.52 (A)	28.72 (A)	N/A	N/A	N/A	N/A	N/A	N/A
Mean s.e.	0.26	0.25	0.19	0.25	0.22	0.18	0.25	0.22	0.17
pval	0.5731	0.0775	0.7188	0.9494	0.2953	0.1686	0.2285	0.1486	0.0005
pval_Bon	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033	0.0033

Appendix C11. Zadoks Maturity QxE Data

Effect	TP159734 hk			TP175699 np			TP191087 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	56.64 (A)			56.7 (A)			56.75 (A)		
2017	56.06 (B)			56.15 (B)			56.21 (B)		
Mean s.e.	0.21			0.2			0.21		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	57.16 (A)	57.95 (A)	56.36 (A)	57.21 (A)	57.99 (A)	56.43 (A)	57.24 (A)	57.99 (A)	56.5 (A)
Poly	55.51 (C)	55.36 (C)	55.66 (B)	55.59 (C)	55.45 (C)	55.74 (B)	55.66 (C)	55.5 (C)	55.83 (B)
Mono	56.39 (B)	56.62 (B)	56.16 (A)	56.47 (B)	56.66 (B)	56.28 (A)	56.53 (B)	56.76 (B)	56.3 (A)
Mean s.e.	0.22	0.24	0.2	0.22	0.23	0.2	0.22	0.25	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0006
Allele									
ll, nn, hh	56.6 (A)	56.9 (A)	56.31 (A)	55.92 (B)	56.28 (B)	55.56 (B)	56.02 (B)	56.35 (B)	55.7 (B)
lm, np, hk	56.8 (A)	57.02 (A)	56.59 (A)	56.93 (A)	57.12 (A)	56.74 (A)	56.12 (B)	56.44 (B)	55.79 (B)
kk	55.64 (B)	56.02 (B)	55.28 (B)	N/A	N/A	N/A	57.3 (A)	57.46 (A)	57.14 (A)
Mean s.e.	0.22	0.24	0.2	0.21	0.23	0.19	0.22	0.25	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	57.29 (AB)	58.05 (AB)	56.53 (AB)	56.84 (B)	57.74 (B)	55.95 (BC)	56.82 (BC)	57.7 (B)	55.94 (B)
Spaced-lm, np, hk	57.51 (A)	58.17 (A)	56.86 (A)	57.57 (A)	58.24 (A)	56.91 (A)	56.98 (BC)	57.89 (AB)	56.07 (B)
Spaced-kk	56.67 (C)	57.64 (B)	55.7 (DE)	N/A	N/A	N/A	57.94 (A)	58.39 (A)	57.48 (A)
Poly-ll, nn, hh	55.81 (D)	55.73 (D)	55.9 (CD)	55.12 (D)	55.05 (E)	55.2 (D)	55.06 (F)	55.04 (D)	55.07 (C)
Poly-lm, np, hk	56.03 (D)	55.88 (D)	56.18 (BCD)	56.07 (C)	55.85 (D)	56.28 (B)	55.25 (F)	55.16 (D)	55.35 (C)
Poly-kk	54.68 (E)	54.46 (E)	54.89 (F)	N/A	N/A	N/A	56.68 (CD)	56.29 (C)	57.07 (A)
Mono-ll, nn, hh	56.71 (C)	56.94 (C)	56.49 (ABC)	55.8 (C)	56.05 (D)	55.54 (CD)	56.19 (DE)	56.3 (C)	56.07 (B)
Mono-lm, np, hk	56.87 (BC)	56.99 (C)	56.74 (A)	57.15 (AB)	57.27 (C)	57.03 (A)	56.12 (E)	56.28 (C)	55.96 (B)
Mono-kk	55.59 (D)	55.94 (D)	55.24 (EF)	N/A	N/A	N/A	57.29 (B)	57.7 (B)	56.86 (A)
Mean s.e.	0.26	0.29	0.26	0.25	0.26	0.23	0.27	0.3	0.27
pval	0.4637	0.1624	0.9087	0.166	0.0579	0.2166	0.6057	0.2106	0.1493
pval_Bon	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038

