DISSERTATION

GENOMIC AND PHENOMIC TOOLS TO AID IN THE UTILIZATION OF EASTERN EUROPEAN AND CENTRAL ASIAN WHEAT GERMPLASM IN U.S. HARD WINTER WHEAT BREEDING

Submitted by

Craig Thomas Beil

Department of Soil and Crop Sciences

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Doctoral Committee:

Advisor: Scott Haley

Patrick Byrne
Courtney Jahn
Adam Heuberger

ABSTRACT

GENOMIC AND PHENOMIC TOOLS TO AID IN THE UTILIZATION OF EASTERN EUROPEAN AND CENTRAL ASIAN WHEAT GERMPLASM IN U.S. HARD WINTER WHEAT BREEDING

There is a tremendous amount of genetic material available for use in plant breeding. The challenge is how to most effectively screen this material and incorporate it into the breeding program in order to create new genetic combinations that are higher yielding and better adapted to stresses in the target environment. Advances in high-throughput single nucleotide polymorphism (SNP) genotyping have enabled powerful genome-wide association studies (GWAS) in diverse collections of germplasm. This has enhanced the ability to identify causal mutations that underlie agronomically important traits. These same SNPs are also valuable for genomic prediction and genomic selection (GS) (Meuwissen et al. 2001) where the genomic estimated breeding value (GEBV) of individuals can be determined. These advancements allow for novel genetic material to be identified and used in a breeding program in order to enhance genetic gain.

Characterization of population structure and genetic relatedness among diverse wheat (*Triticum aestivum* L.) germplasm collections is critical for GWAS and training population development for GS. Cooperative regional and international nurseries are well suited for GWAS and GS studies due to the production of multi-environment phenotypic datasets. In this study I analyzed population structure and genetic diversity of 345 genotypes which included 272 individuals from three years of the Facultative and Winter Wheat Observation Nursery

(FAWWON) and 73 individuals from two years of the U.S. Hard Winter Wheat Southern Regional Performance Nursery (SRPN). The collection was genotyped with SNP markers obtained through genotyping-by-sequencing (GBS). Four subpopulations were identified using a correlated allele frequencies model in the program STRUCTURE. Three subpopulations were characterized as having a high percentage of genotypes from the FAWWON while the fourth subpopulation had a high percentage of genotypes from the SRPN. Wright's fixation index (F_{ST}) values ranged from 0.16 to 0.32 between subpopulations indicating that the subpopulations possess unique alleles. High yielding FAWWON genotypes identified in yield trials across six environments in Colorado represented eight of the 11 countries and breeding programs and were from all four subpopulations. The characterization of population structure within the FAWWON and SRPN will allow breeders to select and test germplasm that is genetically diverse from their own which will help foster the utilization and exchange of germplasm across diverse global winter wheat production regions.

In addition, I analyzed population structure and genetic diversity of 283 genotypes from seven years of the Winter Wheat Eastern European Regional Yield Trial (WWEERYT). The collection was also genotyped with SNP markers obtained via GBS. Seven subpopulations were identified using a correlated allele frequencies model in the program STRUCTURE. A genotype's breeding program of origin, based on four major geographic regions, was closely related to subpopulation assignment. Genotypes of central and eastern European origin were assigned to six of the seven subpopulations, indicating extensive diversity among genotypes from this region. Genotypes from the United States (U.S.) (n=59) were assigned to only two of the seven subpopulations with 52.5% of the genotypes assigned to population F. The lowest value for

Wright's fixation index (F_{ST}=0.20) was observed between a population of predominantly Turkey-CIMMYT-ICARDA genotypes and genotypes from the U.S., indicating a close relationship between genotypes from these two regions. The characterization of population structure and genetic diversity within the WWEERYT nurseries will allow breeders to accurately select and test germplasm that is genetically diverse from their own by targeting germplasm from different subpopulations identified in this study.

One of the main challenges when trying to incorporate genetically diverse germplasm into a breeding program is the adaptation of such germplasm to the biotic and abiotic pressures present in the new environment. Low temperature tolerance is an important characteristic for autumn sown winter wheat in regions with cold winters. Vernalization and photoperiod genes influence adaptation of wheat by regulating the timing of the transition from vegetative to reproductive growth to protect the floral meristem from low temperature injury. I evaluated winter injury of 287 genotypes from the FAWWON in six field environments over three years (2014 to 2016) in Colorado. Entries (experimental lines and varieties) were genotyped with SNP markers obtained through GBS and at known vernalization (*Vrn-A1*, *Vrn-B1*, and *Vrn-D1*) and photoperiod (*Ppd-B1* and *Ppd-D1*) loci using Kompetitive Allele Specific PCR (KASP) assays. Winter injury was observed in five of the six environments. Mean GS prediction accuracies across the five environments using GBS-based SNPs alone as random effects ranged from 0.26 ± 0.01 to 0.74 ± 0.00. Incorporation of alleles at *Vrn-A1*, *Vrn-B1*, and *Vrn-D1* loci as fixed effects in the GS models together with 23,269 GBS markers as random effects provided the highest prediction accuracy with mean GS prediction accuracies ranging from 0.34 ± 0.01 to 0.78 ± 0.00 across the five environments. Genomic selection models incorporating photoperiod alleles as

fixed effects rarely improved GS prediction accuracy. Genomic selection models that incorporate both major and minor genetic factors that influence low temperature tolerance improved the model predictions of identifying genotypes that are best adapted to regions where cold winter temperatures are an important production constraint.

In these studies I was able to identify wheat lines from eastern Europe and central and western Asia that are genetically diverse from wheat lines currently being grown in the central and southern Great Plains in the U.S. Some of these lines showed high and stable grain yield in multiple environments in Colorado. The GS model that was developed in this study will allow for efficient screening of genotypes that would be best adapted to the harsh winter conditions in Colorado and potentially increase winter hardiness through the accumulation of minor alleles by evaluating individuals for their GEBV. It is my hope that the results from this study will assist plant breeders in the U.S. Great Plains, eastern Europe, and central and western Asia in identifying germplasm that is useful in their region and can be used in their breeding programs.

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LITERATURE REVIEW

Germplasm and Its Use in Wheat Breeding

A narrowing genetic base in wheat (*Triticum aestivum* L.) is a serious obstacle to sustaining and improving crop productivity. Reduced diversity results from limited genetic variability and uniform cultivars and increases the vulnerability of wheat to new biotic and abiotic stresses (McCouch et al., 2012). A loss of genetic diversity in wheat initially occurred as a small number of founder populations experienced intense selection for agronomically desirable traits (Tanksley and McCouch, 1997) and again as a limited number of landraces were used to develop today's modern cultivars (Tanksley and McCouch, 1997; van de Wouw et al., 2010). Although intensive plant breeding has been shown to reduce genetic diversity (Fu et al., 2003; Roussel et al., 2004; Warburton et al., 2006), results indicate that this can be averted through the introgression of novel genetic material (Reif et al., 2005; Warburton et al., 2006; Fu et al., 2007). Plant breeders need to be equipped with the right tools to be able to identify and use genetic variation that exists among cultivars, experimental lines, landraces, and wild relatives in order to develop new varieties that will be able to cope with ever changing climatic and management conditions (Frison et al., 2011).

International Winter Wheat Germplasm Nurseries

Beginning in the 1950s and particularly in the 1960s, a looming global food crisis led to rapid advances to formalize international exchange of genetic materials to increase food production and food security in developing countries (Byerlee and Dubin, 2009). This work, originally led by the Rockefeller and Ford Foundations, resulted in the development of

international agricultural research centers such as the Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT) and fostered the exchange of germplasm and knowledge of wheat improvement across developing countries (Byerlee and Dubin, 2009; Nelles, 2011). CIMMYT grew out of a pilot program sponsored by the Mexican government and the Rockefeller Foundation in the 1940s and 1950s and was formally launched as an international organization in 1966 (CIMMYT, 2016). CIMMYT became one of the first international research centers supported through the Consultative Group on International Agricultural Research (CGIAR), which is now made up of 15 independent, international agricultural research organizations (Nelles, 2011; CIMMYT, 2016). CGIAR research is dedicated to reducing rural poverty, increasing food security, improving human health and nutrition, and ensuring sustainable management of natural resources (CIMMYT, 2016). The CGIAR institutes use global genetic resources in inter-country research experiments, known as international nurseries, and serves as an example of open-source collaboration for biological research through free exchange of germplasm and information (Byerlee and Dubin, 2009).

CIMMYT categorized the wheat-growing regions of the world into twelve mega-environments (MEs) based on similarities of biotic and abiotic stresses, cropping systems, and consumer demands (Rajaram et al., 1993; Braun et al., 1996). International germplasm nurseries were established to target a particular set of MEs and have been disseminated by CIMMYT in a system that is known as the International Wheat Improvement Network (IWIN). In the late 1970s and early 1980s, CIMMYT recognized that winter wheat breeding for the developing world remained largely unaddressed. The target area for winter wheat was central and west Asia which covered 15-20 million ha of crop land in Turkey, Iran, central Asia, and the

Caucasus region (CIMMYT, 2012). Turkey was chosen as the location for the main breeding facility due to its diversity of environments and its importance as a major winter wheat producer in the region (CIMMYT, 2012). The CIMMYT winter wheat program in Turkey began cooperating with the International Center for Agricultural Research in the Dry Areas (ICARDA) in 1991 and the Ministry of Agriculture and Rural Affairs of Turkey to form the International Winter Wheat Improvement Program (IWWIP) (Morgounov et al., 2005; CIMMYT, 2012). Although CIMMYT was already testing nurseries of spring wheat on a global scale, nothing was in place for international evaluation of winter wheats (Bedö and Láng, 2010). The United States Department in Agriculture (USDA) in Lincoln, Nebraska and the University of Nebraska organized the International Winter Wheat Performance Nursery (IWWPN) in 1968 and was widely endorsed by wheat breeders and agronomists throughout the winter wheat production regions of the world (Bedö and Láng, 2010). The IWWPN was soon grown cooperatively in 37 countries (Bedö and Láng, 2010). In the 1980s, CIMMYT in Turkey began distribution of their own winter wheat nursery called the International Winter Wheat Screening Nursery (IWWSN) (CIMMYT, 2012). The IWWSN included germplasm from Turkish breeding programs, lines bred by the IWWIP, and lines introduced from programs in other production regions. In 1992, the nursery was transformed into the Facultative and Winter Wheat Observation Nursery (FAWWON) in order to accommodate facultative, or semi-winter growth type, germplasm from ICARDA (CIMMYT, 2012). The IWWIP distributes the FAWWON, comprised of high yielding and advanced breeding lines, to facilitate introduction and exchange of improved germplasm globally for irrigated and dryland production systems (Sharma et al., 2010, 2012). To expand the international exchange of winter wheat germplasm, CIMMYT and Oregon State University

initiated the Winter Wheat Eastern European Regional Yield Trial (WWEERYT) as a separate IWWIP project to evaluate elite lines and varieties from eastern Europe, IWWIP, the Caucus Region, and the United States (Sharma et al., 2014). The genetic diversity of lines in the FAWWON and WWEERYT is assumed to be broad as their pedigrees include not only CIMMYT germplasm parents but also a wide range of genetically unrelated winter wheats from Armenia, Azerbaijan, Bulgaria, Czech Republic, Georgia, Hungary, Iran, Kazakhstan, Kyrgyzstan, Moldova, Romania, Russia, Turkey, Ukraine, United States, Uzbekistan, and other countries.

Regional nursery collections also play an important role in facilitating germplasm exchange among breeding programs. The Great Plains of North America contains one of the world's largest concentrations of wheat production (Graybosch and Peterson, 2012). Each year, public and private breeding programs in the central and southern Great Plains submit their highest performing experimental lines to be part of the Southern Regional Performance Nursery (SRPN) (Graybosch and Peterson, 2010, 2012). The SRPN facilitates evaluation of germplasm for important traits and helps to support the exchange of germplasm among public and private wheat breeding programs. The SRPN is a vital component of maintaining genetic diversity in the Great Plains region. Elite breeding lines tested in international and regional performance nurseries represent the most advanced materials from a collection of breeding programs and bring attention to a pool of genotypes for cultivar release or use as parents in future crosses (Peterson and Pfeiffer, 1989; Graybosch and Peterson, 2010, 2012; Sharma et al., 2010, 2012, 2014).

Genetic Diversity

Understanding the levels and distribution of genetic diversity in germplasm collections allows for the development of strategies for genetic resource management and exploitation. The development of genome-wide association studies (GWAS) to identify quantitative trait loci (QTLs) underlying complex traits has resulted in renewed interest to characterize population structure in wheat collections (Yu et al., 2006). The existence of population structure with unequal allelic distribution within a GWAS panel can result in spurious associations and is the primary obstacle to successful GWAS (Buckler and Thornsberry, 2002; Zhao et al., 2007).

Genetic diversity and population structure have been evaluated in wheat collections using molecular markers, such as random amplified polymorphic DNA (RAPD; Joshi and Nguyen, 1993), restriction fragment length polymorphism (RFLP; Siedler et al., 1994; Kim and Ward, 2000), amplified fragment length polymorphism (AFLP; Barrett and Kidwell, 1998), simple sequence repeats (SSR; Röder et al., 2002; Balfourier et al., 2007; Zhang et al., 2010) and diversity arrays technology (DArT; White et al., 2008; Dreisigacker et al., 2012; Cabrera et al., 2014). Single nucleotide polymorphism (SNP) markers have become the preferred marker for genetic studies due to their greater abundance in the genome and better amenability to high-throughput, low cost genotyping (Varshney et al., 2006).

In population structure experiments, individuals that are genetically similar are grouped together by the identification of distinct clusters of related individuals. The clusters are then examined to determine how they relate to geographic origin or phenotypes of individuals within and between the population groupings. Distance-based methods, which rely on phylogenetic trees, are better suited to exploratory data analysis than to fine statistical

inference. This is because clusters or population groupings are inferred visually (Pritchard et al., 2000). The software program STRUCTURE is a common tool for model-based population analysis and is widely used since it can use a variety of marker types (SSRs, RFLPs, and SNPs) (Pritchard et al., 2000). In the program STRUCTURE, populations are delineated based on individual's genotypes at multiple loci using a Bayesian approach (Pritchard et al., 2000). Using the estimated allele frequencies, it is then possible to assign individuals, of unknown origin, to populations (Rannala and Mountain, 1997). The program TASSEL (Trait Analysis by aSSociation, Evaluation and Linkage; Bradbury et al., 2007) uses a combination of structured association implemented in STRUCTURE (Pritchard et al., 2000) and family relatedness within populations (Yu et al., 2006).

In wheat, several studies have examined genetic diversity by various methods including genetic distance, coefficient of parentage, principal component analysis (PCA), and model-based approaches (Barrett and Kidwell, 1998; Kim and Ward, 2000; Chao et al., 2007; White et al., 2008; Prasad et al., 2009; Hao et al., 2011; Cabrera et al., 2014). Results from these studies have drawn conflicting conclusions. Some studies have shown that populations identified in wheat collections correspond to geographic regions (Kim and Ward, 2000; Balfourier et al., 2007; Chao et al., 2007; Tommasini et al., 2007; Le Couviour et al., 2011; Beil et al., 2017). These results support the notion that genetic diversity existing among wheat germplasm is likely the result of natural and artificial selection regimes due to varying environmental conditions, selection based on different breeding objectives unique to a region, or the exchange of germplasm between programs in a region. Other studies have identified no population structure in wheat (Reif et al., 2011; Benson et al., 2012; Würschum et al., 2013), which can be

explained by the breeding history of wheat. Improved lines are often developed by constant exchange of germplasm between breeding programs thus resulting in a panmictic population. A lack of population structure can also be explained by the collection being comprised of limited geographic diversity. Analyses have also shown that not all accessions of wheat originating from the same geographic region clustered in the same population group (Huang et al., 2002; Prasad et al., 2009; Beil et al., 2017).

Environmental and Genetic Factors Affecting Winter Wheat Adaptation

Low Temperature Tolerance, Vernalization, and Photoperiod

Low-temperature (LT) tolerance is an important breeding objective in autumn sown wheat grown in regions with cold winters, such as the Great Plains of North America and the steppes of Russia and Ukraine (Fowler et al., 1999; Paulsen and Shroyer, 2008; Fowler, 2012). The ability of wheat to survive cold winter temperatures is attributed to morphological and physiological characteristics (Fowler et al., 1981; Gusta and Wisniewski, 2013) as well as genetically determined responses to temperature (*VRN* genes) and photoperiod (*PPD* genes) (Fowler et al., 1996; Limin and Fowler, 2006). Floral meristems are more sensitive to cold damage than vegetative meristems and, therefore, small differences in developmental timing can affect plant response to freezing temperatures (Galiba et al., 2009).

The allelic diversity of vernalization and photoperiod genes has been characterized in several worldwide (Iwaki et al., 2001; Kiss et al., 2014) and regional (Zhang et al., 2008; Grogan et al., 2016) wheat germplasm collections. These analyses have indicated that allelic variation at vernalization loci is closely associated with winter temperatures in the growing region (Iwaki et al., 2001) while allelic variation at photoperiod loci is closely correlated with the growing

regions' latitude (Worland et al., 1994; Grogan et al., 2016). Understanding the genetic factors that control LT tolerance at the molecular level, and identifying genotypes with higher LT tolerance is imperative for further enhancement of LT resistance in winter cereals.

Vernalization

Ancestral wheats delayed their transition from vegetative to reproductive growth until they had been exposed to a period of low, non-freezing temperatures, in a process called vernalization (Distelfeld et al., 2009). Based on differences in their vernalization requirement, wheat cultivars may be classified as winter, facultative, and spring habit types. Spring wheat varieties do not have a vernalization requirement which allows them to flower without any low temperature exposure, and are thus generally sown at a time that minimizes risk of exposure to freezing temperatures (Distelfeld et al., 2009). Winter wheat varieties require exposure to cold temperatures to accelerate flowering and thus are sown in autumn (Distelfeld et al., 2009). This adaptive feature prevents the exposure of sensitive floral meristems to freezing winter temperatures (Distelfeld et al., 2009). Facultative wheats are intermediate to spring and winter wheats and are fall or winter planted in areas where the risk of cold damage is reduced due to milder winter temperatures. For winter wheat, vernalization occurs when temperatures are between 0 and 8 °C (Porter and Gawith, 1999). Gardner and Barnett (1990) reported that winter-type cultivars need a vernalization period of 6-8 weeks to complete spike primordial differentiation while facultative-type cultivars require 2-4 weeks (Rousset et al., 2011).

Vernalization requirements are controlled by at least three sets of genes in wheat (*VRN1*, *VRN2*, and *VRN3*) (Trevaskis et al., 2007; Distelfeld et al., 2009). The most common source of non-winter growth type is a dominant allele within the promoter or the first intron at

one or more *Vrn-1* loci (*Vrn-A1*, *Vrn-B1*, and *Vrn-D1*), located on the long arm of the group 5 chromosomes (Yan et al., 2004a; Fu et al., 2005; Santra et al., 2009; Trevaskis, 2010; Zhang et al., 2012). A dominant vernalization allele at any one of the three genomes is sufficient to confer a spring growth habit while recessive alleles at all three loci are required for winter growth habit (Zhang et al., 2012; Kamran et al., 2014). The dominant *Vrn-A1a* allele has the most dramatic effect in conferring spring growth habit, while dominant, spring alleles at *Vrn-B1* and *Vrn-D1* only partially eliminate the need for cold treatment (Pugsley, 1971, 1972). Thus, genotypes with dominant, spring alleles at *Vrn-B1* and *Vrn-D1* show some slight response to vernalization (Santra et al., 2009). Eagles et al. (2010) showed that spring alleles at the *Vrn-1* loci differ in their effect of reducing heading date with spring alleles at *Vrn-B1* having a lesser effect than spring alleles at *Vrn-A1* and *Vrn-D1*. Pugsley (1983) suggested that facultative wheat would lack a spring allele at the *Vrn-A1* locus, but could have a spring allele at *Vrn-B1* or *Vrn-D1*. Eagles et al. (2009) found that the facultative wheat variety 'Oxley' had winter alleles at *Vrn-A1*, *Vrn-B1*, and *Vrn-D1* suggesting that there are additional genes that influence facultative growth habit.

The *VRN1* gene is a homolog of the Arabidopsis (*Arabidopsis thaliana*) meristem identity gene *APETALA1*, which determines the transition between the production of leaves and flowers at the shoot apical meristem (Danyluk et al., 2003; Trevaskis et al., 2003; Yan et al., 2003). The *VRN1* gene encodes a MADS-box transcription factor that is up-regulated by low temperatures (Trevaskis et al., 2003; Yan et al., 2003). *VRN1* transcripts are present at low basal levels but increase during prolonged cold treatment (Trevaskis et al., 2003; Yan et al., 2003). This response is quantitative, with longer cold treatments inducing higher transcript levels (Danyluk

et al., 2003; Yan et al., 2003). Several mutations have been identified in regulatory regions of the *VRN1* promoter or first intron, which are associated with spring growth habit through the elimination or reduction of the vernalization requirement (Yan et al., 2003; Fu et al., 2005). Chen and Dubcovsky (2012) demonstrated that the key role of the *VRN1* gene is to down-regulate the expression of the floral repressor *VRN2* gene in order to allow floral induction.

To date, eight *Vrn-A1* alleles have been described (Yan et al., 2004a; Dubcovsky et al., 2006). The most common is *Vrn-A1a* which has an insertion of a foldback repetitive element and a duplicated region in the promoter (Yan et al., 2004a). The *Vrn-A1b* allele, which is relatively rare, also shows several SNPs and a deletion in the promoter region (Yan et al., 2004a; Eagles et al., 2009). The *Vrn-A1c* allele has a large deletion in the first intron (Fu et al., 2005). Two winter alleles at *Vrn-A1* (*vrn-A1a, vrn-A1b*) were described in winter wheat cultivars adapted to the Great Plains of the U.S. and showed differences in winter dormancy release (Chen et al., 2009). The *vrn-A1a* allele of 'Jagger' was shown to contribute to earlier dormancy release while the *vrn-A1b* allele was shown to contribute to later dormancy release (Chen et al., 2009). In freezing tolerance studies, the *vrn-A1b* allele showed increased LT tolerance over the *vrn-A1a* allele (Chen et al., 2009). Chen et al. (2009) suggested labeling the alleles as *vrn-A1v* for the allele in 'Jagger' and *vrn-A1w* for the allele in 'Wichita'. These two winter alleles have shown differences in dormancy release and freezing tolerance with the *vrn-A1v* allele having a reduced vernalization requirement compared to the *vrn-A1w* allele (Eagles et al., 2011; Zhu et al., 2014). Although these two alleles were distinguished by a single SNP (Chen et al., 2009), they are also linked to copy number variation with the *vrn-A1v* allele associated with two or fewer copies of the gene and the *vrn-A1w* allele associated with three or more copies (Zhu et

al., 2014). Increased copy number results in greater vernalization requirements and later flowering when the vernalization requirement is only partially fulfilled (Diaz et al., 2012).

Three dominant allelic variants (*Vrn-B1a, Vrn-B1b,* and *Vrn-B1c*) have been described at the *Vrn-B1* locus (Santra et al., 2009; Milec et al., 2012). Similar to the *Vrn-A1c* spring allele, each of the dominant *Vrn-B1* alleles for spring growth habit is characterized by large deletions in the first intron (Fu et al., 2005). The *Vrn-B1b* allele has the same deletion as the *Vrn-B1a* allele plus an additional small deletion (36 bp) identified the spring wheat 'Alpowa' (Santra et al., 2009). The *Vrn-B1c* allele also has a large deletion within the first intron but with different break points than the *Vrn-B1a* or *Vrn-B1b* alleles (Milec et al., 2012). The *Vrn-B1c* allele was found in germplasm from eastern Europe (Milec et al., 2012).

Three alleles have been described at the *Vrn-D1* locus (*Vrn-D1a*, *Vrn-D1b*, and *vrn-D1*). The dominant spring-habit allele is designated as *Vrn-D1a* while the recessive allele, *vrn-D1*, is associated with winter growth habit. As with the *Vrn-A1a* and *Vrn-B1a* alleles, the dominant *Vrn-D1a* allele is characterized by a large deletion in the first intron (Fu et al., 2005). A relatively rare allele, *Vrn-D1b,* is associated with facultative growth habit (Zhang et al., 2012). The *Vrn-D1b* allele has the same deletion in intron 1 as *Vrn-D1a*, and, in addition, possesses a SNP in the promoter region (Zhang et al., 2012). Rousset et al. (2011) identified facultative-types, also referred to as semi-winter or intermediate growth habit types, that had their vernalization requirement met with a 4-week vernalization treatment. This behavior was explained by differences at the *Vrn-D1* locus which had spring alleles (*Vrn-D1a* and *Vrn-D1b*) that maintain a greater response to vernalization than spring alleles at *Vrn-A1* and *Vrn-B1* loci (Rousset et al., 2011).

The *VRN2* gene encodes two linked zinc finger CCT domain genes (*ZCCT1* and *ZCCT2*) that act as flowering repressors and are down-regulated in response to cold temperatures and short days (Yan et al., 2004b). *VRN2* expression decreases when plants are vernalized, whereas expression of *VRN1* increases in response to vernalization (Trevaskis et al., 2007). The *VRN3* gene is located on the short arm of chromosome 7B and is up-regulated by cold temperatures and long days to accelerate the development of the floral meristem (Yan et al., 2006). The *VRN3* gene has been identified as an orthologue of the FLOWERING LOCUS T (FT) gene in *Arabidopsis* (Yan et al, 2006; Cockram et al., 2007). FLOWERING LOCUS T acts as a long distance flowering signal that moves from leaves to apices and promotes flowering in a diversity of plant species by inducing meristem identity genes (Yan et al., 2006). The *VRN3* gene promotes the transcription of *Vrn-1* alleles, thereby overcoming the repression of *VRN2* and accelerating flowering time in wheat (Yan et al., 2006).

Photoperiod

Wheat genotypes are classified as photoperiod sensitive (require long days to flower) or photoperiod insensitive (day length neutral) with ancestral wheats being photoperiod sensitive. The response to photoperiod is controlled primarily by photoperiod genes (*Ppd-A1*, *Ppd-B1*, and *Ppd-D1*), located on the group 2 chromosomes in wheat (Welsh et al., 1973; Law et al., 1978), which are members of the *pseudo-response regulator* (*PPR*) gene family (Worland et al., 1998; Beales et al., 2007). Alleles at *Ppd-D1* have a greater effect on controlling heading date than alleles at *Ppd-B1* which have a greater effect on heading date than alleles at *Ppd-A1* (Scarth and Law, 1984; Worland, 1996; Worland et al., 1998; Grogan et al., 2016). Dominant alleles at photoperiod loci (*Ppd-A1a*, *Ppd-B1a*, and *Ppd-D1a*) confer day length insensitivity and earlier

flowering, whereas wild type, recessive alleles (*Ppd-A1b*, *Ppd-B1b*, and *Ppd-D1b*) confer day length sensitivity and later flowering (Pugsley, 1966; Scarth and Law, 1984). A photoperiod insensitive genotype can transition to reproductive growth when temperature increases in the spring, whereas a photoperiod sensitive genotype remains in the vegetative phase until the day length increases to satisfy the photoperiod requirement.

Among European and Chinese cultivars the major allele for photoperiod insensitivity is the *Ppd-D1a* allele (Worland, 1996; Yang et al., 2009). The *Ppd-D1a* allele contains a 2,089 bp deletion in the promoter region which is associated with photoperiod insensitivity (Beales et al., 2007). The ability of photoperiod insensitive genotypes to flower earlier is advantageous in warmer environments because plants can complete development and grain filling before the onset of high summer temperatures and associated water deficit (Beales et al., 2007). Worland (1996) reported that the *Ppd-D1*a allele had a positive effect on increasing spikelet fertility and thus higher grain set per spike. Langer et al. (2014) observed that the *Ppd-D1a* allele is rare in the United Kingdom, Denmark, Germany, Poland, and Czech Republic germplasm, but is common in French, eastern European, and Russian germplasm. The *Ppd-B1a* allele is characterized by a 308 bp insertion in the 5'-upstream region (Nishida et al., 2013). In wheat, the photoperiod insensitive *Ppd-B1a* allele is carried by the cultivar 'Chinese Spring' (Nishida et al., 2013). It has also been shown that copy number variation in *Ppd-B1* alleles can alter flowering time in plants with a photoperiod sensitive phenotype (Díaz et al., 2012). Grogan et al. (2016) reported that the photoperiod insensitive alleles *Ppd-D1a* and *Ppd-B1a* were present at higher levels in germplasm from the southern plains than those from the central or northern plains in the U.S.

Additional Genes Influencing Low Temperature Tolerance

Any factor that lengthens the vegetative stage, such as an increased vernalization requirement or photoperiod sensitivity, also increases the duration and expression of LT tolerance (Fowler et al. 1996; Mahfoozi et al. 2000; Limin and Fowler 2006). Although the vernalization and photoperiod loci have been shown to influence LT tolerance, studies have associated at least 15 out of 21 different pairs of chromosomes with LT tolerance in wheat (Stushnoff et al., 1984; Sutka, 1994). Increased transcription levels of *COR14b*, *WCS120*, and *CBF* genes are observed in winter cereals when plants are exposed to low temperatures (Crosatti et al., 1995, Sarhan et al., 1997; Medina et al., 1999). The *COR14b* gene encodes a polypeptide that accumulated in the stroma fraction of the chloroplasts, and has been shown to be differentially expressed in cold-tolerant and cold-susceptible plants (Crosatti et al., 2003). The COR14b protein helps to protect the photosynthetic mechanisms from photodamage during light exposure following freezing temperatures (Rapacz et al., 2008). The accumulation of the WCS120 protein also shows a positive correlation with freezing tolerance (Sarhan et al., 1997). WCS120 belongs to the dehydrin group of proteins which are associated with the protection of cells against desiccation of other stresses caused by low-temperature induced dehydration (Sarhan et al., 1997). The *CBF* genes, encode transcription factors that bind to many dehydration-responsive genes and stimulate their transcription (Stockinger et al., 1997). Many of these genes have loci that map to a region known as the FROST RESISTANCE 2 (*Fr*-A2) locus. Dhillon et al. (2010) and Limin and Fowler (2006) showed that allelic variation at *Vrn-1* loci is sufficient to determine differences in LT tolerance among wheat varieties irrespective of alleles at the *Fr-A2* locus.

Genomic Selection

Genomic selection (GS) promises to accelerate the rate of genetic gain in plant breeding for genetically complex traits, including yield, by selecting individuals of high breeding value earlier in the breeding cycle (Crossa et al., 2010; Jannink et al., 2010; Heffner et al., 2011; Burgueño et al., 2012). The GS approach is novel in that individual marker effects are not estimated based on their level of significance, but rather GS simultaneously estimates all genome-wide marker effects to predict an individual's genomic estimated breeding value (GEBV) (Meuwissen et al., 2001; Heffner et al., 2009). As the cost and efficiency of obtaining genomic information on wheat drops below the cost and efficiency of evaluating individuals over years and locations, genomic information can more affordably be leveraged to predict phenotypic performance (Bernardo, 2008; Cobb et al., 2013). This can facilitate a shortening of the breeding cycle and enable earlier selection and intercrossing of early-generation breeding material. Using rapid inbreeding methods such as single seed descent (SSD) or doubled haploids (DH), GS-based cycle time may be reduced to one or two years from the traditional five to seven years as selection of lines prior to field testing allows shortening of the generation interval typical with phenotypic selection (Heffner et al., 2010).

One of the greatest potential advantages of GS is its ability to identify individuals with higher breeding values without the requirement of collecting phenotypes pertaining to those individuals. It has been shown that selection of individuals based on GEBV can substantially increase the rate of genetic gain in plant breeding compared to traditional marker-assisted selection (MAS) or phenotypic selection (Bernardo and Yu, 2007; Heffner et al., 2011). Simulation and empirical GS studies have shown GEBV prediction accuracies high enough to

generate rapid gains in early selection cycles (Meuwissen et al., 2001; Lorenzana and Bernardo, 2009; Jannink et al., 2010).

Training Population

Genomic selection prediction models are developed using a training population consisting of individuals with both genome-wide marker genotypes and phenotypes of interest. These individuals are used to train a model by simultaneously estimating the contribution of marker effects to their phenotypic value. Genomic selection models utilize information gathered from the training population to estimate a breeding value and predict the performance of breeding lines without phenotypes (Cobb et al., 2013).

Dense marker coverage is needed in order to maximize the number of QTL in linkage disequilibrium (LD) with at least one marker, thereby maximizing the number of QTL effects captured by the molecular markers (Heffner et al., 2009; Spindel et al., 2013). The minimum number of markers to achieve this coverage depends on LD decay rates, the size of linkage blocks, population size and structure, recombination, and relatedness between individuals in the training and test populations (Flint-Garcia et al., 2003; De Roos et al., 2009; Hickey et al., 2014). Crossa et al. (2010) were able to show that even with a modest number of molecular markers (n=1447), models for GS can attain relatively high prediction accuracies for traits of economic interest. Overall, increasing marker density has been shown to increase GS prediction accuracy while reducing the number of markers has been shown to result in a small but significant decrease in GS prediction accuracy (Lorenzana and Bernardo, 2009; Heffner et al., 2011). With a large number of genetic markers (Lorenzana and Bernardo, 2009; Heffner et al., 2011) there will often be more effects to be estimated than there are phenotypic data points

for which to estimate them (Heffner et al., 2009). This is known as the 'large *p*, small *n* problem' and is a concern for GS as it can cause over-fitting of the model which exaggerates minor fluctuations in the data (Nakaya and Isobe, 2012) and is due to collinearity between markers (Lorenz et al., 2011). This creates a model that is highly accurate when evaluating the training population but has poor predictive ability when applied to a different test population (Nakaya and Isobe, 2012). This effect can be resolved by scaling down the number of markers analyzed in proportion to the size of the training population. Research has shown that GS models have diminishing returns for additional markers once the populations have reached the point of 'marker saturation' (Lorenzana and Bernardo, 2009; Jannink et al., 2010; Heffner et al., 2011).

One of the most important factors in developing a GS model is the composition of individuals included in the training population set. Prediction accuracies are maximized when the training population and the test population (selection candidates) are closely related (Heffner et al., 2009; Lorenz and Smith, 2015). More closely related individuals share a common ancestry fewer generations back, and, therefore, fewer opportunities for recombination between markers and QTL, thus preserving QTL-marker linkage phases (Lorenz and Smith, 2015). Several studies have shown that training population size has a greater impact on GS prediction accuracy than marker number with a smaller training population size having a strong negative effect on GS prediction accuracy (Heffner et al., 2011; Lorenz et al., 2011). Studies have shown that combining genotypes from multiple populations in order to create a larger training population results in higher prediction accuracies than analysing individual populations with fewer genotypes in the training population (Hayes et al., 2009; Crossa et al., 2010; Asoro et al., 2011; Schulz-Streeck et al., 2012). Yet, Lorenz and Smith (2015) found that using the whole

training population was consistently less predictive than using a subset of the training population selected using only highly related individuals.

Imputation

The development of molecular markers for wheat is a formidable challenge due to wheat's large polyploid genomes. Reducing genome complexity with restriction enzymes coupled with multiplex next-generation-sequencing (NGS) for high-density SNP discovery and genotyping was originally demonstrated with restriction site associated DNA (RAD) tagging (Baird et al., 2008). A more recent development in genotyping technology is genotyping by sequencing (GBS), an adaptation of NGS protocols to simultaneously discover polymorphic markers in populations of interest. This sequence-based genotyping approach reduces ascertainment bias associated with marker discovery panels (Poland and Rife, 2012). Genotyping-by-sequencing was developed as a simple but robust approach for complexity reduction in large complex genomes (Elshire et al., 2011). Genotyping-by-sequencing holds the potential to close the genotyping gap between references of broad interest and mapping or breeding populations of local or specific interest (Spindel et al., 2013). For breeding applications, informative polymorphisms can be discovered as novel germplasm is introduced into the breeding population. The GBS approach targets the genomic sequence flanking restriction enzyme sites to produce a reduced representation of the genome. The original GBS approach used a single restriction enzyme (Elshire et al., 2011), but it has now been developed into a two-enzyme GBS approach (Poland et al., 2012b). DNA barcoded adapters are used to sequence multiple samples in parallel on a single run of NGS platforms (multiplexing). Multiplex sequencing is accomplished by tagging randomly sheared DNA fragments from different

samples with unique, short DNA barcode sequences and pooling samples into a single sequencing reaction.

Depending on the level of multiplexing, GBS in large populations typically results in low sequencing coverage and a large proportion of missing data (Deschamps et al., 2012; Poland et al., 2012a). Depending on the genome, the type of GBS libraries, and the overall size of the datasets, the imputation of missing data has been shown to help increase prediction accuracy (Poland et al., 2012a). The multivariate normal expectation maximization (MVN-EN) algorithm (Dempster et al., 1977) imputes based on the realized relationship matrix (averaged over all markers) and was shown to be more accurate than imputation based on mean allele calls in a population of individuals or giving missing genotypes heterozygous allele calls (Poland et al., 2012a).

Genomic Selection Models

The GS concept encompasses a broad range of methods. Their common feature is to estimate the breeding values of individuals for quantitative traits using whole genome genotypes through the simultaneous estimation of marker effects in a single step. With the increased popularity of GS in plant breeding, numerous models (ridge regression-best linear unbiased prediction, Bayesian regression, kernel regression, and machine learning) have been proposed. A ridge regression-best linear unbiased prediction (RR-BLUP) model makes the assumption that markers are random effects having nonzero effects with equal marker variance (Meuwissen et al., 2001). This assumption does not mean the effects of all markers are equal; rather they are all equally shrunk toward zero (Jannink et al., 2010). By shrinking all marker effects to the same degree and including all markers in the model, the use of RR-BLUP is best

suited for traits controlled by many loci with small effects (Meuwissen et al., 2001; Lorenz et al., 2011). Bayesian models address the simple but likely unrealistic assumptions that all markers have nonzero effects and that markers have equal variance. Bayesian models relax these two assumptions and better model marker effects of differing sizes (Meuwissen et al., 2001). Bayesian models estimate a separate variance for each marker, and the variances are assumed to follow a specified prior distribution (Meuwissen et al., 2001). Meuwissen et al. (2001) proposed two types of prior distribution for marker variances: the first type (BayesA) allowed variance toward zero, but did not permit the value of zero itself, while the second type (BayesB) allowed markers to have a variance of zero. BayesC π assumed common marker variance and allows for some markers to have no effect (Jannink, 2010; Heffner et al., 2011). Meuwissen et al. (2001) concluded that Bayesian methods outperformed RR-BLUP through better estimation of large-effect QTL by allowing for unequal variances. Heffner et al. (2011) compared the accuracy of four different GS models (RR-BLUP, BayesA, BayesB, and BayesC π) and observed only slight differences between their accuracies for 13 different agronomic traits and concluded that GS accuracy was not strongly influenced by model choice. One of the draw backs of the Bayesian approach is its computational complexity which results in long run times (Cobb et al., 2013) which has led many researchers and breeders to rely on the RR-BLUP model.

The best approach for using molecular markers in GS largely depends on the genetic architecture of the trait (Bernardo, 2008). For a given number of markers (N_M), RR-BLUP assumes that each marker accounts for $(1/N_M)^{th}$ of the total genetic variation (V_G). If one of the markers corresponds to a known major gene, the assumption of common variance for the known major gene leads to an underestimation of the estimated effects of the major gene

(Bernardo, 2014). An alternative to the modelling all genes as random effects with equal variance is to model known major genes or QTLs as fixed effects in a model with genome-wide markers as random effects. RR-BLUP models with fixed effects of major genes were shown to provide greater GS prediction accuracy when trait heritability was high and a large percentage of V_G was explained by the major genes (Bernardo, 2014). It was also shown that as the number of training population individuals decreased, it became more advantageous to consider major genes as fixed effects rather than random effects (Bernardo, 2014). These results were consistent whether there was a single major gene or whether there were multiple major genes (Bernardo, 2014). Although treating a major gene as a fixed effect can increase GS prediction accuracy, using a major gene as a fixed effect puts a stronger selection pressure on the major gene which can lead to more drastic changes in gene frequency (Bernardo, 2014).

In this study I expect to identify FAWWON genotypes that are genetically diverse from SRPN genotypes. There will be a number of FAWWON lines that show high and stable yield across some of Colorado's environments. These high yielding FAWWON lines will help to expand the genetic diversity of U.S. hard winter wheat lines currently being grown in the U.S. Great Plains. I expect to see allelic diversity at vernalization and photoperiod loci in FAWWON genotypes that can help to explain differences in low temperature tolerance. Due to the quantitative nature of low temperature tolerance in wheat, I will see that a model with major loci treated as fixed effects in combination with minor loci treated as random effects will result in a high level of GS prediction accuracy.

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HIGH YIELDING FACULTATIVE AND WINTER WHEAT GENOTYPES FROM EASTERN EUROPE AND CENTRAL ASIA CAN INCREASE THE GENETIC DIVERSITY OF U.S. HARD WINTER WHEAT

International exchange of improved germplasm is important in addressing existing and emerging constraints to global wheat (*Triticum aestivum* L.) production. Elite breeding lines tested in international and regional performance nurseries represent the most advanced materials from a collection of breeding programs and bring attention to a pool of genotypes for cultivar release or use as parents in future crosses (Peterson and Pfeiffer, 1989; Graybosch and Peterson, 2010, 2012; Sharma et al., 2010, 2012, 2014). The International Winter Wheat Improvement Program (IWWIP) is a cooperative breeding program between the Ministry of Agriculture and Rural Affairs of Turkey, the International Maize and Wheat Improvement Center (CIMMYT), and the International Center of Agricultural Research in the Dry Areas (ICARDA) (Morgounov et al., 2005). The IWWIP distributes the Facultative and Winter Wheat Observation Nursery (FAWWON) comprised of high yielding, advanced breeding lines to facilitate introduction and exchange of improved germplasm globally for irrigated and dryland production systems (Sharma et al., 2010, 2012).

Regional nursery collections also play an important part in facilitating germplasm exchange among breeding programs. The Great Plains of North America represents one of the world's largest areas of winter wheat production (Graybosch and Peterson, 2012). Each year, public and private breeding programs in the central and southern Great Plains submit their highest performing experimental lines to be part of the Southern Regional Performance Nursery (SRPN) (Graybosch and Peterson, 2010, 2012). The SRPN supports the evaluation and

exchange of germplasm among public and private wheat breeding programs and is a vital component of maintaining genetic diversity in the Great Plains region.

Understanding the levels and distribution of genetic diversity in germplasm collections allows for the development of strategies for genetic resource management and exploitation. The development of genome-wide association studies (GWAS) to identify quantitative trait loci (QTLs) underlying complex traits in large collections has been constrained by population structure in plant genetics (Yu et al., 2006). The existence of subpopulation structure with an unequal allelic distribution within a GWAS panel can result in spurious associations and is the primary obstacle to successful GWAS (Buckler and Thornsberry, 2002; Zhao et al., 2007).

Genomic selection (GS) is a technique that leverages genome-wide DNA markers with plant phenotypes to enable trait prediction earlier in the breeding cycle to potentially accelerate genetic gain for genetically complex traits (Meuwissen et al., 2001; Crossa et al., 2010; Jannink et al., 2010; Burgueño et al., 2012). Genomic selection prediction accuracies may be maximized when the training population and the selection candidates are closely related (Lorenz and Smith, 2015). Using rapid inbreeding methods such as single seed descent (SSD) or doubled haploids (DH), GS-based cycle time in winter wheat may be reduced to one or two years from the traditional five to seven years (Heffner et al., 2010). Genetic gain in early selection cycles may be dramatically high, but rapid cycling using GS may ultimately increase the rate of loss of genetic diversity through a reduction of the effective population size and loss of rare alleles (Jannink, 2010; Heslot et al., 2015). Identification and introgression of new and favorable alleles will be needed to enhance genetic diversity and sustain long-term gains while implementing GS in wheat (Heslot et al., 2015).

Genetic diversity and population structure have been evaluated in wheat collections using molecular markers, such as random amplified polymorphic DNA (RAPD; Joshi and Nguyen, 1993), restriction fragment length polymorphism (RFLP; Siedler et al., 1994; Kim and Ward, 2000), amplified fragment length polymorphism (AFLP; Barrett and Kidwell, 1998), simple sequence repeats (SSR; Röder et al., 2002; Balfourier et al., 2007; Zhang et al., 2010) and diversity arrays technology (DArT; White et al., 2008; Dreisigacker et al., 2012; Cabrera et al., 2014). Single nucleotide polymorphism (SNP) markers have become the preferred marker for genetic studies due to their greater abundance in the genome and amenability to low cost high-throughput genotyping (Varshney et al., 2006).

In wheat, several studies have examined genetic diversity by various methods including genetic distance, coefficient of parentage, principal component analysis (PCA), and model-based approaches (Barrett and Kidwell, 1998; Kim and Ward, 2000; Chao et al., 2007; White et al., 2008; Prasad et al., 2009; Hao et al., 2011; Cabrera et al., 2014). Conclusions from these studies have been somewhat conflicting, with some studies reporting that population structure corresponds to geographic origin (Kim and Ward, 2000; Balfourier et al., 2007; Chao et al., 2007; Tommasini et al., 2007; Le Couviour et al., 2011; Beil et al., 2017) and other studies reporting a lack of population structure (Rief et al., 2011; Benson et al., 2012; Würschum et al., 2013).

Although intensive plant breeding is generally considered to be a practice that leads to reduced genetic diversity (Tanksley and McCouch, 1997; Fu et al., 2003; Roussel et al., 2004; Warburton et al., 2006), results have shown that increased genetic diversity within a breeding population can be achieved through introgression of diverse germplasm (Reif et al., 2005;

Warburton et al., 2006; Fu et al., 2007). Our objectives in this study were to use SNP markers obtained using genotyping-by-sequencing (GBS) to i) identify subpopulation structure among genotypes from the FAWWON and SRPN using a model-based approach, ii) compare subpopulation structure between each genotype's nursery and country of origin, and iii) determine if the highest yielding FAWWON lines from three years of yield trials in Colorado would increase genetic diversity in the U.S. hard winter wheat gene pool.

Materials and Methods

Germplasm and field evaluation

I analysed 345 genotypes, including 272 genotypes from three years of the FAWWON (20th FAWWON, 21st FAWWON, and 22nd FAWWON) and 73 genotypes from two years of the SRPN (2014, 2015). The FAWWON genotypes originated from breeding programs in Bulgaria, Iran, Kazakhstan, Romania, Russia, Syria, Turkey, and The United States (U.S.), and genotypes resulting from collaborations between countries including Turkey-CIMMYT-ICARDA (TCI), Mexico-TCI, and U.S.-TCI. The SRPN included genotypes from public and private breeding programs in Colorado, Nebraska, Kansas, Oklahoma, and Texas. The SRPN was used to represent the level of genetic diversity currently present in the breeding programs in the central and southern Great Plains.

Yield of FAWWON lines was measured in six environments, which included field experiments at both Fort Collins (sprinkler irrigated) and Julesburg (non-irrigated), Colorado in the 2014 (112 genotypes), 2015 (200 genotypes), and 2016 (186 genotypes) growing seasons. Within years, the same genotypes were grown at both locations. All 112 genotypes from the 20th FAWWON that were evaluated in 2014 were evaluated in 2015 with an additional 88

genotypes from the 21st FAWWON. Genotypes with high levels of winter injury at both locations in 2015 were not re-evaluated in 2016. Experiments in 2016 included 69 genotypes from the 20th FAWWON (third year of evaluation), 30 genotypes from the 21st FAWWON (second year of evaluation), and 87 genotypes from the 22nd FAWWON (first year of evaluation). In 2014, genotypes were arranged in an augmented row-column design with the local cultivar 'Byrd' (Haley et al., 2012) as a releated check . In 2015 and 2016, genotypes were arranged in a partially replicated row-column design with Byrd as a repeated check. Randomizations were prepared using the package DiGGer (Coombes, 2009) in R (R Development Core Team, 2014). All experiments were planted in six-row plots, 3.7 m long and 1.8 m wide, with 0.3 m spacing between rows.

Grain yield was measured with an on-combine weighing system and yields were adjusted based on 12% grain moisture. Best linear unbiased predictors (BLUPs) of yield were calculated separately for each environment using ASReml-R (Gilmour et al., 2009; VSN International Ltd., Hemel Hempstead, UK). Data for each environment were analyzed with a series of spatial models that included genotype, row, and column coordinates as random effects, and several different residual error terms specified in the *rcov* argument within ASReml-R. The restricted maximum likelihood (REML) loglikelihood value was used to select the best model. The top 10 yielding FAWWON genotypes, based on BLUPs from each of the six field environments in Colorado, were identified as superior yielding genotypes.

GBS-based SNP genotyping

Genomic DNA was extracted from bulked leaves of 10 one-wk-old seedlings at the single leaf stage in a 96-well format using King Fisher 96 magnetic bead extraction kits on the King

Fisher Flex Purification System (ThermoFisher Scientific Inc., Waltham, MA, U.S.A.). Genotyping-by-sequencing library construction was carried out using the restriction enzymes *PstI and MspI* using a protocol modified from Poland et al. (2012). A single blank was included in each plate at random locations for quality control to ensure library identity. Sequencing was performed at 192-plex on an Illumina Hi-Seq 2000 at the DNA core facility at the University of Missouri in Columbia, MO. Single-nucleotide polymorphism calls were made using the TASSEL-GBSv1 Pipeline (Glaubitz et al., 2014) which is a reference-based SNP calling procedure. The International Wheat Genome Sequencing Consortium (IWGSC) Chromosome Survey Sequence was used as the reference genome (IWGSC, 2014). A subset of SNPs shared between the SRPN and FAWWON genotypes were identified and only this shared subset was used in subsequent analyses.

GBS marker filtering

A total of 21,484 SNP markers was obtained using GBS and shared between the FAWWON and SRPN individuals. A subset of 983 markers from the 21,484 markers was created by filtering out markers with more than 5% missing data. The polymorphism information content (PIC) value for each of the 983 markers was calculated as 1- $\sum_i^n p_i^2$, where p_i is the proportion of the population carrying the *i*th allele (Anderson et al., 1993). For bi-allelic markers such as SNPs, the PIC values can range from 0 (fixation of one allele) to 0.5 (equal allele frequencies). The average PIC for this subset of markers was 0.35 and markers with a PIC value less than 0.25 across all genotypes were removed. This PIC value was used to reduce the GBS marker subset to the most discriminating SNP markers for population structure analysis. Markers that were that were immediately adjacent to each other and had the same PIC value

were reduced to a single marker in order to satisfy the no-linkage assumption for analysis in the software program STRUCTURE 2.3.4 (Pritchard et al., 2000). Chromosome positions were available for all markers retained.

Model-based population structure analysis

The software program STRUCTURE 2.3.4 (Pritchard et al., 2000) was used to assign individuals to subpopulations based on their genotypes at multiple loci using a Bayesian approach and an admixture model with correlated allele frequencies. No external *a priori* information was used with the model for determining population structure. Five independent runs were performed for *K* (subpopulations) values of 2 to 12 for the model. A burn-in period of 15,000 iterations and data collection of 50,000 Markov chain Monte Carlo (MCMC) iterations were determined to be adequate based on the convergence summary statistics. The best separator for the number of subpopulations was determined by selecting the *K* associated with the highest delta *K* value (Evanno et al., 2005) using the program STRUCTURE HARVESTER (Earl, 2012). A series of 25 independent runs were then performed for the selected *K* for the model with a burn-in period of 25,000 iterations and data collection of 100,000 MCMC iterations. Outputs from STRUCTURE were integrated using the program CLUMPP (Jakobsson and Rosenberg, 2007) under the *FullSearch* algorithm to estimate an average membership coefficient (Q-matrix) for each genotype from the 25 independent runs for the optimized *K* value.

Genotypes with membership coefficients greater than or equal to 50% were assigned to a distinct subpopulation. Individuals with less than the minimum membership coefficient value required to be assigned to a single population were classified as “Mixed”. The genetic variation

between subpopulations, expressed as Wright's fixation index (F_{st}), was measured using analysis of molecular variance (AMOVA) implemented in STRUCTURE.

Principal component analysis

Principal component analysis was performed to visualize the dispersion of subpopulations, nursery of origin, and superior genotypes among the FAWWON and SRPN genotypes using SNPs. Eigenvector values for PCA were calculated using the base function 'eigen' in R 3.2.2 (R Development Core Team, 2014) and plotted using the ggplot package (Wickham, 2009) in R. Missing marker data were imputed with the mean marker value using the A.mat function in the rrBLUP package (Endelman, 2011) in R. The markers used for PCA were the same subset used after GBS marker filtering with the addition of the imputed missing markers.

Results and Discussion

SNP markers

There were 491 SNP markers with less than 5% missing data, PIC values greater than 0.25, and not immediately adjacent with each other. These 491 highly polymorphic SNP markers were spread across all seven chromosomes on all three genomes (Figure 2.1). Among the 491 SNPs, 219 were located on B genome chromosomes while 189 were on A genome chromosomes and 83 were on D genome chromosomes. This resulted in an average of 31 SNPs per chromosome for the B genome, 27 for the A genome, and 12 for the D genome. The greatest SNP coverage was on chromosome 5B with 73 SNPs while the lowest coverage was on chromosomes 3D and 4D with one SNP each (Figure 2.1). The distribution of SNP markers

across the three genomes in our study was in agreement with previous studies. Using RFLP markers in a collection of winter wheat genotypes, Siedler et al. (1994) showed that the greatest number of markers was across the B genome while the lowest number of markers was across the D genome. Similar results for hexaploid wheat were reported with SSR markers (Huang et al., 2002; Chao et al., 2007), DArT markers (Dreisigacker et al., 2012), and other GBS-derived SNP markers (Poland et al., 2012).

Subpopulation structure among FAWWON and SRPN genotypes

Clear evidence of population structure was evident among the 345 genotypes. Based on the highest delta K value (Evanno et al., 2005), four unique subpopulations were identified using a correlated allele frequencies model with admixture. Under this model, subpopulations were defined as having a high percentage of genotypes from either the FAWWON or the SRPN. Population A included 54 total genotypes with 96.3% from the FAWWON (Table 2.1), population B included 130 total genotypes with 99.2% from the FAWWON, population C included 32 genotypes exclusively from the FAWWON, and population D included 67 total genotypes with 83.6% from the SRPN and 16.4% from the FAWWON. These results indicate that there are genetic differences between U.S. hard winter wheat genotypes and genotypes found in the FAWWON, and that subpopulation classification agreed closely with the nursery of origin. With only a small amount of overlap between subpopulation assignments between FAWWON and SRPN genotypes, the U.S. hard winter wheat breeding programs in the central and southern Great Plains could increase their genetic diversity by incorporating FAWWON genotypes into their breeding programs. Likewise, the U.S. hard winter wheat gene pool could

serve as an additional source of new genetic diversity for breeding programs in eastern Europe and central and western Asia.

The model-based methods developed by Pritchard et al. (2000) allow for the inclusion of admixed individuals whose genetic composition is drawn from more than one of *K* subpopulations. This assumption fits well with international nursery collections as individuals are often assigned to one or more subpopulations due to a history of germplasm exchange and utilization between different breeding programs. With the potential for genotypes to have partial membership in four subpopulations, some individuals did not show the 50% membership threshold required to be assigned to a single population and thus were classified as Mixed. The Mixed genotypes included 62 individuals from both nurseries with 77.4% from the FAWWON and 22.6% from the SRPN (Table 2.1). The IWWIP makes crosses between the best performing U.S. genotypes and genotypes from eastern European and central and western Asian countries (Morgounov et al., 2012) which could explain the higher proportion of Mixed individuals in the FAWWON compared to the SRPN.

The F_{ST} value, calculated using STRUCTURE, is defined as the degree of correlation of gametes within subpopulations relative to gametes drawn at random from the entire population. The F_{ST} values ranged from 0.16 to 0.32 across the four subpopulations indicating subpopulation differentiation (Table 2.2). The highest F_{ST} value of 0.32 was between population A (n=54) and population C (n=32) despite each of these two subpopulations being almost exclusively FAWWON genotypes. This result was surprising but shows that U.S. hard winter wheats genotypes are not as genetically divergent from the FAWWON genotypes as the subpopulation classifications showed. The three highest F_{ST} values across all subpopulation

combinations were observed for subpopulation C. This may be in part due to its small sample size or possibly due to the uniqueness of the alleles in the germplasm of the subpopulation. Subpopulation C was the only subpopulation that did not have some genotypes from both the FAWWON and the SRPN (Table 2.1). The lowest F_{ST} value observed was 0.16 between subpopulations A and B which both consist of predominantly FAWWON genotypes, indicating that these two subpopulations are more genetically related. Using DArT marker genotyping, Dreisigacker et al. (2012) reported F_{ST} values of 0.11 to 0.73 across five subpopulations of 606 spring wheat lines from 25 years of CIMMYT's Elite Spring Wheat Yield Trial. Cabrera et al. (2014) reported F_{ST} values of 0.16 to 0.57 across five subpopulations of soft winter wheat lines from the eastern U.S. The F_{ST} values between subpopulation D, which included predominantly U.S. hard winter wheat genotypes, and the other subpopulations, which included predominantly FAWWON genotypes, indicate that genotypes from the FAWWON and those from the U.S. hard winter wheat region are unique enough to possess unique alleles.

Subpopulation structure by country

Although genotypes from the FAWWON were assigned to all four subpopulations and the Mixed subpopulation, indicating extensive diversity in this collection, there were differences in subpopulation structure among countries and inter-country collaborations. A majority of genotypes from Kazakhstan and Romania were assigned to subpopulation A while a majority of genotypes from Iran, Mexico-TCI, Russia, TCI, and U.S.-TCI were assigned to subpopulation B (Table 2.3). No country had a majority of their genotypes assigned to population C despite eight of the 11 countries and collaborations having genotypes assigned to subpopulation C. Genotypes from the SRPN were exclusively from the U.S. (U.S.-SRPN) and

were predominantly assigned to subpopulation D which also included the largest percentage of genotypes from Turkey. The assignment of SRPN genotypes to population D is in contrast to the assignment of U.S.-TCI genotypes and U.S. genotypes that were part of the FAWWON (U.S.-FAWWON). The U.S.-TCI genotypes were predominantly assigned to subpopulation B while U.S. genotypes in the FAWWON were predominantly Mixed (Table 2.3). Genotypes from U.S.-TCI, Mexico-TCI, and TCI would be expected to include Mixed individuals due to breeding collaborations between programs while FAWWON genotypes from Iran, Kazakhstan, and the U.S. also had a significant percentage of their genotypes classified as Mixed.

Belgium, Kazakhstan, Mexico-TCI, Romania, and Russia each included only genotypes that were assigned to subpopulations A, B, or C with none assigned to subpopulation D (Table 2.3). These results support previous reports that subpopulation structure of wheat genotypes may be partially explained by geographic origin (Kim and Ward, 2000; Balfourier et al., 2007; Chao et al., 2007; Tommasini et al., 2007; Le Couviour et al., 2011) and support the notion that subpopulation structure within the FAWWON and the SRPN collections is the result of natural or artificial selection due to climatic variables, breeding objectives unique to a program or region, or exchange of germplasm among breeding programs in a region. However, not all genotypes originating from the FAWWON were assigned to only subpopulations A, B, and C. Iran, Syria, and TCI included genotypes assigned to subpopulation D but in very low numbers while Turkey included genotypes assigned to all four subpopulations with its highest number assigned to subpopulation D.

Superior FAWWON genotypes population structure

The top ten yielding FAWWON genotypes were identified in each of six Colorado environments. Due to partial replication of genotypes across years and full replication of genotypes across locations within years, some of the top ten yielding genotypes were the same across environments. This resulted in 46 different FAWWON genotypes being identified as superior for yield performance in Colorado (Table 2.4). These superior yielding genotypes represented each of the four subpopulations with 10 from subpopulation A, 12 from subpopulation B, nine from subpopulation C, five from subpopulation D, and 10 from the Mixed group. This result shows that even genotypes from the subpopulation that is the most genetically distant from the U.S. hard winter wheat lines (subpopulation C) were shown to perform well in Colorado environments. The incorporation of superior yielding FAWWON genotypes into breeding programs in the U.S. southern and central Great Plains can introduce unique and beneficial alleles and increase the genetic diversity in the region. The 46 superior genotypes also represented eight of the 11 countries and collaborations between countries, with genotypes from Kazakhstan, Syria, and Turkey not represented.

Some of the superior yielding FAWWON genotypes showed higher grain yield than locally adapted check varieties in the irrigated environments (Fort Collins) in all three years (Table 2.4). In Fort Collins 2014, eight of the ten superior yielding FAWWON genotypes outperformed the highest yielding check variety. In Fort Collins 2015 and 2016, two of the ten FAWWON genotypes outperformed the highest yielding check variety. However, the superior yielding FAWWON genotypes were less yield-competitive with the locally adapted check varieties in the non-irriagted environments (Julesburg). Although the highest yielding FAWWON

line was lower yielding than a check variety in each Julesburg environment, certain FAWWON lines had higher grain yield than some check varieties each year. The line 20FAWWON.SA.241 was in the top ten for four of the six environments (two irrigated and two rainfed environments). Line 20FAWWON.IRR.95 was in the top ten for each of the three Julesburg environments and line 20FAWWON.SA.243 was in the top ten for three of the six environments representing both irrigated and non-irrigated environments. The divserty of high yielding entries identified here highlights the importance of participating in international and regional nurseries. By submitting lines and growing these nurseries, breeders can identify and provide superior genotypes that can be used in new regions and breeding programs. This will result in increasing the genetic diversity in their own program and the genetic diversity in others.

Principal component analysis

Principal component analysis was used to visualize the relationships among the 345 genotypes from the FAWWON and the SRPN. Principal component one (PC1) explained 7.1% of the variation in the data set while principal component two (PC2) explained 5.1% of the variation, together accounting for 12.2% of the total variation. (Figure 2.2) This is in agreement with other studies in common wheat where the first two principal components accounted for roughly 10% of the total variation present among the genotypes studied (Le Couviour et al., 2011; Würschum et al., 2013; Cabrera et al., 2014).

Under the correlated allele frequencies model, the mean PC scores for FAWWON genotypes were separated from the mean PC scores of U.S. hard winter wheat genotypes across both PC1 and PC2. This is in agreement with the FAWWON and SRPN genotypes being grouped into separate subpopulations. The mean PC scores assigned to subpopulations A and B

were separated from the mean PC scores of subpopulations C and D according to PC1, while the mean PC scores for subpopulations B and C were separated from the mean PC scores of subpopulations A and D according to PC2 (Figure 2.3). The Mixed genotypes are centrally located and are predominantly located in the transition areas separating one subpopulation from another or where genotypes belonging to different subpopulations begin to overlap.

The 46 superior yielding FAWWON genotypes can be found on both sides of PC1 and PC2 (Figure 2.4 and 2.5). This is in agreement with the best performing genotypes being composed of individuals from all four subpopulations and the Mixed group and also from multiple countries and breeding programs. The PCA of superior yielding FAWWON genotypes also demonstrates that they are not concentrated around the SRPN genotypes. This indicates that the in spite of the genetic differences between the two groups (FAWWON and SRPN), FAWWON genotypes with high grain yield under irrigated and non-irrigated production systems in Colorado may be identified. The mean PC scores of the FAWWON genotypes that had superior grain yield exclusively in the irrigated environments (n=22 entries) is separated from the mean PC value of FAWWON genotypes that had superior yield exclusively in the non-irriagted environments (n=18 entries) across PC2 (Figure 2.5). The average PC values for the FAWWON genotypes that performed best under irrigation and those that performed best under non-irriagted conditions indicate that there are different alleles or allelic combinations that allow them to be best adapted to these particular environments. FAWWON genotypes that performed best in both irrigated and non-irrigated environments (n=6 entries) have a mean PC value closer to the mean of those that performed best only in the irrigated environments and is also on the same side of PC1 as the mean value for SRPN genotypes. This may be due to SRPN

genotypes being tested and selected for adaptation to a wide range of environment conditions that include both high yielding and low yielding environments. Further analysis may be able to identify the genes and potential mechanisms that explain why some individuals in the FAWWON are better adapted to irrigated conditions while others are adapted to lower yielding environments.

Tables

Table 2.1. Number and percentage of genotypes from the two nurseries within each subpopulation.

Populations	Number	FAWWON†	SRPN
		———————%———————	
A	54	96.3	3.7
B	130	99.2	0.8
C	32	100.0	0.0
D	67	16.4	83.6
MIXED	62	77.4	22.6

† FAWWON, Facultative and Winter Wheat Observation Nursery;
SRPN, Southern Regional Performance Nursery.

Table 2.2. Wright's fixation index (F_{ST}) pairwise values among four subpopulations identified using the model-based approach in STRUCTURE.

Sub-population	B	C	D
	---------- F_{ST} ----------		
A	0.16	0.32	0.23
B	—	0.24	0.17
C	—	—	0.27

Table 2.3. Country of origin and subpopulation classification of 345 genotypes from the Facultative and Winter Wheat Observation Nursery (FAWWON) and Southern Regional Performance Nursery (SRPN).

		Sub-Population				
Origin†	Total Number	A	B	C	D	MIXED
Bulgaria	3	1	1	1	–	–
Iran	30	–	23	2	1	4
Kazakhstan	5	3	–	1	–	1
Mexico-TCI	11	1	9	–	–	1
Romania	14	8	3	3	–	–
Russia	6	1	3	2	–	–
Syria	1	–	–	–	1	–
TCI	165	37	76	18	6	28
Turkey	7	1	1	2	3	–
U.S.-TCI	25	–	13	3	2	7
U.S.-FAWWON	5				1	4
U.S.-SRPN	73	2	1	0	56	14

† TCI, Turkey-CIMMYT-ICARDA; U.S., United States; FAWWON, Facultative and Winter Wheat Observation Nursery; SRPN, Southern Regional Performance Nursery.

Table 2.4. Grain yield for the top ten yielding FAWWON genotypes and the check genotypes in each of the six tested environments and theit subpopulation assignment.

			Environments†					
Nursery	Entry	Subpopulation	FC 14	JB 14	FC 15	JB15	FC 16	JB 16
			---------- kg ha $^{-1}$ ----------					
20 FAWWON	IRR.106	A		4667				
20 FAWWON	IRR.115	Mixed				4008		
20 FAWWON	IRR.118	Mixed				4990		
20 FAWWON	IRR.12	C	8588	4802				
20 FAWWON	IRR.143	Mixed		4761				5602
20 FAWWON	IRR.15	A						5548
20 FAWWON	IRR.21	C			6725			
20 FAWWON	IRR.22	B			6786			
20 FAWWON	IRR.29	B	7983					
20 FAWWON	IRR.44	C			6765			
20 FAWWON	IRR.45	Mixed	8245			3995		
20 FAWWON	IRR.54	B	8010					
20 FAWWON	IRR.57	A		5145		4808		
20 FAWWON	IRR.59	C	8393					
20 FAWWON	IRR.88	B			7014			
20 FAWWON	IRR.9	B	8252				6813	
20 FAWWON	IRR.95	A		4963		4587		5750
20 FAWWON	IRR.97	A		4607				
20 FAWWON	SA.212	Mixed			6705			
20 FAWWON	SA.222	A		4748			6564	
20 FAWWON	SA.224	C			7425			
20 FAWWON	SA.227	C					6557	
20 FAWWON	SA.231	B			6907			
20 FAWWON	SA.235	B	8306					
20 FAWWON	SA.236	B			6920			
20 FAWWON	SA.238	B	8104					
20 FAWWON	SA.241	Mixed		4654	6927	4109	6584	
20 FAWWON	SA.243	Mixed	7949	4741			6523	
20 FAWWON	SA.256	C		4661				
20 FAWWON	SA.258	C				3907		
20 FAWWON	SA.259	A	7841					
21 FAWWON	IRR.137	D				4889		5932
21 FAWWON	IRR.141	A						5528
21 FAWWON	IRR.143	Mixed				3887		
21 FAWWON	IRR.95	D						5568
21 FAWWON	SA.210	Mixed					6819	
21 FAWWON	SA.234	D			7640			
21 FAWWON	SA.247	D				3995		

21 FAWWON	SA.287	A						5905
21 FAWWON	SA.292	C					6550	
22 FAWWON	IRR.19	B					6658	
22 FAWWON	IRR.32	B					6537	
22 FAWWON	IRR.57	B						4802
22 FAWWON	IRR.69	Mixed						5595
22 FAWWON	IRR.98	D						5710
22 FAWWON	SA.214	A					6597	
Check	Byrd	NA	7720	5098	5589	4795	6671	5750
Check	Denali	NA	7694	5291	7196	4794	6441	6335
Check	Ripper	NA	7963	4299	4324	3649	6557	5878
Check	Antero	NA	7660	5219	6819	5017	6611	6436
Check	Snowmass	NA	6598	4450	6032	4381	6260	5672
FAWWON	Mean		7115	4122	5615	2992	5972	4923

† FC 14, Fort Collins 2014 (irrigated); FC 15, Fort Collins 2015 (irrigated); FC 16, Fort Collins 2016 (irrigated); JB 14, Julesburg 2014 (non-irrigated); JB 15, Julesburg 2015 (non-irrigated); JB 16, Julesburg 2016 (non-irrigated).

Table 2.5. Nursery origin, experimental number, genotype identifier, program origin, superior genotype classification, population assignment, and dendrogram abbreviated identifier of genotypes from the Facultative and Winter Wheat Observation Nursery (FAWWON) and the Southern Regional Performance Nursery (SRPN).

Nursery	Experimental #	Name/CID	Country	State/Program	Superior	Correlated	Dendrogram
SRPN 2014, 2015	CO11D174	Avery	U.S.	CO	No	D	S_1
SRPN 2014, 2015	OK09125	Bentley	U.S.	OK	No	D	S_2
SRPN 2014	CO09W009		U.S.	CO	No	D	S_3
SRPN 2014	CO09W040-F1		U.S.	CO	No	D	S_4
SRPN 2015	CO11D1316W		U.S.	CO	No	D	S_5
SRPN 2015	CO11D1353		U.S.	CO	No	D	S_6
SRPN 2015	CO11D1397		U.S.	CO	No	D	S_7
SRPN 2015	CO11D1539		U.S.	CO	No	D	S_8
SRPN 2015	CO11D1767		U.S.	CO	No	D	S_9
SRPN 2014	CO11D346		U.S.	CO	No	D	S_10
SRPN 2014	KS061406-LN~37	Hot Rod	U.S.	KS	No	MIXED	S_11
SRPN 2014	HV9W09-0746		U.S.	WestBred	No	B	S_12
SRPN 2014	HV9W09-0918		U.S.	WestBred	No	MIXED	S_13
SRPN 2014, 2015	W98-362	Jagalene	U.S.	AgriPro	No	D	S_14
SRPN 2014	KS11HW39-5-4	Joe	U.S.	KS	No	D	S_15
SRPN 2014	KS030887K-6	KanMark	U.S.	KS	No	D	S_16
SRPN 2014, 2015		Kharkof	U.S.	Introduction	No	D	S_17
SRPN 2014	KS050278M-1		U.S.	KS	No	MIXED	S_18
SRPN 2015	KS060084-M-4		U.S.	KS	No	D	S_19
SRPN 2015	KS060106-M-11	Zenda	U.S.	KS	No	D	S_20
SRPN 2015	KS060143-K-2	Larry	U.S.	KS	No	A	S_21
SRPN 2015	KS060371-M-3		U.S.	KS	No	D	S_22
SRPN 2015	KS060476-M-6		U.S.	KS	No	MIXED	S_23
SRPN 2014	KS061406-LN~15		U.S.	KS	No	MIXED	S_24
SRPN 2014	KS061406-LN~26		U.S.	KS	No	MIXED	S_25
SRPN 2014	KS10HW78-1-1		U.S.	KS	No	D	S_26
SRPN 2015	KS11HW15-4-1		U.S.	KS	No	D	S_27
SRPN 2015	KS11HW18-1-6		U.S.	KS	No	D	S_28

SRPN 2015	KS11HW39-5-4	Joe	U.S.	KS	No	D	S_29
SRPN 2014	KS11HW39-6		U.S.	KS	No	D	S_30
SRPN 2015	KS11HW53-1-6		U.S.	KS	No	D	S_31
SRPN 2014, 2015	CO11D446	Langin	U.S.	CO	No	D	S_32
SRPN 2014	LCH09-06		U.S.	Limagrain	No	MIXED	S_33
SRPN 2014	LCH10-187		U.S.	Limagrain	No	D	S_34
SRPN 2014	LCH11-1064		U.S.	Limagrain	No	D	S_35
SRPN 2014	LCH11-109		U.S.	Limagrain	No	MIXED	S_36
SRPN 2015	LCH11-1117		U.S.	Limagrain	No	D	S_37
SRPN 2015	LCH12-012		U.S.	Limagrain	No	D	S_38
SRPN 2015	LCH13-092		U.S.	Limagrain	No	D	S_39
SRPN 2015	LCH13DH-3-31		U.S.	Limagrain	No	D	S_40
SRPN 2015	LCI13DH-14-53W		U.S.	Limagrain	No	D	S_41
SRPN 2015	LCH13DH-20-87	LCS Chrome	U.S.	Limagrain	No	MIXED	S_42
SRPN 2014	LCH11-1130	LCS Pistol	U.S.	Limagrain	No	D	S_43
SRPN 2014	N11MD2157W		U.S.	USDA-NE	No	D	S_44
SRPN 2014	N11MD2172		U.S.	USDA-NE	No	D	S_45
SRPN 2014	NE10478		U.S.	NE	No	D	S_46
SRPN 2014, 2015	NE10507		U.S.	NE	No	D	S_47
SRPN 2014	NE10589	Ruth	U.S.	NE	No	D	S_48
SRPN 2015	NE12429		U.S.	NE	No	D	S_49
SRPN 2015	NE12571		U.S.	NE	No	D	S_50
SRPN 2014	NH11489		U.S.	NE	No	D	S_51
SRPN 2015	NI13706		U.S.	NE	No	MIXED	S_52
SRPN 2014	OK09520		U.S.	OK	No	D	S_53
SRPN 2014, 2015	OK10126		U.S.	OK	No	D	S_54
SRPN 2014, 2015	OK1059060		U.S.	OK	No	MIXED	S_55
SRPN 2014	OK10728W	Stardust	U.S.	OK	No	D	S_56
SRPN 2014	OK10805W		U.S.	OK	No	MIXED	S_57
SRPN 2014, 2015		Scout 66	U.S.	NE	No	D	S_58
SRPN 2014, 2015	TX80GH2875	TAM 107	U.S.	TX	No	D	S_59
SRPN 2014	TX08A001249		U.S.	TX	No	D	S_60

SRPN 2014	TX08V7313		U.S.	TX	No	D	S_61
SRPN 2014	TX09A001194		U.S.	TX	No	D	S_62
SRPN 2014	TX09D1172		U.S.	TX	No	D	S_63
SRPN 2015	TX09V7315		U.S.	TX	No	D	S_64
SRPN 2015	TX09V7352		U.S.	TX	No	D	S_65
SRPN 2015	TX09V7446		U.S.	TX	No	D	S_66
SRPN 2015	TX10A001099		U.S.	TX	No	D	S_67
SRPN 2015	TX11A001295		U.S.	TX	No	D	S_68
SRPN 2015	TX12M4004		U.S.	TX	No	MIXED	S_69
SRPN 2015	TX12M4063		U.S.	TX	No	MIXED	S_70
SRPN 2015	TX12M4065		U.S.	TX	No	D	S_71
SRPN 2015	WB4303		U.S.	WestBred	No	A	S_72
SRPN 2015	WB4462		U.S.	WestBred	No	D	S_73
20FAWWON	IRR-10	TCI011657	TCI		No	B	F_1
20FAWWON	IRR-100	06325G1-2	ROM		No	A	F_2
20FAWWON	IRR-106	*06579G1-1	ROM		Superior	A	F_3
20FAWWON	IRR-11	TCI-02-691	TCI		No	B	F_4
20FAWWON	IRR-114	OR2071681	U.S.	OR	No	MIXED	F_5
20FAWWON	IRR-115	OR2080111H	U.S.	OR	Superior	MIXED	F_6
20FAWWON	IRR-118	Appalachian White	U.S.	NC	Superior	MIXED	F_7
20FAWWON	IRR-12	TCI022028	TCI		Superior	C	F_8
20FAWWON	IRR-13	TCI022063	TCI		No	A	F_9
20FAWWON	IRR-14	TCI022073	TCI		No	C	F_10
20FAWWON	IRR-143	NACIBEY	TCI		Superior	MIXED	F_11
20FAWWON	IRR-15	TCI022086	TCI		Superior	A	F_12
20FAWWON	IRR-16	TCI022086	TCI		No	A	F_13
20FAWWON	IRR-17	TCI022086	TCI		No	C	F_14
20FAWWON	IRR-18	TCI022216	TCI		No	MIXED	F_15
20FAWWON	IRR-19	TC1021013	TCI		No	B	F_16
20FAWWON	IRR-20	TC1021027	TCI		No	B	F_17
20FAWWON	IRR-21	TC1021032	TCI		Superior	C	F_18
20FAWWON	IRR-22	TC1021034	TCI		Superior	B	F_19

20FAWWON	IRR-23	TC1021034	TCI		No	C	F_20
20FAWWON	IRR-24	TC1021068	TCI		No	B	F_21
20FAWWON	IRR-25	TC1021152	TCI		No	B	F_22
20FAWWON	IRR-26	TC1021152	TCI		No	C	F_23
20FAWWON	IRR-27	TC1021162	TCI		No	B	F_24
20FAWWON	IRR-28	TC1021164	TCI		No	B	F_25
20FAWWON	IRR-29	TC1021187	TCI		Superior	B	F_26
20FAWWON	IRR-30	TC1021198	TCI		No	B	F_27
20FAWWON	IRR-31	TC1021243	TCI		No	C	F_28
20FAWWON	IRR-32	TC1021414	TCI		No	C	F_29
20FAWWON	IRR-33	TCI-02-45	TCI		No	B	F_30
20FAWWON	IRR-35	TCI-02-175	TCI		No	B	F_31
20FAWWON	IRR-36	OCW02S155T	U.S.-TCI	OK-TCI	No	MIXED	F_32
20FAWWON	IRR-37	OCW02S155T	U.S.-TCI	OK-TCI	No	D	F_33
20FAWWON	IRR-38	OCW02S155T	U.S.-TCI	OK-TCI	No	C	F_34
20FAWWON	IRR-39	OCW02S369S	U.S.-TCI	OK-TCI	No	B	F_35
20FAWWON	IRR-40	SONMEZ	TUR		No	C	F_36
20FAWWON	IRR-41	OCW02S471S	U.S.-TCI	OK	No	C	F_37
20FAWWON	IRR-42	OCW02S471S	U.S.-TCI	OK	No	B	F_38
20FAWWON	IRR-43	OCW02S484S	U.S.-TCI	OK	No	B	F_39
20FAWWON	IRR-44	OCW02S567S	U.S.-TCI	OK	Superior	C	F_40
20FAWWON	IRR-45	OCW02S567S	U.S.-TCI	OK	Superior	MIXED	F_41
20FAWWON	IRR-46	OCW02S567S	U.S.-TCI	OK	No	B	F_42
20FAWWON	IRR-47	OCW02S596S	U.S.-TCI	OK	No	B	F_43
20FAWWON	IRR-48	OCW02S607S	U.S.-TCI	OK	No	B	F_44
20FAWWON	IRR-49	OCW02S608S	U.S.-TCI	OK	No	B	F_45
20FAWWON	IRR-50	CMSA01M00330S	MEX-TCI		No	B	F_46
20FAWWON	IRR-51	CMSA01M00370T	MEX-TCI		No	B	F_47
20FAWWON	IRR-52	CMSA01M00381T	MEX-TCI		No	B	F_48
20FAWWON	IRR-54	CMSW01WM00578S	MEX-TCI		Superior	B	F_49
20FAWWON	IRR-55	TCI012088	TCI		No	C	F_50
20FAWWON	IRR-56	TCI-02-80	TCI		No	C	F_51

20FAWWON	IRR-57	02106G2-2	TCI		Superior	A	F_52
20FAWWON	IRR-59	TURKOAZ	BUL		Superior	C	F_53
20FAWWON	IRR-60	TEKIRA2	BUL		No	B	F_54
20FAWWON	IRR-69	IRW2000-01 - 246	IR		No	MIXED	F_55
20FAWWON	IRR-7	TCI011031	TCI		No	B	F_56
20FAWWON	IRR-70	1-C-17450	IR	Karadj	No	B	F_57
20FAWWON	IRR-71	1-C-17474	IR	Karadj	No	B	F_58
20FAWWON	IRR-72	1-C-17474	IR	Karadj	No	C	F_59
20FAWWON	IRR-74	1-C-17487	IR	Karadj	No	B	F_60
20FAWWON	IRR-75	1-C-17551	IR	Miandoab	No	B	F_61
20FAWWON	IRR-77	1-C-17560	IR	Karadj	No	B	F_62
20FAWWON	IRR-78	1-C-17603	IR	Karadj	No	C	F_63
20FAWWON	IRR-8	TCI011031	TCI		No	C	F_64
20FAWWON	IRR-85	1-NS 1590	IR	Karadj	No	B	F_65
20FAWWON	IRR-86	1-C-17630	IR	Ardebil	No	MIXED	F_66
20FAWWON	IRR-87	1-C-17630	IR	Ardebil	No	B	F_67
20FAWWON	IRR-88	1-C-17480	IR	Miandoab	Superior	B	F_68
20FAWWON	IRR-89	1-C-17551	IR	Miandoab	No	B	F_69
20FAWWON	IRR-9	TCI011214	TCI		Superior	B	F_70
20FAWWON	IRR-95	OTILIA	ROM		Superior	A	F_71
20FAWWON	IRR-97	06393GP1	ROM		Superior	A	F_72
20FAWWON	IRR-98	05899G01-2	ROM		No	C	F_73
20FAWWON	SA-202	KARAHAN	TUR		No	C	F_74
20FAWWON	SA-206	TC1021032	TCI		No	C	F_75
20FAWWON	SA-207	TC1021068	TCI		No	B	F_76
20FAWWON	SA-208	TC1021160	TCI		No	B	F_77
20FAWWON	SA-209	TC1021180	TCI		No	C	F_78
20FAWWON	SA-210	TC1021198	TCI		No	B	F_79
20FAWWON	SA-212	TC1021243	TCI		Superior	MIXED	F_80
20FAWWON	SA-213	TC1021266	TCI		No	B	F_81
20FAWWON	SA-214	TC1021276	TCI		No	MIXED	F_82
20FAWWON	SA-215	TC1021276	TCI		No	C	F_83

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20FAWWON	SA-221	TCI022086	TCI		No	A	F_85
20FAWWON	SA-222	TCI022108	TCI		Superior	A	F_86
20FAWWON	SA-223	TCI022191	TCI		No	MIXED	F_87
20FAWWON	SA-224	TCI022200	TCI		Superior	C	F_88
20FAWWON	SA-226	TCI022271	TCI		No	B	F_89
20FAWWON	SA-227	TCI022271	TCI		Superior	C	F_90
20FAWWON	SA-228	TCI-02-87	TCI		No	A	F_91
20FAWWON	SA-230	TCI-02-111	TCI		No	B	F_92
20FAWWON	SA-231	TCI-02-129	TCI		Superior	B	F_93
20FAWWON	SA-232	TCI-02-142	TCI		No	MIXED	F_94
20FAWWON	SA-233	TCI-02-26	TCI		No	C	F_95
20FAWWON	SA-235	TCI-02-36	TCI		Superior	B	F_96
20FAWWON	SA-236	TCI-02-913	TCI		Superior	B	F_97
20FAWWON	SA-237	OCW02S262T	U.S.-TCI	OK-TCI	No	B	F_98
20FAWWON	SA-238	OCW02S528S	U.S.-TCI	OK-TCI	Superior	B	F_99
20FAWWON	SA-239	OCW02S567S	U.S.-TCI	OK-TCI	No	B	F_100
20FAWWON	SA-241	OCW02S596S	U.S.-TCI	OK-TCI	Superior	MIXED	F_101
20FAWWON	SA-243	IRW2000-01 - 246	IR		Superior	MIXED	F_102
20FAWWON	SA-244	1-C-17459	IR	Karadj	No	MIXED	F_103
20FAWWON	SA-249	AK-B?BA?	KAZ		No	A	F_104
20FAWWON	SA-251	KARASAY	KAZ		No	C	F_105
20FAWWON	SA-252	ZHADYRA	KAZ		No	A	F_106
20FAWWON	SA-254	NIKIFOR	ROM		No	C	F_107
20FAWWON	SA-256	06659G4-1	ROM		Superior	C	F_108
20FAWWON	SA-257	ELVIRA	RUS	SAR	No	C	F_109
20FAWWON	SA-258	KALACH	RUS	SAR	Superior	C	F_110
20FAWWON	SA-259	SVETOCH	RUS	SAM	Superior	A	F_111
20FAWWON	SA-278	BDME 09 1/K	TUR		No	A	F_112
21FAWWON	IRR-103	MUSTANG/ICIZCE	TCI		No	B	F_113
21FAWWON	IRR-11	SHARK/F4105W2.1	TCI		No	MIXED	F_114
21FAWWON	IRR-113	TX71C8130R/TX81V66	TCI		No	B	F_115

21FAWWON	IRR-116	TX71C8130R/TX81V66	TCI		No	B	F_116
21FAWWON	IRR-119	TX71A983.4/TX69D48	TCI		No	B	F_117
21FAWWON	IRR-122	JI5418/MARAS//SHAR	TCI		No	B	F_118
21FAWWON	IRR-137	43-RWA-94N-74/	TCI		Superior	D	F_119
21FAWWON	IRR-14	ALPU//VP5053	TCI		No	B	F_120
21FAWWON	IRR-141	MINA/KRISTAL	TCI		Superior	A	F_121
21FAWWON	IRR-142	MINA/KRISTAL	TCI		No	A	F_122
21FAWWON	IRR-143	6/YUZHNAYA12	TCI		Superior	MIXED	F_123
21FAWWON	IRR-144	SHAR6/YUZHNAYA12	TCI		No	B	F_124
21FAWWON	IRR-146	CHATELET/GRU-45	TCI		No	A	F_125
21FAWWON	IRR-148	CHATELET/GRU-45	TCI		No	B	F_126
21FAWWON	IRR-150	DORADE-5/DUNAV	TCI		No	D	F_127
21FAWWON	IRR-152	1-68-188//1-60-3	TCI		No	B	F_128
21FAWWON	IRR-157	ID2619/5/GRTPL 6121	TCI		No	B	F_129
21FAWWON	IRR-16	TCI032348	TCI		No	B	F_130
21FAWWON	IRR-161	PALANDOKEN97/LLA	TCI		No	B	F_131
21FAWWON	IRR-163	NGDA146/4/YMH/TO	TCI		No	A	F_132
21FAWWON	IRR-166	SHARK-6/YUZHNAYA1	TCI		No	MIXED	F_133
21FAWWON	IRR-167	88ZHONG218//CTK/V	TCI		No	B	F_134
21FAWWON	IRR-17	OCW02S476S	U.S.-TCI	OK-TCI	No	MIXED	F_135
21FAWWON	IRR-29	TCI031171	TCI		No	B	F_136
21FAWWON	IRR-31	TCI-02-80	TCI		No	B	F_137
21FAWWON	IRR-32	TCI 001409	TCI		No	B	F_138
21FAWWON	IRR-35	TCI-01-117	TCI		No	B	F_139
21FAWWON	IRR-36	TCI-02-475	TCI		No	B	F_140
21FAWWON	IRR-43	OSTROV	ROM		No	A	F_141
21FAWWON	IRR-45	F06325G1-	ROM		No	A	F_142
21FAWWON	IRR-48	F06580G2-1	ROM		No	B	F_143
21FAWWON	IRR-49	F06659G6-1	ROM		No	B	F_144
21FAWWON	IRR-50	F06659G10-1	ROM		No	B	F_145
21FAWWON	IRR-59	NOTA	RUS		No	B	F_146
21FAWWON	IRR-62	1-C-17677	IR	Karadj	No	B	F_147

21FAWWON	IRR-64	1-C-17748	IR	Karadj	No	B	F_148
21FAWWON	IRR-66	1-C-17809	IR	Karadj	No	B	F_149
21FAWWON	IRR-68	1-C-17641	IR	Miandoab	No	B	F_150
21FAWWON	IRR-7	TCI032026	TCI		No	A	F_151
21FAWWON	IRR-71	SHİ≠4414/CROW	IR	Dari	No	B	F_152
21FAWWON	IRR-72	DMITRY	RUS		No	B	F_153
21FAWWON	IRR-75	PROTON	RUS		No	B	F_154
21FAWWON	IRR-76	KIPRA	BUL		No	A	F_155
21FAWWON	IRR-81	SWW1-135	KAZ		No	A	F_156
21FAWWON	IRR-83	SWW1-97	KAZ		No	MIXED	F_157
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21FAWWON	IRR-95	JUP/4/CLLF/3/II14-53	TCI		Superior	D	F_159
21FAWWON	SA-201	GEREK79	TUR		No	B	F_160
21FAWWON	SA-202	KARAHAN	TUR		No	MIXED	F_161
21FAWWON	SA-207	TCI031181	TCI		No	A	F_162
21FAWWON	SA-208	TCI032095	TCI		No	B	F_163
21FAWWON	SA-210	TCI032063	TCI		Superior	MIXED	F_164
21FAWWON	SA-211	TCI031039	TCI		No	B	F_165
21FAWWON	SA-214	TCI032348	TCI		No	B	F_166
21FAWWON	SA-218	TCI031020	TCI		No	D	F_167
21FAWWON	SA-223	TCI032235	TCI		No	MIXED	F_168
21FAWWON	SA-226	TCI031396	TCI		No	B	F_169
21FAWWON	SA-227	TCI032210	TCI		No	A	F_170
21FAWWON	SA-228	TCI031171	TCI		No	MIXED	F_171
21FAWWON	SA-231	TCI031286	TCI		No	B	F_172
21FAWWON	SA-234	TCI031396	TCI		Superior	D	F_173
21FAWWON	SA-243	OK07214	U.S.	OK	No	MIXED	F_174
21FAWWON	SA-247	OK09634	U.S.	OK	Superior	D	F_175
21FAWWON	SA-248	TCI011194-030	TCI		No	A	F_176
21FAWWON	SA-250	1-C-17849	IR	Miandoab	No	B	F_177
21FAWWON	SA-252	PYN/BAU//BONITO	IR	Dari	No	B	F_178
21FAWWON	SA-256	CMSW97WM00399S	TCI		No	MIXED	F_179

21FAWWON	SA-258	TCI97AP-310	TCI	No	B	F_180
21FAWWON	SA-261	TCI04-1	TCI	No	MIXED	F_181
21FAWWON	SA-262	TCI04-324	TCI	No	B	F_182
21FAWWON	SA-263	TCI02-679	TCI	No	MIXED	F_183
21FAWWON	SA-265	TCI02-405	TCI	No	MIXED	F_184
21FAWWON	SA-268	91-142 a 139	TCI	No	B	F_185
21FAWWON	SA-269	TCI 001409	TCI	No	A	F_186
21FAWWON	SA-270	TCI 002133	TCI	No	A	F_187
21FAWWON	SA-271	TCI-01-117	TCI	No	MIXED	F_188
21FAWWON	SA-275	TCI04-1	TCI	No	B	F_189
21FAWWON	SA-276	TCI04-1	TCI	No	A	F_190
21FAWWON	SA-281	TCI032527	TCI	No	B	F_191
21FAWWON	SA-286	TC1021266	TCI	No	MIXED	F_192
21FAWWON	SA-287	TCI022086	TCI	Superior	A	F_193
21FAWWON	SA-288	TCI02-87	TCI	No	A	F_194
21FAWWON	SA-289	TC1021068	TCI	No	B	F_195
21FAWWON	SA-292	TCI 002115	TCI	Superior	C	F_196
21FAWWON	SA-293	TCI031223	TCI	No	A	F_197
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21FAWWON	SA-299	TC1021027	TCI	No	B	F_199
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22FAWWON	IRR-103	SULTAN95	MEX-TCI	No	B	F_201
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22FAWWON	IRR-111	F05906G1-101	ROM	No	A	F_203
22FAWWON	IRR-14	TCI041060	TCI	No	A	F_204
22FAWWON	IRR-18	TCI041237	TCI	No	A	F_205
22FAWWON	IRR-19	TCI041261	TCI	Superior	B	F_206
22FAWWON	IRR-21	TCI041286	TCI	No	MIXED	F_207
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22FAWWON	IRR-26	TCI042153	TCI	No	B	F_209
22FAWWON	IRR-27	TCI042167	TCI	No	A	F_210
22FAWWON	IRR-31	TCI042366	TCI	No	MIXED	F_211

22FAWWON	IRR-32	TCI042619	TCI		Superior	B	F_212
22FAWWON	IRR-33	TCI042632	TCI		No	B	F_213
22FAWWON	IRR-34	TCI042638	TCI		No	A	F_214
22FAWWON	IRR-35	TCI042638	TCI		No	A	F_215
22FAWWON	IRR-41	TCI072152	TCI		No	B	F_216
22FAWWON	IRR-42	OCW05S645S	U.S.-TCI	OK-TCI	No	MIXED	F_217
22FAWWON	IRR-45	OR2052096	U.S.-TCI	OR-TCI	No	MIXED	F_218
22FAWWON	IRR-49	CMSA06WM00018T	MEX-TCI		No	B	F_219
22FAWWON	IRR-52	TCI071325	TCI		No	B	F_220
22FAWWON	IRR-53	TCI072137	TCI		No	B	F_221
22FAWWON	IRR-54	OCW05S626S	U.S.-TCI	OK	No	B	F_222
22FAWWON	IRR-55	TCI071189	TCI		No	B	F_223
22FAWWON	IRR-57	TCI071199	TCI		Superior	B	F_224
22FAWWON	IRR-60	CGWS04WM00054S	MEX-TCI		No	A	F_225
22FAWWON	IRR-66	OCW05S626S	U.S.-TCI	OK-TCI	No	B	F_226
22FAWWON	IRR-67	OCW04S037S	U.S.-TCI	OK-TCI	No	D	F_227
22FAWWON	IRR-68	TCI052118	TCI		No	B	F_228
22FAWWON	IRR-69	OCW05S594T	U.S.-TCI	OK-TCI	Superior	MIXED	F_229
22FAWWON	IRR-7	TCI021034	TCI		No	B	F_230
22FAWWON	IRR-73	TCI052022	TCI		No	B	F_231
22FAWWON	IRR-79	RUMELI	TUR		No	MIXED	F_232
22FAWWON	IRR-8	TCI021034	TCI		No	B	F_233
22FAWWON	IRR-81	CROC_1/AE.SQUARRO	MEX-TCI		No	B	F_234
22FAWWON	IRR-83	1-C-17967	IR	Karadj	No	B	F_235
22FAWWON	IRR-84	1-C-17967	IR	Karadj	No	B	F_236
22FAWWON	IRR-85	1-C-17969	IR	Karadj	No	B	F_237
22FAWWON	IRR-86	1-C-17969	IR	Karadj	No	B	F_238
22FAWWON	IRR-87	1-C-17971	IR	Karadj	No	B	F_239
22FAWWON	IRR-9	TCI02-913	TCI		No	B	F_240
22FAWWON	IRR-92	DH-26-42	IR	Karadj	No	B	F_241
22FAWWON	IRR-93	1-C-17964	IR	Miandoab	No	B	F_242
22FAWWON	IRR-98	1-C-18144	IR	Ardebil	Superior	D	F_243

22FAWWON	SA-202	KARAHAN	TUR		No	MIXED	F_244
22FAWWON	SA-211	TCI041084	TCI		No	A	F_245
22FAWWON	SA-214	TCI041237	TCI		Superior	A	F_246
22FAWWON	SA-217	TCI041347	TCI		No	MIXED	F_247
22FAWWON	SA-218	TCI041374	TCI		No	MIXED	F_248
22FAWWON	SA-221	TCI041505	TCI		No	A	F_249
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22FAWWON	SA-225	TCI042304	TCI		No	A	F_251
22FAWWON	SA-231	TCI042604	TCI		No	MIXED	F_252
22FAWWON	SA-232	TCI042609	TCI		No	B	F_253
22FAWWON	SA-235	TCI042673	TCI		No	A	F_254
22FAWWON	SA-237	TCI042691	TCI		No	B	F_255
22FAWWON	SA-248	TCI051373	TCI		No	MIXED	F_256
22FAWWON	SA-249	TCI051404	TCI		No	B	F_257
22FAWWON	SA-250	TCI051412	TCI		No	B	F_258
22FAWWON	SA-253	TCI052037	TCI		No	B	F_259
22FAWWON	SA-256	TCI052366	TCI		No	MIXED	F_260
22FAWWON	SA-258	TCI052470	TCI		No	A	F_261
22FAWWON	SA-259	TCI052479	TCI		No	A	F_262
22FAWWON	SA-260	TCI051051	TCI		No	A	F_263
22FAWWON	SA-262	TCI071116	TCI		No	A	F_264
22FAWWON	SA-263	TCI071156	TCI		No	B	F_265
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22FAWWON	SA-269	TCI072083	TCI		No	A	F_267
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22FAWWON	SA-274	CGWS04WM00052S	MEX		No	MIXED	F_269
22FAWWON	SA-277	CMSW05WM00013T	MEX		No	B	F_270
22FAWWON	SA-281	OCW05S740S	U.S.-TCI	OK-TCI	No	B	F_271
22FAWWON	SA-294	ICWH970148	SYR		No	D	F_272

† CID, CIMMYT identification for each entry available

‡ Dendrogram ID, a shortened identification for each entry used in Figure 2.6

Figures

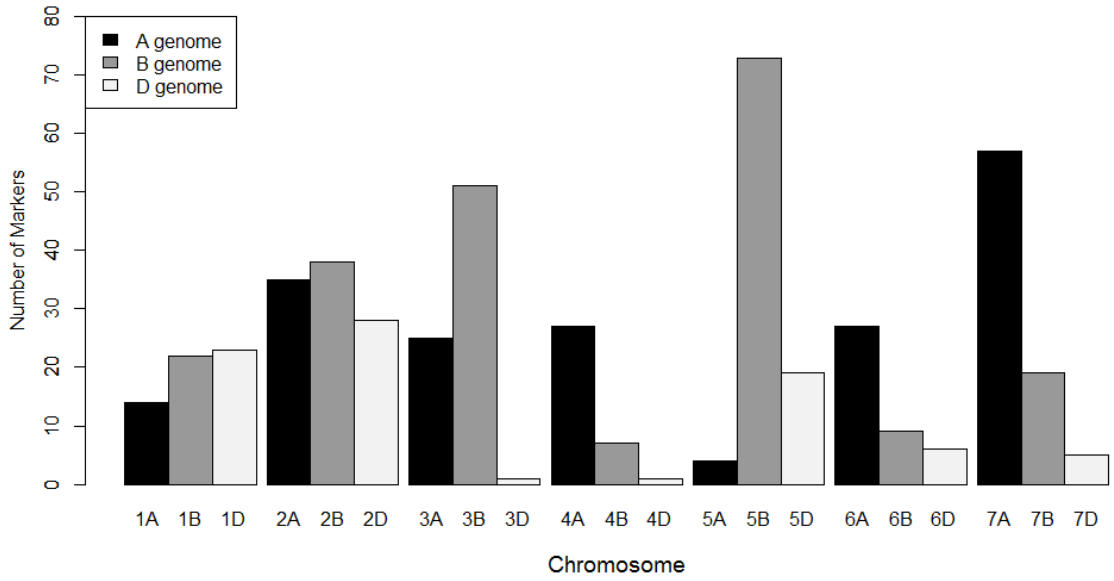

Figure 2.1. Distribution of 491 single nucleotide polymorphism markers across all seven chromosomes on all three genomes of common wheat.