Appendix C11. Zadoks Maturity QxE Data Continued

Effect	TP272027 lm			TP283477 hk			TP302599 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	56.74 (A)			56.55 (A)			56.65 (A)		
2017	56.18 (B)			55.89 (B)			56.08 (B)		
Mean s.e.	0.2			0.21			0.2		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	57.23 (A)	58.02 (A)	56.44 (A)	57.04 (A)	57.88 (A)	56.2 (A)	57.16 (A)	57.93 (A)	56.39 (A)
Poly	55.62 (C)	55.47 (C)	55.77 (B)	55.37 (C)	55.3 (C)	55.44 (B)	55.52 (C)	55.38 (C)	55.66 (B)
Mono	56.52 (B)	56.72 (B)	56.31 (A)	56.26 (B)	56.48 (B)	56.04 (A)	56.42 (B)	56.64 (B)	56.2 (A)
Mean s.e.	0.22	0.24	0.2	0.22	0.24	0.2	0.21	0.24	0.2
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele									
ll, nn, hh	56.93 (A)	57.06 (A)	56.79 (A)	55.26 (B)	55.8 (B)	54.71 (B)	56.33 (B)	56.58 (B)	56.08 (B)
lm, np, hk	55.99 (B)	56.41 (B)	55.56 (B)	56.67 (A)	56.87 (A)	56.47 (A)	56.89 (A)	57.1 (A)	56.68 (A)
kk	N/A	N/A	N/A	56.75 (A)	56.99 (A)	56.5 (A)	55.86 (C)	56.26 (B)	55.47 (C)
Mean s.e.	0.21	0.23	0.19	0.22	0.24	0.2	0.21	0.24	0.2
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	57.67 (A)	58.33 (A)	57.01 (A)	56.3 (DE)	57.41 (B)	55.18 (D)	57.29 (AB)	57.95 (AB)	56.64 (AB)
Spaced-lm, np, hk	56.79 (B)	57.71 (B)	55.87 (C)	57.43 (A)	58.1 (A)	56.75 (A)	57.57 (A)	58.3 (A)	56.84 (A)
Spaced-kk	N/A	N/A	N/A	57.39 (AB)	58.13 (A)	56.65 (A)	56.61 (CD)	57.53 (BC)	55.68 (D)
Poly-ll, nn, hh	56.04 (C)	55.71 (E)	56.36 (B)	54.3 (G)	54.42 (D)	54.18 (E)	55.59 (F)	55.54 (F)	55.64 (DE)
Poly-lm, np, hk	55.21 (D)	55.24 (F)	55.18 (D)	55.9 (E)	55.65 (C)	56.15 (BC)	56.07 (E)	55.85 (EF)	56.28 (BC)
Poly-kk	N/A	N/A	N/A	55.91 (E)	55.82 (C)	56 (C)	54.9 (G)	54.75 (G)	55.05 (E)
Mono-ll, nn, hh	57.07 (B)	57.16 (C)	56.99 (A)	55.17 (F)	55.57 (C)	54.77 (DE)	56.12 (DE)	56.26 (DE)	55.98 (CD)
Mono-lm, np, hk	55.96 (C)	56.29 (D)	55.63 (CD)	56.68 (CD)	56.87 (B)	56.5 (AB)	57.04 (BC)	57.16 (C)	56.93 (A)
Mono-kk	N/A	N/A	N/A	56.94 (BC)	57.02 (B)	56.85 (A)	56.09 (DEF)	56.49 (D)	55.68 (DE)
Mean s.e.	0.24	0.26	0.23	0.26	0.29	0.26	0.26	0.28	0.25
pval	0.6279	0.427	0.778	0.4257	0.4885	0.5149	0.2413	0.1376	0.341
pval_Bon	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038