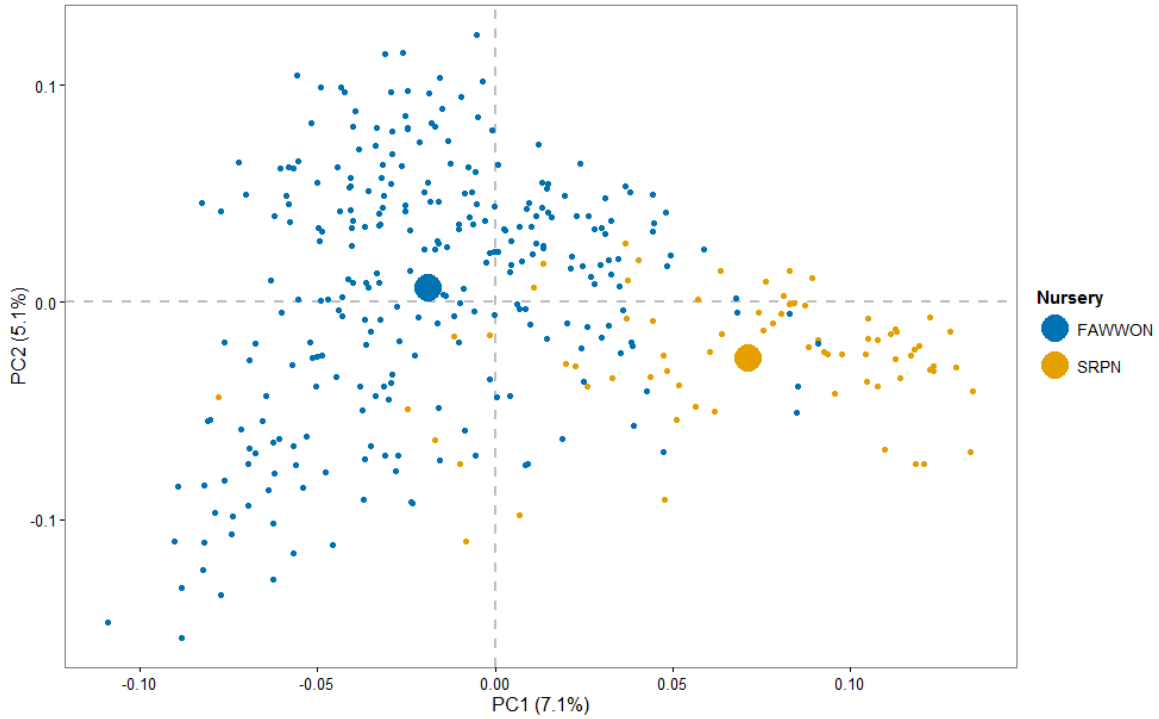

Figure 2.2. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 491 single nucleotide polymorphism markers. Nursery origin is shown for each genotype. The smaller circles show each individual genotype's nursery of origin while the larger circles show the average eigenvector values among all genotypes for a nursery collection.

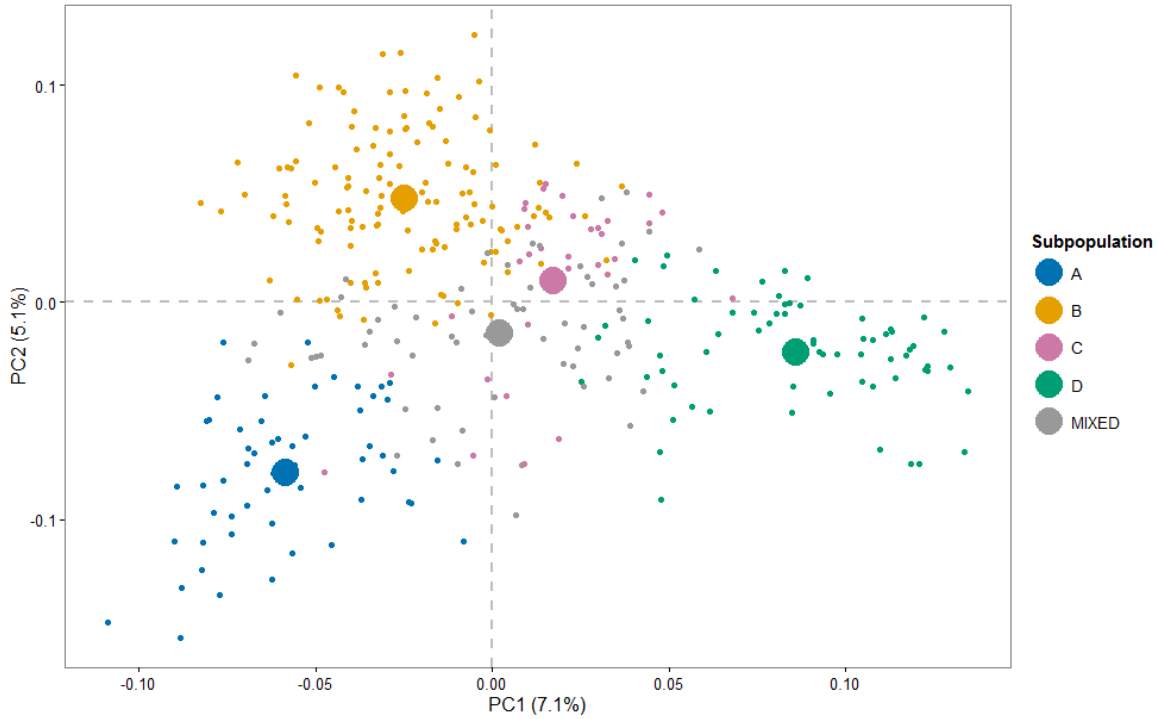

Figure 2.3. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 491 single nucleotide polymorphism markers. Subpopulation assignment is shown for each FAWWON and U.S. hard winter wheat genotype under the correlated allele frequencies model. The smaller circles show each individual genotype and their subpopulation assignment while the larger circles show the average eigenvector values among all genotypes for a subpopulation.

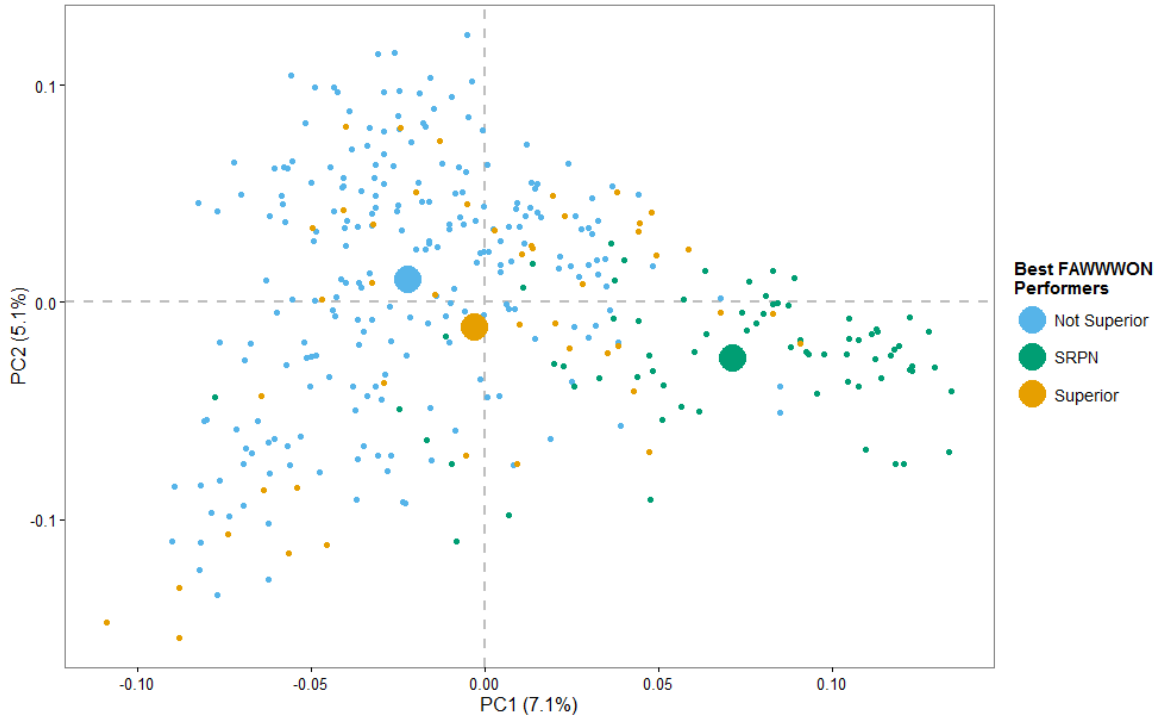

Figure 2.4. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 491 single nucleotide polymorphism markers for the 46 superior performing FAWWON genotypes from six environments in Colorado. The smaller circles show each individual genotype while the larger circles shows the average eigenvector values among all superior genotypes from the FAWWON as well as the U.S. hard winter wheat genotypes (SRPN).

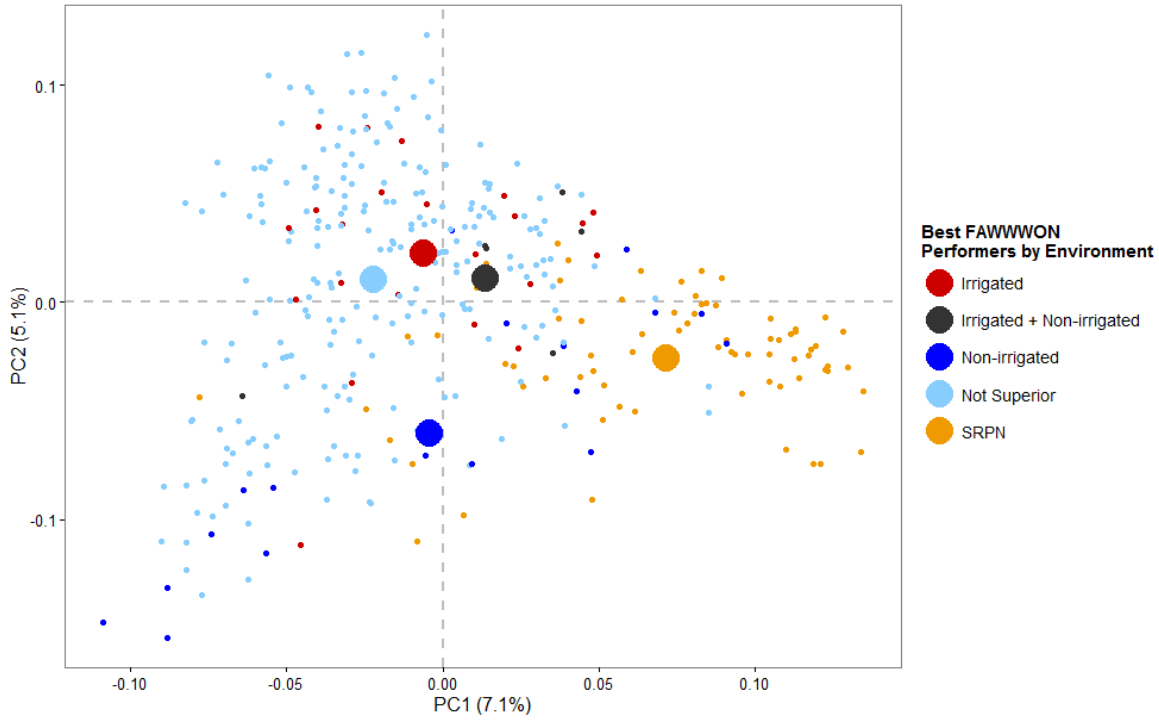

Figure 2.5. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 491 single nucleotide polymorphism markers for the 46 superior performing FAWWON genotypes under the environment (irrigated , non-irrigated, or irrigated and non-irrigated) that they performed best under. The smaller circles show each individual genotype while the larger circles shows the average eigenvector values among all superior genotypes from the FAWWON as well as the U.S. hard winter wheat genotypes (SRPN).

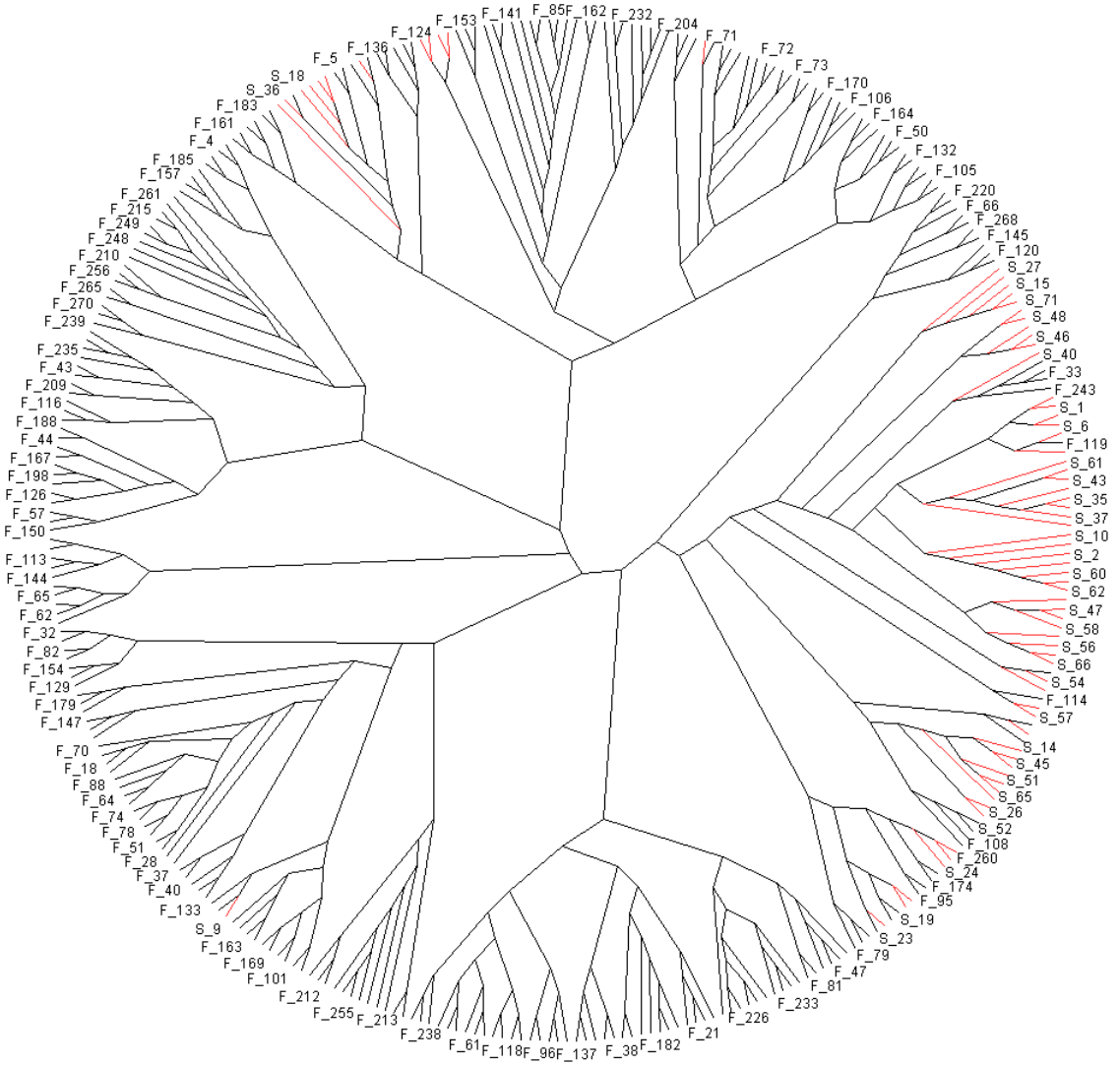

Figure 2.6. Hierarchical clustering based on Euclidean genetic distance between each genotype from the Facultative and Winter Wheat Observation Nursery (FAWWON) in black and each genotype from the Southern Regional Performance Nursery (SRPN) in red based on 491 SNP markers.

REFERENCES

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POPULATION STRUCTURE AND GENETIC DIVERSITY ANALYSIS OF GERMPLASM FROM THE WINTER WHEAT EASTERN EUROPEAN REGIONAL YIELD TRIAL (WWEERYT)[1]

International exchange of improved germplasm is important in addressing existing and emerging constraints to global wheat (*Triticum aestivum* L.) production. Elite breeding lines tested in international performance nurseries represent the most advanced materials from a collection of breeding programs and best showcase a pool of genotypes for cultivar release or use as parents in future crosses (Peterson and Pfeiffer, 1989; Sharma et al., 2010, 2012, 2014). The International Winter Wheat Improvement Program (IWWIP) is a cooperative breeding program between the Ministry of Agriculture and Rural Affairs of Turkey, the International Maize and Wheat Improvement Center (CIMMYT), and the International Center of Agricultural Research in the Dry Areas (ICARDA) (Morgounov et al., 2005). The IWWIP distributes observation nurseries and yield trials comprising high yielding, advanced breeding lines to facilitate introduction and exchange of improved germplasm in developing countries for irrigated and dryland production systems (Sharma et al., 2010, 2012). To expand the international exchange of winter wheat germplasm, CIMMYT and Oregon State University initiated the Winter Wheat Eastern European Regional Yield Trial (WWEERYT) as a separate IWWIP project to evaluate elite lines and varieties from eastern Europe, IWWIP, the Caucus Region, and the United States (Sharma et al., 2014). Sharma et al. (2014) identified high yielding

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and stable genotypes in the WWEERYT, using genotype and genotype x environment (GGE) biplot analysis (Yan et al., 2000), that performed well in test locations in central and western Asia (CWA), central and eastern Europe (CEE), and the United States (USA).

The development of genome-wide association studies (GWAS) to identify quantitative trait loci (QTLs) underlying complex traits has resulted in renewed interest to characterize population structure in wheat collections (Yu et al., 2006). The existence of subpopulation structure with an unequal allelic distribution within a GWAS panel can result in spurious associations and is the primary obstacle to successful GWAS (Buckler and Thornsberry, 2002; Zhao et al., 2007). Genomic selection (GS) is a technique that leverages genome-wide DNA markers with plant phenotypes to enable trait prediction earlier in the breeding cycle to potentially accelerate genetic gain for genetically complex traits (Meuwissen et al., 2001; Crossa et al., 2010; Jannink et al., 2010; Burgueño et al., 2012). Genomic selection prediction accuracies have been shown to be maximized when the training population and the selection candidates are closely related (Lorenz and Smith, 2015). Using rapid inbreeding methods such as single seed descent (SSD) or doubled haploids (DH), GS-based cycle time may be reduced to one or two years from the traditional five to seven years (Heffner et al., 2010). Genetic gain in early selection cycles may be dramatically high, but rapid cycling using GS may ultimately increase the rate of loss of genetic diversity through a reduction of the effective population size and loss of rare alleles (Jannink, 2010; Heslot et al., 2015). Identification and introgression of new and favorable alleles will be needed to enhance genetic diversity and sustain long-term gains while implementing GS in wheat (Heslot et al., 2015).

Genetic diversity and population structure have been evaluated in wheat collections level using molecular markers, such as random amplified polymorphic DNA (RAPD; Joshi and Nguyen, 1993), restriction fragment length polymorphism (RFLP; Siedler et al., 1994; Kim and Ward, 2000), amplified fragment length polymorphism (AFLP; Barrett and Kidwell, 1998), simple sequence repeats (SSR; Röder et al., 2002; Balfourier et al., 2007; Zhang et al., 2010) and diversity arrays technology (DArT; White et al., 2008; Dreisigacker et al., 2012; Cabrera et al., 2014). Single nucleotide polymorphism (SNP) markers have become the preferred marker for genetic studies due to their greater abundance in the genome and better amenability to high-throughput genotyping (Varshney et al., 2006).

In wheat, several studies have examined genetic diversity by various methods including genetic distance, coefficient of parentage, principal component analysis (PCA), and model-based approaches (Barrett and Kidwell, 1998; Kim and Ward, 2000; Chao et al., 2007; White et al., 2008; Prasad et al., 2009; Hao et al., 2011; Cabrera et al., 2014). Results from these studies have drawn conflicting conclusions with some studies showing that populations identified in wheat collections often correspond to geographic regions (Kim and Ward 2000; Balfourier et al., 2007; Chao et al., 2007; Tommasini et al., 2007; Le Couviour et al., 2011) while other studies have claimed no population structure in wheat (Reif et al., 2011; Benson et al., 2012; Würschum et al., 2013).

Although intensive plant breeding is generally considered to be a practice that leads to reduced genetic diversity (Tanksley and McCouch, 1997), results have shown that plant breeders can avert a narrowing germplasm base and subsequently increase genetic diversity within their breeding population through introgression of diverse germplasm (Reif et al., 2005).

International exchange of elite germplasm is important in addressing existing and emerging constraints to global wheat production by responding positively to changing climates, pests, diseases, and consumer preferences. Our objectives were to use SNP markers obtained using genotyping-by-sequencing (GBS) to i) identify subpopulation structure among genotypes from seven years of the WWEERYT using a model-based approach, ii) compare subpopulation structure between regions, countries, and states, and iii) characterize subpopulation structure and genetic relatedness among previously-identified superior-performing genotypes from the WWEERYT.

Materials and Methods

WWEERYT Germplasm

I analysed 283 winter wheat genotypes from seven years of the WWEERYT nursery in our study. Genotypes included released cultivars and elite experimental lines from four major winter wheat regions and 16 countries. One hundred thirty-eight genotypes were from central and eastern Europe (CEE), 48 were from central and western Asia (CWA), 38 were from Turkey-CIMMYT-ICARDA (TCI), and 59 were from the USA.

Superior genotypes from the WWEERYT collections were previously identified based on high and stable yield performance, resistance to leaf rust (*Puccinia triticina* Erikss.), stripe rust (*Puccinia striiformis* Westend. F. sp. *tritici* Eriks.), and stem rust (*Puccinia graminis* Pers. F. sp. *tritici* Eriks. & E. Henn.), and several agronomic traits (Sharma et al., 2014). Sharma et al. (2014) identified 56 superior genotypes from eight years of the WWEERYT, but a seed sample was available for only 35 of the 56 superior genotypes. These 35 genotypes were further analyzed in

this study to determine if their superior performance was associated with their subpopulation classification or program of origin.

SNP Genotyping

Genomic DNA was extracted from bulked leaves of 10 one-wk-old seedlings at the single leaf stage using a 96-well format (King Fisher 96 magnetic bead extraction kit) on the King Fisher Flex Purification System (Thermo Fisher Scientific Inc., Waltham, MA USA). Genotyping-by-sequencing library construction was carried out using the restriction enzymes *PstI-MspI* and a protocol modified from Poland et al. (2012). A single blank was included in each plate at random locations for quality control to ensure that libraries were not switched during preparation and sequencing. All libraries were 192-plexed. The sequencing was performed on an Illumina Hi-Seq 2000 at the DNA core facility at the University of Missouri in Columbia, MO. Single-nucleotide polymorphism calls were made using the TASSEL-Pipeline (Bradbury et al., 2007) which uses a reference SNP calling procedure. An Ensembl Plant assembly for wheat was used as the reference (Kersey et al., 2013).

GBS Marker Filtering

A total of 75,254 SNP markers were obtained using GBS. A subset of 1,724 markers was created by filtering out markers with more than 10% missing data. The average polymorphism information content (PIC) for this subset of markers was 0.25. The PIC was calculated as 1-$\sum_i^n p_i^2$, where p_i is the proportion of the population carrying the *i*th allele (Anderson et al., 1993). For bi-allelic markers such as SNPs, the PIC values can range from 0 (fixation of one allele) to 0.5 (equal allele frequencies). Markers with a PIC value less than 0.35 across all

genotypes were removed. This high PIC value was used to further reduce the GBS marker subset to the most discriminating SNP markers for population structure analysis. Markers that were immediately adjacent to each other and had the same PIC value were reduced to a single marker in order to satisfy the no-linkage assumption for analysis in the software program STRUCTURE 2.3.4 (Pritchard et al., 2000). Chromosome positions were available for all markers retained.

Model-Based Population Structure Analysis

The software program STRUCTURE 2.3.4 was used to assign individuals to subpopulations based on their genotypes at multiple loci using a Bayesian approach. Two models with different allele frequency assumptions were used: Model 1 was an admixture model with correlated allele frequencies and Model 2 was an admixture model with independent allele frequencies (Pritchard et al., 2000). No external *a priori* information was used with either model for determining population structure.

Five independent runs were performed for *K* (subpopulations) values of 1 to 12 for both models. A burn-in period of 10,000 iterations and data collection of 50,000 Markov chain Monte Carlo (MCMC) iterations were determined to be adequate based on the convergence summary statistics. The best separator for the number of subpopulations was determined by selecting the *K* associated with the highest delta *K* value (Evanno et al., 2005) using the program STRUCTURE HARVESTER (Earl, 2012). A series of 25 independent runs were then performed for the selected *K* for each model with a burn-in period of 25,000 iterations and data collection of 100,000 MCMC iterations. Outputs from STRUCTURE were integrated using the program CLUMPP (Jakobsson and Rosenberg, 2007) under the *FullSearch* algorithm to estimate an

average membership coefficient (Q-matrix) for each genotype from the 25 independent runs for the optimized *K* value.

Genotypes with membership coefficients greater than or equal to 50% were assigned to a distinct subpopulation. Under Model 1, individuals with less than the minimum membership coefficient value required to be assigned to a single population were classified as "Mixed". The genetic variation between subpopulations, expressed as Wright's fixation index (F_{st}), was tested using analysis of molecular variance (AMOVA) implemented in STRUCTURE to measure genetic diversity between the subpopulation gene pools.

Principal Component Analysis

Principal component analysis was performed to visualize the dispersion of subpopulations, program of origin, and superior genotypes among the 283 WWEERYT genotypes using SNPs. Eigenvector values for PCA were calculated using the base function 'eigen' in R 3.2.2 (R Development Core Team, 2014) and plotted using the ggplot package (Wickham, 2009) in R. Missing marker data were imputed using the multivariate normal expectation maximization (MVN-EM) method (Dempster et al., 1977) using the A.mat function in the rrBLUP package (Endelman, 2011) in R. The markers used for PCA were the same subset used after GBS marker filtering.

Results and Discussion

SNP Markers

There were 548 GBS SNP markers with less than 10% missing data, with PIC values greater than 0.35, and not in linkage disequilibrium with each other. These 548 highly

polymorphic SNP markers were spread across all seven chromosomes on all three genomes (Figure 3.1). The B genome had the greatest number of SNPs with 280 followed by the A genome with 189 and the D genome with 79. This resulted in an average of 40 SNPs per chromosome for the B genome, 27 for the A genome, and 11 for the D genome. Chromosome 5B had the highest coverage with 70 SNPs and chromosome 4D had the lowest coverage with two SNPs (Figure 3.1). The distribution of GBS-derived SNP markers in our study was in agreement with previous studies. Using RFLP markers in a collection of winter wheat genotypes, Siedler et al. (1994) showed that the B genome had the greatest number of polymorphic loci and the D genome had the lowest number of markers. Similar results with hexaploid wheat were reported with SSR markers (Huang et al., 2002; Chao et al., 2007), DArT markers (Dreisigacker et al., 2012), and other GBS-derived SNP markers (Poland et al., 2012).

Population Structure Present by Region

Clear evidence of population structure in the WWEERYT collections of genotypes was observed. Based on the highest delta K values (Evanno et al., 2005), seven unique subpopulations were identified with Model 1 and two unique subpopulations were identified with Model 2. Under Model 1, subpopulations tended to be defined by a high percentage of genotypes from one of the four geographic regions. Populations D and G included genotypes exclusively from CEE (Table 3.1). Although populations C and F included genotypes from three of the four geographic regions, 85.7% of the genotypes in populations C were from TCI and 77.5% of the genotypes in population F were from the USA (Table 3.1). Under Model 1, population E was the only subpopulation composed of genotypes from each of the four geographic regions with 53.6% from CEE, 35.7% from USA, 7.1% from CWA, and 3.6% from TCI

(Table 3.1). The model-based methods developed by Pritchard et al. (2000) allowed for the inclusion of admixed individuals whose genetic composition is drawn from more than one of *K* subpopulations. This assumption fits well with international nursery collections such as the WWEERYT, as individuals are often assigned to one or more subpopulations due to germplasm exchange and crosses being made with genotypes from different breeding programs. With the potential for genotypes to have partial membership in up to seven subpopulations, many individuals did not have the 50% membership threshold to be assigned to a single population and thus were classified as Mixed. Under Model 1, Mixed individuals (n=109) included genotypes from all four regions with 45.0% from CEE, 21.1% from CWA, 17.4% from TCI, and 16.5% from USA (Table 3.1). Regions with a higher percentage of genotypes classified as Mixed would potentially have a wider germplasm base as their material is composed of germplasm from multiple subpopulations rather than from a single population.

The F_{ST} was calculated using STRUCTURE and varied across subpopulations. F_{ST} is defined as the correlation of gametes within subpopulations relative to gametes drawn at random from the entire population. I observed F_{ST} values greater than zero between subpopulations for Model 1, which suggested subpopulation differentiation. The F_{ST} values for Model 1 ranged from 0.20 to 0.56 (Table 3.2). Under Model 1, the highest F_{ST} value of 0.56 was between population A (n=3) and population D (n=10), possibly due to their smaller sample sizes. The F_{ST} value of 0.20 under Model 1 was between a population of predominantly TCI genotypes and a population of predominantly USA genotypes indicating that these two subpopulations are more genetically related. Using DArT marker genotyping, Dreisigacker et al. (2012) reported F_{ST} values of 0.11 to 0.73 across five subpopulations of 606 spring wheat lines from 25 years of CIMMYT's

Elite Spring Wheat Yield Trial. Cabrera et al. (2014) reported F_{ST} values of 0.16 to 0.57 across five subpopulations of soft winter wheat lines from the eastern USA.

Population Structure Further Evident by Country and State Within a Region

Genotypes of CEE origin included 138 genotypes from seven different countries (Table 3.3.). While genotypes of CEE origin were assigned to six of the seven subpopulations under Model 1, indicating extensive diversity present among genotypes from this region, there were clear differences in population structure within and among countries from this region. Genotypes from the Czech Republic were found in only two subpopulations with the majority in population E. Genotypes from Hungary that were not classified as Mixed were found predominantly in population G while 86.4% of Romanian genotypes were also found in population G (Table 3.3). This is in contrast to Russian genotypes found in population B and the majority of Ukrainian genotypes found in populations B and D (Table 3.3). Genotypes of CWA origin were composed of 48 genotypes from seven different countries (Table 3.3). While genotypes of CWA origin were found in four of the seven populations, only a small percentage of genotypes exclusively from Kazakhstan were found in population C and a small percentage of genotypes from Kazakhstan and Uzbekistan were found in population E (Table 3.3). Genotypes from CWA were predominantly found in population B or had high percentages of Mixed genotypes. Genotypes of USA origin were present in only two of the seven subpopulations. Under Model 1, genotypes of USA origin showed the narrowest diversity with 52.5% of the genotypes being assigned to a single subpopulation (population F) while also having the lowest percentage of Mixed individuals among the four regions. This trend is even more defined when examining germplasm by state origin. Genotypes from Colorado and Nebraska were found

exclusively in population F and without any genotypes classified as Mixed. Genotypes from Texas, Kansas, and Oklahoma were also found exclusively in population F but with some genotypes classified as Mixed. Genotypes from Oregon were the only USA genotypes found in population E showing separation from the genotypes from the Great Plains wheat region in the USA. Genotypes of TCI origin were not included in Figure 3 or explored any further since they could not be further separated into country or state of origin.

These results support previous reports that subpopulation structure of wheat genotypes correspond to geographic regions (Kim and Ward 2000; Balfourier et al., 2007; Chao et al., 2007; Tommasini et al., 2007; Le Couviour et al., 2011) and support the notion that subpopulation structure within the WWEERYT collections is the result of natural or artificial selection due to climatic variables, breeding objectives unique to a region, or exchange of germplasm between breeding programs in a region. Under Model 1, genotypes from a particular geographic region were assigned at a higher frequency to specific subpopulations. However, not all genotypes originating from the same geographic region were appropriated to the same population or limited to a single population, in agreement with previous reports (Huang et al., 2002; Prasad et al., 2009).

Superior Genotypes Show Less Population Structure

Of the 35 superior genotypes described by Sharma et al. (2014), under Model 1 eight were assigned to population B, four to population D, five to population E, four to population F, six to population G, and eight as Mixed (Table 3.4). None of the superior genotypes were assigned to populations A and C. The lack of superior genotypes from population A may be due to its small population size (n=3). The 35 superior genotypes were from all four major regions

with 26 from CEE, one from CWA, four from TCI, and four from USA. These 35 superior genotypes represented all seven countries from CEE, Kazakhstan from CWA, and Kansas, Nebraska, Oregon, and Texas from the USA. The combined results from the Sharma et al. (2014) paper and this study show that genotypes that have high and stable yield across a range of growing environments can be found from different geographic regions and from different subpopulations. This highlights the importance of screening international nurseries in order to identify superior genotypes that can be used in new regions and breeding programs since geographic origin and subpopulation classification do not provide a clear means for efficiently identifying the best subset of genotypes for wide adaptation.

Principal Component Analysis Displays Relatedness but Does not Define Subpopulations

Principal component analysis was used to visualize the relationships among the 283 WWEERYT genotypes. Principal component one (PC1) explained 9.4% of the variation in the data set while principal component two (PC2) explained 4.7% of the variation, together accounting for 14.1% of the total variation. This is in agreement with other studies in common wheat where the first two principal components accounted for roughly 10% of the total variation present among the genotypes studied (Le Couviour et al., 2011; Würschum et al., 2013; Cabrera et al., 2014).

Under Model 1, the mean PC scores assigned to populations A, C, E, and F were separated from the mean PC scores of populations B, D, and G according to PC1 (Figure 3.2). The subpopulation assignment based on Model 1 was not as readily inferred based on PC1 or PC2 position using PCA and was due to the overlap of several subpopulations determined in STRUCTURE. Thus, subpopulation assignment based solely on PCA is not recommended for

assignment of individuals using the correlated allele frequencies model. In common wheat, model-based and PCA approaches have produced similar results when assessing genetic diversity (Chao et al., 2010; Zhang et al., 2010; Le Couviour et al., 2011; Cabrera et al., 2014).

The mean PC scores of genotypes from CEE and CWA were on one side of the PC1 axis while the mean PC scores of genotypes from TCI and USA were on the other side of the PC1 axis (Figure 3.3). Each region of origin included some outlier genotypes that could be found on the opposing side of the PC1 axis with TCI and USA genotypes having fewer outliers than genotypes of CEE and CWA origin. These PCA results agree closely with the percentages of genotypes found in each subpopulation for each geographic region for Model 1. The superior performing genotypes as identified by Sharma et al. (2014) can be found on both sides of PC1 (Figure 3.4). This is in agreement with the best performing genotypes being composed of genotypes from all four geographic regions.

Conclusions

The recent expansion of GWAS studies in crop plants to identify QTL underlying complex traits requires increased knowledge of population structure in germplasm sets. Information gathered from model-based and PCA approaches can also help to identify individuals for genomic selection training population development. In summary, this study shows that there is reasonable genetic diversity in international winter wheat gene pools with some regions having greater diversity than others, and that SNP markers obtained via GBS are effective for assessment of genetic diversity and population structure analyses in wheat. Characterization and screening of international nurseries shows promise to facilitate introduction of beneficial alleles from other countries into gene pools with the potential to broaden wheat genetic

diversity within a breeding program or across a region. The population structure and genetic diversity analysis provided here will help foster the development of strategies for genetic resource management and exploitation across multiple winter wheat growing regions.

Tables

Table 3.1. Number and percentage of genotypes from four geographic regions within each subpopulation for the correlated allele frequencies (Model 1).

Model 1 Populations	n	CEE†	CWA‡	TCI§	USA¶
		---------- percent (%) ----------			
A	3	0.0	66.7	33.3	0.0
B	51	60.8	39.2	0.0	0.0
C	14	7.1	7.1	85.7	0.0
D	10	100.0	0.0	0.0	0.0
E	28	53.6	7.1	3.6	35.7
F	40	10.0	0.0	12.5	77.5
G	28	100.0	0.0	0.0	0.0
Mixed	109	45.0	21.1	17.4	16.5

† central and eastern Europe
‡ central and western Asia
§ Turkey-CIMMYT-ICARDA
¶ United States

Table 3.2. Wright's fixation index (F_{st}) pairwise values among seven subpopulations determined in the model-based approach in STRUCTURE under the model assumptions of correlated allele frequencies (Model 1).

	B	**C**	**D**	**E**	**F**	**G**
A	0.50	0.47	0.56	0.48	0.49	0.54
B	-	0.27	0.23	0.28	0.33	0.22
C		-	0.33	0.20	0.20	0.31
D			-	0.33	0.34	0.32
E				-	0.24	0.32
F					-	0.31

Table 3.3. Percentage distribution of each country/state for three of the four geographic regions across subpopulations for Model 1.

Region	Country/State†	n	A	B	C	D	E	F	G	Mixed
CEE	BUL	30	–	33.3	–	3.3	10.0	–	3.3	50.0
CEE	CZE	10	–	–	–	–	70.0	10.0	–	20.0
CEE	HUN	26	–	3.8	–	–	7.7	3.8	30.8	53.8
CEE	MOL	9	–	22.2	11.1	11.1	–	11.1	–	44.4
CEE	ROM	22	–	4.5	–	–	4.5	–	86.4	4.5
CEE	RUS	12	–	66.7	–	–	–	–	–	33.3
CEE	UKR	29	–	31.0	–	27.6	6.9	3.4	–	31.0
CWA	ARM	3	–	33.3	–	–	–	–	–	66.7
CWA	AZB	4	25.0	25.0	–	–	–	–	–	50.0
CWA	GEO	1	–	–	–	–	–	–	–	100.0
CWA	KAZ	15	–	66.7	6.7	–	6.7	–	–	20.0
CWA	KYR	10	–	20.0	–	–	–	–	–	80.0
CWA	TUR	5	–	20.0	–	–	–	–	–	80.0
CWA	UZB	10	10.0	50.0	–	–	10.0	–	–	30.0
USA	CO	5	–	–	–	–	–	100.0	–	–
USA	KS	10	–	–	–	–	–	60.0	–	40.0
USA	NE	5	–	–	–	–	–	100.0	–	–
USA	OK	12	–	–	–	–	–	33.3	–	66.7
USA	OR	14	–	–	–	–	71.4	–	–	28.6
USA	TX	13	–	–	–	–	–	84.6	–	15.4

† BUL=Bulgaria, CZE=Czech Republic, HUN=Hungary, MOL=Republic of Moldova, ROM=Romania, RUS=Russia, UKR=Ukraine, ARM=Armenia, AZB=Azerbaijan, GEO=Georgia, KAZ=Kazakhstan, KYR=Kyrgyzstan, TUR=Turkey, UZB=Uzbekistan, CO=Colorado, KS=Kansas, NE=Nebraska, OK=Oklahoma, OR=Oregon, TX=Texas

Table 3.4. Total number and percentage of genotypes assigned for each subpopulation for Model 1 by percentage of superior genotypes from each of the four geographic regions.

Model 1 Populations	n	CEE†	CWA‡	TCI§	USA¶
		---------- percent (%) ----------			
A	0	0.0	0.0	0.0	0.0
B	8	87.5	12.5	0.0	0.0
C	0	0.0	0.0	0.0	0.0
D	4	100.0	0.0	0.0	0.0
E	5	80.0	0.0	0.0	20.0
F	4	0.0	0.0	25.0	75.0
G	6	100.0	0.0	0.0	0.0
MIXED	8	62.5	0.0	37.5	0.0
Total (n)		26	1	4	4

† central and eastern Europe
‡ central and western Asia
§ Turkey-CIMMYT-ICARDA
¶ United States

Figures

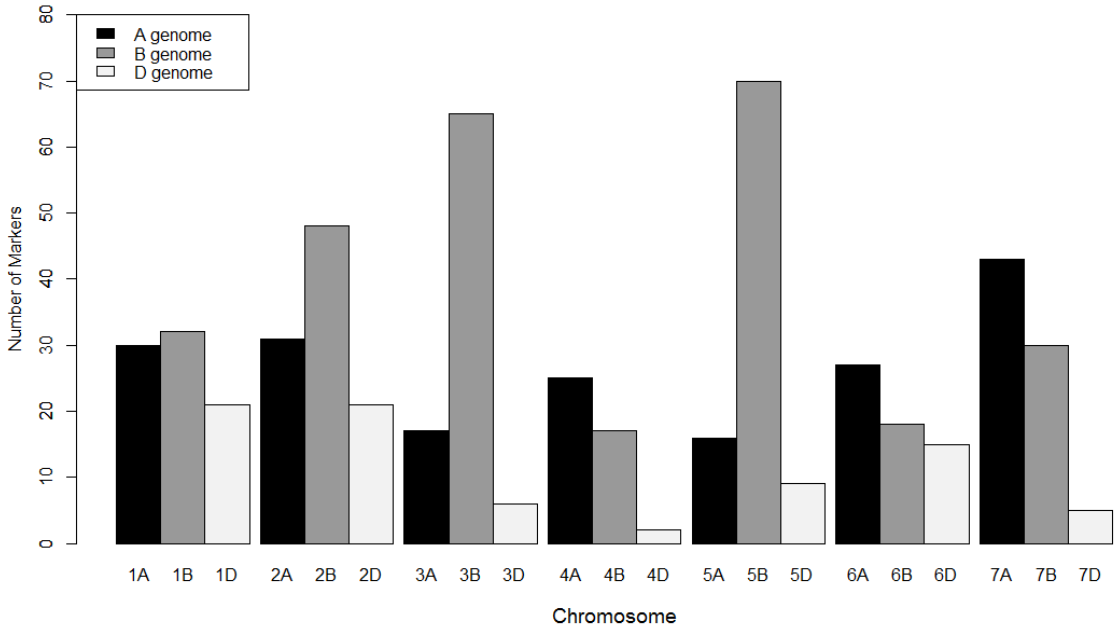

Figure 3.1. Distribution of 548 single nucleotide polymorphism markers across all seven chromosomes on all three genomes of common wheat.

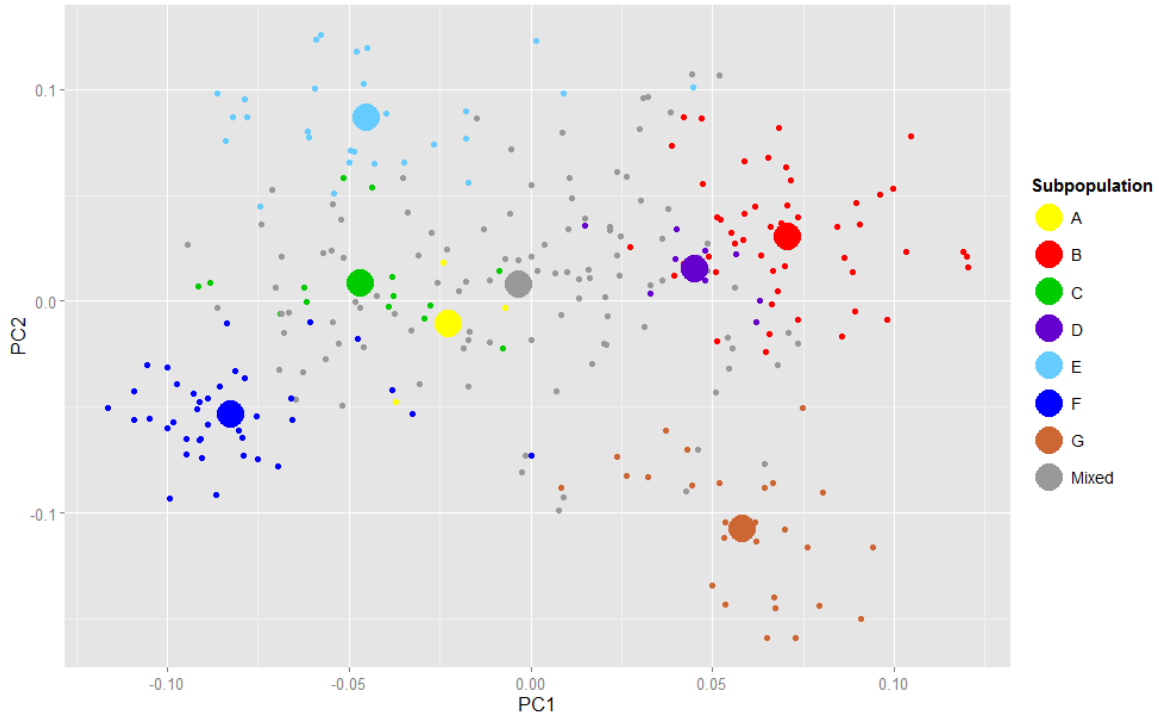

Figure 3.2. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 548 single nucleotide polymorphism markers. Population assignment is shown for each WWEERYT genotype under the correlated allele frequencies model with membership coefficients greater than or equal to 50% (Model 1). The smaller circles show each individual genotype and their subpopulation assignment while the larger circles show the average eigenvector values among all genotypes for a subpopulation.

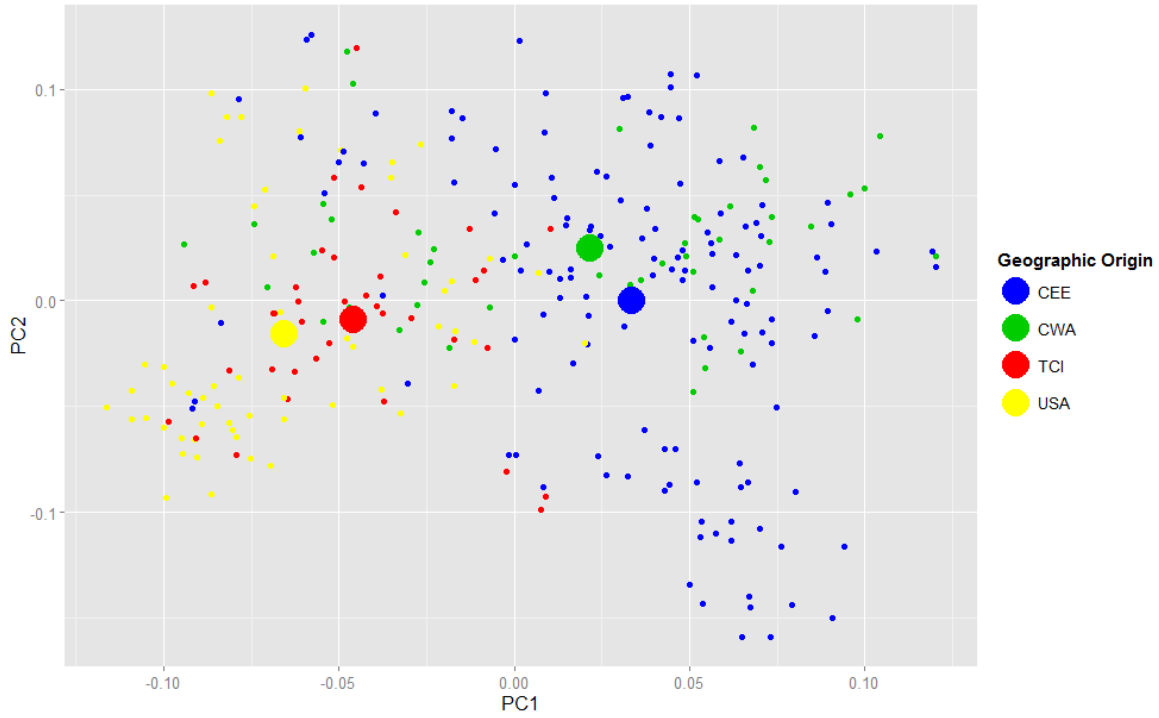

Figure 3.3. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 548 single nucleotide polymorphism markers. Geographic region of origin with each genotype color-coded based on passport data assigning it to one of four geographic regions. The smaller circles show each individual genotype while the larger circles show the average eigenvector values among all genotypes for a region.

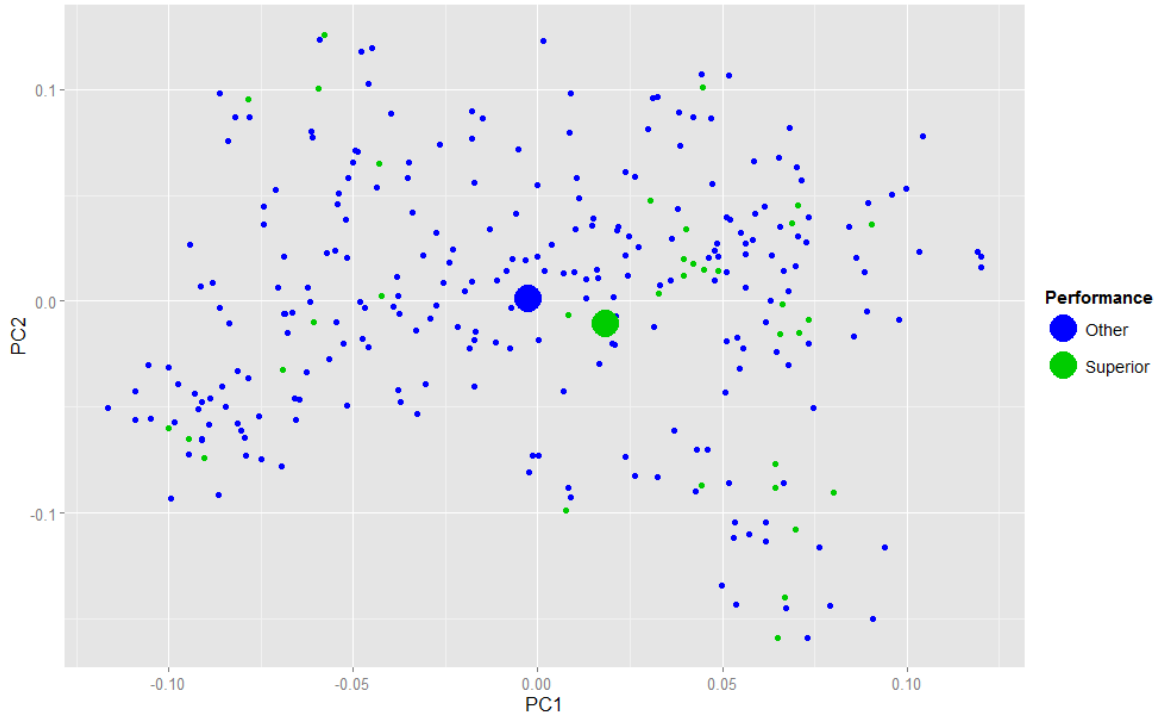

Figure 3.4. Principal component analysis displaying the eigenvector values for PC1 and PC2 using 548 single nucleotide polymorphism markers. Thirty-five of the best performing genotypes from seven years of WWEERYT trials are identified. The smaller circles show each individual genotype while the larger circles show the average eigenvector values among all genotypes for the best performing individuals and the other individuals.

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GENOMIC SELECTION FOR WINTER INJURY AMONG A DIVERSE COLLECTION OF FACULTATIVE AND WINTER WHEAT GENOTYPES

Winter injury is an important abiotic constraint for hard winter wheat (*Triticum aestivum* L.) in the Great Plains of North America (Paulsen and Shroyer, 2008; Fowler, 2012). Cold tolerant plants are able to survive the freezing winter temperatures and prevent damage to plant tissues that can negatively impact yield potential (Galiba et al., 2009). Vernalization, the process of prolonged exposure to low temperature to accelerate flowering, is vital for winter wheat as it protects sensitive floral organs from exposure to freeze damage during winter and early spring (Fowler et al., 1996; Distelfeld et al., 2009; Galiba et al., 2009). Based on differences in the vernalization requirement, wheat cultivars may be classified as winter, facultative, and spring habit types. Winter-types require a vernalization period of 6-8 weeks at 4 °C to complete spike primordia differentiation (Gardner and Barnett, 1990), facultative-types need only 2-4 weeks (Rousset el al., 2011), and spring-types complete spike primordia differentiation without any low temperature exposure.

The cause of spring growth type is a mutation within the promoter or the first intron at one or more *Vrn-1* loci (*Vrn-A1, Vrn-B1,* and *Vrn-D1*), located on the long arm of the group 5 chromosomes (Yan et al., 2004; Fu et al., 2005; Santra et al., 2009; Trevaskis, 2010; Zhang et al., 2012). A dominant *Vrn-A1* allele is sufficient to cause spring growth habit while recessive alleles at all three loci are required for winter growth habit (Zhang et al., 2012; Kamran et al., 2014). The dominant *Vrn-A1a* allele has the most dramatic effect on the development of spring growth habit, while dominant alleles at the *Vrn-B1* and *Vrn-D1* loci only partially reduce the need for

cold treatment (Pugsley, 1971, 1972). Thus, genotypes with the dominant alleles at *Vrn-B1* and *Vrn-D1* show some slight response to vernalization (Santra et al., 2009).

In addition to the vernalization requirement, the transition from vegetative to reproductive development may be influenced by response to day length. Photoperiod response is controlled primarily by alleles at two photoperiod loci (*Ppd-B1* and *Ppd-D1*) located on the short arm of the group 2 chromosomes in wheat (Law et al., 1978; Scarth and Law, 1984; Worland et al., 1998; Cockram et al., 2007). Dominant alleles at photoperiod loci confer day length insensitivity (or 'day-length neutral') and earlier flowering while recessive alleles confer day length sensitivity and later flowering (Pugsley, 1966; Scarth and Law, 1984). Any factor that maintains the plant in the vegetative stage, such as a vernalization requirement or photoperiod sensitivity, increases low temperature tolerance by maintaining low temperature tolerance genes in an up-regulated state (Fowler et al., 1996; Mahfoozi et al., 2000; Limin and Fowler, 2006). Although alleles at vernalization and photoperiod loci exert a major effect on low temperature response through the timing of the transition from vegetative to reproductive development, at least 15 of hexaploid wheat's 21 chromosomes have been associated with low temperature tolerance (Stushnoff et al., 1984; Sutka, 1994). Additionally, multiple morphological and physiological characteristics have been shown to influence low temperature response (Fowler et al., 1981; Gusta and Wisniewski, 2013).

The International Winter Wheat Improvement Program (IWWIP) is a cooperative breeding program between the Ministry of Agriculture and Rural Affairs of Turkey, the International Maize and Wheat Improvement Center (CIMMYT), and the International Center of Agricultural Research in the Dry Areas (ICARDA) (Morgounov et al., 2005). The IWWIP

distributes the Facultative and Winter Wheat Observation Nursery (FAWWON) to breeding programs around the world (Rajaram et al., 1993; Morgounov et al., 2012). Elite breeding lines distributed through international performance nurseries facilitate the introduction and exchange of improved germplasm between developing and developed countries (Peterson and Pfeiffer, 1989; Sharma et al., 2014). As the cost of obtaining genetic markers drops below the cost of evaluating individuals over years and locations, genomic information can more affordably be leveraged to predict phenotypic performance (Bernardo, 2008; Cobb et al., 2013). This will assist in identifying individuals that are best adapted to regions where severe winter conditions are an important production constraint.

Genomic selection (GS) is a technique that leverages genome-wide DNA markers with plant phenotypes to enable trait prediction earlier in the breeding cycle and potentially accelerate genetic gain for genetically complex traits (Heffner et al., 2009; Crossa et al., 2010; Jannink et al., 2010; Burgueño et al., 2012). Genomic selection involves the estimation of an individual's breeding value based on genome-wide marker effects using a training population consisting of individuals with both marker genotypes and trait phenotypes (Meuwissen et al., 2001). A GS prediction model would be particularly useful for low temperature tolerance since this phenotype may not be available for evaluation in all environments or growing seasons. Ridge regression best linear unbiased prediction (RR-BLUP) is a common method used for GS (Whittaker et al., 2000; Endelman, 2011). The best way of using molecular markers in GS largely depends on the genetic architecture of the trait (Bernardo, 2008). For a given number of markers (N_M), RR-BLUP assumes that each marker accounts for $(1/N_M)^{th}$ of genetic variation (V_G). If one of the markers corresponds to a known major gene, the assumption of common

variance for the known major gene leads to an underestimation of the estimated effects of the major gene (Bernardo, 2014). An alternative to the RR-BLUP model is to model any known major quantitative trait loci (QTL) as having fixed effects while keeping the unknown minor QTL as random effects. Several studies have shown an improvement in GS prediction accuracy when trait-associated or functional markers are included as fixed effects in a GS model (Bernardo, 2014; Daetwyler, 2014; Moore et al., 2017).

In this study I examined the effectiveness of GS prediction of low temperature tolerance in a collection of individuals from the FAWWON using winter injury as the phenotype of interest. The objectives of this study were to i) compare GS prediction accuracy with vernalization and photoperiod alleles as fixed effects to a GS approach where only genome wide single nucleotide polymorphism (SNP) markers were treated as random effects and ii) identify the vernalization and photoperiod loci that provide the greatest increase in GS prediction of winter injury when used as fixed effects in a mixed effects GS model.

Materials and Methods

Germplasm, experimental layout, and phenotypic evaluation

Genotypes from three years of the FAWWON were included in these experiments (n=287 individuals), including individuals from the 20th FAWWON, 21st FAWWON, and 22nd FAWWON. All accessions included in this study are elite genotypes representing released cultivars and experimental lines. The FAWWON genotypes represented breeding programs from Turkey-CIMMYT-ICARDA (TCI), United States (U.S.), Iran, Romania, Kazakhstan, Russia, Bulgaria, Turkey, and Syria. Six total environments were used, which included field experiments at both Fort Collins (sprinkler irrigated) and Julesburg (non-irrigated) Colorado in the 2014 (112

genotypes), 2015 (200 genotypes), and 2016 (186 genotypes) growing seasons. Within years, the same genotypes were grown at both locations. All 112 genotypes from the 20th FAWWON that were evaluated in 2014 were evaluated in 2015 with an additional 88 genotypes from the 21st FAWWON. Genotypes with high levels of winter injury at both locations in 2015 were not re-evaluated in 2016. Experiments in 2016 included 69 genotypes from the 20th FAWWON (third year of evaluation), 30 genotypes from the 21st FAWWON (second year of evaluation), and 87 genotypes from the 22nd FAWWON (first year of evaluation). In 2014, genotypes were arranged in an augmented row-column design with the local cultivar 'Byrd' (Haley et al., 2012) as a repeated check. In 2015 and 2016, genotypes were arranged in a partially replicated row-column design with Byrd as a repeated check. Randomizations were prepared using the package DiGGer (Coombes, 2009) in R (R Development Core Team, 2014). All experiments were planted in six-row plots, 3.7 m long and 1.8 m wide, with 0.3 m spacing between rows. The planting dates for the six environments were: October 3, 2013 for Fort Collins 2014; September 25, 2013 for Julesburg 2014; September 24, 2014 for Fort Collins 2015; September 17, 2014 for Julesburg 2015; September 25, 2015 for Fort Collins 2016; and September 15, 2015 for Julesburg 2016.

Plant emergence in the field experiments was visually assessed approximately two months after planting (Zadoks stage 15; Zadoks et al., 1974) to ensure that subsequent winter injury ratings were not misclassified due to poor germination or non-uniform emergence. Uniform germination and excellent fall plant stands were observed at all locations. Winter injury was visually assessed in early spring (Zadoks stage 25) on a 0 percent (no injury) to 100 percent (all dead plants) scale.

GBS-based SNP genotyping

Genomic DNA was extracted from bulked leaves of 10 one-wk-old seedlings at the single leaf stage in a 96-well format using King Fisher 96 magnetic bead extraction kits on the King Fisher Flex Purification System (ThermoFisher Scientific Inc., Waltham, MA, U.S.A.). Genotyping-by-sequencing library construction was carried out using the restriction enzymes *PstI* and *MspI* using a protocol modified from Poland et al. (2012). A single blank was included at random positions in each plate for quality control to ensure library identity. Sequencing was performed at 192-plex on an Illumina Hi-Seq 2000 at the DNA core facility at the University of Missouri in Columbia, MO. Single-nucleotide polymorphism (SNP) calls were made using the TASSEL-GBSv1 Pipeline (Glaubitz et al., 2014), which is a reference-based SNP calling procedure. The International Wheat Genome Sequencing Consortium (IWGSC) Chromosome Survey Sequence was used as the reference genome (IWGSC, 2014). Missing marker data were imputed using the multi-variate normal expectation maximization (MVN-EM) method (Dempster et al., 1977) within the A.mat function in the rrBLUP package (Endelman, 2011) in R. The GS analysis used 23,269 SNPs based on markers having less than 30% missing data across the set of FAWWON genotypes.

KASP marker analysis

Genotypes at three vernalization loci and two photoperiod loci were obtained from Kompetitive Allele Specific PCR (KASP) assays done using the same DNA samples used for GBS library preparation. Polymorphisms were identified using LGC Genomics (http://www.lgcgroup.com) KASP system fluorescent assays. Polymerase chain reaction (PCR) was run on Bio-Rad C1000 thermal cyclers (Bio Rad, Hercules, CA, U.S.A.) using a reaction

volume of 8.0 µl, consisting of 4 µl KASP V4.0 2x master mix with 0.11 µl KASP assay mix, and 4 µl of template DNA (20 ng μl^{-1}). Thermal cycling conditions included a hot-start activation and initial denaturation at 94 °C for 15 min followed by 10 cycles of step-down amplification involving 20 s of denaturation at 94 °C, 60 s of annealing, and extension at 65 °C (decreasing 0.6 °C per cycle). This was followed by 26 cycles of amplification involving 20 s of denaturation at 94 °C and 60 s of annealing/extension at 57 °C. This protocol included 3 recycles, each consisting of 3 cycles of a 20 s denaturation at 94 °C and a 60 s annealing/extension at 57 °C. Fluorescence was read on a Bio-Rad CFX96 Touch Real-Time Detection System and genotypes were assigned using Bio-Rad CFX Manager 2.1 (Bio Rad, Hercules, CA, U.S.A.).

Kompetitive Allele Specific PCR assays were acquired from published sequences to distinguish alleles at the *Vrn-A1*, *Vrn-B1*, *Vrn-D1*, *Ppd-B1*, and *Ppd-D1* loci. A single KASP assay was used to distinguish between two winter alleles at *Vrn-A1* (Chen et al., 2009), designated as *vrn-A1w* and *vrn-A1v* by Eagles et al. (2011), that show differences in dormancy release and low temperature tolerance. Three different KASP assays were used to distinguish three known spring alleles (*Vrn-B1a, Vrn-B1b,* and *Vrn-B1c*) from the winter allele (*vrn-B1*) at *Vrn-B1* (Santra et al., 2009). The spring (*Vrn-D1*) and winter (*vrn*-D1) alleles at *Vrn-D1* were distinguished using a single KASP assay (Fu et al., 2005). Spring alleles at *Vrn-A1* were not assayed since the dominant *Vrn-A1a* allele has the most dramatic effect on the development of spring growth habit (Pugsley, 1971, 1972; Santra et al., 2009; Eagles et al., 2010), and true spring wheat types were not part of the FAWWON collection.

The photoperiod sensitive allele (*Ppd-B1b*) at *Ppd-B1* was determined using an assay that detects the 'Chinese Spring' photoperiod insensitive (*Ppd-B1a*) allele (Beales et al., 2007).

The photoperiod insensitive (*Ppd-D1a*) and sensitive (*Ppd-D1b*) alleles at *Ppd-D1* were distinguished using a KASP assay that detects a deletion upstream of the coding region responsible for the photoperiod insensitive or 'Ciano 67'-type allele (Beales et al., 2007).

Statistical analysis

Best linear unbiased predictors (BLUPs) of winter injury were calculated separately for each environment using ASReml-R (VSN International Ltd., Hemel Hempstead, UK). Data for each environment were analyzed with a series of spatial models that included genotype, row, and column coordinates as random effects, and several different residual error terms specified in the *rcov* argument within ASReml-R (Gilmour et al., 2009). The restricted maximum likelihood (REML) loglikelihood value was used to select the best model.

In order to obtain BLUPs of each genotype for a combined analysis across all environments, winter injury data from the FAWWON trials were analyzed with ASReml-R using a two-stage procedure (Piepho et al., 2008). In the first stage, data from individual environments were analyzed with a series of spatial models as described above. The restricted maximum likelihood (REML) loglikelihood value was used to select the best model as done previously. Best linear unbiased estimates (BLUEs) from the first stage of the analysis were then subject to a combined analysis over environments with environments and genotypes as random effects. Environment specific error variance weights were calculated for each environment and utilized with the weights argument within the ASReml call. The weightings were calculated as (Reps/Trial EMS)/Average EMS, where Reps is the number of replications for each trial, Trial EMS is the error mean square for each trial, and the Average EMS is the average of the error mean squares over the five trials where winter injury was observed.

Genomic selection prediction accuracies of three different models were compared: the Fixed effects model used only KASP assay allele calls at the three vernalization and two photoperiod loci as fixed effects; the Random effects model used the 23,269 GBS SNP markers as random effects; and the Mixed effects model used both KASP markers as fixed effects and GBS SNP markers as random effects. Genomic estimated breeding values (GEBVs) were calculated using rrBLUP (Endelman, 2011) in R using the following model:

$$y = X\beta + Z\mu + \varepsilon$$

where X is the design matrix (n x p) allocating fixed effect values to individuals and β as a vector (p x 1) of fixed effects, Z is a design matrix (n x p) for random effects allocating marker values to individuals, μ is a vector of random effects, and ε is a vector of errors with a variance σ_ε^2.

Five-fold cross validation was used to assess model accuracy by assigning genotypes to one of five folds and using four of the folds to train the model and predict the GEBVs for the fifth fold for validation. The GS accuracy was calculated as the correlation between the GEBVs and phenotype BLUPs for individuals in the validation set. To compute model accuracy, 300 cycles of cross validation were performed and the average correlation was determined. The standard error of the mean prediction accuracy was calculated as the standard deviation divided by the square root of the number of cross validation cycles.

Results and Discussion

Winter injury variation across environments

Relatively little winter injury was observed in 2014 with none recorded at Fort Collins and an average of 15.2% at Julesburg (maximum of 98.9%) (Figure 4.1). In 2015, significant

winter injury was observed at both locations with average winter injury of 45.7% (maximum of 99.7%) at Fort Collins and 84.4% (maximum of 100%) at Julesburg. In 2016, observed winter injury was more similar to that observed in 2014, with average winter injury of 2.6% (maximum of 89.4%) at Fort Collins and 9.2% (maximum 71.9%) at Julesburg. The degree and consistency of winter injury observed across the six environments indicate that the FAWWON includes individuals with different levels of sensitivity to freezing temperatures. This may be due to the nursery including both facultative and winter habit wheats and their respective differences in vernalization requirements. Screening methods that do not require field evaluations would help to identify individuals that are not low temperature tolerant and thus not adapted to a particular growing region without the need for a costly season-long field evaluation that may not provide differential winter injury (as observed for Fort Collins 2014).

Allelic diversity at vernalization and photoperiod loci

The 287 FAWWON individuals were genotyped for alleles at three vernalization loci and two photoperiod loci (Table 4.1). The *Vrn-A1* KASP assay identified 73 individuals as homozygous for the *vrn-A1v* allele and 214 individuals as homozygous for the *vrn-A1w* allele. These two winter alleles are responsible for differences in dormancy release and freezing tolerance with the *vrn-A1v* allele showing reduced vernalization requirement compared to the *vrn-A1w* allele (Eagles et al., 2011; Zhu et al., 2014). These alleles are also associated with copy number variation with the *vrn-A1v* allele having two or fewer copies of the gene and the *vrn-A1w* allele having three or more copies (Zhu et al., 2014). Increased copy number results in a greater vernalization requirement and later flowering when the vernalization requirement is only partially met (Diaz et al., 2012). The *Vrn-B1a* KASP assay identified 102 individuals

homozygous for the *Vrn-B1a* spring allele, 146 individuals homozygous for the *vrn-B1* winter allele, and 39 individuals as heterozygous. The *Vrn-B1b* KASP assay identified nine individuals homozygous for the *Vrn-B1b* spring allele, 276 genotypes homozygous for the *vrn-B1* winter allele, and two individuals as heterozygous. None of the individuals evaluated had the *Vrn-B1c* allele. The *Vrn-D1* KASP assay identified 70 individuals as homozygous for the *Vrn-D1* spring allele and 217 individuals homozygous for the *vrn-D1* winter allele.

Allelic diversity of vernalization genes has been characterized in several worldwide (Iwaki et al., 2001; Kiss et al., 2014) and regional collections (Zhang et al., 2008; Grogan et al., 2016) of wheat. These analyses have indicated that allelic variation at vernalization loci is closely associated with winter temperatures in the growing region (Iwaki et al., 2001). Grogan et al. (2016) did not detect any spring-habit alleles at *Vrn-A1*, *Vrn-B1*, or *Vrn-D1* loci in a collection of contemporary and historic winter wheat individuals from the U.S. Great Plains. This suggests that strict selection pressure has been placed on true winter wheat types with a long vernalization requirement, but also demonstrates a high degree of genetic uniformity for vernalization alleles present in U.S. hard winter wheat germplasm. International nursery collections such as the FAWWON could be used to introduce vernalization alleles with slight differences in vernalization requirements that may allow for adaptation to different growing conditions in the U.S. Great Plains.

The *Ppd-B1* KASP assay identified four individuals homozygous for the photoperiod insensitive *Ppd-B1a* allele and 283 individuals homozygous for the photoperiod sensitive *Ppd-B1b* allele. The *Ppd-D1* KASP assay identified 217 individuals homozygous for the *Ppd-D1a* photoperiod insensitive allele, 68 individuals homozygous for the photoperiod sensitive *Ppd-*

D1b allele, and two as heterozygous. Studies in the U.S. northern Great Plains found that photoperiod insensitive lines were earlier to head and shorter in stature than their photoperiod sensitive counterparts (Busch et al., 1984; Marshall et al., 1989). In a collection of contemporary and historic winter wheat genotypes grown in the U.S. Great Plains, 57% carried the sensitive *Ppd-B1b* allele and 43% carried the insensitive *Ppd-B1a* allele, while 71% carried the photoperiod sensitive allele *Ppd-D1b* and 29% carried the insensitive *Ppd-D1a* allele (Grogan et al., 2016). The ratios of photoperiod sensitive to insensitive alleles between the FAWWON individuals in this study and the individuals from the U.S. Great Plains in the study by Grogan et al. (2016) are significantly different for both *Ppd-B1* and *Ppd-D1*. This could influence adaptation of FAWWON individuals in the U.S. Great Plains. Understanding the genetic factors that control low temperature tolerance at the molecular level is imperative for early screening to help foster the utilization and exchange of FAWWON germplasm across diverse global winter wheat production regions.

Among the 287 FAWWON individuals, 17 unique haplotypes were observed when considering the vernalization KASP assay results (Table 4.2). The most common haplotypes were Vrn-A1, w/Vrn-B1b, winter/Vrn-B1b, winter/Vrn-B1c, winter/Vrn-D1, winter (79 entries, 27.5%) which represents true winter habit types with all winter alleles; Vrn-A1, w/Vrn-B1a, spring/Vrn-B1b, winter/Vrn-B1c, winter/Vrn-D1, winter (56 entries, 19.5%) which represents a non-winter wheat growth type with a single spring allele at the *Vrn-B1* locus; and Vrn-A1, v/Vrn-B1a, winter/Vrn-B1b, winter/Vrn-B1c, winter/Vrn-D1, winter (36 entries, 12.5%) which represents a reduced vernalization winter type. There was a reduced vernalization or spring allele in a homozygous state at one or more vernalization loci in 187 (65%) of the FAWWON

individuals. Multiple reduced vernalization or spring alleles in a homozygous state were found in 54 (18.8%) of the FAWWON individuals (Table 4.2). The transition from vegetative to reproductive growth is a critical development switch and key adaptive trait. Any factor that maintains the plant in the vegetative stage, such as increased vernalization requirement or photoperiod sensitivity, also increases the duration and expression of low temperature tolerance (Fowler et al., 1996; Mahfoozi et al., 2000; Limin and Fowler, 2006). Allelic differences at these vernalization and photoperiod loci may help identify FAWWON individuals that are more susceptible to low temperatures found in the U.S. Great Plains.

Genomic selection prediction accuracies

Genomic selection could only be done using data from five of the six environments due to the lack of winter injury at Fort Collins 2014. Prediction accuracies for the Fixed effects model, where only genotypes at vernalization and photoperiod loci were used as fixed effects, ranged from 0.26 ± 0.01 to 0.57 ± 0.01 across the five environments and the combined data set (Figure 4.2). Prediction accuracies for the Random effects model, where the 23,269 SNP markers were treated as random effects, ranged from 0.26 ± 0.01 to 0.74 ± 0.01 across the five environments and the combined data set (Figure 4.2). The GS prediction accuracies observed in this study were comparable to Zhao et al. (2013) who reported a GS prediction accuracy of 0.58 for frost tolerance in wheat.

Prediction accuracies for the Random effects model were greater than the Fixed effects model in 2014, 2015, and the combined data set (Figure 4.2a, b, & d). In 2016, prediction accuracies for winter injury with the Random and Fixed effects models were not different (Figure 4.2c). These results indicate that even with a few known major QTL controlling low

temperature tolerance, modeling genome wide marker effects helps to explain a greater portion of the phenotypic variance for the trait than only modeling known major genes. The results for 2014, 2015, and the combined data set support the hypothesis that low temperature tolerance is controlled by more genes than just the major vernalization and photoperiod loci evaluated in this study.

Single factor fixed effect models

Each vernalization and photoperiod locus was individually treated as a fixed effect, while also modeling the 23,269 SNP markers as random effects, to determine the effect of each locus on GS prediction accuracy of winter injury in the Mixed effects model. When the alleles at *Vrn-A1* were treated as fixed effects, an increase in GS prediction accuracy above the Random effects model was observed for Julesburg 2014 (Figure 4.2a), Fort Collins 2015 and Julesburg 2015 (Figure 4.2b), and the combined data set (Figure 4.2d). Modeling the alleles at *Vrn-A1* as fixed effects in the Mixed effects model resulted in reduced GS prediction accuracy compared to the Random effects model for Fort Collins 2016 and Julesburg 2016 (Figure 4.2c). Using alleles at *Vrn-A1* as a fixed effect, the greatest increase in prediction accuracy above the Random effects model was from 0.61 ± 0.00 to 0.68 ± 0.00 (11.5%) for Julesburg 2014 (Figure 4.2a).

A Mixed effects model with alleles at *Vrn-B1* treated as fixed effects showed slightly reduced prediction accuracy compared to the Random effects model for Julesburg 2014 (Figure 4.2a), Fort Collins 2015 (Figure 4.2b), and Fort Collins 2016 (Figure 4.2c). Eagles et al. (2010) reported that spring alleles at the *Vrn-1* loci do not reduce heading date equally with *Vrn-B1* having a smaller effect than *Vrn-A1* and *Vrn-D1*. These results agree with this our study, as

when treated as a fixed effect *Vrn-B1* was not consistently or highly effective in increasing GS prediction accuracy above the Random effects model prediction accuracy.

A Mixed effects model with alleles at *Vrn-D1* treated as fixed effects showed increased prediction accuracy compared to the Random effects model in the combined data set (Figure 4.2d) and each environment except Julesburg 2015, where no difference in prediction accuracy was observed (Figure 4.2a, b, & c). The greatest increase in prediction accuracy was observed for Julesburg 2016 where accuracy increased 36% from 0.36 ± 0.01 to 0.49 ± 0.01 (Figure 4.2c). The results presented here highlight the importance of genotyping individuals at *Vrn-D1* when screening for low temperature tolerance as it was shown to be the most consistent vernalization locus for increasing GS prediction accuracy and the locus with the single greatest effect in increasing prediction accuracy. Zhang et al. (2012) also reported that facultative wheats show sequence variation at the *Vrn-D1* locus.

No improvement in GS prediction accuracy was observed in the combined data or in the individual environments when either photoperiod allele was used as a fixed effect (Figure 4.2). For Fort Collins 2016, the Mixed effects models with alleles at *Ppd-B1* or *Ppd-D1* as fixed effects decreased GS prediction accuracy (Figure 4.2c). Although, photoperiod genes influence the timing of the transition from vegetative to reproductive growth (Cockram et al., 2007) they did not appear to be associated with variation in winter injury among individuals from the FAWWON.

Multi-factor fixed effects models

A Mixed effects model with alleles at all three vernalization loci as fixed effects and 23,269 GBS SNPs as random effects was evaluated to determine their combined effect on GS

prediction accuracy compared to the Random effects model and the best single locus Fixed effects model. Using all three loci as fixed effects resulted in a greater GS prediction accuracy above the Random effects model in all five environments and the combined data set (Figure 4.3a, b, c & d). The greatest increase in prediction accuracy (38.9%) observed was from 0.36 ± 0.01 to 0.50 ± 0.01 for Julesburg 2016 (Figure 4.3c). This model outperformed or performed the same as the best single locus Fixed effects model for each environment and the combined data set (Figure 4.3).

A Mixed effects model with alleles at both photoperiod loci as fixed effects and the GBS SNP markers as random effects showed similar prediction accuracy as the Random effects model for each environment and the combined data set (Figure 4.3), in agreement with that observed for the Mixed effects model with individual photoperiod loci as fixed effects. While the Mixed effects model with all vernalization and photoperiod loci as fixed effects and SNP markers as random effects showed higher prediction accuracy than the Random effects model in some environments, it showed no higher prediction accuracy than the Mixed effects model with vernalization loci together as fixed effects (Figure 4.3).

Mixed effects models were shown to be effective in accounting for major and minor genetics effects and provided the most accurate estimates of GEBV for low temperature tolerance in this collection of FAWWON lines. Identifying genotypes with high GEBV for winter hardiness could help identify individuals best adapted to regions with severe cold where only spring wheat types can be grown. A shift to over wintering wheat types with higher cold tolerance in these areas would help to increase wheat yields as winter wheat types generally

have greater yield potential than spring wheat due to an extended growing season (Randhawa et al., 2013).

Conclusions

This collection of genotypes from the FAWWON include both facultative and winter wheat types with considerable variation for both low temperature sensitivity and allelic diversity at the major vernalization loci. While field winter survival ability is considered the ultimate test of a cultivar's winter hardiness, obtaining such data from field trials is costly and often hampered by the lack of differential winter injury in a particular growing environment. Because of this limitation, GS can be an effective method for prediction of low temperature tolerance among germplasm collections. An understanding of the underlying genetic controls, and how to optimize GS models for predicting low temperature tolerance, is important for plant breeders to target germplasm to different production regions with variable environmental conditions.

The mixed effects model approach to GS allows for known vernalization loci with large effects to be included in a model with genome wide SNP markers for unknown smaller effect QTLs. Genomic selection using all three vernalization loci as fixed effects in combination with genome wide SNP markers appears to be the most effective method for predicting low temperature tolerance in this collection.

Tables

Table 4.1. Description of the vernalization (Vrn) and photoperiod (Ppd) alleles and their predicted phenotypes.

Locus	Allele	Phenotype
Vrn-A1	*vrn-A1w*	winter growth habit, higher freezing tolerance, Wichita-type
	vrn-A1v	winter growth habit, reduced freezing tolerance, Veery-type
Vrn-B1	*Vrn-B1a*	spring growth habit
	Vrn-B1b	spring growth habit
	Vrn-B1c	spring growth habit
	vrn-B1	winter growth habit
Vrn-D1	*Vrn-D1*	spring growth habit
	vrn-D1	winter growth habit
Ppd-B1	*Ppd-B1a*	photoperiod insensitive
	Ppd-B1b	photoperiod sensitive
Ppd-D1	*Ppd-D1a*	photoperiod insensitive
	Ppd-D1b	photoperiod sensitive

Table 4.2. Summary of haplotypes of 287 individuals from the Facultative and Winter Wheat Observation Nursery (FAWWON) based on Kompetitive Allele Specific PCR assays at the vernalization loci.

n	Vrn-A1†	Vrn-B1a	Vrn-B1b	Vrn-B1c	Vrn-D1
79	w	Winter	Winter	Winter	Winter
27	w	Winter	Winter	Winter	Spring
56	w	Spring	Winter	Winter	Winter
16	w	Spring	Winter	Winter	Spring
4	w	Spring	Spring	Winter	Winter
1	w	Spring	Het	Winter	Winter
20	w	Het	Winter	Winter	Winter
9	w	Het	Winter	Winter	Spring
1	w	Het	Het	Winter	Winter
1	w	Het	Spring	Winter	Winter
36	v	Winter	Winter	Winter	Winter
4	v	Winter	Winter	Winter	Spring
12	v	Spring	Winter	Winter	Winter
9	v	Spring	Winter	Winter	Spring
4	v	Spring	Spring	Winter	Winter
5	v	Het	Winter	Winter	Spring
3	v	Het	Winter	Winter	Winter

† The Vrn-A1 KASP assay results are designated as ‘v’ for reduced vernalization and ‘w’ for regular vernalization winter alleles. The Vrn-B1a, Vrn-B1b, Vrn-B1c, and Vrn-D1 KASP assay results are designated as Spring (no vernalization requirement) and Winter (vernalization requirement). Heterozygous allele calls are designated with ‘Het’.

Table 4.3. Description of Kompetitive Allele Specific PCR (KASP) assays used to genotype 287 individuals from the Facultative and Winter Wheat Observation Nursery (FAWWON) for alleles at major vernalization and photoperiod loci.

Locus	Allele(s) assayed	Primer name	Label	Primer Sequence	Control Genotypes
Vrn-A1	*vrn-A1v*	Vrn-A1_AL1	FAM	CAACTCCTTGAGATTCAAAGATTCAAG	Jagger
	vrn-A1w	Vrn-A1_AL2	HEX	GCAACTCCTTGAGATTCAAAGATTCAAA	Above, 2174
		Vrn-A1_C1		CATCCTGCATCTGCAGGCATCTC	
Vrn-B1	*vrn-B1*	Vrn-B1_D_A2	FAM	GGCAGCTAATGTGGGGTAGTCT	Jagger, Above
		Vrn-B1_D_C1s		ATTCGTATTGCTAGCTCCGGCCAT	
	Vrn-B1a	Vrn-B1_I_ALG	HEX	CAACCTCCACGGTTTCAAAAAGTAG	Exchange
		Vrn-B1_I_C1		ATATTTACTAAGCAGCGGTCATTCCGAT	
Vrn-B1	*vrn-B1*	Vrn-B1_B_AL1	FAM	GCGCAAGCGGGAGCTACATG	Jagger, Above
	Vrn-B1b	Vrn-B1_B_AL2	HEX	GCGCAAGCGGGAGCTACATC	Alpowa
		Vrn-B1_B_C1		GCCATGAACAACAAAGGGGGTGGT	
Vrn-B1	*vrn-B1*	Vrn-B1_C_AL1	FAM	CCTAAACAGGGGCAGAACACTG	Jagger, Above
	Vrn-B1c	Vrn-B1_C_AL2	HEX	CCTAAACAGGGGCAGAACACTA	Lutescens 62
		Vrn-B1_C_C1		GACCCCAGGGCCTATGAATGTAATT	
Vrn-D1	*vrn-D1*	Vrn-D1_AL1	FAM	ATCATTCGAATTGCTAGCTCCGG	Jagger, Above
	Vrn-D1a	Vrn-D1_AL2	HEX	ATCATTCGAATTGCTAGCTCCGC	Norin 61, Chinese Spring
		Vrn-D1_C		GCCTGAACGCCTAGCCTGTGTA	
Ppd-B1	*Ppd-B1a*	Ppd-B1_A_AL1	FAM	GACGTTATGAACGCTTGGCA	Chinese Spring
	Ppd-B1b	Ppd-B1_A_AL2	HEX	CCGTTTTCGCGGCCTT	Chihoku Komugi
		Ppd-B1_A_C		GGGTTCGTCGGGAGCTGT	
Ppd-D1	*Ppd-D1a*	Ppd-D1_A_AL1	FAM	CAAGGAAGTATGAGCAGCGGTT	Ciano67
	Ppd-D1b	Ppd-D1_A_AL2	HEX	AAGAGGAAACATGTTGGGGTCC	Chinese Spring
		Ppd-D1_A_C		GCCTCCCACTACACTGGGC	

Table 4.4. Genotypes of 287 individuals from the Facultative and Winter Wheat Observation Nursery (FAWWON) at vernalization and photoperiod loci based on Kompetitive Allele Specific PCR (KASP) assays. FAWWON ID represents the nursery code (20th, 21st, 22nd FAWWON), the type of nursery (IRR for irrigated, SA for semi-arid), and the nursery entry number. The OTHER ID represents the individual's CIMMYT ID, cultivar name, or cross.