Appendix C11. Zadoks Maturity QxE Data Continued

Effect	TP44922 hk			TP641846 hk			TP652187 hk		
	AY	2016	2017	AY	2016	2017	AY	2016	2017
Year									
2016	56.68 (A)			56.73 (A)			56.8 (A)		
2017	56.19 (B)			56.18 (B)			56.32 (B)		
Mean s.e.	0.21			0.2			0.2		
pval	<.0001			<.0001			<.0001		
Environment									
Spaced	57.27 (A)	58.03 (A)	56.51 (A)	57.23 (A)	58.02 (A)	56.45 (A)	57.3 (A)	58.03 (A)	56.57 (A)
Poly	55.61 (C)	55.43 (C)	55.8 (B)	55.64 (C)	55.49 (C)	55.79 (B)	55.74 (C)	55.56 (C)	55.92 (B)
Mono	56.42 (B)	56.59 (B)	56.25 (A)	56.5 (B)	56.68 (B)	56.32 (A)	56.64 (B)	56.81 (B)	56.46 (A)
Mean s.e.	0.22	0.25	0.2	0.21	0.23	0.2	0.22	0.24	0.21
pval	<.0001	<.0001	0.0002	<.0001	<.0001	0.0001	<.0001	<.0001	0.0003
Allele									
ll, nn, hh	57.02 (A)	57.05 (A)	57 (A)	55.65 (C)	56.18 (C)	55.13 (C)	57.31 (A)	57.37 (A)	57.25 (A)
lm, np, hk	56.45 (B)	56.81 (A)	56.08 (B)	56.62 (B)	56.85 (B)	56.38 (B)	56.42 (B)	56.78 (B)	56.07 (B)
kk	55.83 (C)	56.19 (B)	55.48 (C)	57.1 (A)	57.15 (A)	57.04 (A)	55.95 (C)	56.26 (C)	55.63 (C)
Mean s.e.	0.22	0.25	0.2	0.21	0.23	0.19	0.22	0.24	0.21
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele									
Spaced-ll, nn, hh	57.68 (A)	58.24 (A)	57.12 (A)	56.39 (D)	57.44 (B)	55.34 (E)	57.87 (A)	58.36 (A)	57.37 (A)
Spaced-lm, np, hk	57.15 (B)	57.96 (A)	56.35 (BC)	57.37 (B)	58.06 (A)	56.68 (BC)	57.19 (BC)	58.02 (AB)	56.37 (BC)
Spaced-kk	56.97 (BC)	57.89 (A)	56.05 (CD)	57.94 (A)	58.55 (A)	57.33 (A)	56.83 (BCD)	57.7 (BC)	55.97 (CDE)
Poly-ll, nn, hh	56.46 (C)	56.12 (C)	56.79 (AB)	54.82 (F)	54.86 (F)	54.79 (E)	56.63 (CDE)	56.33 (D)	56.92 (AB)
Poly-lm, np, hk	55.59 (D)	55.55 (D)	55.63 (D)	55.77 (E)	55.6 (E)	55.94 (D)	55.66 (F)	55.63 (E)	55.69 (EF)
Poly-kk	54.8 (E)	54.63 (E)	54.98 (E)	56.31 (D)	56 (DE)	56.63 (BC)	54.94 (G)	54.73 (F)	55.16 (F)
Mono-ll, nn, hh	56.94 (BC)	56.79 (B)	57.08 (A)	55.75 (E)	56.24 (D)	55.26 (E)	57.44 (AB)	57.41 (C)	57.46 (A)
Mono-lm, np, hk	56.6 (C)	56.93 (B)	56.27 (BC)	56.71 (CD)	56.89 (C)	56.52 (C)	56.41 (DE)	56.68 (D)	56.15 (CD)
Mono-kk	55.73 (D)	56.04 (CD)	55.41 (DE)	57.04 (BC)	56.9 (BC)	57.17 (AB)	56.07 (EF)	56.34 (D)	55.77 (DEF)
Mean s.e.	0.26	0.3	0.26	0.25	0.28	0.25	0.28	0.29	0.27
pval	0.0903	0.0313	0.4607	0.9496	0.7016	0.9925	0.6254	0.2247	0.9268
pval_Bon	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038