FAWWON ID	OTHER ID	VRN-A1	VRN-B1a	VRN-B1b	VRN-B1c	VRN-D1	PPD-B1	PPD-D1
20FAWWON.IRR.7	TCI011031	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.8	TCI011031	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.9	TCI011214	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.10	TCI011657	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.11	TCI-02-691	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.12	TCI022028	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.13	TCI022063	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.IRR.14	TCI022073	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.15	TCI022086	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.IRR.16	TCI022086	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.IRR.17	TCI022086	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.IRR.18	TCI022216	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.19	TC1021013	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.20	TC1021027	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.21	TC1021032	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.22	TC1021034	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.23	TC1021034	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.24	TC1021068	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.25	TC1021152	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.26	TC1021152	w	Het	Winter	Winter	Winter	b	a
20FAWWON.IRR.27	TC1021162	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.28	TC1021164	w	Spring	Winter	Winter	Winter	b	b
20FAWWON.IRR.29	TC1021187	w	Spring	Winter	Winter	Winter	a	a
20FAWWON.IRR.30	TC1021198	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.31	TC1021243	v	Winter	Winter	Winter	Winter	b	b

20FAWWON.IRR.32	TC1021414	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.IRR.33	TCI-02-45	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.35	TCI-02-175	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.36	OCW02S155T	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.37	OCW02S155T	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.38	OCW02S155T	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.39	OCW02S369S	w	Het	Winter	Winter	Winter	b	a
20FAWWON.IRR.40	SONMEZ	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.41	OCW02S471S	w	Het	Winter	Winter	Winter	b	a
20FAWWON.IRR.42	OCW02S471S	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.43	OCW02S484S	w	Winter	Winter	Winter	Spring	b	b
20FAWWON.IRR.44	OCW02S567S	v	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.45	OCW02S567S	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.46	OCW02S567S	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.47	OCW02S596S	v	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.48	OCW02S607S	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.49	OCW02S608S	v	Spring	Winter	Winter	Spring	b	b
20FAWWON.IRR.50	CMSA01M00330S	v	Spring	Winter	Winter	Spring	b	a
20FAWWON.IRR.51	CMSA01M00370T	v	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.52	CMSA01M00381T	v	Spring	Winter	Winter	Spring	b	a
20FAWWON.IRR.54	CMSW01WM00578S	v	Winter	Winter	Winter	Spring	b	b
20FAWWON.IRR.55	TCI012088	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.56	TCI-02-80	w	Spring	Winter	Winter	Winter	b	b
20FAWWON.IRR.57	02106G2-2	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.59	TURKOAZ	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.60	TEKIRA2	v	Spring	Winter	Winter	Spring	b	a
20FAWWON.IRR.69	IRW2000-01 - 246	w	Spring	Winter	Winter	Spring	b	a
20FAWWON.IRR.70	1-C-17450	v	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.71	1-C-17474	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.IRR.72	1-C-17474	w	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.74	1-C-17487	w	Winter	Winter	Winter	Winter	b	a

20FAWWON.IRR.75	1-C-17551	w	Spring	Winter	Winter	Spring	b	a
20FAWWON.IRR.77	1-C-17560	w	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.78	1-C-17603	w	Het	Winter	Winter	Winter	b	a
20FAWWON.IRR.85	1-NS 1590	v	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.86	1-C-17630	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.87	1-C-17630	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.88	1-C-17480	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.89	1-C-17551	w	Het	Winter	Winter	Spring	b	a
20FAWWON.IRR.95	OTILIA	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.97	06393GP1	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.98	05899G01-2	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.100	06325G1-2	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.106	06579G1-1	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.IRR.114	OR2071681	v	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.115	OR2080111H	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.118	Appalachian White	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.IRR.143	NACIBEY	v	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.202	KARAHAN	v	Spring	Spring	Winter	Winter	b	b
20FAWWON.SA.206	TC1021032	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.207	TC1021068	w	Spring	Winter	Winter	Spring	b	a
20FAWWON.SA.208	TC1021160	v	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.209	TC1021180	v	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.210	TC1021198	w	Spring	Winter	Winter	Spring	b	b
20FAWWON.SA.212	TC1021243	w	Winter	Winter	Winter	Spring	b	b
20FAWWON.SA.213	TC1021266	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.SA.214	TC1021276	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.215	TC1021276	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.218	TC1021350	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.221	TCI022086	w	Winter	Winter	Winter	Spring	b	a
20FAWWON.SA.222	TCI022108	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.223	TCI022191	w	Spring	Winter	Winter	Spring	b	a

20FAWWON.SA.224	TCI022200	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.226	TCI022271	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.227	TCI022271	w	Het	Winter	Winter	Winter	b	a
20FAWWON.SA.228	TCI-02-87	v	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.230	TCI-02-111	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.SA.231	TCI-02-129	w	Spring	Spring	Winter	Winter	b	b
20FAWWON.SA.232	TCI-02-142	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.233	TCI-02-26	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.SA.235	TCI-02-36	w	Spring	Winter	Winter	Winter	b	b
20FAWWON.SA.236	TCI-02-913	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.237	OCW02S262T	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.238	OCW02S528S	w	Spring	Winter	Winter	Winter	b	a
20FAWWON.SA.239	OCW02S567S	v	Spring	Winter	Winter	Winter	b	a
20FAWWON.SA.241	OCW02S596S	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.243	IRW2000-01 - 246	w	Winter	Winter	Winter	Winter	b	b
20FAWWON.SA.244	1-C-17459	w	Het	Winter	Winter	Winter	b	a
20FAWWON.SA.249	AK-B?BA?	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.251	KARASAY	w	Het	Winter	Winter	Winter	b	b
20FAWWON.SA.252	ZHADYRA	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.254	NIKIFOR	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.256	06659G4-1	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.257	ELVIRA	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.258	KALACH	w	Winter	Winter	Winter	Winter	b	a
20FAWWON.SA.259	SVETOCH	w	Winter	Winter	Winter	Winter	b	Het
20FAWWON.SA.278	BDME 09 1/K	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.7	TCI032026	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.9	TCI031361	w	Het	Winter	Winter	Winter	b	b
21FAWWON.IRR.11	SHARK/F4105W2.1//CHARA/3/MERCAN-1	v	Spring	Winter	Winter	Winter	b	b
21FAWWON.IRR.14	ALPU//VP5053 (WA#FM/201/23*2/GS50A)	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.16	TCI032348	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.17	OCW02S476S	w	Spring	Winter	Winter	Winter	b	a

21FAWWON.IRR.29	TCI031171	w	Het	Spring	Winter	Winter	b	a
21FAWWON.IRR.31	TCI-02-80	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.32	TCI 001409	v	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.35	TCI-01-117	v	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.36	TCI-02-475	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.43	OSTROV	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.45	F06325G1-	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.48	F06580G2-1	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.49	F06659G6-1	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.50	F06659G10-1	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.52	F07270G2	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.59	NOTA	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.62	1-C-17677	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.64	1-C-17748	v	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.66	1-C-17809	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.68	1-C-17641	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.71	SH??4414/CROW//ATT?LA	w	Spring	Het	Winter	Winter	b	a
21FAWWON.IRR.72	DMITRY	v	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.75	PROTON	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.76	KIPRA	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.81	SWW1-135	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.83	SWW1-97	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.95	JUP/4/CLLF/3/II14-53/ODIN//CI134431/ …	w	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.103	MUSTANG/ICIZCE	w	Spring	Winter	Winter	Winter	b	b
21FAWWON.IRR.113	TX71C8130R/TX81V6610/3/RL6010/…	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.116	TX71C8130R/TX81V6610/3/RL6010/…	v	Winter	Winter	Winter	Spring	b	a
21FAWWON.IRR.119	TX71A983.4/TX69D4812//PYN/3/VPM/…	v	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.122	JI5418/MARAS//SHARK/F4105W2.1	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.137	43-RWA-94N-74/F6038W12.1	w	Winter	Winter	Winter	Winter	b	b
21FAWWON.IRR.141	MINA/KRISTAL	v	Spring	Winter	Winter	Winter	b	b
21FAWWON.IRR.142	MINA/KRISTAL	w	Winter	Winter	Winter	Spring	b	b

21FAWWON.IRR.143	SHARK-6/YUZHNAYA12/7/ID2619…	w	Winter	Winter	Winter	Winter	b	b
21FAWWON.IRR.144	SHARK-6/YUZHNAYA12/7/ID2619…	w	Winter	Winter	Winter	Winter	b	b
21FAWWON.IRR.146	CHATELET/GRU-45	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.148	CHATELET/GRU-45	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.150	DORADE-5/DUNAV	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.152	1-68-188//1-60-3/Tonichi 81…	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.IRR.157	ID2619/5/GRTPL 6121…	w	Het	Winter	Winter	Winter	b	a
21FAWWON.IRR.161	PALANDOKEN97/ATTILLA	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.IRR.163	NGDA146/4/YMH/TOB//MCD/3/LIRA…	w	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.166	SHARK-6/YUZHNAYA12/7/ID2619…	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.IRR.167	88ZHONG218//CTK/VEE/3/KVZ/GV//PR…	v	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.201	GEREK79	v	Het	Winter	Winter	Winter	b	a
21FAWWON.SA.202	KARAHAN	v	Spring	Spring	Winter	Winter	b	b
21FAWWON.SA.207	TCI031181	w	Winter	Winter	Winter	Spring	b	b
21FAWWON.SA.208	TCI032095	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.210	TCI032063	w	Winter	Winter	Winter	Winter	b	a
21FAWWON.SA.211	TCI031039	w	Winter	Winter	Winter	Winter	b	b
21FAWWON.SA.214	TCI032348	w	Het	Winter	Winter	Spring	b	a
21FAWWON.SA.218	TCI031020	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.223	TCI032235	v	Spring	Winter	Winter	Winter	b	b
21FAWWON.SA.226	TCI031396	w	Spring	Winter	Winter	Winter	b	b
21FAWWON.SA.227	TCI032210	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.228	TCI031171	w	Winter	Winter	Winter	Winter	b	a
21FAWWON.SA.231	TCI031286	v	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.234	TCI031396	w	Spring	Winter	Winter	Winter	b	b
21FAWWON.SA.243	OK07214	w	Het	Winter	Winter	Spring	b	a
21FAWWON.SA.247	OK09634	v	Winter	Winter	Winter	Winter	b	b
21FAWWON.SA.248	TCI011194-030	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.250	1-C-17849	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.SA.252	PYN/BAU//BONITO	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.256	CMSW97WM00399S	v	Winter	Winter	Winter	Winter	b	a

21FAWWON.SA.258	TCI97AP-310	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.261	TCI04-1	v	Spring	Winter	Winter	Winter	b	b
21FAWWON.SA.262	TCI04-324	w	Spring	Winter	Winter	Spring	b	a
21FAWWON.SA.263	TCI02-679	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.265	TCI02-405	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.268	91-142 a 139	v	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.269	TCI 001409	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.270	TCI 002133	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.271	TCI-01-117	w	Spring	Spring	Winter	Winter	b	a
21FAWWON.SA.275	TCI04-1	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.276	TCI04-1	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.281	TCI032527	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.SA.286	TC1021266	w	Het	Winter	Winter	Winter	b	b
21FAWWON.SA.287	TCI022086	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.288	TCI02-87	v	Winter	Winter	Winter	Winter	b	a
21FAWWON.SA.289	TC1021068	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.292	TCI 002115	w	Winter	Winter	Winter	Winter	b	b
21FAWWON.SA.293	TCI031223	w	Winter	Winter	Winter	Spring	b	a
21FAWWON.SA.297	TC1021243	w	Spring	Winter	Winter	Winter	b	a
21FAWWON.SA.299	TC1021027	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.7	TCI021034	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.8	TCI021034	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.9	TCI02-913	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.10	TCI041031	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.14	TCI041060	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.18	TCI041237	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.19	TCI041261	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.20	TCI041261	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.21	TCI041286	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.22	TCI041496	v	Spring	Spring	Winter	Winter	b	a
22FAWWON.IRR.23	TCI041505	w	Spring	Winter	Winter	Winter	b	a

22FAWWON.IRR.25	TCI042153	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.26	TCI042153	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.27	TCI042167	w	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.31	TCI042366	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.32	TCI042619	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.33	TCI042632	v	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.34	TCI042638	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.35	TCI042638	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.41	TCI072152	w	Spring	Spring	Winter	Winter	b	a
22FAWWON.IRR.42	OCW05S645S	v	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.45	OR2052096	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.48	TCI051145	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.49	CMSA06WM00018T	v	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.51	TCI071259	w	Winter	Winter	Winter	Winter	a	a
22FAWWON.IRR.52	TCI071325	v	Winter	Winter	Winter	Spring	b	a
22FAWWON.IRR.53	TCI072137	w	Spring	Winter	Winter	Winter	b	b
22FAWWON.IRR.54	OCW05S626S	w	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.55	TCI071189	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.57	TCI071199	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.60	CGWS04WM00054S	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.66	OCW05S626S	w	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.67	OCW04S037S	w	Winter	Winter	Winter	Spring	b	a
22FAWWON.IRR.68	TCI052118	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.69	OCW05S594T	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.70	OCW05S626S	w	Het	Winter	Winter	Winter	b	a
22FAWWON.IRR.71	TCI071078	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.73	TCI052022	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.79	RUMELI	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.81	CROC_1/AE.SQUARROSA(224)//OPATA	w	Het	Winter	Winter	Spring	b	Het
22FAWWON.IRR.83	1-C-17967	v	Spring	Winter	Winter	Spring	a	a
22FAWWON.IRR.84	1-C-17967	v	Spring	Winter	Winter	Spring	a	a

22FAWWON.IRR.85	1-C-17969	w	Spring	Winter	Winter	Spring	b	a
22FAWWON.IRR.86	1-C-17969	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.87	1-C-17971	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.89	1-C-18034	v	Spring	Winter	Winter	Winter	b	a
22FAWWON.IRR.92	DH-26-42	v	Spring	Winter	Winter	Spring	b	a
22FAWWON.IRR.93	1-C-17964	w	Spring	Winter	Winter	Spring	b	a
22FAWWON.IRR.95	1-C-18077	v	Het	Winter	Winter	Spring	b	a
22FAWWON.IRR.98	1-C-18144	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.IRR.103	SULTAN95	w	Spring	Winter	Winter	Winter	b	b
22FAWWON.IRR.108	F06521GP3	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.IRR.111	F05906G1-101	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.202	KARAHAN	v	Spring	Spring	Winter	Winter	b	b
22FAWWON.SA.211	TCI041084	w	Het	Winter	Winter	Winter	b	a
22FAWWON.SA.214	TCI041237	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.SA.217	TCI041347	w	Het	Winter	Winter	Winter	b	a
22FAWWON.SA.218	TCI041374	w	Het	Winter	Winter	Winter	b	a
22FAWWON.SA.221	TCI041505	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.SA.223	TCI041548	w	Spring	Spring	Winter	Winter	b	b
22FAWWON.SA.225	TCI042304	w	Het	Het	Winter	Winter	b	a
22FAWWON.SA.230	TCI042565	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.SA.231	TCI042604	w	Winter	Winter	Winter	Spring	b	b
22FAWWON.SA.232	TCI042609	w	Spring	Winter	Winter	Winter	b	b
22FAWWON.SA.235	TCI042673	w	Het	Winter	Winter	Winter	b	b
22FAWWON.SA.237	TCI042691	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.SA.239	TCI051038	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.243	TCI051257	v	Winter	Winter	Winter	Winter	b	b
22FAWWON.SA.248	TCI051373	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.249	TCI051404	v	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.250	TCI051412	w	Winter	Winter	Winter	Spring	b	b
22FAWWON.SA.253	TCI052037	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.256	TCI052366	w	Het	Winter	Winter	Spring	b	b

22FAWWON.SA.258	TCI052470	w	Spring	Winter	Winter	Spring	b	a
22FAWWON.SA.259	TCI052479	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.SA.260	TCI051051	w	Winter	Winter	Winter	Spring	b	b
22FAWWON.SA.262	TCI071116	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.263	TCI071156	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.265	TCI071310	w	Het	Winter	Winter	Spring	b	b
22FAWWON.SA.269	TCI072083	w	Het	Winter	Winter	Spring	b	b
22FAWWON.SA.270	CGSW05B00011T	w	Spring	Winter	Winter	Spring	b	a
22FAWWON.SA.273	CGWS04WM00048S	w	Het	Winter	Winter	Winter	b	a
22FAWWON.SA.274	CGWS04WM00052S	w	Het	Winter	Winter	Winter	b	a
22FAWWON.SA.277	CMSW05WM00013T	w	Winter	Winter	Winter	Winter	b	b
22FAWWON.SA.281	OCW05S740S	w	Winter	Winter	Winter	Winter	b	a
22FAWWON.SA.282	WSX0400302	w	Spring	Winter	Winter	Winter	b	a
22FAWWON.SA.294	ICWH970148	w	Winter	Winter	Winter	Winter	b	b

Figures

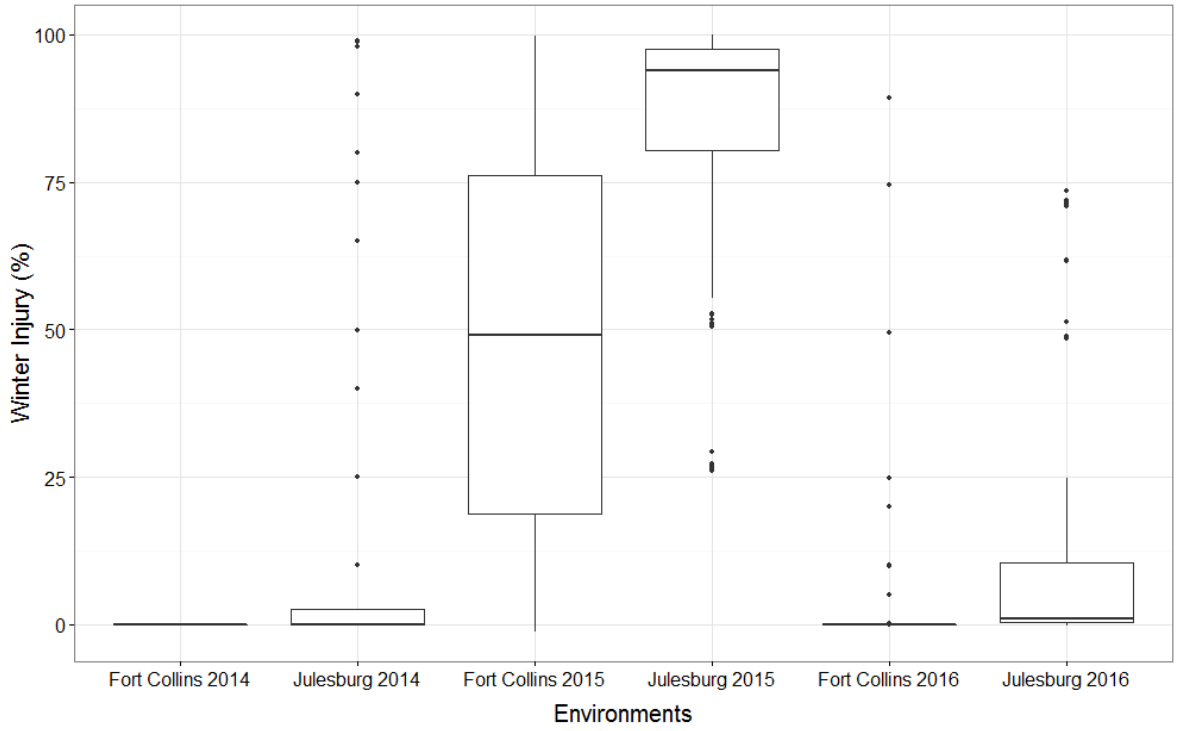

Figure 4.1. Distribution of best linear unbiased predictors (BLUPs) for winter injury observed for individuals from the Facultative and Winter Wheat Observation Nursery (FAWWON) for each of the six field environments.

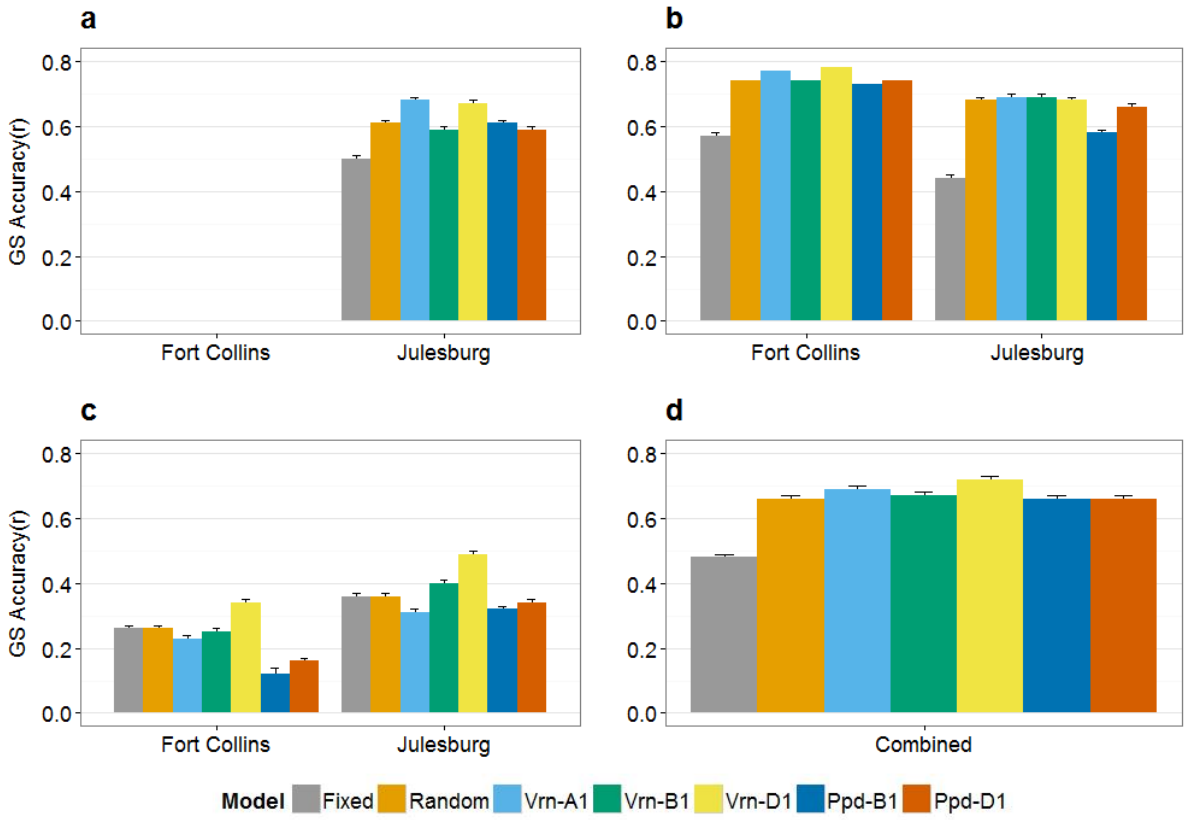

Figure 4.2. Genomic selection prediction accuracies using three vernalization and two photoperiod loci in a fixed-only model, genotyping-by-sequencing (GBS) derived SNP markers in a random-only model, and GBS markers together with single vernalization (*Vrn-A1*, *Vrn-B1*, and *Vrn-D1*) and single photoperiod (*Ppd-B1* and *Ppd-D1*) loci as fixed effects in a mixed effects model for a) Julesburg 2014, b) Fort Collins and Julesburg 2015, c) Fort Collins and Julesburg 2016, and d) combined over all environments.

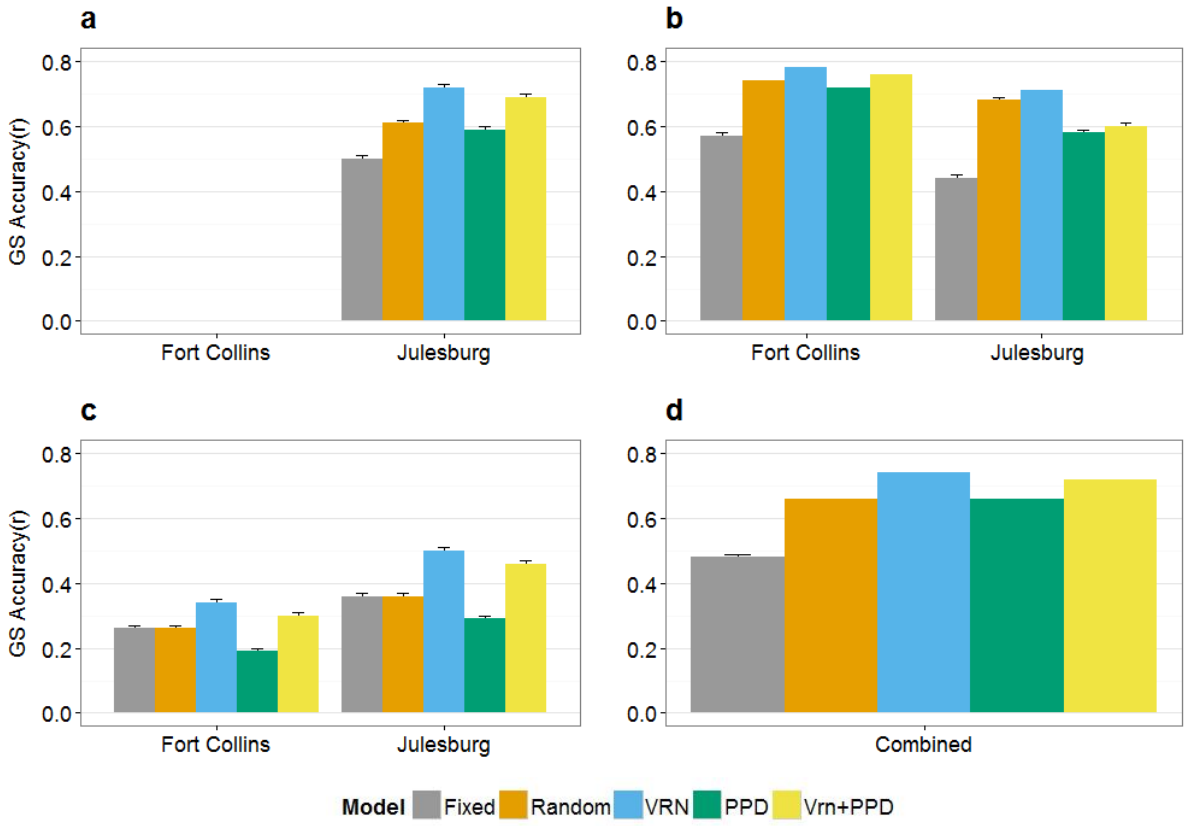

Figure 4.3. Genomic selection prediction accuracies using three vernalization and two photoperiod loci in a fixed-only model, genotyping-by-sequencing (GBS) derived SNP markers in a random-only model, and GBS markers together with all three vernalization (VRN), two photoperiod (PPD) loci, and vernalization and photoperiod loci (VRN+PPD) as fixed effects in a mixed effects model for a) Julesburg 2014, b) Fort Collins and Julesburg 2015, c) Fort Collins and Julesburg 2016, and d) combined over all environments.

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APPENDICES

Supplemental Text

Supplemental Text S5.1

GENOMIC SELECTION PREDICTION ACCURACY FOR GRAIN YIELD IN WHEAT IS IMPROVED WITH NORMALIZED DIFFERENCE VEGETATION INDEX AND HEADING DATE

Genomic selection (GS) promises to accelerate the rate of genetic gain in wheat (*Triticum aestivum* L.) for genetically complex traits, including grain yield (Araus et al., 2002; Jannink et al., 2010; Heffner et al., 2011). Genomic selection prediction models are developed using a training population of individuals with both trait phenotypes and marker genotypes to estimate genome-wide marker effects (Meuwissen et al., 2001; Lorenz et al., 2011). The GS model then uses the marker effects to calculate a genomic estimated breeding value (GEBV) for selection candidates that are genotyped but not phenotyped (Lorenz et al., 2011; Cobb et al., 2013). This technique allows for indirect selection of individuals for quantitative traits prior to phenotyping allowing for earlier selection and thus enhanced selection gains per unit of time and cost (Bernardo and Yu, 2007; Heffner et al., 2010). As the cost and efficiency of obtaining genomic information on wheat drops below the cost and efficiency of phenotyping individuals over years and locations, genomic information can more affordably be leveraged to predict phenotypic performance (Bernardo, 2008; Cobb et al., 2013). This can facilitate a shortening of

the breeding cycle and enable earlier selection and intercrossing of early-generation breeding material.

In order to utilize genomic information for GS applications it needs to be carefully and comprehensively linked to phenotypes observed in representative environments (Furbank and Tester, 2011). Current genomic prediction models typically use a single phenotypic trait even though new varieties of crops are evaluated for their performance across multiple traits. In plant breeding, indirect selection for the primary trait using a correlated secondary trait is often used when the primary trait is difficult or expensive to measure. Examples from wheat breeding include selection for reduced plant height to improve harvest index and lodging resistance and selection for higher protein concentration to improve quality. Selection using secondary traits is advantageous when the secondary trait is highly heritable, has a high genetic correlation with the target trait, and is inexpensive to measure relative to the target trait.

High throughput phenotyping techniques that measure spectral radiation reflectance from crop canopies show promise for differentiating and selecting superior genotypes (Aparicio et al., 2000; Raun et al., 2001; Royo et al., 2003). Measurements of spectral radiation reflected by crop canopies at specific wavelengths in the visible (VIS, 400-700 nm) and near-infrared (NIR, 750-1300 nm) regions of the electromagnetic spectrum provide a reflectance signature for each genotype due to absorption contrasts between spectral radiation regions (Reynolds et al., 1999). These spectral reflectance signatures can estimate simultaneously, and in a rapid nondestructive manner, a variety of morphological and physiological traits (Pask et al., 2012; Reynolds et al., 2012).

Spectral reflectance indices (SRI) were developed on the basis of ratios or differences between reflectances observed at different wavelengths (Araus, 1996; Araus et al., 2001). Among the most commonly used vegetation indices is the normalized difference vegetation index (NDVI; Araus, 1996; Araus et al., 2001). The NDVI indices are associated with component traits of grain yield and have yielded estimates of chlorophyll content (Baber et al., 2006), green biomass (Babar et al., 2006; Marti et al., 2007), percent ground cover (Mullan and Reynolds, 2010), nitrogen status (Wright Jr et al., 2005), green leaf duration (Lopes and Reynolds, 2012), and grain yield (Aparicio et al., 2000; Araus, 1996; Raun et al., 2001; Royo et al., 2003). Large NDVI values are associated with greater biomass accumulation and more rapid growth when measured during the vegetative phase and longer grain filling duration and delayed leaf senescence when measured during the grain filling phase (Barber et al., 2006).

Strong correlations between NDVI measurements and grain yield have been shown at heading (Babar et al., 2006), anthesis (Aparicio et al., 2000), and grain filling in wheat (Babar et al., 2006a, 2006b; Royo et al., 2003). Passioura et al. (1993) suggested that the overriding factor determining grain yield in wheat in a Mediterranean environment is the development of leaf area through time. Rather than using NDVI at a single time point or growth stage, multiple NDVI measurements taken over the course of a growing season would allow seasonal profiles of genotypes to be developed that show crop emergence, maturation, and senescence (Bartholome, 1988; Prasad and Carver, 2007). Researchers have found that NDVI measurements averaged across multiple growth stages of wheat provide a higher correlation with grain yield than any individual growth stage measurement (Labus et al., 2002; Babar et al., 2006; Prasad et al., 2007; Gutierrez et al., 2010). Although mean measurement values have

become standard practice, Pinter Jr. et al. (1981) and Rudorff et al. (1990) plotted the trajectory of NDVI throughout the growing season and verified that the area under the spectral curve was closely related to final grain yield. Prasad et al. (2007) and Babar et al. (2006) showed that mean index values averaged over several growth stages could provide a higher correlation with grain yield compared with any individual growth stage.

The prospect of future genetic improvements through the use of SRI to identify and track physiological traits provides plant breeding programs with new opportunities to examine genetic diversity, improve crop stress response, and increase yield potential. Incorporating secondary traits into a multivariate GS model has been shown to produce higher prediction accuracies than a univariate model using yield data alone (Calus et al., 2011; Jia et al., 2012; Pszczola et al., 2013; Rutkoski et al., 2016). Using NDVI as a secondary trait has been shown to increase GS prediction accuracies (Rutkoski et al., 2016). Although including NDVI as a secondary trait is not new, a direct comparison of using mean NDVI measurements to area under the NDVI curve in a multivariate genomic selection model has not been done. The main objectives of this study were i) to compare the GS prediction accuracies for yield using single-trait genomic selection to multi-trait genomic selection models with different secondary trait phenotypes and ii) to determine the best cumulative NDVI phenotype for summarizing multiple NDVI time point measurements for increasing GS prediction of yield in different environments.

Materials and Methods

Germplasm and experimental layout

Genotypes from three years of the Facultative and Winter Wheat Observation Nursery (FAWWON) were included in these experiments (n=287 individuals), including individuals from

the 20th FAWWON, 21st FAWWON, and 22nd FAWWON. All individuals included in this study are elite genotypes representing released cultivars and experimental lines. The FAWWON individuals represented breeding programs from Turkey-CIMMYT-ICARDA (TCI), United States (U.S.), Iran, Romania, Kazakhstan, Russia, Bulgaria, Turkey, and Syria. Six total environments were used, which included field experiments at both Fort Collins (sprinkler irrigated) and Julesburg (rainfed) Colorado in the 2014 (112 genotypes), 2015 (200 genotypes), and 2016 (186 genotypes). Within years, the same genotypes were grown at both locations. All 112 genotypes from the 20th FAWWON that were evaluated in 2014 were evaluated in 2015 with an additional 88 genotypes from the 21st FAWWON. Genotypes with high levels of winter injury at both locations in 2015 were not re-evaluated in 2016. Experiments in 2016 included 69 genotypes from the 20th FAWWON (third year of evaluation), 30 genotypes from the 21st FAWWON (second year of evaluation), and 87 genotypes from the 22nd FAWWON (first year of evaluation). Due to winter injury observed in several of the environments, each environment had a different number of FAWWON individuals with NDVI and yield data. In 2014, genotypes were arranged in an augmented row-column design with the local cultivar 'Byrd' (Haley et al., 2012) as a repeated check. In Fort Collins 2014, 112 individuals were used for GS analysis while in Julesburg 2014 only 99 individuals were used for GS analysis. In 2015 and 2016, genotypes were arranged in a partially replicated row-column design with repeated checks. Randomizations were prepared using the package DiGGer (Coombes, 2009) in R (R Development Core Team, 2014). In Fort Collins 2015, 170 individuals were used for GS analysis while in Julesburg 2015 only 67 individuals were used for GS analysis. In Fort Collins 2016, 181 individuals were used for GS analysis while in Julesburg 2016 172 individuals were used for GS

analysis. All experiments were planted in six-row plots, 3.7 m long and 1.8 m wide, with 0.3 m spacing between rows.

Phenotypic measurements

Grain yield was measured with an on-combine weighing system and yields were adjusted based on 12% grain moisture. Plant height was measured from the ground to the top of the spikes (excluding awns) at physiological maturity and was the average measurement from three locations within each plot. Heading date was recorded as the number of calendar days from January 1 until 50% of the spikes had fully extended from the leaf sheath.

Spectral reflectance measurements were collected using a CropCircle ACS-470 handheld optical sensor (Holland scientific, Inc.) mounted to a handheld boom. The CropCircle was set to record 10 values per sec (10 Hz) and measurements were taken by centering the sensor 1 m above the canopy and walking the length of the plot. An average of 30-40 measurement readings were collected per plot. This resulted in a data point being collected every 10.5 cm along the length of plot. The spectral characteristics of the Crop Circle ACS-470 are user configurable and allowed the use of three different 12.5 mm diameter interference filters (550nm, 670nm, 760nm). Normalized difference vegetation index based on the difference between NIR (760nm) and red reflectance (670nm) resulted in a red-NDVI (RNDVI) measurement while the difference between NIR (760nm) and green reflectance (550nm) resulted in a green-NDVI (GNDVI) measurement. The reflectance measurements were taken between 1030 and 1400 h under sunny, dry conditions. Two measurement readings were taken on each collection date at a minimum of 1 h apart and were averaged to give a single reflectance reading per plot per collection day.

Cumulative NDVI phenotypes

Only NDVI measurement dates after January 1 were used for analyses as this best represented the greenup and growth of the genotypes following vernalization and overwintering. In 2014, there were eight NDVI measurement time points in Fort Collins and Julesburg (Table 1). In 2015, there were 10 NDVI measurement time points in Fort Collins and nine NDVI measurement time points in Julesburg. In 2016, there were eight NDVI measurement time points in both Fort Collins and in Julesburg. The data from NDVI measurements were grouped into vegetative (VEG) and grain filling (GF) growth stages based on the collection date. Collection dates before the average heading date at each location were classified as a "VEG" phenotype and NDVI collection dates after the heading date were classified as a "GF" phenotype. There were four to five NDVI measurements per VEG or GF growth stage within each environment.

To evaluate the best use of the NDVI data across a growing season, two different methods were used to summarize multiple NDVI time points. The first was to use the mean of the NDVI measurements for the VEG, GF, and full season (FULL). The RNDVI and GNDVI phenotypes under this method were renamed as MEAN-RNDVI-VEG, MEAN-RNDVI-GF, MEAN-RNDVI-FULL MEAN-GNDVI-VEG, MEAN-GNDVI-GF, and MEAN-GNDVI-FULL according to the data summary method, NDVI phenotype used, and growth stage classification. Phenotypes for NDVI were also evaluated by calculating the area under the curve (AUC). The AUC was calculated as:

$$\mathrm{Ak} = \sum_{i=1}^{Ni-1} \frac{(yi1 + yi2)}{2} (ti2 - ti1)$$

where $yi1$ is the NDVI value for first collection date, $yi2$ is the NDVI value for the second collection date, $ti1$ is the date in Julian days of the first collection sample and $ti2$ is the date in Julian days of the second collection sample. The AUC between adjacent collection time points was calculated independently and then summed based on the duration of interest. The AUC was calculated for each genotype for the entire growing season (FULL). The RNDVI and GNDVI phenotypes under this method were renamed as AUC-RNDVI-VEG, AUC-RNDVI-GF, AUC-RNDVI-FULL, AUC-GNDVI-VEG, AUC-GNDVI-GF, and AUC-GNDVI-FULL according to the data summary method, NDVI phenotype used, and growth stage classification.

GBS-Based SNP genotyping

Genomic DNA was extracted from bulked leaves of 10 one-wk-old seedlings at the single leaf stage in a 96-well format using King Fisher 96 magnetic bead extraction kits on the King Fisher Flex Purification System (ThermoFisher Scientific Inc., Waltham, MA, U.S.A.). Genotyping-by-sequencing library construction was carried out using the restriction enzymes *PstI* and *MspI* using a protocol modified from Poland et al. (2012). A single blank was included at random positions in each plate for quality control to ensure library identity. Sequencing was performed at 192-plex on an Illumina Hi-Seq 2000 at the DNA core facility at the University of Missouri in Columbia, MO. Single-nucleotide polymorphism (SNP) calls were made using the TASSEL-GBSv1 Pipeline (Glaubitz et al. 2014) which is a reference-based SNP calling procedure. The International Wheat Genome Sequencing Consortium (IWGSC) Chromosome Survey Sequence was used as the reference genome (IWGSC, 2014). Missing marker data were imputed using the multi-variate normal expectation maximization (MVN-EM) method (Dempster et al., 1977) within the A.mat function in the rrBLUP package (Endelman, 2011) in R. Due to different

numbers of individuals being present in each of the six environments, different missing marker values were used in order to provide roughly 42,000 to 44,000 of GBS SNP markers for GS analysis (Table S2).

Statistical analysis of field data

Best linear unbiased predictors (BLUPs) of each phenotype were calculated separately for each environment using the ASReml-R package (VSN International Ltd., Hemel Hempstead, UK) in R. Data for each environment were analyzed with a series of spatial models that included genotype, row, and column coordinates as random effects, and several different residual error terms specified in the *rcov* argument within ASReml-R (Gilmour et al., 2009). The restricted maximum likelihood (REML) loglikelihood value was used to select the best model.

Model choice-variance

The genomic estimated breeding values (GEBVs) were calculated for the univariate model using RR-BLUP (Meuwissen et al. 2001; Endelman 2011) with the following model:

$$y = \mathrm{WG}\mu + \varepsilon$$

where y is a vector of phenotypic values (BLUPs) for individuals; W is a design matrix relating genotypes to phenotypes (y); G is the genotype matrix for bi-allelic SNPs under an additive model; μ is a vector of marker effects, and ε is a vector of errors with a variance σ_{ε}^{2}.

Accuracies for the multivariate model used grain yield only on the training set and the secondary trait on both the training and test sets. The multivariate GS model was run in ASReml-R and was done by fitting the phenotypic observations of multiple traits simultaneously in a multivariate mixed linear model:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix}$$

where $y_1$is a vector of BLUPs for grain yield and $y_2$is a vector of BLUPS for the secondary trait of interest; X is the fixed effects design matrix, $\mu_1$is a vector of fixed effects for grain yield and $\mu_2$is a vector of fixed effects for the secondary trait of interest, Z is the random effects design matrix, which is the same for each trait, $a_1$is a vector of additive genetic effects for grain yield and $a_2$is a vector of additive genetic effects for the secondary trait of interest, and $\varepsilon_1$is a vector of residuals for grain yield and $\varepsilon_2$is a vector of residuals for the secondary trait. The genomic relationship matrix was estimated according to equation 15 in Endelman and Jannink (2012) using the A.mat function in rrBLUP (Endelman, 2011).

Five-fold cross validation was used to assess model accuracy by assigning genotypes to one of five folds and using four of the folds to train the model and predict the GEBVs for the fifth fold for validation. The GS accuracy was calculated as the correlation between the GEBVs and phenotype BLUPs for individuals in the validation set. To compute model accuracy, 300 cycles of cross validation were performed and the average correlation was determined. The standard error of the mean prediction accuracy was calculated as the standard deviation divided by the square root of the number of cross validation cycles.

The model statement in ASreml-R was written as:

Model <- asreml(fixed=cbind(Yield1,Trait2)~trait, random=~giv(genotype,var=T), ginverse=list(genotype=Ainv), data=Data2, rcov=~units:us(trait))

Results and Discussion

Prediction accuracies of yield

The GS prediction accuracies for yield in a univariate GS model were consistently higher in Julesburg (non-irrigated) than in Fort Collins (irrigated) within years and between years (Table S3). Crossa et al. (2010) observed that the estimates of marker effects in GS models were different across environments, indicating that genotype x environment (GxE) interaction is an important component in GS prediction models. González-Camacho et al. (2012) were able to obtain moderately high accuracies in well-watered and high yielding environments and lower predictive accuracies under drought stress and low-yield environments. I observed a difference in prediction accuracies across environments, but with the rainfed environments (Julesburg) providing higher GS prediction accuracies than in the irrigated environment (Fort Collins) across all three years. This is particularly surprising since the Julesburg environments consistently had fewer genotypes for GS analysis due to differential winter injury that was observed at this location. Results from previous studies have consistently shown that increasing the number of individuals in a training population should lead to higher GS prediction accuracies. Our results support Crossa et al. (2010) who reported that GxE is an important consideration in developing GS models. This emphasizes the need to better understand environmental factors and which environments should be included in the training population for GS model predictions. Our results contradict those from González-Camacho et al. (2012). It appears that the higher yielding environment (Fort Collins) has the most to gain from using a multivariate GS model approach with secondary traits as a univariate model only using yield data provided lower prediction accuracies than the lower yielding, rainfed environment (Julesburg).

Heading date as a secondary trait

Heading date was positively correlated with yield in Fort Collins across all three years. The phenotypic correlation between heading date and yield was 0.46 for Fort Collins 2014, 0.41 in 2015, and 0.12 in 2016. In Fort Collins 2014, incorporating heading date as a secondary trait into the multivariate GS model on both the training and test populations increased the prediction accuracy of yield from 0.14 to 0.42 (200%) (Table S3). In Fort Collins 2015, incorporating heading date as a secondary trait increased the prediction accuracy of yield from 0.37 to 0.41 (10.8%). In Fort Collins 2016, heading date reduced the prediction accuracy of yield from 0.33 to 0.12 (-63.6%). These results highlight the importance of using only a secondary trait in a multi-trait GS model when the secondary trait has a moderate correlation to the trait of interest.

Heading date was negatively correlated with yield In Julesburg across all three years. The phenotypic correlation between heading date and yield was -0.21 in 2014, -0.45 in 2015, and -0.16 in 2015. The negative correlation between yield and heading date resulted in negative prediction accuracies for yield when used in the multi-trait GS model (Table S3). Inverting the heading dates provided heading dates that were positively correlated yield but did not increase the GS prediction accuracies above the prediction accuracies of yield in the univariate model. Using the inverted heading dates in Julesburg 2016, the model was never able to converge and provide a GS prediction accuracy for this environment. At this time I am not sure how to best use a highly negatively correlated trait in a multi-trait GS model.

Optimizing the heading date of lines so that they do not coincide with a period of water deficit or extreme heat or early spring freeze has been shown to be an effective strategy in

improving yield under low water conditions (Araus et al., 2002). In this study I found that incorporating the heading date into a multivariate GS model was more effective in an irrigated environment than in a non-irrigated environment (Julesburg). With the positive correlations between heading date and yield in Fort Collins, the multivariate model was able to use the additional information of heading date timing and increase the prediction accuracy of yield. This is promising that a simple phenotype, heading date, which is typically collected on lines in a breeding program, can be used to increase GS predictions of yield in certain environments. In the non-irrigated environments heading date was negatively correlated with yield indicating that genotypes that matured earlier were able to avoid the late season heat and stress. Heading date as a secondary trait was not effective in these environments.

Plant Height as a secondary trait

Plant height was positively correlated with yield in Fort Collins across all three years. The phenotypic correlation between plant height and yield was 0.17 for Fort Collins 2014, 0.49 in 2015, and 0.05 in 2016. In Fort Collins 2014 using plant height as a secondary trait increased the GS prediction accuracy of yield from 0.14 to 0.20 (42%), in Fort Collins 2015 it was increased from 0.37 to 0.47 (27%), but in Fort Collins 2016 it decreased from 0.33 to 0.08 (-75.8%) (Table S3). The phenotypic correlation between plant height and yield was 0.01 for Julesburg 2014, -0.03 in 2015, and -0.27 in 2016. In Julesburg 2014, plant height used as a secondary trait decreased the GS prediction accuracies of yield from 0.58 to 0.01, and in Julesburg 2015 decreased the GS prediction accuracy of yield from 0.56 to 0.01. In Julesburg 2016, the prediction accuracy was decreased from 0.46 to -0.20.

Again, these data show that using a secondary trait with a low correlation with the primary trait can negatively impact the GS prediction accuracy in a multi-trait GS model. With a correlation of near zero between the primary and secondary trait a multi-trait GS model will provide a prediction accuracy of near zero for the trait of interest. Plant height does not appear to be as reliable of a secondary trait for multi-trait GS analysis in the FAWWON germplasm. This may be due to the diversity of genotypes in the collection where both tall and short varieties can be either high yielding or low yielding. Plant height may be an appropriate secondary trait in a breeding program that has a population more targeted to the region where small differences in plant height may be more correlated to differences in yield. These results highlight the need to examine the data before using it in a multi-trait GS model and the need to find cheap, reliable phenotypes that provide a consistently high, positive correlation with the primary trait.

Mean Cumulative NDVI phenotypes as secondary traits

I feel that a method that accounts for the seasonal variability in leaf area using spectral reflectance values over most of the growing season is a better and more robust phenotype than a single date or single growth stage and would better assist in GS predictions for grain yield in wheat. Two methods were compared to determine the best cumulative NDVI phenotype for summarizing multiple NDVI time point measurements for increasing the GS prediction of yield. Rutkoski et al. (2016) observed increases in GS prediction accuracy by as much as 70% when mean NDVI phenotypes were incorporated into a multivariate GS model on the training and test populations. Rutkoski et al. (2016) found that the correlation between the secondary traits and yield as well as the heritability of the secondary traits were the primary drivers for

increasing prediction accuracy. But, they concluded that the expected gain in accuracy due to a set of secondary traits is difficult to predict.

The MEAN-VEG, MEAN-GF, and MEAN-FULL phenotypes for both RNDVI and GNDVI helped to increase the GS prediction accuracies of yield in Fort Collins 2014 (Table S4). The FULL mean RNDVI and GNDVI phenotypes increased GS prediction accuracy of yield in Fort Collins 2015. The FULL mean RNDVI phenotypes increased GS prediction accuracy of yield in Fort Collins 2016. In Fort Collins the RNDVI phenotypes averaged across the entire growing season was the most consistent secondary NDVI phenotype in increasing the GS prediction accuracy of yield when used in a multivariate GS model. This highlights that there are important changes in the plant canopy structure that are occurring during the entire growing season that must be accounted for in order to create the best multi trait GS model when using NDVI as a secondary trait for yield. The mean RNDVI phenotypes for the full growing season increased prediction accuracies from 0.14 to 0.25 (78.6%) in Fort Collins 2014, 0.37 to 0.44 (18.9%) in Fort Collins 2015, and from 0.33 to 0.35 (6.1%) in Fort Collins 2016.

The MEAN-VEG-RNDVI and MEAN-VEG-GNDVI phenotypes increased the GS prediction accuracies of yield in Julesburg 2014 (Table S4). The MEAN-VEG-RNDVI and MEAN-FULL-RNDVI phenotypes increased GS prediction accuracy of yield in Julesburg 2015. The MEAN-VEG-GNDVI and MEAN-FULL-GNDVI phenotypes increased GS prediction accuracy of yield in Julesburg 2016. In Julesburg, the NDVI phenotype most consistent across the three years was the MEAN-VEG-RNDVI or the MEAN-VEG-GNDVI as both increased the prediction accuracy of yield in two of three growing seasons. There was no single mean NDVI phenotype that increased the GS prediction accuracy of yield all three years. These data show that in Julesburg (non-irrigated)

NDVI phenotypes are only needed from early spring growth to heading in order to provide a mean NDVI phenotype that can help increase the prediction accuracy of yield. While the literature suggests that in wheat, the later developmental stages appear to be the most appropriate time to utilize SRI to discriminate for crop productivity (Aparicio et al., 2000; Babar et al., 2006; Naser, 2012) the results showed that multiple early season measurements provided the greatest increase in GS prediction accuracy of grain yield. Our results indicate that determining key growth stages for SRI measurements may not need to be identified as a mean NDVI value provides a similar correlation to grain yield as the best single time point estimate (data not shown). This provides the technician or researcher with a tremendous amount of flexibility in terms of collection times as key physiological stages do not have to be directly measured for NDVI to be a valuable secondary phenotype.

The AUC NDVI phenotypes were not as effective in increasing the GS prediction accuracies of yield in Fort Collins. There was no single phenotype that was consistent across all three growing seasons in Fort Collins. In 2014 only the AUC-GF-RNDVI and AUC-GF-GNDVI phenotypes increased the prediction accuracies of yield above the level for the univariate model (Table S5). In Fort Collins 2015, none of the AUC phenotypes increased the prediction accuracy of yield. In Fort Collins 2016, the AUC-FULL-RNDVI and AUC-FULL-RNDVI phenotypes increased the prediction accuracy of yield.

The AUC NDVI phenotypes were very effective in increasing the GS prediction accuracies of yield in Julesburg (non-irrigated). This is in agreement with Rutkoski et al. (2016) who observed that the multivariate GS model with secondary traits lead to the greatest percent increase in accuracy in the drought environment.

Measuring spectral reflectance appears to be a practical means of adopting physiological trait selection for crop improvement within a breeding program. The use of field portable spectroradiometers capable of collecting multiple indices allowed for a quick and easy comparison of these indices under the same experimental conditions in terms of their correlation to yield. The development and examination of reliable screening techniques is necessary in order to make indirection selection more efficient. Rutkoski et al. (2016) and Pszczola et al. (2013) observed no improvement in prediction accuracy when secondary traits were only recorded and modeled on the training set. Based on simulation, including secondary traits only on the training set can improve accuracy when the heritability of the trait of interest is low and heritability of the secondary traits are high (Jia et al., 2012). Because breeding lines have to be grown in the field for seed increase, there would only be a marginal additional cost of high-throughput phenotyping of lines already present in the field.

Conclusion

Genomic selection's ability to predict the breeding value of an individual based on the composition of its marker set is emerging as an important procedure for improving complex quantitative traits in plants. This paper shows that a relatively small number of diverse genotypes with NDVI and traditional plant breeding phenotypes can help increase the GS prediction accuracy of yield across environments. Plant height, heading date, RNDVI, and GNDVI could be excellent secondary traits for multi-trait GS in wheat because of their high heritabilities, genetic correlations with yield, and their relative ease in being measured on lines prior to harvest.

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Supplemental Tables

Supplemental Table S5.1. Red normalized difference vegetation index (RNDVI) and green normalized difference vegetation index (GNDVI) collection dates into growth stages across the six measured environments.

	Fort Collins 2014			Julesburg 2014		
Collection Day	Date	Julian Day	Growth	Date	Julian Day	Growth
1	19-Apr	109	VEG	20-Apr	110	VEG
2	14-May	134	VEG	15-May	135	VEG
3	28-May	148	VEG	27-May	147	VEG
4	1-Jun	152	VEG	2-Jun	153	VEG
5	7-Jun	158	GF	6-Jun	157	GF
6	18-Jun	169	GF	17-Jun	168	GF
7	28-Jun	179	GF	27-Jun	178	GF
8	11-Jul	192	GF	10-Jul	191	GF

	Fort Collins 2015			Julesburg 2015		
Collection Day	Date	Julian Day	Growth	Date	Julian Day	Growth
1	6-Nov	NA	-	8-Nov	NA	-
2	13-Feb	44	VEG	16-Feb	47	VEG
3	27-Mar	86	VEG	29-Mar	88	VEG
4	22-Apr	112	VEG	-	-	
5	12-May	132	VEG	28-Apr	118	VEG
6	31-May	151	VEG	14-May	134	VEG
7	4-Jun	155	GF	29-May	149	VEG
8	17-Jun	168	GF	5-Jun	156	GF
9	23-Jun	174	GF	14-Jun	165	GF
10	1-Jul	182	GF	24-Jun	175	GF
11	20-Jul	207	GF	2-Jul	183	GF

	Fort Collins 2016			Julesburg 2016		
Collection Day	Date	Julian Day	Growth	Date	Julian Day	Growth
1	14-Nov	NA	-	15-Nov	NA	-
2	11-Mar	71	VEG	10-Mar	70	VEG
3	8-Apr	99	VEG	9-Apr	100	VEG
4	6-May	127	VEG	5-May	126	VEG
5	20-May	141	VEG	22-May	143	VEG
6	2-Jun	154	GF	3-Jun	155	GF
7	14-Jun	166	GF	15-Jun	167	GF
8	25-Jun	177	GF	24-Jun	176	GF
9	6-Jul	188	GF	8-Jul	190	GF

Supplemental Table S5.2. Number of single nucleotide polymorphism (SNP) markers used for genomic selection analysis in each of the 6 environments and the missing marker percentage threshold used to obtain that number of SNP markers.

Location	Year	Missing Marker %	# of SNPs
Fort Collins	2014	30	42,055
Julesburg	2014	30	44,365
Fort Collins	2015	35	43,992
Julesburg	2015	25	44,890
Fort Collins	2016	50	42,451
Julesburg	2016	50	44,041

Supplemental Table S5.3. Genomic selection (GS) model prediction accuracies for yield. The 'Yield' column is when only yield was used in a univariate GS model. The phenotypes listed in the table give the prediction accuracies for grain yield when they were used as secondary traits in a multi-trait GS prediction model.

Environment		Yield	Height	Heading Date
Fort Collins 2014	MTGS	0.14	0.20	0.42
	S.E.	0.01	0.01	0.01
Julesburg 2014	MTGS	0.58	0.01	-0.14
	S.E.	0.01	0.01	0.01
Fort Collins 2015	MTGS	0.37	0.47	0.41
	S.E.	0.01	0.01	0.01
Julesburg 2015	MTGS	0.56	0.01	-0.42
	S.E.	0.01	0.02	0.01
Fort Collins 2016	MTGS	0.33	0.08	0.12
	S.E.	0.01	0.01	0.01
Julesburg 2016	MTGS	0.46	-0.20	-0.14
	S.E.	0.01	0.01	0.01

Supplemental Table S5.4. Genomic selection (GS) model prediction accuracies for yield. The 'Yield' column is when only yield was used in a univariate GS model. The phenotypes listed in the table are normalized difference vegetation indicies (NDVI) using mean values to give the prediction accuracies for grain yield when they were used as secondary traits in a multi-trait GS prediction model.

			MEAN NDVI					
Environment		Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NVDI	FULL-G.NDVI
Fort Collins 2014	MTGS	0.14	0.15	0.34	0.25	0.21	0.31	0.26
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2014	MTGS	0.58	0.69	0.08	0.25	0.62	0.08	0.54
	S.E.	0.01	0.01	0.02	0.02	0.01	0.01	0.01
Fort Collins 2015	MTGS	0.37	0.29	0.36	0.44	0.36	0.31	0.38
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2015	MTGS	0.56	0.71	-0.01	0.59	-0.21	0.45	-0.11
	S.E.	0.01	0.02	0.02	0.02	0.00	0.02	0.02
Fort Collins 2016	MTGS	0.33	0.30	0.28	0.35	0.33	0.07	0.26
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2016	MTGS	0.46	0.20	0.39	0.44	0.52	0.43	0.52
	S.E.	0.01	0.02	0.01	0.01	0.02	0.01	0.02

Supplemental Table S5.5. Genomic selection (GS) model prediction accuracies for yield. The 'Yield' column is when only yield was used in a univariate GS model. The phenotypes listed in the table are normalized difference vegetation indicies (NDVI) using area under the curve (AUC) to give the prediction accuracies for grain yield when they were used as secondary traits in a multi-trait GS prediction model.

			AUC NDVI					
Environment		Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
Fort Collins 2014	MTGS	0.14	-0.07	0.23	-0.02	-0.05	0.19	-0.03
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2014	MTGS	0.58	0.65	0.15	0.69	0.66	0.17	0.70
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Fort Collins 2015	MTGS	0.37	0.20	0.16	0.27	0.05	-0.05	0.21
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2015	MTGS	0.56	0.80	0.59	0.81	0.79	0.48	0.23
	S.E.	0.01	0.01	0.01	0.00	0.01	0.01	0.03
Fort Collins 2016	MTGS	0.33	0.29	0.30	0.34	0.32	0.22	0.36
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Julesburg 2016	MTGS	0.46	0.46	0.22	0.48	0.48	0.38	0.58
	S.E.	0.01	0.01	0.01	0.01	0.01	0.01	0.01

Supplemental Table S5.6. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) for Fort Collins 2014.

		AUC					
ID	Yield	VEGR.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X20FAWWON.IRR.7	97.39	21.52	17.87	43.62	23.31	17.72	44.79
X20FAWWON.IRR.8	103.44	20.78	18.42	43.09	22.84	17.97	44.39
X20FAWWON.IRR.9	122.67	21.35	17.12	43.05	23.31	17.56	44.83
X20FAWWON.IRR.10	90.14	21.46	19.42	44.97	23.24	18.59	46.11
X20FAWWON.IRR.11	98.93	20.81	17.54	42.93	22.74	17.42	43.79
X20FAWWON.IRR.12	127.71	22.10	19.27	45.72	23.45	18.48	45.36
X20FAWWON.IRR.13	104.06	20.48	17.30	41.54	22.85	17.72	43.64
X20FAWWON.IRR.14	109.35	20.86	18.99	43.41	22.84	18.23	44.38
X20FAWWON.IRR.15	108.01	20.53	18.38	43.05	22.83	18.05	44.52
X20FAWWON.IRR.16	109.32	21.44	18.93	44.96	23.18	18.00	45.41
X20FAWWON.IRR.17	107.86	21.36	18.78	44.52	23.40	18.50	45.93
X20FAWWON.IRR.18	105.16	21.24	19.20	44.83	23.03	18.44	45.24
X20FAWWON.IRR.19	103.00	21.31	18.37	44.14	23.10	17.95	44.75
X20FAWWON.IRR.20	107.44	21.75	18.75	45.10	23.25	18.37	45.31
X20FAWWON.IRR.21	94.93	21.64	18.09	44.12	23.20	17.60	44.76
X20FAWWON.IRR.22	103.89	21.63	17.97	44.32	23.38	17.72	45.27
X20FAWWON.IRR.23	114.38	22.31	18.98	46.06	23.84	18.51	46.73
X20FAWWON.IRR.24	102.19	21.33	17.06	43.02	22.98	16.92	43.20
X20FAWWON.IRR.25	101.87	20.69	18.69	43.36	22.71	18.03	44.17
X20FAWWON.IRR.26	91.49	21.96	17.81	44.73	23.45	17.61	45.10
X20FAWWON.IRR.27	114.34	21.46	19.39	45.18	23.22	18.71	45.62
X20FAWWON.IRR.28	110.48	21.81	18.19	44.74	23.48	18.12	45.49
X20FAWWON.IRR.29	118.66	22.70	19.96	47.45	23.93	19.18	47.17
X20FAWWON.IRR.30	107.29	22.21	18.81	45.61	23.56	18.29	45.67
X20FAWWON.IRR.31	107.33	20.91	18.98	43.88	22.94	18.77	45.42
X20FAWWON.IRR.32	99.95	21.84	18.45	44.85	23.33	17.46	44.60

X20FAWWON.IRR.33	105.15	20.44	18.21	42.68	22.76	18.22	43.97
X20FAWWON.IRR.35	111.84	21.00	18.94	44.11	22.95	18.06	44.65
X20FAWWON.IRR.36	108.54	21.63	19.46	45.56	23.34	19.09	45.95
X20FAWWON.IRR.37	96.06	21.97	19.72	46.59	23.38	18.47	46.02
X20FAWWON.IRR.38	102.78	20.47	17.70	42.20	22.68	18.34	44.15
X20FAWWON.IRR.39	96.37	21.39	19.27	44.72	22.99	18.22	45.06
X20FAWWON.IRR.40	103.30	21.37	18.73	44.09	23.24	18.21	45.05
X20FAWWON.IRR.41	110.67	21.70	19.65	45.67	23.31	18.78	45.88
X20FAWWON.IRR.42	112.86	22.18	19.36	46.09	23.68	19.01	46.85
X20FAWWON.IRR.43	96.78	20.77	17.07	41.97	22.61	16.90	42.91
X20FAWWON.IRR.44	113.01	21.70	19.43	45.64	23.40	18.50	46.25
X20FAWWON.IRR.45	122.64	21.65	18.77	44.84	23.34	18.00	44.91
X20FAWWON.IRR.46	96.72	19.93	17.64	41.51	22.21	17.39	42.45
X20FAWWON.IRR.47	107.27	20.82	18.36	43.23	23.06	18.03	44.52
X20FAWWON.IRR.48	103.02	21.53	18.36	44.47	23.25	18.23	45.62
X20FAWWON.IRR.49	108.28	21.28	19.84	44.97	23.27	19.34	46.52
X20FAWWON.IRR.50	107.27	21.16	19.03	44.22	22.96	18.42	44.51
X20FAWWON.IRR.51	93.19	21.31	19.04	44.65	23.11	18.86	45.67
X20FAWWON.IRR.52	99.76	19.88	17.56	41.65	22.33	17.58	42.74
X20FAWWON.IRR.54	119.11	20.50	19.03	43.55	22.94	18.80	45.75
X20FAWWON.IRR.55	99.75	21.51	19.46	45.27	23.27	18.73	45.89
X20FAWWON.IRR.56	111.78	22.17	19.10	45.94	23.72	18.61	46.25
X20FAWWON.IRR.57	109.76	19.53	18.14	40.83	22.28	18.44	43.20
X20FAWWON.IRR.59	124.83	21.54	19.43	45.09	23.34	19.16	45.92
X20FAWWON.IRR.60	97.10	21.52	18.26	44.48	23.23	17.99	44.98
X20FAWWON.IRR.69	114.50	20.83	18.20	43.38	22.91	17.73	44.22
X20FAWWON.IRR.70	104.56	19.88	17.08	40.87	22.43	17.57	43.31
X20FAWWON.IRR.71	97.54	21.05	18.25	43.18	22.93	17.65	44.19
X20FAWWON.IRR.72	103.69	21.27	18.87	44.65	23.19	18.52	45.49
X20FAWWON.IRR.74	103.05	21.48	18.72	44.69	23.17	17.85	44.55
X20FAWWON.IRR.75	110.47	20.06	18.26	42.23	22.47	18.15	43.97

X20FAWWON.IRR.77	81.84	22.05	18.16	45.14	23.59	18.29	45.81
X20FAWWON.IRR.78	112.35	21.49	19.33	45.45	23.27	18.68	46.05
X20FAWWON.IRR.85	96.84	21.46	18.29	44.18	23.18	18.11	45.20
X20FAWWON.IRR.86	112.77	21.92	18.37	44.96	23.61	17.98	46.10
X20FAWWON.IRR.87	109.65	21.39	18.28	44.34	23.23	18.00	44.85
X20FAWWON.IRR.88	102.49	20.93	18.58	43.51	23.04	18.12	44.53
X20FAWWON.IRR.89	111.93	21.56	19.17	44.90	23.22	18.66	45.18
X20FAWWON.IRR.95	115.72	19.48	18.88	41.53	22.10	18.62	43.48
X20FAWWON.IRR.97	109.81	20.80	18.51	43.55	23.11	18.52	45.38
X20FAWWON.IRR.98	95.09	20.42	18.44	42.45	22.67	18.40	44.31
X20FAWWON.IRR.100	87.58	21.51	19.83	45.59	23.16	18.94	46.31
X20FAWWON.IRR.106	108.11	20.78	19.95	44.40	22.90	19.43	45.46
X20FAWWON.IRR.114	104.97	21.14	20.29	45.28	23.13	19.43	46.20
X20FAWWON.IRR.115	110.16	21.57	18.92	44.82	23.39	18.55	45.84
X20FAWWON.IRR.118	89.89	20.41	17.63	42.26	22.80	17.66	44.14
X20FAWWON.IRR.143	84.03	22.16	18.25	45.32	23.54	17.86	45.15
X20FAWWON.SA.202	103.51	21.58	19.21	44.89	23.32	18.16	45.36
X20FAWWON.SA.206	98.22	21.68	17.75	44.26	23.33	17.50	44.69
X20FAWWON.SA.207	101.11	21.08	17.52	42.84	23.01	17.31	43.76
X20FAWWON.SA.208	98.52	21.09	18.89	44.06	23.12	18.59	45.23
X20FAWWON.SA.209	102.66	20.49	18.74	42.89	22.61	18.08	43.87
X20FAWWON.SA.210	112.13	20.14	16.84	40.90	22.56	17.19	43.07
X20FAWWON.SA.212	99.81	21.35	18.09	43.96	23.38	18.67	45.93
X20FAWWON.SA.213	110.38	19.78	18.70	42.13	22.33	18.34	43.78
X20FAWWON.SA.214	116.42	20.68	20.01	44.40	22.81	18.87	45.19
X20FAWWON.SA.215	115.75	20.99	19.80	44.60	22.94	18.80	45.11
X20FAWWON.SA.218	98.10	21.71	18.37	44.42	23.23	17.75	44.79
X20FAWWON.SA.221	109.08	20.87	19.05	44.03	22.91	18.61	44.95
X20FAWWON.SA.222	112.76	20.59	18.57	43.06	22.84	18.18	44.52
X20FAWWON.SA.223	102.55	20.87	17.93	42.98	22.94	17.71	44.24
X20FAWWON.SA.224	105.61	22.26	17.96	45.21	23.63	17.40	45.16

X20FAWWON.SA.226	106.33	20.17	17.01	41.10	22.61	17.29	43.09
X20FAWWON.SA.227	109.96	21.76	18.54	44.99	23.46	18.08	46.21
X20FAWWON.SA.228	111.39	22.22	19.73	46.13	23.67	18.73	46.44
X20FAWWON.SA.230	94.29	20.92	18.78	44.08	22.99	17.99	44.86
X20FAWWON.SA.231	109.77	20.65	19.03	43.42	22.88	18.43	45.09
X20FAWWON.SA.232	109.61	22.28	18.63	45.60	23.59	17.91	45.62
X20FAWWON.SA.233	112.12	21.24	18.73	43.80	23.11	18.23	44.89
X20FAWWON.SA.235	123.51	20.97	19.17	43.95	22.84	18.05	44.49
X20FAWWON.SA.236	99.40	22.82	19.38	47.16	23.94	18.46	46.80
X20FAWWON.SA.237	112.68	22.95	20.39	48.31	24.10	19.02	48.00
X20FAWWON.SA.238	120.55	20.84	18.66	43.67	22.77	17.90	44.09
X20FAWWON.SA.239	102.80	20.35	17.97	42.26	22.67	17.93	43.78
X20FAWWON.SA.241	112.77	21.00	19.90	44.95	22.96	19.13	45.81
X20FAWWON.SA.243	118.15	21.69	19.76	45.59	23.48	19.21	46.29
X20FAWWON.SA.244	96.86	20.91	18.38	43.69	23.06	18.54	45.12
X20FAWWON.SA.249	101.68	21.37	19.42	44.91	23.09	19.02	45.41
X20FAWWON.SA.251	97.54	22.47	19.28	46.64	23.95	19.29	47.94
X20FAWWON.SA.252	104.08	21.85	19.90	46.00	23.40	19.65	46.69
X20FAWWON.SA.254	103.85	20.55	18.10	42.81	22.89	18.13	44.58
X20FAWWON.SA.256	108.45	20.82	17.90	43.16	22.94	18.24	44.83
X20FAWWON.SA.257	100.06	21.05	18.33	43.62	22.88	17.46	43.94
X20FAWWON.SA.258	95.84	22.87	18.29	46.31	24.17	18.19	47.29
X20FAWWON.SA.259	116.59	21.84	19.97	46.01	23.49	18.98	46.40
X20FAWWON.SA.278	109.73	20.67	18.20	43.12	22.95	18.36	44.37
Byrd	114.81	21.81	19.69	45.64	23.42	18.78	45.66
Denali	114.36	19.92	19.75	43.23	22.48	18.91	44.45
Ripper	118.42	22.21	19.56	46.32	23.69	18.86	46.52
Snowmass	98.11	20.01	18.62	42.23	22.37	17.79	43.32
Antero	113.90	21.46	19.36	45.08	23.32	18.76	45.83

Supplemental Table S5.7. Mean normalized difference vegetation indice (NDVI) values for Fort Collins 2014.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X20FAWWON.IRR.7	0.53	0.51	0.52	0.56	0.52	0.54
X20FAWWON.IRR.8	0.52	0.53	0.52	0.55	0.53	0.54
X20FAWWON.IRR.9	0.52	0.48	0.51	0.56	0.51	0.54
X20FAWWON.IRR.10	0.53	0.55	0.54	0.57	0.54	0.56
X20FAWWON.IRR.11	0.52	0.51	0.52	0.56	0.51	0.53
X20FAWWON.IRR.12	0.55	0.55	0.55	0.57	0.53	0.55
X20FAWWON.IRR.13	0.50	0.49	0.49	0.55	0.51	0.53
X20FAWWON.IRR.14	0.54	0.55	0.54	0.57	0.54	0.55
X20FAWWON.IRR.15	0.51	0.52	0.51	0.56	0.52	0.54
X20FAWWON.IRR.16	0.53	0.54	0.53	0.57	0.53	0.55
X20FAWWON.IRR.17	0.53	0.53	0.53	0.57	0.53	0.55
X20FAWWON.IRR.18	0.53	0.54	0.54	0.56	0.54	0.55
X20FAWWON.IRR.19	0.53	0.52	0.53	0.57	0.52	0.54
X20FAWWON.IRR.20	0.55	0.53	0.55	0.57	0.53	0.55
X20FAWWON.IRR.21	0.54	0.52	0.54	0.57	0.52	0.55
X20FAWWON.IRR.22	0.54	0.52	0.53	0.57	0.52	0.55
X20FAWWON.IRR.23	0.56	0.54	0.56	0.59	0.54	0.57
X20FAWWON.IRR.24	0.53	0.49	0.51	0.55	0.50	0.52
X20FAWWON.IRR.25	0.52	0.54	0.53	0.55	0.53	0.54
X20FAWWON.IRR.26	0.54	0.50	0.53	0.57	0.51	0.54
X20FAWWON.IRR.27	0.54	0.55	0.54	0.57	0.53	0.55
X20FAWWON.IRR.28	0.55	0.52	0.54	0.58	0.53	0.56
X20FAWWON.IRR.29	0.56	0.57	0.56	0.58	0.55	0.57
X20FAWWON.IRR.30	0.56	0.53	0.55	0.58	0.53	0.56
X20FAWWON.IRR.31	0.53	0.54	0.53	0.56	0.54	0.56
X20FAWWON.IRR.32	0.54	0.53	0.54	0.56	0.52	0.54
X20FAWWON.IRR.33	0.51	0.51	0.50	0.55	0.52	0.52

X20FAWWON.IRR.35	0.52	0.55	0.53	0.56	0.52	0.54
X20FAWWON.IRR.36	0.54	0.55	0.55	0.57	0.55	0.56
X20FAWWON.IRR.37	0.55	0.55	0.55	0.57	0.53	0.55
X20FAWWON.IRR.38	0.51	0.50	0.50	0.56	0.53	0.54
X20FAWWON.IRR.39	0.54	0.56	0.54	0.56	0.54	0.55
X20FAWWON.IRR.40	0.53	0.54	0.53	0.56	0.53	0.55
X20FAWWON.IRR.41	0.55	0.55	0.55	0.57	0.54	0.56
X20FAWWON.IRR.42	0.55	0.55	0.55	0.58	0.55	0.57
X20FAWWON.IRR.43	0.52	0.50	0.51	0.55	0.51	0.53
X20FAWWON.IRR.44	0.53	0.55	0.54	0.57	0.55	0.56
X20FAWWON.IRR.45	0.54	0.53	0.54	0.56	0.52	0.54
X20FAWWON.IRR.46	0.50	0.50	0.49	0.53	0.50	0.51
X20FAWWON.IRR.47	0.51	0.52	0.51	0.55	0.52	0.54
X20FAWWON.IRR.48	0.54	0.53	0.54	0.57	0.54	0.56
X20FAWWON.IRR.49	0.53	0.56	0.54	0.56	0.56	0.56
X20FAWWON.IRR.50	0.53	0.54	0.53	0.55	0.53	0.54
X20FAWWON.IRR.51	0.54	0.55	0.54	0.57	0.54	0.56
X20FAWWON.IRR.52	0.49	0.50	0.49	0.54	0.51	0.52
X20FAWWON.IRR.54	0.51	0.54	0.52	0.56	0.54	0.55
X20FAWWON.IRR.55	0.54	0.55	0.54	0.56	0.54	0.56
X20FAWWON.IRR.56	0.55	0.54	0.55	0.58	0.54	0.56
X20FAWWON.IRR.57	0.49	0.51	0.49	0.54	0.51	0.52
X20FAWWON.IRR.59	0.54	0.55	0.55	0.57	0.55	0.56
X20FAWWON.IRR.60	0.54	0.52	0.54	0.57	0.51	0.54
X20FAWWON.IRR.69	0.52	0.52	0.52	0.56	0.52	0.54
X20FAWWON.IRR.70	0.51	0.48	0.49	0.55	0.51	0.53
X20FAWWON.IRR.71	0.53	0.51	0.52	0.56	0.51	0.54
X20FAWWON.IRR.72	0.53	0.54	0.54	0.57	0.54	0.55
X20FAWWON.IRR.74	0.53	0.53	0.53	0.57	0.51	0.54
X20FAWWON.IRR.75	0.51	0.52	0.51	0.55	0.53	0.54
X20FAWWON.IRR.77	0.55	0.51	0.54	0.58	0.52	0.55

X20FAWWON.IRR.78	0.54	0.55	0.55	0.57	0.55	0.56
X20FAWWON.IRR.85	0.54	0.52	0.53	0.57	0.53	0.55
X20FAWWON.IRR.86	0.54	0.53	0.54	0.58	0.53	0.56
X20FAWWON.IRR.87	0.53	0.52	0.53	0.57	0.52	0.54
X20FAWWON.IRR.88	0.52	0.53	0.52	0.55	0.52	0.53
X20FAWWON.IRR.89	0.54	0.55	0.54	0.57	0.54	0.55
X20FAWWON.IRR.95	0.51	0.54	0.52	0.55	0.55	0.54
X20FAWWON.IRR.97	0.52	0.53	0.53	0.56	0.54	0.55
X20FAWWON.IRR.98	0.53	0.53	0.53	0.57	0.54	0.56
X20FAWWON.IRR.100	0.54	0.57	0.55	0.57	0.56	0.57
X20FAWWON.IRR.106	0.53	0.57	0.55	0.56	0.56	0.56
X20FAWWON.IRR.114	0.53	0.58	0.55	0.57	0.55	0.56
X20FAWWON.IRR.115	0.53	0.54	0.53	0.57	0.53	0.55
X20FAWWON.IRR.118	0.50	0.50	0.50	0.56	0.52	0.53
X20FAWWON.IRR.143	0.54	0.52	0.53	0.57	0.51	0.54
X20FAWWON.SA.202	0.54	0.55	0.55	0.56	0.53	0.55
X20FAWWON.SA.206	0.54	0.51	0.53	0.57	0.51	0.54
X20FAWWON.SA.207	0.53	0.50	0.52	0.56	0.51	0.53
X20FAWWON.SA.208	0.52	0.54	0.53	0.57	0.53	0.55
X20FAWWON.SA.209	0.52	0.54	0.53	0.55	0.53	0.54
X20FAWWON.SA.210	0.50	0.47	0.48	0.55	0.50	0.52
X20FAWWON.SA.212	0.52	0.52	0.51	0.56	0.54	0.55
X20FAWWON.SA.213	0.50	0.53	0.51	0.54	0.53	0.53
X20FAWWON.SA.214	0.53	0.57	0.55	0.56	0.54	0.55
X20FAWWON.SA.215	0.54	0.56	0.55	0.57	0.54	0.55
X20FAWWON.SA.218	0.55	0.53	0.54	0.56	0.52	0.55
X20FAWWON.SA.221	0.52	0.54	0.53	0.55	0.54	0.54
X20FAWWON.SA.222	0.52	0.53	0.52	0.56	0.52	0.54
X20FAWWON.SA.223	0.53	0.51	0.52	0.56	0.52	0.54
X20FAWWON.SA.224	0.55	0.51	0.54	0.57	0.50	0.54
X20FAWWON.SA.226	0.51	0.49	0.50	0.55	0.50	0.53

X20FAWWON.SA.227	0.54	0.53	0.54	0.58	0.53	0.56
X20FAWWON.SA.228	0.56	0.56	0.57	0.58	0.55	0.57
X20FAWWON.SA.230	0.51	0.53	0.52	0.55	0.53	0.54
X20FAWWON.SA.231	0.52	0.55	0.53	0.56	0.54	0.55
X20FAWWON.SA.232	0.55	0.53	0.55	0.58	0.52	0.55
X20FAWWON.SA.233	0.53	0.53	0.53	0.56	0.52	0.54
X20FAWWON.SA.235	0.54	0.55	0.54	0.56	0.53	0.55
X20FAWWON.SA.236	0.57	0.55	0.57	0.59	0.53	0.57
X20FAWWON.SA.237	0.57	0.58	0.58	0.60	0.55	0.58
X20FAWWON.SA.238	0.52	0.54	0.53	0.55	0.52	0.53
X20FAWWON.SA.239	0.51	0.51	0.51	0.55	0.51	0.53
X20FAWWON.SA.241	0.53	0.56	0.55	0.56	0.55	0.56
X20FAWWON.SA.243	0.54	0.56	0.55	0.57	0.55	0.56
X20FAWWON.SA.244	0.52	0.52	0.52	0.56	0.53	0.55
X20FAWWON.SA.249	0.53	0.56	0.54	0.55	0.55	0.55
X20FAWWON.SA.251	0.57	0.55	0.57	0.59	0.56	0.58
X20FAWWON.SA.252	0.54	0.56	0.55	0.57	0.56	0.56
X20FAWWON.SA.254	0.51	0.52	0.51	0.56	0.53	0.54
X20FAWWON.SA.256	0.52	0.51	0.52	0.56	0.53	0.54
X20FAWWON.SA.257	0.53	0.53	0.53	0.56	0.51	0.54
X20FAWWON.SA.258	0.56	0.53	0.55	0.58	0.54	0.57
X20FAWWON.SA.259	0.54	0.57	0.56	0.56	0.54	0.56
X20FAWWON.SA.278	0.51	0.52	0.51	0.56	0.53	0.54
Byrd	0.54	0.55	0.54	0.56	0.53	0.55
Denali	0.50	0.56	0.52	0.54	0.55	0.54
Ripper	0.54	0.55	0.55	0.57	0.54	0.56
Snowmass	0.50	0.52	0.50	0.54	0.51	0.52
Antero	0.54	0.55	0.54	0.57	0.53	0.55
Byrd4	0.54	0.55	0.55	0.57	0.54	0.55

Supplemental Table S5.8. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) for Julesburg 2014.

		AUC					
ID	Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X20FAWWON.IRR.7	60.47	16.43	13.22	31.14	20.04	15.45	37.78
X20FAWWON.IRR.8	48.41	16.07	11.56	27.74	19.98	14.46	36.32
X20FAWWON.IRR.9	68.46	21.54	13.32	35.34	22.44	15.54	40.16
X20FAWWON.IRR.10	67.95	9.45	12.81	24.75	16.45	15.39	34.81
X20FAWWON.IRR.11	55.22	15.18	13.53	30.64	19.13	15.56	37.28
X20FAWWON.IRR.12	71.40	19.93	12.88	33.72	21.84	15.13	38.83
X20FAWWON.IRR.13	63.24	18.76	12.19	31.48	21.35	14.91	38.40
X20FAWWON.IRR.14	49.09	10.89	13.00	25.42	17.14	15.41	35.17
X20FAWWON.IRR.15	65.70	18.68	13.00	32.64	21.32	15.37	38.84
X20FAWWON.IRR.16	63.14	16.99	13.31	31.98	20.38	15.59	38.35
X20FAWWON.IRR.17	62.88	15.77	12.93	30.22	20.05	15.46	37.91
X20FAWWON.IRR.18	66.33	21.54	13.17	35.62	22.89	15.53	40.44
X20FAWWON.IRR.19	64.16	19.30	12.11	32.22	21.63	14.77	38.37
X20FAWWON.IRR.20	60.01	17.21	12.48	30.76	20.11	14.86	37.07
X20FAWWON.IRR.21	54.18	19.72	12.28	31.55	21.28	14.76	37.68
X20FAWWON.IRR.22	57.76	14.64	13.66	30.91	19.39	15.72	37.90
X20FAWWON.IRR.23	58.54	17.23	12.75	30.83	20.49	15.15	37.82
X20FAWWON.IRR.24	57.32	16.58	12.49	30.11	20.02	14.90	37.05
X20FAWWON.IRR.25	60.39	17.16	13.09	31.73	20.42	15.35	38.05
X20FAWWON.IRR.26	59.94	19.00	12.96	32.78	21.01	15.24	38.59
X20FAWWON.IRR.27	53.41	13.04	13.60	29.37	18.44	15.81	37.13
X20FAWWON.IRR.29	61.67	16.03	13.19	31.62	20.36	15.50	38.32
X20FAWWON.IRR.30	53.38	16.86	12.33	30.02	20.28	14.92	37.40
X20FAWWON.IRR.31	57.27	15.13	13.50	30.40	19.08	15.85	37.87
X20FAWWON.IRR.32	52.34	12.89	13.23	27.98	18.12	15.50	36.20
X20FAWWON.IRR.33	58.45	11.07	13.42	27.11	17.46	15.91	36.51

X20FAWWON.IRR.35	61.17	14.16	13.58	29.93	18.88	15.72	37.32
X20FAWWON.IRR.36	60.30	21.34	12.60	34.41	22.73	15.27	39.81
X20FAWWON.IRR.37	62.47	22.13	12.92	35.51	23.02	15.65	40.73
X20FAWWON.IRR.38	64.82	21.19	12.97	34.66	22.63	15.65	40.29
X20FAWWON.IRR.39	55.56	16.44	13.20	31.28	19.96	15.41	37.83
X20FAWWON.IRR.40	60.97	17.49	12.76	31.60	20.83	15.12	38.00
X20FAWWON.IRR.41	62.21	18.62	13.36	34.01	21.27	15.63	39.39
X20FAWWON.IRR.42	64.57	22.59	13.05	35.61	22.73	15.57	40.46
X20FAWWON.IRR.43	54.00	11.98	12.72	26.53	17.72	15.16	35.55
X20FAWWON.IRR.44	60.98	18.69	12.44	31.47	21.24	14.95	37.99
X20FAWWON.IRR.45	62.70	19.11	12.65	32.40	21.09	15.06	38.41
X20FAWWON.IRR.46	64.85	20.16	13.11	34.41	21.72	15.23	39.07
X20FAWWON.IRR.47	58.50	11.66	13.18	27.19	17.60	15.67	36.27
X20FAWWON.IRR.48	59.18	15.70	13.19	30.81	20.14	15.65	38.30
X20FAWWON.IRR.49	54.64	12.63	12.77	27.54	18.58	15.48	36.56
X20FAWWON.IRR.55	61.31	16.58	12.02	28.57	20.23	14.72	36.69
X20FAWWON.IRR.56	55.73	15.54	13.65	31.42	19.62	15.90	38.37
X20FAWWON.IRR.57	76.48	20.32	12.92	34.16	22.40	15.30	39.71
X20FAWWON.IRR.59	64.52	18.38	12.22	31.53	21.35	14.93	38.52
X20FAWWON.IRR.69	53.93	15.95	12.57	28.90	19.61	14.96	36.48
X20FAWWON.IRR.71	51.51	9.30	12.70	24.17	16.50	15.29	34.56
X20FAWWON.IRR.74	58.87	18.87	12.39	32.15	21.70	14.97	38.60
X20FAWWON.IRR.78	45.92	9.56	13.76	25.75	16.37	15.90	35.11
X20FAWWON.IRR.85	47.62	14.21	12.50	27.65	18.50	15.12	36.27
X20FAWWON.IRR.86	67.31	19.69	12.89	33.70	21.86	15.36	39.46
X20FAWWON.IRR.87	59.83	18.32	12.66	31.54	21.14	15.32	38.48
X20FAWWON.IRR.88	59.03	16.22	13.68	31.23	19.78	15.67	37.84
X20FAWWON.IRR.95	73.79	21.75	13.94	36.48	22.54	15.97	40.80
X20FAWWON.IRR.97	68.51	18.12	12.99	32.31	21.17	15.41	38.86
X20FAWWON.IRR.98	63.86	19.54	12.37	32.16	21.76	14.97	38.58
X20FAWWON.IRR.100	62.29	19.21	12.40	31.59	21.52	14.83	38.01

X20FAWWON.IRR.106	69.41	18.90	13.05	32.88	21.76	15.59	39.45
X20FAWWON.IRR.114	65.02	16.14	14.13	32.80	19.95	16.17	39.11
X20FAWWON.IRR.115	63.22	19.79	12.57	33.26	22.09	15.02	38.93
X20FAWWON.IRR.118	61.76	23.54	12.63	35.78	23.71	15.16	40.58
X20FAWWON.IRR.143	70.77	25.65	13.58	39.86	24.51	15.69	42.17
X20FAWWON.SA.202	60.45	17.43	13.69	33.02	20.61	15.82	38.98
X20FAWWON.SA.206	53.69	20.52	12.08	32.69	22.13	14.78	38.57
X20FAWWON.SA.207	60.64	16.29	11.67	28.48	19.89	14.51	36.47
X20FAWWON.SA.208	51.87	13.50	13.05	27.56	18.09	15.44	36.13
X20FAWWON.SA.209	66.32	18.16	13.20	32.83	21.04	15.49	38.92
X20FAWWON.SA.210	60.61	15.49	13.35	30.48	18.97	15.55	37.38
X20FAWWON.SA.212	56.96	17.51	14.06	33.99	20.81	16.01	39.47
X20FAWWON.SA.213	61.76	17.06	13.11	31.74	20.58	15.38	38.31
X20FAWWON.SA.214	62.49	16.96	13.13	31.64	20.31	15.34	37.92
X20FAWWON.SA.215	65.15	18.22	13.54	33.12	21.02	15.69	38.93
X20FAWWON.SA.218	64.47	22.07	14.37	38.09	22.64	16.21	41.24
X20FAWWON.SA.221	63.83	17.75	12.37	30.49	20.90	15.11	37.95
X20FAWWON.SA.222	70.59	22.14	12.54	34.84	23.06	14.95	39.69
X20FAWWON.SA.223	56.85	14.65	12.83	29.01	18.86	15.22	36.68
X20FAWWON.SA.224	63.02	22.85	13.16	37.21	23.07	15.34	40.63
X20FAWWON.SA.226	55.79	15.34	12.55	28.89	19.54	15.27	37.13
X20FAWWON.SA.227	57.01	16.53	11.92	28.19	19.92	14.77	36.58
X20FAWWON.SA.228	68.16	19.02	13.83	34.42	21.09	15.94	39.64
X20FAWWON.SA.230	62.91	19.04	12.47	31.96	21.65	15.10	38.61
X20FAWWON.SA.231	63.55	16.81	13.18	32.24	20.67	15.40	38.61
X20FAWWON.SA.232	54.92	16.02	12.75	29.90	19.78	15.03	36.85
X20FAWWON.SA.235	60.69	18.47	12.45	31.28	20.89	14.89	37.90
X20FAWWON.SA.236	59.27	19.77	13.30	34.75	21.71	15.56	39.75
X20FAWWON.SA.237	63.93	22.16	13.69	36.23	22.50	15.57	40.10
X20FAWWON.SA.238	57.47	14.84	12.28	28.67	19.41	14.93	36.78
X20FAWWON.SA.241	69.16	21.71	13.48	35.67	22.88	15.66	40.41

X20FAWWON.SA.243	70.48	22.71	13.57	37.19	23.42	15.76	41.18
X20FAWWON.SA.244	58.77	16.22	13.38	31.92	20.39	15.65	38.62
X20FAWWON.SA.249	63.64	23.20	12.89	35.97	23.27	15.59	40.80
X20FAWWON.SA.251	67.17	25.65	14.31	40.63	24.67	16.59	43.57
X20FAWWON.SA.252	66.74	23.03	14.20	38.25	23.23	16.28	41.68
X20FAWWON.SA.254	66.56	19.80	12.86	33.72	21.89	15.31	39.47
X20FAWWON.SA.256	69.32	19.90	12.52	32.83	21.84	15.02	38.84
X20FAWWON.SA.257	61.43	21.72	11.42	32.20	22.52	14.59	38.79
X20FAWWON.SA.258	64.99	22.52	12.40	34.84	23.19	15.01	40.02
X20FAWWON.SA.259	60.85	20.85	12.29	32.55	22.32	14.90	38.83
X20FAWWON.SA.278	66.45	19.08	13.27	32.82	21.22	15.51	38.89
Byrd	75.84	23.72	13.20	37.74	23.64	15.38	41.19
Denali	78.67	22.94	13.31	37.01	23.40	15.59	41.23
Ripper	63.94	20.09	10.81	30.73	21.84	14.15	37.78
Snowmass	66.17	22.25	13.23	36.25	22.53	15.19	39.97
Antero	77.59	24.72	12.93	38.53	24.06	15.35	41.57

Supplemental Table S5.9. Mean normalized difference vegetation indice (NDVI) values for Julesburg 2014.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X20FAWWON.IRR.7	0.44	0.39	0.41	0.52	0.46	0.49
X20FAWWON.IRR.8	0.38	0.36	0.37	0.47	0.44	0.46
X20FAWWON.IRR.9	0.44	0.39	0.40	0.53	0.46	0.49
X20FAWWON.IRR.10	0.28	0.39	0.37	0.44	0.46	0.47
X20FAWWON.IRR.11	0.38	0.40	0.39	0.46	0.45	0.46
X20FAWWON.IRR.12	0.47	0.38	0.42	0.54	0.46	0.49
X20FAWWON.IRR.13	0.40	0.36	0.38	0.51	0.45	0.48
X20FAWWON.IRR.14	0.34	0.38	0.39	0.48	0.46	0.48
X20FAWWON.IRR.15	0.45	0.38	0.41	0.52	0.46	0.50
X20FAWWON.IRR.16	0.43	0.40	0.41	0.51	0.46	0.48
X20FAWWON.IRR.17	0.38	0.39	0.39	0.48	0.45	0.47
X20FAWWON.IRR.18	0.51	0.39	0.44	0.55	0.46	0.50
X20FAWWON.IRR.19	0.49	0.37	0.43	0.55	0.45	0.50
X20FAWWON.IRR.20	0.39	0.36	0.38	0.47	0.45	0.46
X20FAWWON.IRR.21	0.48	0.35	0.42	0.53	0.45	0.49
X20FAWWON.IRR.22	0.35	0.40	0.39	0.48	0.46	0.48
X20FAWWON.IRR.23	0.45	0.38	0.41	0.53	0.46	0.49
X20FAWWON.IRR.24	0.41	0.37	0.40	0.51	0.45	0.48
X20FAWWON.IRR.25	0.38	0.39	0.38	0.49	0.45	0.47
X20FAWWON.IRR.26	0.42	0.39	0.40	0.51	0.45	0.48
X20FAWWON.IRR.27	0.36	0.41	0.40	0.49	0.47	0.49
X20FAWWON.IRR.29	0.41	0.39	0.40	0.51	0.46	0.49
X20FAWWON.IRR.30	0.40	0.37	0.39	0.50	0.45	0.48
X20FAWWON.IRR.31	0.35	0.40	0.38	0.49	0.46	0.48
X20FAWWON.IRR.32	0.36	0.39	0.39	0.47	0.46	0.48
X20FAWWON.IRR.33	0.32	0.39	0.37	0.47	0.46	0.47
X20FAWWON.IRR.35	0.35	0.40	0.38	0.45	0.45	0.46

X20FAWWON.IRR.36	0.53	0.38	0.44	0.56	0.46	0.50
X20FAWWON.IRR.37	0.50	0.39	0.43	0.56	0.46	0.51
X20FAWWON.IRR.38	0.45	0.39	0.41	0.53	0.46	0.49
X20FAWWON.IRR.39	0.39	0.39	0.40	0.49	0.46	0.48
X20FAWWON.IRR.40	0.43	0.38	0.41	0.51	0.46	0.48
X20FAWWON.IRR.41	0.46	0.39	0.42	0.53	0.46	0.50
X20FAWWON.IRR.42	0.51	0.40	0.44	0.56	0.46	0.51
X20FAWWON.IRR.43	0.31	0.37	0.36	0.45	0.46	0.46
X20FAWWON.IRR.44	0.44	0.37	0.41	0.52	0.46	0.49
X20FAWWON.IRR.45	0.46	0.39	0.42	0.54	0.46	0.50
X20FAWWON.IRR.46	0.46	0.40	0.42	0.53	0.46	0.49
X20FAWWON.IRR.47	0.30	0.40	0.36	0.46	0.45	0.47
X20FAWWON.IRR.48	0.40	0.39	0.40	0.51	0.46	0.49
X20FAWWON.IRR.49	0.32	0.37	0.36	0.46	0.46	0.47
X20FAWWON.IRR.55	0.36	0.35	0.37	0.48	0.45	0.46
X20FAWWON.IRR.56	0.41	0.40	0.42	0.51	0.47	0.50
X20FAWWON.IRR.57	0.47	0.39	0.42	0.54	0.46	0.50
X20FAWWON.IRR.59	0.45	0.36	0.41	0.54	0.45	0.49
X20FAWWON.IRR.69	0.43	0.38	0.41	0.51	0.45	0.48
X20FAWWON.IRR.71	0.27	0.39	0.35	0.43	0.45	0.46
X20FAWWON.IRR.74	0.44	0.37	0.40	0.52	0.45	0.49
X20FAWWON.IRR.78	0.30	0.40	0.38	0.45	0.47	0.47
X20FAWWON.IRR.85	0.33	0.38	0.37	0.47	0.46	0.47
X20FAWWON.IRR.86	0.44	0.37	0.41	0.52	0.46	0.49
X20FAWWON.IRR.87	0.39	0.37	0.38	0.51	0.45	0.48
X20FAWWON.IRR.88	0.42	0.40	0.42	0.51	0.47	0.49
X20FAWWON.IRR.95	0.47	0.42	0.43	0.52	0.45	0.48
X20FAWWON.IRR.97	0.43	0.38	0.41	0.53	0.46	0.49
X20FAWWON.IRR.98	0.44	0.38	0.40	0.52	0.45	0.49
X20FAWWON.IRR.100	0.47	0.38	0.41	0.53	0.45	0.49
X20FAWWON.IRR.106	0.48	0.39	0.43	0.54	0.46	0.50

X20FAWWON.IRR.114	0.42	0.41	0.42	0.52	0.47	0.50
X20FAWWON.IRR.115	0.49	0.37	0.42	0.54	0.46	0.50
X20FAWWON.IRR.118	0.51	0.37	0.43	0.56	0.46	0.50
X20FAWWON.IRR.143	0.53	0.41	0.44	0.56	0.46	0.50
X20FAWWON.SA.202	0.43	0.41	0.42	0.52	0.46	0.49
X20FAWWON.SA.206	0.44	0.37	0.40	0.52	0.45	0.48
X20FAWWON.SA.207	0.36	0.35	0.37	0.48	0.45	0.47
X20FAWWON.SA.208	0.37	0.38	0.40	0.49	0.46	0.48
X20FAWWON.SA.209	0.39	0.39	0.39	0.50	0.45	0.48
X20FAWWON.SA.210	0.37	0.40	0.39	0.49	0.46	0.48
X20FAWWON.SA.212	0.43	0.42	0.42	0.52	0.46	0.49
X20FAWWON.SA.213	0.41	0.39	0.40	0.51	0.46	0.49
X20FAWWON.SA.214	0.43	0.39	0.41	0.52	0.46	0.49
X20FAWWON.SA.215	0.48	0.40	0.44	0.54	0.47	0.51
X20FAWWON.SA.218	0.46	0.42	0.42	0.53	0.46	0.50
X20FAWWON.SA.221	0.41	0.38	0.39	0.52	0.45	0.49
X20FAWWON.SA.222	0.51	0.37	0.43	0.56	0.45	0.50
X20FAWWON.SA.223	0.38	0.38	0.39	0.49	0.45	0.48
X20FAWWON.SA.224	0.47	0.39	0.42	0.54	0.46	0.49
X20FAWWON.SA.226	0.39	0.38	0.39	0.50	0.46	0.48
X20FAWWON.SA.227	0.38	0.35	0.37	0.49	0.44	0.47
X20FAWWON.SA.228	0.49	0.42	0.45	0.55	0.47	0.51
X20FAWWON.SA.230	0.39	0.36	0.38	0.51	0.45	0.48
X20FAWWON.SA.231	0.42	0.38	0.40	0.52	0.46	0.49
X20FAWWON.SA.232	0.42	0.37	0.40	0.50	0.46	0.48
X20FAWWON.SA.235	0.43	0.38	0.40	0.52	0.45	0.49
X20FAWWON.SA.236	0.47	0.40	0.43	0.54	0.46	0.50
X20FAWWON.SA.237	0.50	0.39	0.44	0.56	0.46	0.51
X20FAWWON.SA.238	0.38	0.36	0.38	0.49	0.45	0.48
X20FAWWON.SA.241	0.50	0.39	0.44	0.56	0.46	0.51
X20FAWWON.SA.243	0.51	0.39	0.44	0.56	0.46	0.51

X20FAWWON.SA.244	0.42	0.39	0.41	0.52	0.46	0.49
X20FAWWON.SA.249	0.53	0.39	0.44	0.57	0.46	0.52
X20FAWWON.SA.251	0.53	0.44	0.45	0.57	0.47	0.52
X20FAWWON.SA.252	0.51	0.40	0.45	0.56	0.47	0.51
X20FAWWON.SA.254	0.47	0.38	0.42	0.54	0.46	0.50
X20FAWWON.SA.256	0.43	0.37	0.40	0.50	0.45	0.47
X20FAWWON.SA.257	0.49	0.36	0.42	0.55	0.45	0.50
X20FAWWON.SA.258	0.47	0.36	0.41	0.54	0.46	0.49
X20FAWWON.SA.259	0.46	0.36	0.41	0.51	0.45	0.48
X20FAWWON.SA.278	0.42	0.39	0.40	0.51	0.45	0.48
Byrd	0.51	0.39	0.44	0.55	0.45	0.50
Denali	0.52	0.39	0.46	0.57	0.47	0.52
Ripper	0.46	0.33	0.40	0.52	0.44	0.48
Snowmass	0.48	0.39	0.42	0.53	0.45	0.49
Antero	0.53	0.39	0.44	0.57	0.45	0.51
Byrd4	0.53	0.39	0.45	0.56	0.45	0.51

Supplemental Table S5.10. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) for Fort Collins 2015.