Appendix C11. Zadoks Maturity QxE Data Continued

		TP764084 hk			TP875227 lm		
Effect		AY	2016	2017	AY	2016	2017
<u>Year</u>							
	2016	56.68 (A)			56.73 (A)		
	2017	56.04 (B)			56.17 (B)		
	Mean s.e.	0.19			0.2		
	pval	<.0001			<.0001		
<u>Environment</u>							
	Spaced	57.12 (A)	57.93 (A)	56.32 (A)	57.22 (A)	57.99 (A)	56.44 (A)
	Poly	55.52 (C)	55.4 (C)	55.63 (B)	55.62 (C)	55.48 (C)	55.76 (B)
	Mono	56.44 (B)	56.7 (B)	56.17 (A)	56.5 (B)	56.71 (B)	56.29 (A)
	Mean s.e.	0.21	0.23	0.19	0.22	0.24	0.19
	pval	<.0001	<.0001	0.0002	<.0001	<.0001	<.0001
<u>Allele</u>							
	ll, nn, hh	56.43 (B)	56.75 (B)	56.11 (B)	56.98 (A)	57.11 (A)	56.85 (A)
	lm, np, hk	56.9 (A)	57.09 (A)	56.71 (A)	55.91 (B)	56.34 (B)	55.48 (B)
	kk	55.75 (C)	56.19 (C)	55.31 (C)	N/A	N/A	N/A
	Mean s.e.	0.21	0.23	0.19	0.21	0.23	0.18
	pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
<u>Env. X Allele</u>							
	Spaced-ll, nn, hh	57.27 (AB)	57.99 (AB)	56.56 (AB)	57.64 (A)	58.27 (A)	57.01 (A)
	Spaced-lm, np, hk	57.56 (A)	58.29 (A)	56.83 (A)	56.8 (B)	57.72 (B)	55.88 (C)
	Spaced-kk	56.54 (C)	57.51 (BC)	55.56 (D)	N/A	N/A	N/A
	Poly-ll, nn, hh	55.73 (E)	55.69 (F)	55.77 (CD)	56.14 (C)	55.83 (D)	56.45 (B)
	Poly-lm, np, hk	56.1 (CDE)	55.91 (EF)	56.29 (BC)	55.1 (D)	55.13 (E)	55.07 (D)
	Poly-kk	54.73 (F)	54.62 (G)	54.84 (E)	N/A	N/A	N/A
	Mono-ll, nn, hh	56.29 (CD)	56.59 (D)	55.99 (BCD)	57.17 (B)	57.24 (C)	57.09 (A)
	Mono-lm, np, hk	57.04 (B)	57.08 (C)	57 (A)	55.84 (C)	56.18 (D)	55.49 (CD)
	Mono-kk	55.98 (DE)	56.44 (DE)	55.52 (DE)	N/A	N/A	N/A
	Mean s.e.	0.25	0.28	0.26	0.25	0.26	0.22
	pval	0.3966	0.2716	0.4131	3233	0.2173	0.3281
	pval_Bon	0.0038	0.0038	0.0038	0.0038	0.0038	0.0038

Appendix C11. Zadoks Maturity QxE Data Continued

Effect	TP902986 np			TP743845 hk		
	AY	2016	2017	AY	2016	2017
Year						
2016	56.72 (A)			56.71 (A)		
2017	56.18 (B)			56.17 (B)		
Mean s.e.		0.2			0.2	
pval	<.0001			<.0001		
Environment						
Spaced	57.22 (A)	57.99 (A)	56.46 (A)	57.22 (A)	57.99 (A)	56.44 (A)
Poly	55.61 (C)	55.46 (C)	55.77 (B)	55.62 (C)	55.47 (C)	55.76 (B)
Mono	56.51 (B)	56.7 (B)	56.31 (A)	56.49 (B)	56.67 (B)	56.31 (A)
Mean s.e.		0.22	0.23		0.21	0.24
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Allele						
ll, nn, hh	55.96 (B)	56.32 (B)	55.61 (B)	57.11 (A)	57.16 (A)	57.06 (A)
lm, np, hk	56.93 (A)	57.12 (A)	56.75 (A)	56.56 (B)	56.81 (B)	56.31 (B)
kk	N/A	N/A	N/A	55.65 (C)	56.16 (C)	55.14 (C)
Mean s.e.		0.2	0.22		0.21	0.24
pval	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Env. X Allele						
Spaced-ll, nn, hh	56.86 (B)	57.74 (B)	55.97 (BC)	57.95 (A)	58.51 (A)	57.38 (A)
Spaced-lm, np, hk	57.59 (A)	58.24 (A)	56.94 (A)	57.32 (B)	58.04 (A)	56.6 (C)
Spaced-kk	N/A	N/A	N/A	56.38 (D)	57.43 (B)	55.34 (E)
Poly-ll, nn, hh	55.12 (D)	55.03 (E)	55.21 (D)	56.34 (D)	56.05 (D)	56.63 (BC)
Poly-lm, np, hk	56.11 (C)	55.89 (D)	56.33 (B)	55.71 (E)	55.53 (E)	55.9 (D)
Poly-kk	N/A	N/A	N/A	54.8 (F)	54.84 (F)	54.76 (E)
Mono-ll, nn, hh	55.91 (C)	56.17 (D)	55.65 (C)	57.05 (BC)	56.93 (BC)	57.16 (AB)
Mono-lm, np, hk	57.1 (B)	57.23 (C)	56.97 (A)	56.65 (CD)	56.87 (C)	56.44 (C)
Mono-kk	N/A	N/A	N/A	55.77 (E)	56.22 (D)	55.33 (E)
Mean s.e.		0.25	0.25		0.26	0.29
pval		0.3923	0.1581		0.9351	0.692
pval_Bon		0.0038	0.0038		0.0038	0.0038