		AUC					
ID	Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X21FAWWON.SA.288	75.78	50.24	20.65	73.07	55.91	23.86	82.42
X20FAWWON.SA.227	84.93	48.68	21.10	72.47	55.24	24.14	81.94
X20FAWWON.IRR.42	93.62	51.28	20.96	74.89	57.05	24.66	84.26
X20FAWWON.SA.215	98.14	49.73	21.74	74.48	55.51	24.30	82.34
X21FAWWON.IRR.157	80.70	45.79	21.22	70.10	52.81	23.75	79.43
X20FAWWON.SA.223	90.51	43.17	19.80	65.50	51.57	22.89	77.41
X20FAWWON.IRR.12	92.05	48.73	20.76	72.17	54.92	23.64	81.09
X21FAWWON.IRR.81	58.38	47.57	20.93	71.74	55.05	24.57	82.18
X21FAWWON.SA.258	72.57	42.91	20.46	65.93	51.28	23.28	76.99
X20FAWWON.SA.231	102.69	46.94	22.32	72.69	54.26	24.92	81.87
X20FAWWON.IRR.100	73.90	47.64	20.51	70.72	54.20	23.94	80.91
X21FAWWON.SA.207	84.44	53.34	21.02	77.05	58.35	23.46	84.69
X21FAWWON.IRR.142	76.80	48.86	20.23	71.33	55.09	23.33	80.95
X21FAWWON.IRR.59	86.23	39.43	23.02	66.04	49.52	24.94	77.23
X21FAWWON.IRR.152	71.98	45.46	20.58	68.72	53.10	23.95	79.47
X20FAWWON.SA.230	65.64	44.03	20.38	67.30	51.82	23.88	78.61
X20FAWWON.SA.243	91.10	50.21	21.26	74.13	55.98	24.66	83.04
X20FAWWON.IRR.95	75.62	49.57	20.32	72.03	56.22	23.81	82.44
X21FAWWON.SA.275	54.76	45.20	19.42	66.98	52.74	23.60	78.73
X21FAWWON.IRR.9	89.94	45.36	22.30	71.25	53.19	24.54	80.11
X21FAWWON.SA.250	80.87	43.67	22.39	70.17	52.14	24.61	79.64
X20FAWWON.IRR.55	78.22	47.10	20.78	70.35	53.99	23.81	80.45
X21FAWWON.SA.297	62.35	47.24	21.36	71.29	53.63	24.67	80.50
X21FAWWON.SA.261	81.57	48.61	19.65	70.58	54.77	23.45	80.56
X20FAWWON.IRR.46	87.30	51.27	21.19	74.91	56.46	24.16	82.85
X21FAWWON.IRR.116	79.34	41.34	21.01	65.69	50.18	24.15	76.81

X21FAWWON.IRR.36	62.41	40.04	22.56	66.49	49.60	25.39	77.70
X21FAWWON.IRR.7	80.59	49.16	20.81	72.51	55.43	23.96	81.92
X21FAWWON.IRR.122	73.68	43.91	19.13	65.35	52.09	22.90	77.64
X21FAWWON.SA.201	76.07	53.77	21.49	77.78	57.81	25.81	86.00
X21FAWWON.SA.292	85.87	41.29	20.35	64.57	50.21	23.45	76.51
X20FAWWON.IRR.36	77.13	54.21	22.58	79.69	58.57	25.37	86.52
X21FAWWON.IRR.141	90.22	49.61	20.74	73.35	55.80	24.70	83.18
X20FAWWON.IRR.115	89.56	51.81	20.60	74.98	57.31	23.03	83.27
X20FAWWON.SA.278	83.96	46.12	21.24	70.28	53.48	25.07	80.96
X21FAWWON.SA.228	98.42	46.08	20.77	69.87	53.42	23.46	79.65
X21FAWWON.IRR.29	77.81	48.41	21.36	72.59	54.99	25.11	82.49
X20FAWWON.SA.241	102.95	51.91	21.46	76.26	57.48	24.48	84.63
X21FAWWON.SA.234	113.56	52.38	19.90	74.69	57.44	23.10	82.95
X21FAWWON.SA.243	79.66	52.71	21.93	77.42	58.50	25.48	86.08
X20FAWWON.IRR.25	72.31	44.62	20.25	67.98	52.88	23.90	79.64
X20FAWWON.IRR.18	85.58	50.91	21.03	74.42	56.43	24.33	83.23
X21FAWWON.IRR.166	80.88	48.74	20.40	71.41	54.74	23.70	80.75
X21FAWWON.SA.252	86.33	43.23	19.31	64.91	51.23	22.64	76.69
X20FAWWON.IRR.23	99.08	51.22	21.13	75.13	57.03	23.51	83.66
X21FAWWON.SA.263	73.82	41.16	21.27	65.85	50.47	24.40	77.56
X20FAWWON.IRR.19	90.73	49.06	21.33	73.02	55.43	24.19	82.39
X20FAWWON.IRR.97	86.35	48.92	20.00	71.17	55.67	23.69	82.05
X20FAWWON.SA.206	79.91	45.58	21.66	70.58	52.98	24.02	79.96
X20FAWWON.SA.207	78.37	40.72	20.03	64.02	49.75	23.05	75.91
X20FAWWON.IRR.114	89.93	52.66	22.83	78.97	58.09	25.17	85.99
X20FAWWON.IRR.37	85.23	48.27	23.15	74.69	54.95	27.40	84.35
X21FAWWON.IRR.76	61.38	44.91	22.18	70.03	52.77	25.04	80.44
X21FAWWON.IRR.71	86.21	48.00	19.46	69.95	54.87	23.73	80.97
X20FAWWON.SA.209	76.50	42.27	22.03	67.77	50.95	24.97	78.62
X21FAWWON.IRR.148	81.36	49.08	20.34	71.91	55.25	23.73	81.54
X20FAWWON.IRR.118	70.97	52.12	20.03	74.52	58.01	24.32	84.68

X20FAWWON.SA.252	85.80	53.45	20.44	76.26	58.09	24.26	84.96
X21FAWWON.SA.270	77.58	43.37	21.27	67.60	51.55	24.19	78.60
X20FAWWON.IRR.33	81.58	43.57	22.44	69.66	51.97	25.28	80.20
X20FAWWON.IRR.43	71.37	42.05	19.36	64.06	50.58	23.10	76.10
X20FAWWON.IRR.7	90.62	45.41	21.15	69.37	52.75	24.11	79.58
X20FAWWON.SA.244	70.07	44.33	21.52	68.68	52.09	24.89	79.28
X21FAWWON.IRR.146	80.66	42.58	20.38	65.94	51.17	23.87	77.72
X20FAWWON.IRR.28	85.18	38.98	22.42	65.08	48.58	25.01	76.39
X20FAWWON.IRR.57	83.91	49.41	21.43	73.80	56.07	25.00	83.51
X21FAWWON.SA.202	79.50	49.05	21.31	73.17	55.04	24.03	81.85
X20FAWWON.SA.210	86.47	42.66	19.93	65.55	50.83	23.23	76.80
X21FAWWON.SA.248	78.20	52.10	21.27	76.19	57.64	24.04	84.39
X20FAWWON.IRR.86	92.86	55.58	21.56	79.68	59.48	24.19	86.29
X21FAWWON.SA.247	80.87	52.69	21.60	76.97	57.80	24.41	84.92
X21FAWWON.SA.223	79.95	44.57	19.97	67.24	51.91	22.81	77.18
X21FAWWON.IRR.49	70.93	45.30	19.49	67.14	52.34	23.10	78.39
X20FAWWON.IRR.41	81.61	50.69	21.61	75.02	55.93	24.68	83.10
X21FAWWON.SA.256	63.36	47.53	19.16	68.65	53.94	22.43	79.23
X21FAWWON.SA.271	69.84	40.07	20.14	63.21	49.23	22.80	75.21
X20FAWWON.IRR.22	100.93	41.09	21.61	66.37	50.53	24.72	77.77
X21FAWWON.SA.287	75.85	50.64	21.84	75.38	56.69	25.31	84.42
X21FAWWON.SA.231	86.04	46.71	21.56	71.29	53.85	24.11	80.67
X20FAWWON.IRR.24	81.22	39.42	20.10	62.53	48.82	23.02	74.72
X21FAWWON.IRR.137	91.88	54.39	21.26	77.86	59.16	24.14	85.85
X21FAWWON.SA.265	73.94	38.98	21.21	63.75	48.52	24.14	75.91
X20FAWWON.SA.237	99.31	53.39	22.05	78.60	58.95	23.86	85.62
X21FAWWON.IRR.143	90.26	52.64	20.04	74.99	57.57	22.80	83.06
X21FAWWON.IRR.163	82.50	48.99	20.16	71.73	55.12	23.47	81.27
X21FAWWON.SA.269	73.85	44.86	21.18	69.11	52.57	24.79	80.00
X20FAWWON.SA.221	66.03	47.67	20.54	70.75	54.54	24.43	81.16
X20FAWWON.IRR.32	90.31	43.30	21.24	67.74	51.46	24.05	78.40

X20FAWWON.SA.259	89.91	51.44	20.84	74.78	57.29	23.71	83.78
X21FAWWON.IRR.144	84.70	46.19	20.91	69.72	53.19	24.59	80.36
X20FAWWON.IRR.40	87.67	46.97	21.63	71.60	53.57	24.02	80.46
X20FAWWON.IRR.56	98.92	44.07	21.43	68.65	52.28	24.04	79.19
X20FAWWON.IRR.15	83.04	48.79	21.36	72.69	54.92	24.56	82.00
X20FAWWON.IRR.27	84.73	41.00	22.64	67.75	50.48	25.16	78.53
X20FAWWON.SA.226	90.21	47.00	20.68	70.29	53.75	23.52	80.30
X21FAWWON.IRR.43	77.52	51.67	22.53	77.03	57.34	25.12	84.89
X21FAWWON.IRR.48	86.36	37.74	21.26	62.93	47.78	24.08	75.16
X21FAWWON.SA.226	84.89	46.55	20.51	69.97	53.58	22.90	79.41
X21FAWWON.IRR.103	95.44	46.25	21.58	71.02	53.51	24.20	80.63
X21FAWWON.IRR.52	80.88	47.28	19.35	68.80	54.12	22.91	79.54
X20FAWWON.SA.235	78.30	43.27	19.32	65.30	50.87	21.85	76.14
X20FAWWON.SA.228	77.48	53.24	22.95	79.01	58.18	25.46	86.22
X20FAWWON.SA.249	82.73	50.71	21.19	74.48	56.15	24.46	83.10
X20FAWWON.IRR.49	88.70	43.23	22.15	69.00	51.93	26.00	80.28
X20FAWWON.SA.251	86.33	52.66	21.25	76.53	57.74	24.67	85.14
X20FAWWON.IRR.48	85.47	41.13	21.36	65.85	50.06	24.13	77.23
X20FAWWON.SA.202	82.45	47.34	20.43	70.63	53.87	23.81	80.07
X21FAWWON.SA.286	87.75	49.20	20.53	72.25	55.70	24.33	82.62
X20FAWWON.IRR.106	87.19	50.96	20.41	74.13	57.03	24.31	83.90
X20FAWWON.IRR.85	56.84	40.98	19.52	62.96	49.64	23.34	75.55
X21FAWWON.IRR.17	82.16	48.63	20.57	72.27	55.39	24.28	82.50
X20FAWWON.IRR.69	75.28	39.28	20.34	63.46	48.83	23.58	75.52
X20FAWWON.IRR.98	83.11	52.62	20.76	75.98	57.70	23.72	84.34
X21FAWWON.IRR.14	90.67	37.12	21.82	63.15	47.38	23.93	74.67
X20FAWWON.IRR.10	83.31	42.93	20.86	66.88	51.46	23.84	78.08
X20FAWWON.SA.218	83.21	49.84	22.18	75.29	55.82	24.54	83.28
X21FAWWON.IRR.150	75.17	48.08	21.02	71.54	54.33	25.07	81.46
X21FAWWON.SA.211	88.75	49.98	20.40	72.74	56.06	23.51	82.02
X21FAWWON.SA.293	80.93	48.23	20.14	70.71	54.67	23.17	80.66

X20FAWWON.SA.222	89.66	53.73	21.52	77.73	58.58	24.00	85.03
X20FAWWON.SA.232	87.66	48.20	19.87	70.55	54.53	22.40	79.59
X21FAWWON.IRR.75	87.80	41.79	21.16	66.16	50.49	23.93	77.42
X20FAWWON.IRR.59	89.15	47.99	20.56	71.13	54.49	23.98	80.67
X21FAWWON.SA.299	79.07	44.40	20.60	67.97	52.17	23.87	78.52
X20FAWWON.IRR.21	100.04	48.57	20.52	71.74	54.60	23.38	80.48
X21FAWWON.IRR.83	74.58	52.75	20.36	75.08	57.74	24.31	84.27
X21FAWWON.SA.218	74.91	48.07	20.48	70.85	54.43	23.58	80.67
X20FAWWON.IRR.38	83.90	48.26	21.12	72.21	55.00	25.06	82.62
X20FAWWON.IRR.143	72.71	53.49	20.66	76.79	58.50	23.92	84.96
X20FAWWON.IRR.44	100.60	49.86	19.95	72.36	55.55	22.66	81.08
X20FAWWON.SA.236	102.94	48.51	22.51	74.44	55.11	24.79	82.45
X20FAWWON.IRR.17	73.71	47.80	21.78	72.63	54.49	24.45	81.94
X21FAWWON.IRR.95	95.18	53.00	22.12	78.06	58.55	25.03	86.27
X20FAWWON.IRR.20	69.57	48.92	20.20	71.73	55.29	23.74	81.59
X20FAWWON.IRR.26	80.01	44.18	21.00	68.15	52.07	24.39	79.00
X20FAWWON.SA.214	90.89	44.91	22.28	70.63	52.79	24.65	80.37
X21FAWWON.IRR.62	90.30	40.27	21.61	65.25	50.08	24.27	77.20
X20FAWWON.IRR.35	83.70	36.37	23.03	63.59	46.45	24.98	74.50
X21FAWWON.SA.210	94.15	48.12	20.70	71.57	55.03	24.14	81.52
X21FAWWON.IRR.31	84.23	43.82	21.85	69.39	52.03	24.79	79.52
X20FAWWON.IRR.88	104.26	54.32	21.78	78.83	59.05	24.57	86.13
X21FAWWON.SA.208	67.24	41.66	20.41	65.18	50.81	23.15	76.93
X20FAWWON.SA.213	94.52	44.18	20.66	67.65	51.83	23.61	78.40
X21FAWWON.IRR.16	79.69	44.31	21.82	69.33	52.56	24.21	79.55
X20FAWWON.IRR.16	77.31	46.14	21.37	70.79	53.40	24.89	80.80
X20FAWWON.SA.224	110.44	48.42	21.06	72.28	54.85	23.58	80.95
X20FAWWON.SA.254	72.96	50.35	20.29	72.90	56.47	23.70	82.94
X20FAWWON.IRR.87	96.84	52.18	21.61	76.56	57.54	24.13	84.31
X20FAWWON.IRR.11	89.18	45.31	20.98	69.37	52.71	23.83	79.43
X20FAWWON.SA.208	79.96	45.58	21.52	70.03	53.15	24.60	80.34

X21FAWWON.IRR.50	88.39	47.59	20.52	70.88	54.45	23.29	80.85
X21FAWWON.SA.281	92.38	35.86	22.70	62.53	47.27	24.50	74.52
X20FAWWON.IRR.31	92.51	39.37	22.67	65.99	49.46	24.71	77.10
X20FAWWON.SA.212	99.73	48.10	19.81	70.20	54.63	23.19	80.55
X20FAWWON.IRR.29	96.39	47.01	20.32	69.77	54.15	23.55	80.34
X21FAWWON.SA.276	74.41	45.27	21.70	69.90	52.70	24.63	79.72
X20FAWWON.IRR.14	81.04	44.02	20.80	67.86	52.61	23.35	78.66
X20FAWWON.IRR.39	98.62	46.94	21.41	71.72	54.10	23.95	81.06
X20FAWWON.IRR.30	82.52	47.05	20.91	70.86	53.81	23.96	80.52
X20FAWWON.IRR.13	85.16	47.21	21.07	70.87	54.41	24.60	81.52
X20FAWWON.IRR.74	91.44	47.40	20.89	71.03	54.31	23.45	80.61
X20FAWWON.IRR.9	98.58	52.17	21.62	76.53	57.21	24.33	84.08
X20FAWWON.IRR.8	84.43	48.14	20.41	71.21	54.38	23.29	80.60
X20FAWWON.IRR.45	89.91	49.85	20.66	72.96	55.56	23.36	81.67
X21FAWWON.SA.227	87.88	43.45	21.00	67.69	52.12	24.24	79.26
X20FAWWON.SA.238	85.26	45.56	21.53	70.22	52.47	23.94	79.18
X20FAWWON.SA.256	73.95	51.70	19.97	73.48	57.26	24.03	83.40
X21FAWWON.SA.289	71.69	40.30	20.31	63.58	49.25	23.45	75.52
X20FAWWON.SA.258	77.75	51.81	20.12	74.03	57.56	24.15	83.84
X21FAWWON.IRR.68	82.17	38.12	20.90	62.37	47.90	24.21	74.90
X20FAWWON.SA.257	83.02	52.62	19.71	74.24	57.48	22.89	82.87
Snowmass	89.69	52.08	19.75	74.63	56.90	22.85	82.49
Ripper	64.29	53.98	20.69	77.31	58.72	24.58	85.95
Antero	101.40	54.60	21.58	79.00	59.29	24.31	86.34
Denali	107.01	56.03	21.82	80.74	60.69	24.69	88.21
Byrd	83.13	55.85	21.39	80.38	60.01	24.28	87.06

Supplemental Table S5.11. Mean normalized difference vegetation indice (NDVI) values for Fort Collins 2015.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X21FAWWON.SA.288	0.48	0.48	0.48	0.54	0.53	0.54
X20FAWWON.SA.227	0.47	0.48	0.48	0.54	0.54	0.54
X20FAWWON.IRR.42	0.47	0.48	0.47	0.53	0.54	0.54
X20FAWWON.SA.215	0.46	0.48	0.47	0.53	0.53	0.53
X21FAWWON.IRR.157	0.44	0.49	0.47	0.51	0.53	0.53
X20FAWWON.SA.223	0.43	0.47	0.45	0.52	0.52	0.52
X20FAWWON.IRR.12	0.46	0.48	0.47	0.52	0.53	0.53
X21FAWWON.IRR.81	0.46	0.47	0.47	0.52	0.53	0.53
X21FAWWON.SA.258	0.41	0.47	0.45	0.50	0.52	0.52
X20FAWWON.SA.231	0.44	0.49	0.47	0.51	0.54	0.53
X20FAWWON.IRR.100	0.44	0.47	0.46	0.52	0.52	0.53
X21FAWWON.SA.207	0.52	0.48	0.49	0.56	0.53	0.54
X21FAWWON.IRR.142	0.44	0.45	0.44	0.51	0.52	0.51
X21FAWWON.IRR.59	0.40	0.52	0.47	0.50	0.55	0.53
X21FAWWON.IRR.152	0.48	0.49	0.48	0.54	0.53	0.54
X20FAWWON.SA.230	0.42	0.49	0.46	0.51	0.53	0.53
X20FAWWON.SA.243	0.46	0.48	0.47	0.53	0.54	0.53
X20FAWWON.IRR.95	0.47	0.46	0.46	0.53	0.53	0.53
X21FAWWON.SA.275	0.42	0.47	0.45	0.51	0.53	0.52
X21FAWWON.IRR.9	0.44	0.49	0.47	0.52	0.54	0.52
X21FAWWON.SA.250	0.43	0.49	0.46	0.50	0.54	0.52
X20FAWWON.IRR.55	0.44	0.46	0.45	0.52	0.53	0.52
X21FAWWON.SA.297	0.45	0.48	0.47	0.52	0.53	0.53
X21FAWWON.SA.261	0.43	0.45	0.44	0.52	0.52	0.52
X20FAWWON.IRR.46	0.48	0.48	0.47	0.54	0.53	0.53
X21FAWWON.IRR.116	0.41	0.48	0.46	0.50	0.53	0.52
X21FAWWON.IRR.36	0.40	0.51	0.47	0.49	0.55	0.53

X21FAWWON.IRR.7	0.46	0.48	0.47	0.53	0.53	0.53
X21FAWWON.IRR.122	0.42	0.45	0.44	0.51	0.51	0.52
X21FAWWON.SA.201	0.49	0.48	0.48	0.55	0.55	0.54
X21FAWWON.SA.292	0.38	0.46	0.43	0.48	0.52	0.51
X20FAWWON.IRR.36	0.50	0.49	0.49	0.54	0.55	0.54
X21FAWWON.IRR.141	0.45	0.47	0.46	0.52	0.54	0.53
X20FAWWON.IRR.115	0.48	0.48	0.47	0.54	0.52	0.53
X20FAWWON.SA.278	0.42	0.47	0.45	0.51	0.54	0.53
X21FAWWON.SA.228	0.46	0.49	0.48	0.53	0.53	0.53
X21FAWWON.IRR.29	0.48	0.49	0.48	0.54	0.54	0.54
X20FAWWON.SA.241	0.51	0.49	0.50	0.56	0.54	0.55
X21FAWWON.SA.234	0.49	0.47	0.48	0.54	0.52	0.53
X21FAWWON.SA.243	0.49	0.49	0.49	0.55	0.55	0.54
X20FAWWON.IRR.25	0.43	0.48	0.46	0.51	0.53	0.53
X20FAWWON.IRR.18	0.48	0.47	0.47	0.54	0.54	0.53
X21FAWWON.IRR.166	0.44	0.46	0.45	0.52	0.52	0.52
X21FAWWON.SA.252	0.42	0.47	0.44	0.50	0.52	0.52
X20FAWWON.IRR.23	0.53	0.49	0.50	0.56	0.54	0.54
X21FAWWON.SA.263	0.40	0.48	0.45	0.49	0.53	0.52
X20FAWWON.IRR.19	0.47	0.48	0.48	0.54	0.54	0.54
X20FAWWON.IRR.97	0.47	0.47	0.47	0.54	0.53	0.54
X20FAWWON.SA.206	0.43	0.48	0.46	0.51	0.54	0.52
X20FAWWON.SA.207	0.42	0.48	0.46	0.51	0.52	0.52
X20FAWWON.IRR.114	0.51	0.51	0.51	0.56	0.55	0.55
X20FAWWON.IRR.37	0.47	0.51	0.49	0.54	0.57	0.56
X21FAWWON.IRR.76	0.42	0.49	0.46	0.51	0.54	0.53
X21FAWWON.IRR.71	0.45	0.47	0.46	0.52	0.52	0.53
X20FAWWON.SA.209	0.47	0.50	0.48	0.52	0.55	0.53
X21FAWWON.IRR.148	0.49	0.48	0.48	0.55	0.53	0.54
X20FAWWON.IRR.118	0.50	0.47	0.48	0.56	0.53	0.55
X20FAWWON.SA.252	0.50	0.48	0.48	0.55	0.54	0.54

X21FAWWON.SA.270	0.45	0.50	0.48	0.52	0.54	0.54
X20FAWWON.IRR.33	0.43	0.49	0.47	0.51	0.56	0.53
X20FAWWON.IRR.43	0.41	0.45	0.44	0.51	0.52	0.51
X20FAWWON.IRR.7	0.45	0.48	0.46	0.52	0.54	0.53
X20FAWWON.SA.244	0.43	0.48	0.46	0.52	0.54	0.53
X21FAWWON.IRR.146	0.40	0.47	0.44	0.50	0.54	0.52
X20FAWWON.IRR.28	0.41	0.50	0.46	0.50	0.55	0.52
X20FAWWON.IRR.57	0.49	0.48	0.48	0.55	0.54	0.55
X21FAWWON.SA.202	0.45	0.48	0.46	0.52	0.53	0.53
X20FAWWON.SA.210	0.42	0.48	0.45	0.50	0.52	0.52
X21FAWWON.SA.248	0.50	0.49	0.49	0.55	0.53	0.54
X20FAWWON.IRR.86	0.50	0.48	0.49	0.55	0.54	0.54
X21FAWWON.SA.247	0.47	0.50	0.48	0.54	0.54	0.54
X21FAWWON.SA.223	0.42	0.47	0.45	0.50	0.51	0.51
X21FAWWON.IRR.49	0.42	0.46	0.44	0.51	0.53	0.52
X20FAWWON.IRR.41	0.48	0.49	0.48	0.53	0.54	0.54
X21FAWWON.SA.256	0.44	0.46	0.46	0.52	0.52	0.52
X21FAWWON.SA.271	0.41	0.48	0.45	0.50	0.53	0.52
X20FAWWON.IRR.22	0.46	0.49	0.48	0.53	0.54	0.54
X21FAWWON.SA.287	0.48	0.48	0.47	0.55	0.55	0.54
X21FAWWON.SA.231	0.44	0.47	0.46	0.52	0.54	0.52
X20FAWWON.IRR.24	0.41	0.47	0.44	0.50	0.52	0.51
X21FAWWON.IRR.137	0.50	0.48	0.49	0.55	0.54	0.55
X21FAWWON.SA.265	0.42	0.49	0.46	0.51	0.54	0.53
X20FAWWON.SA.237	0.53	0.50	0.51	0.56	0.54	0.55
X21FAWWON.IRR.143	0.47	0.47	0.47	0.54	0.52	0.53
X21FAWWON.IRR.163	0.44	0.48	0.46	0.52	0.53	0.53
X21FAWWON.IRR.11						
X21FAWWON.SA.269	0.42	0.48	0.46	0.51	0.55	0.53
X20FAWWON.SA.221	0.43	0.46	0.45	0.51	0.53	0.52
X20FAWWON.IRR.32	0.42	0.47	0.45	0.50	0.54	0.52

X20FAWWON.SA.259	0.48	0.48	0.48	0.55	0.53	0.54
X21FAWWON.IRR.144	0.46	0.49	0.47	0.54	0.55	0.54
X20FAWWON.IRR.40	0.44	0.49	0.47	0.51	0.54	0.53
X20FAWWON.IRR.56	0.43	0.49	0.46	0.51	0.54	0.52
X20FAWWON.IRR.15	0.44	0.48	0.46	0.52	0.54	0.53
X20FAWWON.IRR.27	0.41	0.50	0.46	0.50	0.55	0.53
X20FAWWON.SA.226	0.44	0.48	0.47	0.52	0.54	0.53
X21FAWWON.IRR.43	0.52	0.51	0.51	0.56	0.55	0.56
X21FAWWON.IRR.48	0.39	0.49	0.45	0.49	0.55	0.52
X21FAWWON.SA.226	0.44	0.47	0.45	0.51	0.52	0.51
X21FAWWON.IRR.103	0.46	0.50	0.48	0.53	0.54	0.54
X21FAWWON.IRR.52	0.48	0.46	0.46	0.53	0.52	0.52
X20FAWWON.SA.235	0.44	0.46	0.45	0.51	0.52	0.52
X20FAWWON.SA.228	0.49	0.49	0.48	0.54	0.55	0.54
X20FAWWON.SA.249	0.47	0.49	0.48	0.53	0.53	0.54
X20FAWWON.IRR.49	0.44	0.50	0.47	0.52	0.55	0.54
X20FAWWON.SA.251	0.49	0.49	0.49	0.55	0.54	0.55
X20FAWWON.IRR.48	0.40	0.49	0.46	0.50	0.54	0.53
X20FAWWON.SA.202	0.43	0.47	0.45	0.51	0.53	0.52
X21FAWWON.SA.286	0.46	0.47	0.47	0.54	0.54	0.54
X20FAWWON.IRR.106	0.47	0.47	0.47	0.54	0.53	0.54
X20FAWWON.IRR.85	0.40	0.48	0.45	0.50	0.52	0.52
X21FAWWON.IRR.17	0.45	0.47	0.46	0.53	0.54	0.53
X20FAWWON.IRR.69	0.39	0.49	0.45	0.50	0.53	0.52
X20FAWWON.IRR.98	0.49	0.48	0.47	0.53	0.53	0.53
X21FAWWON.IRR.14	0.40	0.50	0.46	0.49	0.54	0.52
X20FAWWON.IRR.10	0.43	0.47	0.45	0.51	0.53	0.52
X20FAWWON.SA.218	0.45	0.48	0.47	0.52	0.54	0.53
X21FAWWON.IRR.150	0.46	0.48	0.47	0.52	0.54	0.53
X21FAWWON.SA.211	0.45	0.46	0.45	0.53	0.52	0.52
X21FAWWON.SA.293	0.45	0.46	0.45	0.52	0.53	0.52

X20FAWWON.SA.222	0.50	0.48	0.49	0.55	0.53	0.54
X20FAWWON.SA.232	0.46	0.47	0.46	0.52	0.51	0.52
X21FAWWON.IRR.75	0.41	0.49	0.46	0.50	0.53	0.52
X20FAWWON.IRR.59	0.45	0.47	0.46	0.52	0.53	0.52
X21FAWWON.SA.299	0.43	0.48	0.46	0.51	0.53	0.52
X20FAWWON.IRR.21	0.48	0.47	0.47	0.53	0.52	0.53
X21FAWWON.IRR.83	0.49	0.49	0.48	0.55	0.54	0.55
X21FAWWON.SA.218	0.47	0.48	0.47	0.54	0.53	0.54
X20FAWWON.IRR.38	0.44	0.48	0.47	0.52	0.54	0.54
X20FAWWON.IRR.143	0.52	0.47	0.49	0.55	0.53	0.53
X20FAWWON.IRR.44	0.47	0.47	0.47	0.54	0.52	0.53
X20FAWWON.SA.236	0.52	0.50	0.50	0.54	0.54	0.53
X20FAWWON.IRR.17	0.48	0.50	0.49	0.54	0.54	0.54
X21FAWWON.IRR.95	0.51	0.50	0.49	0.56	0.54	0.55
X20FAWWON.IRR.20	0.47	0.46	0.47	0.53	0.52	0.53
X20FAWWON.IRR.26	0.42	0.48	0.45	0.50	0.53	0.52
X20FAWWON.SA.214	0.46	0.51	0.49	0.52	0.55	0.54
X21FAWWON.IRR.62	0.43	0.49	0.46	0.52	0.54	0.53
X20FAWWON.IRR.35	0.38	0.52	0.46	0.48	0.55	0.52
X21FAWWON.SA.210	0.44	0.47	0.46	0.52	0.52	0.53
X21FAWWON.IRR.31	0.42	0.49	0.46	0.51	0.54	0.52
X20FAWWON.IRR.88	0.52	0.50	0.50	0.56	0.54	0.55
X21FAWWON.SA.208	0.41	0.48	0.45	0.50	0.53	0.52
X20FAWWON.SA.213	0.44	0.48	0.46	0.52	0.54	0.53
X21FAWWON.IRR.16	0.41	0.48	0.45	0.51	0.54	0.52
X20FAWWON.IRR.16	0.43	0.48	0.46	0.52	0.54	0.53
X20FAWWON.SA.224	0.50	0.49	0.49	0.55	0.53	0.54
X20FAWWON.SA.254	0.46	0.46	0.46	0.53	0.53	0.53
X20FAWWON.IRR.87	0.51	0.50	0.50	0.56	0.54	0.55
X20FAWWON.IRR.11	0.46	0.49	0.48	0.52	0.54	0.53
X20FAWWON.SA.208	0.43	0.47	0.46	0.52	0.54	0.53

X21FAWWON.IRR.50	0.46	0.48	0.47	0.52	0.53	0.53
X21FAWWON.SA.281	0.38	0.50	0.45	0.49	0.54	0.52
X20FAWWON.IRR.31	0.45	0.51	0.48	0.53	0.55	0.54
X20FAWWON.SA.212	0.44	0.46	0.45	0.53	0.53	0.52
X20FAWWON.IRR.29	0.47	0.48	0.48	0.54	0.53	0.54
X21FAWWON.SA.276	0.44	0.48	0.47	0.52	0.54	0.53
X20FAWWON.IRR.14	0.43	0.48	0.46	0.52	0.52	0.53
X20FAWWON.IRR.39	0.46	0.50	0.48	0.53	0.54	0.54
X20FAWWON.IRR.30	0.48	0.49	0.49	0.54	0.54	0.54
X20FAWWON.IRR.13	0.44	0.47	0.46	0.53	0.54	0.53
X20FAWWON.IRR.74	0.47	0.48	0.48	0.53	0.53	0.53
X20FAWWON.IRR.9	0.50	0.49	0.49	0.54	0.54	0.54
X20FAWWON.IRR.8	0.47	0.48	0.47	0.53	0.53	0.53
X20FAWWON.IRR.45	0.46	0.46	0.46	0.53	0.53	0.52
X21FAWWON.SA.227	0.41	0.48	0.46	0.51	0.54	0.53
X20FAWWON.SA.238	0.43	0.48	0.46	0.51	0.53	0.52
X20FAWWON.SA.256	0.50	0.47	0.47	0.56	0.53	0.54
X21FAWWON.SA.289	0.39	0.47	0.44	0.48	0.52	0.51
X20FAWWON.SA.258	0.49	0.48	0.48	0.55	0.53	0.54
X21FAWWON.IRR.68	0.37	0.48	0.44	0.48	0.53	0.52
X20FAWWON.SA.257	0.50	0.47	0.47	0.54	0.52	0.53
Snowmass	0.49	0.47	0.47	0.54	0.52	0.52
Ripper	0.51	0.48	0.49	0.56	0.55	0.55
Antero	0.51	0.48	0.49	0.56	0.54	0.55
Denali	0.52	0.48	0.50	0.57	0.55	0.55
Byrd	0.55	0.50	0.52	0.57	0.54	0.56

Supplemental Table S5.12. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) for Julesburg 2015.

		AUC					
ID	Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X20FAWWON.SA.227	24.09	28.06	8.78	39.62	42.13	20.23	65.18
X20FAWWON.IRR.42	30.72	28.83	10.15	41.50	43.09	21.11	66.99
X20FAWWON.IRR.100	53.19	37.24	10.34	51.08	46.65	20.81	70.58
X21FAWWON.SA.207	53.46	37.54	11.30	54.20	46.73	21.27	70.83
X20FAWWON.SA.243	56.44	41.25	11.58	56.90	49.06	21.09	73.53
X20FAWWON.IRR.95	68.21	39.65	11.65	55.33	48.34	21.19	72.98
X20FAWWON.IRR.55	31.66	29.26	9.02	41.21	42.59	19.90	65.45
X21FAWWON.SA.261	33.60	30.84	9.75	43.57	43.01	20.75	66.41
X20FAWWON.IRR.46	43.87	34.73	10.99	50.22	44.76	20.70	68.68
X21FAWWON.IRR.7	33.94	28.64	9.61	41.45	42.36	20.69	66.04
X21FAWWON.SA.292	30.60	27.47	8.78	39.41	42.50	20.00	65.41
X20FAWWON.IRR.36	56.64	37.33	11.19	52.11	46.07	21.60	70.79
X21FAWWON.IRR.141	36.38	31.81	8.95	44.10	44.31	20.33	67.76
X20FAWWON.IRR.115	59.57	39.25	10.98	54.78	47.81	21.44	72.06
X21FAWWON.SA.228	41.23	26.10	10.77	40.32	41.38	20.16	64.35
X20FAWWON.SA.241	61.07	38.49	11.82	54.76	47.92	21.90	73.01
X21FAWWON.SA.234	33.29	28.01	10.41	41.93	41.60	20.23	65.16
X21FAWWON.SA.243	47.69	36.23	10.35	48.86	46.40	20.90	70.60
X20FAWWON.IRR.18	49.03	40.01	11.59	55.40	48.50	21.77	73.27
X20FAWWON.IRR.19	34.11	33.06	9.21	45.44	44.16	19.84	67.18
X20FAWWON.IRR.97	49.29	32.75	10.61	46.84	44.28	21.56	68.60
X20FAWWON.SA.206	33.15	30.28	9.89	42.37	41.91	20.67	65.28
X20FAWWON.IRR.37	47.56	32.13	10.63	46.38	44.82	21.80	69.81
X20FAWWON.SA.209	40.85	32.58	10.07	45.70	44.04	20.43	67.79
X20FAWWON.IRR.118	74.19	46.82	12.26	64.05	51.95	21.98	77.76
X20FAWWON.SA.252	49.88	43.90	11.94	59.48	49.75	22.74	76.10

X20FAWWON.SA.244	31.14	30.96	8.80	45.60	43.41	19.95	66.19
X20FAWWON.IRR.57	71.51	37.97	9.77	51.87	47.63	20.35	71.51
X21FAWWON.SA.202	27.88	28.86	10.22	42.51	42.35	20.68	66.26
X20FAWWON.IRR.86	47.04	33.89	10.76	49.18	45.67	20.68	69.80
X21FAWWON.SA.247	59.39	37.73	11.12	53.01	48.22	21.39	73.03
X20FAWWON.IRR.41	40.38	36.40	10.59	52.63	46.22	21.46	70.77
X21FAWWON.SA.287	27.43	24.31	9.03	35.82	39.64	20.09	62.28
X21FAWWON.IRR.137	72.79	45.35	10.60	59.42	50.40	20.51	74.41
X20FAWWON.SA.237	47.17	34.54	12.50	50.40	45.03	21.54	70.04
X21FAWWON.IRR.143	57.83	38.57	10.98	53.89	47.48	20.74	71.32
X21FAWWON.IRR.163	37.67	27.86	9.88	41.29	43.05	20.61	66.52
X20FAWWON.SA.259	50.53	42.43	10.83	57.69	48.86	20.62	73.29
X21FAWWON.IRR.144	33.96	23.82	10.18	36.43	40.08	20.95	63.75
X20FAWWON.IRR.15	37.28	30.18	9.79	43.73	43.21	20.89	66.44
X20FAWWON.SA.226	22.97	29.21	9.39	40.80	41.84	20.60	64.92
X21FAWWON.IRR.43	22.69	24.77	9.25	37.11	41.64	20.64	64.66
X20FAWWON.SA.249	54.29	41.90	12.76	59.58	48.96	23.35	75.79
X20FAWWON.SA.251	52.58	46.73	11.76	63.00	51.01	23.12	77.74
X20FAWWON.IRR.106	40.49	35.04	9.91	48.15	45.67	20.54	69.30
X20FAWWON.IRR.98	49.12	37.13	10.37	51.00	46.19	20.90	70.26
X21FAWWON.IRR.150	36.69	25.03	9.25	37.36	41.64	21.14	65.56
X20FAWWON.SA.222	43.17	31.09	9.53	43.64	43.94	20.16	66.74
X20FAWWON.IRR.59	33.76	30.56	9.68	43.30	43.62	19.96	66.53
X20FAWWON.IRR.21	39.39	29.24	10.82	44.12	42.93	21.00	66.97
X21FAWWON.IRR.83	47.03	32.95	9.89	46.29	44.90	20.67	69.28
X20FAWWON.IRR.38	37.31	31.51	9.00	42.84	43.76	21.38	68.13
X20FAWWON.IRR.143	35.69	32.68	10.17	46.88	44.46	20.57	67.90
X20FAWWON.IRR.44	49.44	30.83	10.62	45.25	43.06	20.77	66.79
X21FAWWON.IRR.95	53.72	42.40	10.73	57.47	49.89	21.21	74.20
X21FAWWON.SA.210	57.13	36.90	11.72	53.79	46.41	21.09	70.90
X20FAWWON.SA.213	39.54	31.17	9.93	44.06	43.53	20.19	67.67

X20FAWWON.SA.224	25.08	31.43	10.12	44.75	42.89	20.52	66.14
X20FAWWON.SA.254	49.73	35.62	10.82	49.95	45.69	21.44	70.12
X20FAWWON.IRR.87	31.98	31.29	11.41	45.81	44.04	21.95	69.02
X20FAWWON.IRR.13	39.49	33.24	9.49	45.17	44.52	19.96	67.96
X20FAWWON.IRR.74	28.69	33.71	11.51	48.45	44.73	20.77	69.17
X20FAWWON.IRR.9	47.62	29.21	10.51	42.52	42.26	20.79	66.41
X20FAWWON.IRR.45	59.43	36.08	12.09	52.97	46.15	21.82	70.83
X20FAWWON.SA.256	55.04	38.65	10.33	52.05	47.52	20.79	71.63
X20FAWWON.SA.258	58.13	44.94	11.18	60.23	50.60	21.42	75.52
X20FAWWON.SA.257	53.98	44.73	9.95	59.58	50.76	21.11	74.73
Snowmass	65.14	44.44	9.78	58.23	49.94	19.91	73.11
Ripper	54.26	44.26	9.01	57.53	50.17	20.22	74.00
Antero	74.61	46.56	11.97	62.46	51.81	21.17	76.29
Denali	71.30	44.69	10.79	59.63	50.80	21.18	75.57
Byrd	71.28	44.78	10.25	59.35	50.53	20.33	74.12

Supplemental Table S5.13. Mean normalized difference vegetation indice (NDVI) values for Julesburg 2015.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GFG.NDVI	FULL-G.NDVI
X20FAWWON.SA.227	0.33	0.35	0.32	0.44	0.47	0.45
X20FAWWON.IRR.42	0.36	0.38	0.37	0.47	0.49	0.48
X20FAWWON.IRR.100	0.42	0.35	0.41	0.48	0.49	0.49
X21FAWWON.SA.207	0.42	0.39	0.42	0.48	0.49	0.49
X20FAWWON.SA.243	0.48	0.40	0.46	0.52	0.50	0.52
X20FAWWON.IRR.95	0.43	0.40	0.43	0.49	0.50	0.50
X20FAWWON.IRR.55	0.35	0.32	0.35	0.45	0.47	0.45
X21FAWWON.SA.261	0.36	0.36	0.36	0.46	0.48	0.47
X20FAWWON.IRR.46	0.43	0.39	0.42	0.48	0.48	0.48
X21FAWWON.IRR.7	0.33	0.35	0.34	0.44	0.47	0.45
X21FAWWON.SA.292	0.33	0.33	0.33	0.45	0.47	0.45
X20FAWWON.IRR.36	0.43	0.41	0.41	0.48	0.50	0.49
X21FAWWON.IRR.141	0.37	0.33	0.36	0.46	0.48	0.47
X20FAWWON.IRR.115	0.45	0.41	0.43	0.50	0.49	0.50
X21FAWWON.SA.228	0.30	0.40	0.33	0.43	0.46	0.44
X20FAWWON.SA.241	0.45	0.42	0.44	0.51	0.51	0.51
X21FAWWON.SA.234	0.35	0.36	0.36	0.45	0.48	0.46
X21FAWWON.SA.243	0.41	0.36	0.39	0.48	0.49	0.49
X20FAWWON.IRR.18	0.46	0.43	0.44	0.51	0.50	0.51
X20FAWWON.IRR.19	0.40	0.35	0.38	0.47	0.48	0.48
X20FAWWON.IRR.97	0.38	0.38	0.38	0.47	0.50	0.48
X20FAWWON.SA.206	0.36	0.36	0.36	0.45	0.48	0.46
X20FAWWON.IRR.37	0.37	0.37	0.37	0.46	0.50	0.48
X20FAWWON.SA.209	0.38	0.36	0.37	0.46	0.48	0.47
X20FAWWON.IRR.118	0.52	0.44	0.48	0.53	0.50	0.52
X20FAWWON.SA.252	0.51	0.44	0.47	0.53	0.51	0.52
X20FAWWON.SA.244	0.37	0.33	0.35	0.45	0.46	0.44

X20FAWWON.IRR.57	0.43	0.34	0.40	0.49	0.48	0.49
X21FAWWON.SA.202	0.34	0.37	0.36	0.45	0.49	0.47
X20FAWWON.IRR.86	0.41	0.38	0.40	0.48	0.48	0.48
X21FAWWON.SA.247	0.41	0.40	0.41	0.50	0.50	0.50
X20FAWWON.IRR.41	0.42	0.37	0.41	0.48	0.49	0.49
X21FAWWON.SA.287	0.29	0.33	0.30	0.41	0.45	0.42
X21FAWWON.IRR.137	0.48	0.39	0.44	0.51	0.48	0.50
X20FAWWON.SA.237	0.41	0.43	0.43	0.48	0.50	0.49
X21FAWWON.IRR.143	0.45	0.40	0.42	0.50	0.48	0.49
X21FAWWON.IRR.163	0.36	0.37	0.35	0.46	0.48	0.47
X20FAWWON.SA.259	0.49	0.39	0.45	0.51	0.47	0.49
X21FAWWON.IRR.144	0.29	0.38	0.32	0.43	0.48	0.45
X20FAWWON.IRR.15	0.34	0.37	0.35	0.45	0.48	0.46
X20FAWWON.SA.226	0.34	0.36	0.34	0.44	0.47	0.45
X21FAWWON.IRR.43	0.31	0.34	0.32	0.44	0.47	0.45
X20FAWWON.SA.249	0.46	0.44	0.46	0.50	0.51	0.51
X20FAWWON.SA.251	0.50	0.44	0.47	0.52	0.51	0.52
X20FAWWON.IRR.106	0.41	0.36	0.39	0.48	0.48	0.48
X20FAWWON.IRR.98	0.46	0.37	0.43	0.50	0.49	0.50
X21FAWWON.IRR.150	0.32	0.35	0.32	0.45	0.48	0.46
X20FAWWON.SA.222	0.35	0.35	0.35	0.45	0.47	0.46
X20FAWWON.IRR.59	0.37	0.35	0.36	0.47	0.47	0.47
X20FAWWON.IRR.21	0.36	0.41	0.37	0.46	0.48	0.47
X21FAWWON.IRR.83	0.37	0.35	0.36	0.47	0.48	0.47
X20FAWWON.IRR.38	0.35	0.35	0.33	0.45	0.48	0.47
X20FAWWON.IRR.143	0.39	0.37	0.38	0.47	0.48	0.47
X20FAWWON.IRR.44	0.38	0.38	0.39	0.47	0.49	0.48
X21FAWWON.IRR.95	0.46	0.38	0.43	0.51	0.49	0.50
X21FAWWON.SA.210	0.43	0.41	0.43	0.48	0.49	0.49
X20FAWWON.SA.213	0.35	0.36	0.36	0.45	0.48	0.47
X20FAWWON.SA.224	0.37	0.35	0.38	0.45	0.48	0.47

X20FAWWON.SA.254	0.41	0.39	0.40	0.48	0.50	0.49
X20FAWWON.IRR.87	0.38	0.42	0.40	0.47	0.50	0.49
X20FAWWON.IRR.13	0.38	0.35	0.37	0.47	0.48	0.48
X20FAWWON.IRR.74	0.40	0.41	0.41	0.47	0.49	0.48
X20FAWWON.IRR.9	0.35	0.39	0.36	0.45	0.48	0.46
X20FAWWON.IRR.45	0.42	0.43	0.43	0.49	0.51	0.50
X20FAWWON.SA.256	0.43	0.38	0.41	0.50	0.49	0.50
X20FAWWON.SA.258	0.49	0.40	0.46	0.52	0.50	0.51
X20FAWWON.SA.257	0.49	0.37	0.44	0.52	0.48	0.50
Snowmass	0.49	0.36	0.44	0.52	0.48	0.50
Ripper	0.48	0.34	0.42	0.51	0.47	0.49
Antero	0.50	0.42	0.47	0.53	0.50	0.52
Denali	0.50	0.40	0.45	0.53	0.49	0.51
Byrd	0.50	0.38	0.45	0.52	0.48	0.50

Supplemental Table S5.14. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) for Fort Collins 2016.