Appendix D. Estimates of QTL effects (α, γ) as a percentage of population mean where α is difference between QTL alleles of the M26 parent and γ is difference between QTL alleles of the M35 parent

Trait	Linkage group	Spaced	Polyculture	Monoculture	Mean	QxE	Bonferroni
MASS	1	(0.01, -0.3)	(0, 0.02)	(0.01, -0.33)**	(0.01, -0.3)	NS	0.0031
MASS	6	(-0.03, 0)	(-0.01, 0.01)	(-0.13, 0.12)**	(-0.08, 0.09)	NS	0.0031
MASS	10	(-0.08, 0.09)**	(-0.02, 0.02)*	(0.01, 0.01)*	(-0.04, 0.04)**	<.0001	0.0031
MASS	11	(-0.01, -0.02)	(0, -0.02)*	(0, -0.01)**	(0, -0.01)	NS	0.0031
MASS	14	(-0.01, -0.08)*	(0.01, -0.02)	(0, -0.01)**	(0, -0.03)*	0.0004	0.0031
MASS	15	(-0.11, 0.02)	(-0.01, -0.01)	(-0.13, 0.11)**	(-0.08, 0.04)	0.0007	0.0031
TILE	10	(-3.13, 2.15)**	(-3.92, 2.72)**	(-3.69, 2.8)*	(-3.24, 2.34)**	NS	0.0033
TILE	11	(2.32, 0.54)*	(2.84, -1.97)*	(2.78, -2.74)*	(2.61, -2.28)**	NS	0.0033
TICR	1	(31.42, -563.82)	(0.58, -32.17)	(1.09, -79.75)**	(12.03, -199.51)	NS	0.0033
TICR	8	(34.5, 29.51)**	(2.66, 11.88)	(0.4, 5.66)	(10.43, 6.09)*	NS	0.0033
ZAMA	16	(-0.4, 0.38)**	(2.73, -5.06)	(-0.29, -1.19)	(-0.43, 0.29)*	NS	0.0038
CP	6	(0.13, -0.12)*	(0.18, 0.15)**	(0.08, 0.08)*	(0.13, 0.07)**	NS	0.0083
NDF	10	(-0.42, 0.53)**	(-0.36, 0.64)**	(-0.3, 0.73)**	(-0.35, 0.57)**	NS	0.0033
NDF	15	(-0.08, 0.43)	(-0.09, 0.24)	(-0.04, 0.81)**	(-0.05, 0.51)	NS	0.0033
NDF	16	(0.44, -0.62)*	(0.18, -0.48)	(0.44, -0.73)**	(0.38, -0.61)**	NS	0.0033
ADF	10	(-0.21, 0.27)**	(-0.24, 0.44)**	(-0.14, 0.43)**	(-0.05, 0.45)**	NS	0.0033
ADF	16	(0.24, -0.32)*	(0.1, -0.3)	(0.26, -0.43)**	(0.23, -0.36)**	NS	0.0033
IVTD	10	(0.3, -0.51)**	(0.39, -0.41)**	(0.59, -0.76)**	(0.33, -0.48)**	NS	0.0033
IVTD	14	(-0.24, 0.46)*	(-0.14, 0.4)*	(-0.08, 0.56)**	(-0.23, 0.48)**	NS	0.0033
IVTD	18	(0.18, 0.53)*	(0.36, 0.49)**	(0.24, 0.56)	(0.25, 0.48)**	NS	0.0033
NDFD	5	(0.19, 0.19)**	(0.14, 0.48)*	(0.08, 0.33)	(0.21, 0.4)*	NS	0.0026
NDFD	9	(-0.17, -0.78)**	(0.27, -0.85)**	(0.16, -0.64)	(0.22, -0.74)**	NS	0.0026
NDFD	10	(0.25, -0.35)	(0.29, -0.09)	(0.47, -0.49)**	(0.32, -0.27)	0.0003	0.0026
NDFD	11	(-0.4, -0.34)**	(-0.47, -0.39)*	(-0.41, 0.03)	(-0.4, -0.25)*	NS	0.0026
NDFD	18	(0.37, 0.51)*	(0.5, 0.49)**	(0.41, 0.49)*	(0.4, 0.51)**	NS	0.0026

* 5% Significance level linkage group wide

** 5% Significance level genome wide

Values were determined by evaluating 192 full-sib genets during 2016 and 2017 near Logan, UT, USA.