		AUC					
ID	Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X22FAWWON.IRR.85	76.68	34.46	13.48	55.33	38.59	18.18	64.87
X22FAWWON.IRR.53	77.54	35.55	14.14	57.82	39.62	18.49	66.66
X22FAWWON.IRR.87	82.04	41.39	15.00	65.15	42.29	19.08	70.05
X22FAWWON.IRR.71	94.59	40.61	15.68	65.41	42.20	19.36	70.48
X22FAWWON.IRR.48	88.96	37.75	16.20	63.03	40.69	19.31	68.74
X22FAWWON.IRR.10	86.47	38.90	16.68	64.73	40.94	19.14	68.74
X22FAWWON.SA.221	91.98	39.33	15.00	62.89	41.76	18.21	68.60
X22FAWWON.IRR.9	87.10	41.19	18.47	69.08	42.30	20.27	71.20
X22FAWWON.IRR.68	86.58	39.09	15.93	64.11	41.55	19.59	69.93
X22FAWWON.IRR.95	89.54	36.56	13.39	57.89	40.27	18.33	67.05
X22FAWWON.IRR.26	95.24	43.24	18.90	72.09	43.26	20.23	72.42
X22FAWWON.IRR.18	92.38	42.30	17.79	69.82	42.80	19.61	71.41
X22FAWWON.IRR.32	97.20	40.95	16.26	66.49	42.29	19.09	70.13
X22FAWWON.IRR.54	82.68	34.60	15.06	57.64	38.27	18.71	65.11
X22FAWWON.SA.232	81.52	37.52	16.75	62.39	40.53	18.71	67.59
X22FAWWON.SA.249	91.04	39.71	17.39	66.18	41.85	20.40	70.96
X22FAWWON.SA.235	81.02	39.54	15.25	63.32	41.68	18.30	68.61
X22FAWWON.IRR.103	83.69	34.70	14.77	57.18	39.23	18.89	66.48
X22FAWWON.IRR.81	77.77	38.02	14.56	61.09	40.58	19.39	68.55
X22FAWWON.SA.281	84.89	42.47	17.59	69.92	42.62	19.47	71.00
X22FAWWON.IRR.93	86.22	38.29	15.31	62.07	40.24	18.81	67.48
X22FAWWON.SA.214	98.11	40.39	18.18	67.98	41.94	19.89	70.51
X22FAWWON.SA.243	78.07	37.18	15.29	60.81	40.42	18.71	67.52
X22FAWWON.SA.260	84.54	40.60	16.11	66.18	42.23	19.43	70.74
X22FAWWON.IRR.21	85.13	38.21	16.22	63.84	40.76	19.47	69.13
X22FAWWON.SA.225	82.66	39.13	16.54	64.70	41.07	18.75	68.30

X22FAWWON.IRR.86	89.77	41.39	14.80	64.90	42.60	19.25	70.58
X20FAWWON.SA.231	87.80	39.75	15.23	64.21	41.59	18.86	69.31
X21FAWWON.IRR.137	89.85	39.59	14.41	63.39	41.86	18.40	69.29
X22FAWWON.SA.294	85.45	39.51	15.60	64.04	41.41	18.57	68.69
X22FAWWON.SA.263	88.08	37.98	17.20	63.84	40.69	19.93	68.93
X22FAWWON.IRR.98	89.77	42.03	15.53	67.37	42.95	18.87	71.01
X22FAWWON.SA.262	92.74	39.84	15.76	64.14	41.85	18.52	68.95
X22FAWWON.IRR.66	86.25	39.36	15.40	64.00	40.65	18.85	68.15
X22FAWWON.IRR.31	92.29	44.10	17.28	71.39	44.13	19.41	72.60
X22FAWWON.IRR.111	83.23	43.11	16.18	69.03	43.24	19.78	71.93
X22FAWWON.IRR.57	86.47	41.86	15.21	66.67	42.69	19.32	71.09
X22FAWWON.IRR.49	89.91	42.54	17.29	70.12	42.73	19.91	71.89
X22FAWWON.IRR.79	87.94	36.64	14.63	59.87	40.28	19.21	68.23
X22FAWWON.IRR.60	80.38	43.00	15.89	68.48	42.92	18.82	70.68
X22FAWWON.IRR.55	87.32	39.54	16.30	64.87	41.57	19.65	69.98
X22FAWWON.IRR.19	99.02	42.20	15.68	66.68	42.78	18.52	69.91
X22FAWWON.IRR.70	86.72	36.50	14.48	58.89	39.60	18.26	66.08
X22FAWWON.SA.239	85.52	36.29	16.14	60.52	39.87	18.57	66.74
X22FAWWON.SA.248	86.52	37.97	15.77	62.38	40.41	18.36	67.29
X22FAWWON.SA.202	86.42	37.99	15.22	61.87	40.71	18.60	67.99
X22FAWWON.IRR.108	86.26	35.35	15.31	58.66	39.62	20.06	68.15
X22FAWWON.IRR.35	83.59	39.29	14.53	61.71	41.47	18.51	68.37
X22FAWWON.IRR.22	84.43	35.72	13.15	56.24	39.38	17.35	64.77
X22FAWWON.SA.218	82.80	35.64	14.89	59.18	38.99	18.18	65.67
X22FAWWON.SA.282	90.39	38.78	14.81	62.15	41.41	18.06	68.16
X22FAWWON.IRR.41	86.02	36.30	14.34	58.79	39.40	18.29	66.05
X22FAWWON.SA.230	91.05	37.49	15.97	62.16	40.51	18.62	67.73
X22FAWWON.IRR.23	83.23	38.06	13.77	60.39	41.00	17.87	67.52
X22FAWWON.IRR.20	95.89	40.74	15.46	65.40	42.20	18.63	69.61
X22FAWWON.SA.223	84.16	39.84	17.52	67.19	40.91	18.41	68.03
X22FAWWON.IRR.14	88.16	38.43	15.28	62.47	40.88	18.82	68.24

X22FAWWON.SA.253	88.67	42.46	16.99	69.36	42.95	19.00	71.08
X22FAWWON.IRR.8	88.22	41.19	16.05	66.67	42.16	19.08	70.26
X22FAWWON.IRR.83	90.15	37.97	14.65	61.31	40.17	17.88	66.64
X22FAWWON.SA.237	85.70	40.96	16.27	66.55	42.02	18.77	69.46
X22FAWWON.SA.258	84.63	34.36	14.88	57.57	38.41	17.61	64.29
X22FAWWON.IRR.42	87.98	40.34	16.88	66.93	41.21	19.16	69.24
X22FAWWON.IRR.25	89.32	39.98	16.65	66.20	41.34	19.62	69.72
X22FAWWON.IRR.34	83.72	39.87	15.31	63.80	42.00	18.67	69.37
X22FAWWON.IRR.27	87.22	42.43	16.14	68.29	42.83	18.87	70.67
X22FAWWON.SA.259	89.94	40.11	15.75	64.64	41.53	18.88	68.97
X22FAWWON.IRR.45	95.44	37.85	16.04	62.61	40.72	19.21	68.62
X22FAWWON.SA.231	80.60	38.22	15.56	62.22	40.42	18.35	67.17
X22FAWWON.IRR.73	87.21	37.31	14.91	60.84	40.41	18.43	67.50
X22FAWWON.SA.256	81.38	37.75	14.63	61.06	40.14	18.33	66.96
X22FAWWON.SA.274	88.49	39.19	16.00	64.39	41.06	18.81	68.56
X22FAWWON.IRR.51	97.44	40.05	17.09	65.71	42.08	20.02	70.66
X22FAWWON.SA.277	79.07	40.65	15.79	65.10	41.77	18.90	69.16
X22FAWWON.IRR.67	84.84	36.69	12.94	57.42	39.59	17.37	65.21
X22FAWWON.SA.265	87.03	36.12	15.18	59.22	39.66	18.44	66.43
X22FAWWON.SA.269	86.56	38.50	14.79	61.79	40.27	17.68	66.29
X22FAWWON.IRR.69	92.31	40.73	15.63	66.06	42.42	19.28	70.88
X22FAWWON.SA.250	83.20	38.11	16.63	63.06	40.39	18.93	67.52
X22FAWWON.IRR.52	81.56	35.61	14.10	57.83	39.48	18.41	66.26
X22FAWWON.SA.270	89.01	36.17	14.79	59.19	39.80	19.01	67.00
X22FAWWON.SA.211	89.56	38.49	16.88	64.44	40.66	19.29	68.50
X22FAWWON.IRR.33	93.81	39.87	14.38	62.58	41.53	17.72	67.75
X22FAWWON.IRR.7	91.36	42.71	16.24	68.14	43.12	19.01	71.15
X22FAWWON.SA.217	85.88	39.11	16.43	64.77	41.38	18.82	69.12
X22FAWWON.SA.273	88.39	36.30	15.74	60.57	39.32	18.82	66.45
X20FAWWON.IRR.100	91.64	40.45	14.85	64.13	42.20	19.05	69.91
X20FAWWON.IRR.106	90.53	37.78	17.00	63.80	40.88	20.26	69.80

X20FAWWON.IRR.11	91.33	39.19	16.12	64.36	40.68	18.87	68.21
X20FAWWON.IRR.114	80.87	40.06	15.04	64.02	41.98	18.88	69.72
X20FAWWON.IRR.115	88.59	38.55	15.36	62.74	41.11	18.90	68.83
X20FAWWON.IRR.118	85.62	38.96	15.62	63.75	41.85	19.00	69.87
X20FAWWON.IRR.12	91.34	35.04	16.86	59.98	38.99	19.13	66.31
X20FAWWON.IRR.13	92.27	38.71	14.36	61.27	41.31	18.37	68.16
X20FAWWON.IRR.143	90.93	41.25	15.88	66.88	42.10	18.55	69.73
X20FAWWON.IRR.15	92.64	36.68	15.33	60.33	39.81	19.42	67.71
X20FAWWON.IRR.18	85.93	38.14	15.77	62.67	40.92	19.21	68.82
X20FAWWON.IRR.19	93.87	39.58	15.63	64.18	41.66	18.74	69.23
X20FAWWON.IRR.21	91.24	40.47	15.93	65.54	41.81	18.42	68.95
X20FAWWON.IRR.22	93.19	40.95	16.04	66.24	42.19	19.11	70.16
X20FAWWON.IRR.23	94.15	41.06	16.40	66.56	42.40	19.25	70.60
X20FAWWON.IRR.29	96.04	42.45	16.70	68.81	43.04	19.60	71.69
X20FAWWON.IRR.31	89.41	35.40	15.28	59.09	39.18	18.62	66.37
X20FAWWON.IRR.32	87.48	39.68	15.11	64.02	40.84	18.56	68.09
X20FAWWON.IRR.36	89.76	40.02	15.68	65.11	41.71	19.76	70.39
X20FAWWON.IRR.37	84.26	36.56	14.18	59.09	40.08	19.51	68.20
X20FAWWON.IRR.38	91.35	38.71	14.42	61.34	41.56	19.61	69.67
X20FAWWON.IRR.39	90.77	41.72	16.39	67.77	42.25	18.98	70.17
X20FAWWON.IRR.40	92.96	39.80	15.08	63.64	41.34	18.31	68.23
X20FAWWON.IRR.41	89.00	41.91	16.87	68.81	42.38	19.59	71.04
X20FAWWON.IRR.42	95.63	41.07	16.08	66.65	42.51	19.74	71.25
X20FAWWON.IRR.44	95.25	39.57	14.90	62.87	41.60	18.13	68.20
X20FAWWON.IRR.45	90.39	39.10	15.57	63.24	41.26	18.58	68.54
X20FAWWON.IRR.46	92.79	39.65	15.12	63.34	41.61	18.34	68.43
X20FAWWON.IRR.49	87.11	36.09	16.34	61.23	39.23	20.44	68.28
X20FAWWON.IRR.55	84.16	36.79	14.75	59.44	40.11	18.57	67.06
X20FAWWON.IRR.56	94.54	37.07	15.99	61.72	40.10	18.89	67.66
X20FAWWON.IRR.57	93.43	36.73	15.36	60.65	40.55	19.49	68.72
X20FAWWON.IRR.59	87.82	35.59	15.93	60.61	39.40	19.10	67.17

X20FAWWON.IRR.7	84.76	36.35	14.41	59.20	39.89	18.34	66.83
X20FAWWON.IRR.74	92.09	38.22	17.75	65.12	41.14	19.37	69.19
X20FAWWON.IRR.86	86.25	40.05	14.71	63.57	41.77	18.54	69.08
X20FAWWON.IRR.87	84.48	37.53	14.33	60.37	40.48	18.31	67.45
X20FAWWON.IRR.88	86.89	40.82	15.60	65.48	42.07	18.80	69.62
X20FAWWON.IRR.9	101.31	38.95	16.90	64.84	40.92	19.65	69.32
X20FAWWON.IRR.95	86.53	36.75	16.37	61.82	40.25	19.64	68.63
X20FAWWON.IRR.97	81.30	34.71	15.50	58.16	39.24	19.79	67.41
X20FAWWON.IRR.98	90.52	40.99	16.67	67.40	42.29	19.66	70.85
X20FAWWON.SA.206	82.31	41.60	15.22	66.23	42.10	18.41	69.36
X20FAWWON.SA.209	93.83	36.89	16.03	61.29	40.02	19.12	67.66
X20FAWWON.SA.210	94.96	36.76	14.95	60.66	39.58	18.36	66.58
X20FAWWON.SA.212	91.39	38.36	16.15	63.38	40.67	18.90	68.20
X20FAWWON.SA.213	90.37	31.95	16.12	55.23	37.62	19.20	64.96
X20FAWWON.SA.214	93.00	38.98	17.91	66.05	41.42	19.65	69.87
X20FAWWON.SA.215	91.94	38.13	16.52	63.23	40.63	19.25	68.41
X20FAWWON.SA.222	97.61	37.89	15.50	61.96	40.76	18.80	68.24
X20FAWWON.SA.223	88.43	41.06	14.26	63.80	42.49	18.50	69.56
X20FAWWON.SA.224	90.75	41.20	16.60	67.23	41.88	18.58	69.07
X20FAWWON.SA.226	86.58	40.07	14.67	63.44	41.83	18.65	69.02
X20FAWWON.SA.227	97.52	39.19	16.48	65.02	41.23	19.06	68.98
X20FAWWON.SA.232	95.32	42.29	15.89	67.43	42.55	18.18	69.49
X20FAWWON.SA.236	90.20	41.16	18.30	69.30	42.13	19.93	70.94
X20FAWWON.SA.237	93.47	44.80	18.35	73.35	44.49	19.86	73.69
X20FAWWON.SA.241	97.92	38.23	16.30	63.57	40.91	19.58	69.20
X20FAWWON.SA.243	96.96	40.13	17.04	66.63	42.19	19.90	71.00
X20FAWWON.SA.244	88.75	38.33	15.49	62.90	40.83	18.96	68.65
X20FAWWON.SA.249	90.66	40.92	18.38	68.68	41.92	20.36	70.78
X20FAWWON.SA.251	80.35	40.91	16.79	67.15	42.06	19.99	70.74
X20FAWWON.SA.252	83.59	38.99	17.20	65.18	41.02	19.89	69.47
X20FAWWON.SA.254	86.25	36.85	15.76	61.08	40.23	19.26	68.13

X20FAWWON.SA.256	90.12	38.46	15.09	62.07	41.03	19.16	68.77
X20FAWWON.SA.257	90.10	37.18	16.66	63.26	40.05	19.02	67.72
X20FAWWON.SA.258	86.69	39.12	16.00	64.55	41.21	19.39	69.62
X20FAWWON.SA.259	87.10	39.60	16.67	65.76	41.37	18.92	68.97
X21FAWWON.IRR.103	85.18	29.90	15.28	52.73	36.32	19.04	63.57
X21FAWWON.IRR.14	80.11	33.50	15.34	57.19	37.54	18.33	64.08
X21FAWWON.IRR.141	87.39	41.01	15.70	66.22	42.50	19.66	71.30
X21FAWWON.IRR.143	92.44	40.96	16.57	66.60	42.40	19.02	70.44
X21FAWWON.IRR.144	85.03	33.74	15.82	57.22	38.60	18.77	65.65
X21FAWWON.IRR.150	89.25	39.54	13.69	61.22	41.98	19.21	69.66
X21FAWWON.IRR.163	91.33	35.59	16.15	60.68	39.71	19.20	67.64
X21FAWWON.IRR.43	91.53	40.20	15.77	65.13	41.62	18.97	69.25
X21FAWWON.IRR.50	94.00	36.11	13.63	57.73	40.00	18.24	66.67
X21FAWWON.IRR.62	85.05	38.29	14.88	62.13	40.12	18.56	67.27
X21FAWWON.IRR.7	90.69	38.05	14.22	60.49	40.76	18.61	67.85
X21FAWWON.IRR.75	91.15	40.44	15.03	64.32	41.88	18.86	69.51
X21FAWWON.IRR.83	94.79	38.27	16.03	62.92	41.32	19.82	69.91
X21FAWWON.IRR.9	83.88	39.49	15.17	63.26	41.26	18.72	68.57
X21FAWWON.IRR.95	95.05	41.88	15.81	67.41	42.90	19.39	71.52
X21FAWWON.SA.202	84.02	38.50	15.45	62.64	41.01	18.76	68.49
X21FAWWON.SA.207	93.23	43.67	15.77	69.23	43.32	18.68	70.84
X21FAWWON.SA.210	101.45	38.53	16.39	63.61	41.33	18.84	68.76
X21FAWWON.SA.211	89.60	38.78	15.60	62.73	41.49	18.50	68.62
X21FAWWON.SA.227	77.45	33.85	14.05	55.75	38.48	18.20	64.97
X21FAWWON.SA.228	91.33	39.51	17.72	65.62	41.77	19.61	70.05
X21FAWWON.SA.234	95.25	38.47	15.48	62.73	40.63	18.48	67.52
X21FAWWON.SA.243	89.27	40.15	15.52	64.63	41.86	19.28	70.03
X21FAWWON.SA.247	92.17	40.54	14.91	64.98	42.40	19.11	70.77
X21FAWWON.SA.261	93.71	37.21	15.66	60.93	40.65	19.02	68.04
X21FAWWON.SA.281	86.43	39.90	15.70	64.72	40.99	18.64	68.33
X21FAWWON.SA.286	87.39	38.40	14.98	61.88	41.36	19.46	69.29

X21FAWWON.SA.287	92.12	36.95	15.83	61.21	39.96	19.30	67.74
X21FAWWON.SA.292	97.44	39.00	15.15	63.08	41.30	18.91	69.17
Snowmass	93.09	40.00	15.23	64.52	41.23	17.98	67.92
Ripper	97.53	43.46	15.02	68.21	43.58	18.63	71.30
Antero	98.34	41.74	15.70	66.88	43.05	19.00	71.15
Denali	95.78	41.06	15.83	66.34	42.80	19.46	71.41
Byrd	99.21	40.55	15.60	65.56	42.17	18.49	69.58

Supplemental Table S5.15. Mean normalized difference vegetation indice (NDVI) values for Fort Collins 2016.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
X22FAWWON.IRR.85	0.51	0.38	0.44	0.56	0.42	0.54
X22FAWWON.IRR.53	0.52	0.42	0.47	0.58	0.44	0.56
X22FAWWON.IRR.87	0.59	0.43	0.51	0.61	0.45	0.59
X22FAWWON.IRR.71	0.59	0.44	0.51	0.61	0.45	0.58
X22FAWWON.IRR.48	0.55	0.46	0.51	0.59	0.46	0.58
X22FAWWON.IRR.10	0.58	0.48	0.53	0.60	0.45	0.58
X22FAWWON.SA.221	0.60	0.42	0.51	0.62	0.43	0.58
X22FAWWON.IRR.9	0.61	0.55	0.58	0.61	0.48	0.60
X22FAWWON.IRR.68	0.57	0.45	0.51	0.61	0.46	0.59
X22FAWWON.IRR.95	0.54	0.41	0.47	0.59	0.43	0.56
X22FAWWON.IRR.26	0.64	0.53	0.58	0.63	0.47	0.61
X22FAWWON.IRR.18	0.62	0.49	0.56	0.61	0.45	0.59
X22FAWWON.IRR.32	0.61	0.48	0.54	0.62	0.45	0.59
X22FAWWON.IRR.54	0.54	0.44	0.49	0.57	0.45	0.56
X22FAWWON.SA.232	0.55	0.46	0.51	0.58	0.43	0.56
X22FAWWON.SA.249	0.58	0.50	0.54	0.61	0.48	0.60
X22FAWWON.SA.235	0.56	0.43	0.50	0.60	0.43	0.57
X22FAWWON.IRR.103	0.51	0.44	0.47	0.57	0.45	0.56
X22FAWWON.IRR.81	0.55	0.40	0.48	0.58	0.45	0.57
X22FAWWON.SA.281	0.62	0.50	0.56	0.62	0.45	0.59
X22FAWWON.IRR.93	0.56	0.42	0.49	0.58	0.43	0.56
X22FAWWON.SA.214	0.60	0.52	0.56	0.61	0.47	0.60
X22FAWWON.SA.243	0.54	0.43	0.49	0.58	0.44	0.56
X22FAWWON.SA.260	0.59	0.45	0.52	0.61	0.45	0.59
X22FAWWON.IRR.21	0.56	0.47	0.52	0.59	0.46	0.58
X22FAWWON.SA.225	0.58	0.49	0.53	0.60	0.45	0.58
X22FAWWON.IRR.86	0.59	0.41	0.50	0.61	0.45	0.59

X20FAWWON.SA.231	0.59	0.44	0.52	0.61	0.44	0.58
X21FAWWON.IRR.137	0.58	0.42	0.51	0.61	0.44	0.58
X22FAWWON.SA.294	0.59	0.44	0.52	0.61	0.44	0.58
X22FAWWON.SA.263	0.56	0.50	0.53	0.59	0.47	0.59
X22FAWWON.IRR.98	0.63	0.47	0.55	0.63	0.45	0.60
X22FAWWON.SA.262	0.58	0.43	0.50	0.60	0.43	0.57
X22FAWWON.IRR.66	0.58	0.45	0.52	0.59	0.45	0.57
X22FAWWON.IRR.31	0.63	0.48	0.56	0.63	0.45	0.60
X22FAWWON.IRR.111	0.61	0.45	0.54	0.62	0.46	0.59
X22FAWWON.IRR.57	0.61	0.44	0.53	0.62	0.45	0.59
X22FAWWON.IRR.49	0.61	0.47	0.54	0.61	0.46	0.59
X22FAWWON.IRR.79	0.53	0.43	0.47	0.58	0.45	0.57
X22FAWWON.IRR.60	0.62	0.45	0.54	0.61	0.44	0.59
X22FAWWON.IRR.55	0.58	0.46	0.52	0.61	0.46	0.59
X22FAWWON.IRR.19	0.62	0.44	0.53	0.62	0.44	0.59
X22FAWWON.IRR.70	0.54	0.42	0.48	0.58	0.43	0.56
X22FAWWON.SA.239	0.55	0.46	0.50	0.59	0.43	0.57
X22FAWWON.SA.248	0.56	0.46	0.51	0.59	0.44	0.57
X22FAWWON.SA.202	0.55	0.43	0.49	0.59	0.44	0.57
X22FAWWON.IRR.108	0.51	0.43	0.47	0.57	0.47	0.58
X22FAWWON.IRR.35	0.55	0.42	0.49	0.59	0.44	0.57
X22FAWWON.IRR.22	0.53	0.37	0.45	0.58	0.41	0.55
X22FAWWON.SA.218	0.52	0.41	0.46	0.56	0.42	0.55
X22FAWWON.SA.282	0.57	0.42	0.49	0.60	0.42	0.57
X22FAWWON.IRR.41	0.54	0.42	0.48	0.58	0.43	0.56
X22FAWWON.SA.230	0.55	0.44	0.50	0.59	0.44	0.57
X22FAWWON.IRR.23	0.54	0.40	0.47	0.59	0.42	0.56
X22FAWWON.IRR.20	0.60	0.45	0.52	0.62	0.44	0.58
X22FAWWON.SA.223	0.59	0.49	0.54	0.59	0.43	0.57
X22FAWWON.IRR.14	0.56	0.42	0.49	0.59	0.44	0.57
X22FAWWON.SA.253	0.61	0.46	0.54	0.61	0.43	0.58

X22FAWWON.IRR.8	0.59	0.46	0.53	0.61	0.45	0.58
X22FAWWON.IRR.83	0.55	0.41	0.48	0.58	0.42	0.55
X22FAWWON.SA.237	0.58	0.46	0.52	0.60	0.44	0.58
X22FAWWON.SA.258	0.52	0.43	0.47	0.57	0.41	0.54
X22FAWWON.IRR.42	0.59	0.48	0.53	0.60	0.45	0.58
X22FAWWON.IRR.25	0.60	0.49	0.55	0.61	0.46	0.59
X22FAWWON.IRR.34	0.59	0.44	0.51	0.61	0.44	0.58
X22FAWWON.IRR.27	0.62	0.49	0.56	0.62	0.45	0.59
X22FAWWON.SA.259	0.58	0.44	0.51	0.59	0.44	0.57
X22FAWWON.IRR.45	0.55	0.45	0.50	0.59	0.45	0.58
X22FAWWON.SA.231	0.54	0.43	0.49	0.58	0.43	0.56
X22FAWWON.IRR.73	0.54	0.42	0.48	0.58	0.43	0.56
X22FAWWON.SA.256	0.54	0.42	0.48	0.58	0.43	0.56
X22FAWWON.SA.274	0.59	0.45	0.52	0.60	0.44	0.58
X22FAWWON.IRR.51	0.58	0.48	0.53	0.61	0.47	0.59
X22FAWWON.SA.277	0.59	0.44	0.52	0.60	0.44	0.58
X22FAWWON.IRR.67	0.52	0.37	0.44	0.57	0.41	0.54
X22FAWWON.SA.265	0.51	0.42	0.47	0.57	0.43	0.55
X22FAWWON.SA.269	0.55	0.40	0.47	0.58	0.41	0.55
X22FAWWON.IRR.69	0.60	0.45	0.53	0.62	0.45	0.59
X22FAWWON.SA.250	0.57	0.47	0.52	0.59	0.44	0.57
X22FAWWON.IRR.52	0.52	0.40	0.46	0.57	0.43	0.56
X22FAWWON.SA.270	0.54	0.43	0.49	0.59	0.45	0.57
X22FAWWON.SA.211	0.57	0.48	0.53	0.59	0.45	0.58
X22FAWWON.IRR.33	0.57	0.41	0.49	0.59	0.41	0.56
X22FAWWON.IRR.7	0.61	0.45	0.53	0.62	0.44	0.59
X22FAWWON.SA.217	0.58	0.47	0.52	0.61	0.44	0.58
X22FAWWON.SA.273	0.53	0.43	0.48	0.56	0.43	0.55
X20FAWWON.IRR.100	0.58	0.42	0.50	0.61	0.45	0.58
X20FAWWON.IRR.106	0.56	0.47	0.51	0.60	0.47	0.59
X20FAWWON.IRR.11	0.56	0.45	0.51	0.59	0.44	0.57

X20FAWWON.IRR.114	0.57	0.44	0.50	0.60	0.45	0.58
X20FAWWON.IRR.115	0.57	0.45	0.51	0.60	0.45	0.58
X20FAWWON.IRR.118	0.57	0.43	0.50	0.60	0.44	0.58
X20FAWWON.IRR.12	0.49	0.48	0.48	0.55	0.44	0.55
X20FAWWON.IRR.13	0.58	0.41	0.49	0.61	0.43	0.57
X20FAWWON.IRR.143	0.61	0.45	0.53	0.61	0.43	0.58
X20FAWWON.IRR.15	0.53	0.43	0.48	0.58	0.45	0.57
X20FAWWON.IRR.18	0.57	0.46	0.52	0.60	0.45	0.58
X20FAWWON.IRR.19	0.58	0.45	0.52	0.61	0.45	0.58
X20FAWWON.IRR.21	0.60	0.46	0.53	0.61	0.44	0.58
X20FAWWON.IRR.22	0.60	0.46	0.53	0.61	0.45	0.59
X20FAWWON.IRR.23	0.61	0.47	0.54	0.62	0.45	0.59
X20FAWWON.IRR.29	0.62	0.48	0.55	0.62	0.46	0.60
X20FAWWON.IRR.31	0.54	0.44	0.49	0.58	0.44	0.56
X20FAWWON.IRR.32	0.57	0.42	0.50	0.59	0.43	0.57
X20FAWWON.IRR.36	0.59	0.46	0.52	0.61	0.47	0.60
X20FAWWON.IRR.37	0.54	0.42	0.48	0.58	0.46	0.58
X20FAWWON.IRR.38	0.57	0.42	0.50	0.60	0.46	0.59
X20FAWWON.IRR.39	0.60	0.48	0.54	0.61	0.45	0.58
X20FAWWON.IRR.40	0.58	0.43	0.51	0.60	0.43	0.57
X20FAWWON.IRR.41	0.60	0.47	0.54	0.61	0.46	0.59
X20FAWWON.IRR.42	0.61	0.46	0.54	0.62	0.47	0.60
X20FAWWON.IRR.44	0.58	0.42	0.50	0.60	0.42	0.57
X20FAWWON.IRR.45	0.56	0.44	0.50	0.59	0.44	0.57
X20FAWWON.IRR.46	0.58	0.44	0.51	0.60	0.43	0.57
X20FAWWON.IRR.49	0.52	0.45	0.49	0.57	0.48	0.58
X20FAWWON.IRR.55	0.53	0.42	0.47	0.57	0.43	0.56
X20FAWWON.IRR.56	0.56	0.45	0.50	0.59	0.43	0.57
X20FAWWON.IRR.57	0.56	0.43	0.49	0.60	0.46	0.58
X20FAWWON.IRR.59	0.53	0.45	0.49	0.58	0.45	0.57
X20FAWWON.IRR.7	0.54	0.43	0.48	0.58	0.44	0.56

X20FAWWON.IRR.74	0.57	0.49	0.53	0.60	0.45	0.58
X20FAWWON.IRR.86	0.58	0.41	0.50	0.61	0.43	0.57
X20FAWWON.IRR.87	0.55	0.42	0.49	0.59	0.43	0.57
X20FAWWON.IRR.88	0.59	0.43	0.51	0.61	0.44	0.58
X20FAWWON.IRR.9	0.56	0.46	0.51	0.59	0.46	0.58
X20FAWWON.IRR.95	0.53	0.46	0.49	0.58	0.46	0.58
X20FAWWON.IRR.97	0.51	0.45	0.48	0.57	0.46	0.57
X20FAWWON.IRR.98	0.62	0.47	0.55	0.62	0.46	0.60
X20FAWWON.SA.206	0.61	0.44	0.53	0.61	0.43	0.58
X20FAWWON.SA.209	0.55	0.46	0.50	0.59	0.44	0.57
X20FAWWON.SA.210	0.54	0.43	0.49	0.58	0.43	0.56
X20FAWWON.SA.212	0.57	0.45	0.51	0.59	0.44	0.57
X20FAWWON.SA.213	0.48	0.45	0.47	0.56	0.45	0.56
X20FAWWON.SA.214	0.57	0.50	0.53	0.60	0.46	0.59
X20FAWWON.SA.215	0.54	0.47	0.50	0.58	0.45	0.57
X20FAWWON.SA.222	0.53	0.43	0.48	0.58	0.44	0.57
X20FAWWON.SA.223	0.59	0.41	0.50	0.61	0.43	0.58
X20FAWWON.SA.224	0.60	0.47	0.54	0.60	0.44	0.58
X20FAWWON.SA.226	0.58	0.43	0.51	0.60	0.44	0.58
X20FAWWON.SA.227	0.58	0.47	0.53	0.60	0.45	0.58
X20FAWWON.SA.232	0.62	0.46	0.54	0.62	0.43	0.58
X20FAWWON.SA.236	0.61	0.52	0.57	0.61	0.47	0.60
X20FAWWON.SA.237	0.64	0.51	0.58	0.64	0.46	0.61
X20FAWWON.SA.241	0.56	0.47	0.51	0.60	0.46	0.58
X20FAWWON.SA.243	0.59	0.49	0.54	0.61	0.47	0.60
X20FAWWON.SA.244	0.56	0.43	0.50	0.60	0.44	0.58
X20FAWWON.SA.249	0.61	0.53	0.57	0.61	0.48	0.60
X20FAWWON.SA.251	0.61	0.47	0.54	0.61	0.47	0.60
X20FAWWON.SA.252	0.57	0.49	0.53	0.60	0.47	0.59
X20FAWWON.SA.254	0.54	0.44	0.49	0.59	0.45	0.58
X20FAWWON.SA.256	0.57	0.42	0.50	0.60	0.44	0.57

X20FAWWON.SA.257	0.56	0.46	0.51	0.59	0.44	0.57
X20FAWWON.SA.258	0.58	0.46	0.52	0.60	0.45	0.58
X20FAWWON.SA.259	0.58	0.49	0.53	0.60	0.45	0.58
X21FAWWON.IRR.103	0.45	0.42	0.43	0.54	0.44	0.54
X21FAWWON.IRR.14	0.50	0.43	0.46	0.55	0.43	0.54
X21FAWWON.IRR.141	0.59	0.44	0.52	0.61	0.46	0.59
X21FAWWON.IRR.143	0.59	0.48	0.53	0.61	0.45	0.59
X21FAWWON.IRR.144	0.49	0.45	0.47	0.56	0.44	0.56
X21FAWWON.IRR.150	0.55	0.40	0.47	0.60	0.45	0.58
X21FAWWON.IRR.163	0.53	0.46	0.49	0.58	0.45	0.57
X21FAWWON.IRR.43	0.58	0.46	0.52	0.60	0.45	0.58
X21FAWWON.IRR.50	0.54	0.37	0.45	0.58	0.42	0.56
X21FAWWON.IRR.62	0.56	0.42	0.49	0.58	0.43	0.56
X21FAWWON.IRR.7	0.55	0.41	0.48	0.59	0.44	0.57
X21FAWWON.IRR.75	0.59	0.42	0.50	0.60	0.44	0.57
X21FAWWON.IRR.83	0.56	0.45	0.51	0.60	0.46	0.59
X21FAWWON.IRR.9	0.57	0.43	0.50	0.60	0.44	0.58
X21FAWWON.IRR.95	0.61	0.46	0.54	0.62	0.46	0.60
X21FAWWON.SA.202	0.56	0.44	0.50	0.59	0.44	0.57
X21FAWWON.SA.207	0.63	0.46	0.55	0.62	0.44	0.59
X21FAWWON.SA.210	0.55	0.44	0.50	0.59	0.43	0.57
X21FAWWON.SA.211	0.56	0.43	0.50	0.60	0.43	0.57
X21FAWWON.SA.227	0.51	0.40	0.45	0.57	0.42	0.55
X21FAWWON.SA.228	0.57	0.48	0.53	0.61	0.45	0.59
X21FAWWON.SA.234	0.57	0.45	0.51	0.60	0.43	0.57
X21FAWWON.SA.243	0.59	0.43	0.51	0.61	0.45	0.58
X21FAWWON.SA.247	0.59	0.41	0.50	0.61	0.44	0.58
X21FAWWON.SA.261	0.56	0.46	0.51	0.60	0.45	0.58
X21FAWWON.SA.281	0.58	0.46	0.52	0.59	0.44	0.57
X21FAWWON.SA.286	0.57	0.45	0.51	0.60	0.47	0.59
X21FAWWON.SA.287	0.53	0.45	0.49	0.58	0.45	0.57

X21FAWWON.SA.292	0.56	0.43	0.49	0.59	0.44	0.58
Snowmass	0.59	0.43	0.51	0.60	0.42	0.57
Ripper	0.62	0.43	0.52	0.62	0.44	0.58
Antero	0.60	0.44	0.52	0.62	0.44	0.59
Denali	0.60	0.46	0.53	0.62	0.46	0.60
Byrd	0.60	0.45	0.53	0.62	0.43	0.58

Supplemental Table S5.16. Grain yield and normalized difference vegetation indice (NDVI) values for area under the curve (AUC) in Julesburg 2016.

		AUC					
ID	Yield	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
22 FAWWON-IRR-85	53.71	42.21	13.50	63.10	50.11	17.81	74.88
22 FAWWON-IRR-53	74.08	53.30	13.88	75.22	55.09	17.93	80.83
22 FAWWON-IRR-87	63.91	50.24	14.75	73.31	53.52	18.72	79.33
22 FAWWON-IRR-71	72.10	48.70	14.80	71.77	53.04	18.17	78.86
22 FAWWON-IRR-48	73.50	49.29	14.58	71.92	53.29	18.10	78.48
22 FAWWON-IRR-10	82.14	54.62	14.90	78.24	55.85	17.79	81.25
22 FAWWON-SA-221	64.74	48.82	13.96	70.28	53.55	17.30	78.67
22 FAWWON-IRR-9	75.59	56.86	15.90	83.15	57.41	17.96	83.98
22 FAWWON-IRR-68	67.45	48.77	14.07	70.86	53.08	17.76	78.16
22 FAWWON-IRR-95	68.80	46.34	13.65	67.11	52.19	17.93	77.24
22 FAWWON-IRR-26	76.49	54.63	15.56	79.04	55.87	17.71	81.58
22 FAWWON-IRR-18	73.32	54.15	14.89	77.63	56.25	18.32	81.94
22 FAWWON-IRR-32	76.22	53.53	15.14	76.87	55.25	18.02	80.72
22 FAWWON-SA-232	71.27	51.85	14.50	75.06	54.95	17.53	80.20
22 FAWWON-SA-249	74.48	52.26	15.23	76.43	54.97	18.44	81.54
22 FAWWON-SA-235	66.33	47.86	14.73	70.93	52.72	18.41	78.17
22 FAWWON-IRR-103	68.33	51.29	14.34	73.42	54.17	17.89	79.46
22 FAWWON-SA-281	69.59	50.67	15.25	74.41	53.58	17.96	78.93
22 FAWWON-IRR-93	69.40	48.62	14.18	70.68	52.61	17.44	77.52
22 FAWWON-SA-214	77.74	54.07	15.85	79.39	56.27	18.57	82.78
22 FAWWON-SA-243	65.40	49.19	15.33	73.36	53.54	17.74	79.23
22 FAWWON-SA-260	70.77	51.34	14.48	74.55	54.76	18.66	80.62
22 FAWWON-IRR-21	69.31	47.79	15.05	72.07	53.36	18.62	79.69
22 FAWWON-SA-225	59.89	51.42	14.99	75.36	54.33	17.70	79.59
22 FAWWON-IRR-86	66.51	49.00	13.40	70.35	53.53	18.01	78.81
20FAWWON-SA-231	71.09	49.48	14.14	71.81	53.29	17.88	78.60

21FAWWON-IRR-137	88.15	54.55	14.44	78.02	56.36	17.84	82.28
22 FAWWON-SA-294	60.81	51.66	15.33	76.26	54.08	18.51	80.24
22 FAWWON-SA-263	66.80	51.36	15.29	75.43	54.32	18.21	79.95
22 FAWWON-IRR-98	84.89	53.47	14.53	76.40	55.27	18.26	80.99
22 FAWWON-SA-262	78.42	51.93	14.61	74.39	54.62	18.02	79.89
22 FAWWON-IRR-66	61.55	49.64	14.65	72.61	53.32	17.90	78.45
22 FAWWON-IRR-31	64.25	52.21	14.34	74.56	54.65	17.81	79.67
22 FAWWON-IRR-111	71.40	53.10	15.11	77.57	55.91	18.74	82.34
22 FAWWON-IRR-57	86.61	56.77	15.13	81.10	57.01	18.56	83.25
22 FAWWON-IRR-49	81.92	58.08	15.40	82.96	57.63	18.72	84.16
22 FAWWON-IRR-79	80.19	51.65	14.86	74.98	54.79	18.72	80.98
22 FAWWON-IRR-60	69.06	52.54	14.13	75.03	54.40	17.34	79.22
22 FAWWON-IRR-55	71.36	46.60	15.30	70.70	52.11	18.40	78.26
22 FAWWON-IRR-19	79.99	54.46	14.45	76.39	55.28	17.58	79.79
22 FAWWON-IRR-70	66.91	48.80	15.01	72.82	52.91	18.31	78.75
22 FAWWON-SA-239	72.61	52.52	15.77	78.25	55.46	18.74	81.95
22 FAWWON-SA-248	69.38	49.37	14.83	73.17	53.46	18.13	78.84
22 FAWWON-SA-202	69.76	51.03	14.21	73.14	54.32	18.02	79.44
22 FAWWON-IRR-108	71.94	48.98	14.58	71.73	54.07	18.29	80.35
22 FAWWON-IRR-35	69.18	51.49	14.40	74.08	54.70	18.28	80.10
22 FAWWON-IRR-22	60.08	46.92	14.34	69.00	51.82	17.33	76.19
22 FAWWON-SA-282	64.90	49.05	14.23	71.29	53.91	17.51	79.23
22 FAWWON-IRR-41	68.99	46.53	14.56	69.21	51.49	17.39	76.43
22 FAWWON-SA-230	59.49	48.92	13.83	69.97	52.73	17.77	77.19
22 FAWWON-IRR-23	60.91	50.82	14.48	73.43	54.34	17.80	79.53
22 FAWWON-IRR-20	78.60	55.02	14.12	77.49	56.28	17.58	81.50
22 FAWWON-SA-223	56.87	52.67	15.07	76.37	54.68	18.33	79.74
22 FAWWON-IRR-14	75.27	49.72	14.48	72.67	54.12	17.92	79.72
22 FAWWON-SA-253	75.34	51.47	14.72	75.24	54.69	18.19	80.59
22 FAWWON-IRR-8	77.88	53.39	14.61	76.17	55.12	18.05	80.37
22 FAWWON-SA-237	74.02	53.60	15.52	78.67	55.86	18.29	81.85

22 FAWWON-IRR-42	76.54	52.82	15.35	77.72	54.35	18.25	80.35
22 FAWWON-IRR-25	74.18	52.07	15.05	76.01	54.43	18.25	79.84
22 FAWWON-IRR-34	66.75	49.14	14.72	72.20	53.47	17.78	78.85
22 FAWWON-IRR-27	78.17	53.87	15.27	78.16	55.44	17.93	80.86
22 FAWWON-SA-259	70.75	49.65	14.66	73.12	53.41	18.20	79.38
22 FAWWON-IRR-45	76.49	49.11	14.48	71.71	53.56	17.95	79.21
22 FAWWON-SA-231	66.24	50.37	14.98	74.31	53.62	17.53	79.06
22 FAWWON-SA-274	67.99	50.60	14.12	72.24	53.29	17.58	77.86
22 FAWWON-IRR-51	81.07	52.60	15.79	77.38	55.42	19.37	82.39
22 FAWWON-SA-277	60.39	49.15	14.21	70.80	53.08	17.36	77.94
22 FAWWON-IRR-84	59.48	43.49	14.38	65.86	50.19	17.79	75.33
22 FAWWON-SA-265	70.36	51.08	15.17	74.96	54.20	17.89	79.67
22 FAWWON-SA-269	75.88	46.51	14.50	69.60	51.49	17.81	76.54
22 FAWWON-IRR-69	83.17	58.28	15.09	82.84	58.66	18.99	85.83
22 FAWWON-SA-250	60.97	48.20	14.62	71.31	52.77	17.93	77.96
22 FAWWON-IRR-52	79.25	50.34	14.76	73.55	54.26	18.31	80.39
22 FAWWON-SA-270	68.10	51.29	15.06	75.36	54.20	19.05	80.70
22 FAWWON-SA-211	66.74	53.59	14.92	77.27	55.34	17.90	80.58
22 FAWWON-IRR-33	81.40	55.62	14.61	78.29	55.79	17.72	80.73
22 FAWWON-IRR-7	81.08	55.86	15.15	80.03	56.74	18.38	82.62
22 FAWWON-SA-217	63.21	49.24	14.80	72.00	53.62	17.58	78.36
22 FAWWON-SA-273	63.85	49.17	14.38	72.30	52.90	17.77	78.03
20FAWWON-IRR-100	79.11	52.16	14.07	74.50	55.07	18.02	80.56
20FAWWON-IRR-106	75.86	54.12	15.45	78.86	56.11	18.73	83.00
20FAWWON-IRR-11	72.54	53.40	14.33	76.24	54.93	18.14	80.42
20FAWWON-IRR-114	77.32	52.86	15.81	78.30	55.86	18.91	82.86
20FAWWON-IRR-115	81.93	52.56	14.56	75.59	55.36	18.10	81.18
20FAWWON-IRR-118	77.84	56.90	14.76	80.75	58.03	18.62	84.42
20FAWWON-IRR-12	74.25	51.07	14.34	74.24	54.38	17.90	79.97
20FAWWON-IRR-13	74.21	51.16	14.05	73.33	54.15	17.94	79.67
20FAWWON-IRR-143	83.32	50.26	15.17	74.04	53.94	17.93	79.62

20FAWWON-IRR-15	82.53	48.16	14.35	70.71	52.64	18.83	78.64
20FAWWON-IRR-18	79.23	51.12	15.04	74.95	54.67	18.13	80.83
20FAWWON-IRR-19	78.15	49.40	14.38	71.48	53.67	17.88	78.81
20FAWWON-IRR-21	66.07	49.20	14.25	71.70	53.03	17.71	77.93
20FAWWON-IRR-22	77.24	51.32	15.08	75.14	54.11	18.27	79.88
20FAWWON-IRR-23	81.53	53.50	15.06	78.13	55.87	18.00	81.93
20FAWWON-IRR-29	68.30	51.06	14.85	74.56	54.36	18.32	80.19
20FAWWON-IRR-31	77.84	47.59	14.76	70.90	52.46	18.66	78.38
20FAWWON-IRR-36	78.94	57.96	15.06	81.87	57.45	19.05	83.99
20FAWWON-IRR-37	81.75	54.13	15.42	78.87	56.22	19.61	84.00
20FAWWON-IRR-38	78.40	53.84	14.44	76.11	55.81	18.71	82.31
20FAWWON-IRR-39	81.06	52.73	15.61	77.25	54.98	18.48	81.15
20FAWWON-IRR-40	80.34	52.01	14.56	74.50	54.39	17.92	79.09
20FAWWON-IRR-41	69.93	51.90	15.25	76.06	54.62	18.56	80.81
20FAWWON-IRR-42	75.30	49.67	14.46	72.04	53.36	18.40	79.13
20FAWWON-IRR-44	81.06	55.03	14.92	79.02	56.90	18.68	83.18
20FAWWON-IRR-45	75.26	49.56	14.25	71.91	53.63	17.81	78.92
20FAWWON-IRR-46	74.79	50.72	14.65	73.94	54.64	17.73	79.77
20FAWWON-IRR-49	66.74	46.74	15.06	70.06	51.96	19.27	78.47
20FAWWON-IRR-55	69.77	51.54	14.36	74.06	54.59	17.93	79.99
20FAWWON-IRR-56	79.51	50.83	14.87	74.40	54.50	18.64	80.59
20FAWWON-IRR-57	79.19	50.64	14.17	72.82	54.98	18.42	80.62
20FAWWON-IRR-59	72.44	49.78	14.68	73.17	54.03	18.08	79.60
20FAWWON-IRR-7	74.39	49.49	14.34	71.86	53.29	17.83	78.45
20FAWWON-IRR-74	69.79	54.60	15.87	79.10	56.04	18.10	81.60
20FAWWON-IRR-86	78.24	53.83	14.52	76.61	55.66	17.87	81.01
20FAWWON-IRR-87	70.77	48.92	14.24	71.39	53.45	17.83	78.77
20FAWWON-IRR-88	71.82	54.31	14.68	77.77	55.39	18.30	81.23
20FAWWON-IRR-9	78.93	48.68	15.20	72.33	52.61	18.48	78.78
20FAWWON-IRR-95	85.45	51.97	14.88	75.85	55.23	18.09	81.48
20FAWWON-IRR-97	80.41	47.44	14.93	70.88	53.32	18.96	80.01

20FAWWON-IRR-98	76.51	51.54	15.50	76.33	54.76	18.41	81.38
20FAWWON-SA-206	74.01	53.51	14.29	75.94	55.20	17.59	80.37
20FAWWON-SA-209	73.27	51.90	14.95	75.87	54.84	18.25	80.92
20FAWWON-SA-210	75.45	45.69	14.94	69.42	51.07	18.40	76.62
20FAWWON-SA-212	67.96	50.03	14.36	73.58	53.61	17.95	78.94
20FAWWON-SA-213	57.18	45.18	14.05	66.64	50.56	17.47	75.01
20FAWWON-SA-214	79.00	54.25	15.47	78.59	56.01	18.43	81.96
20FAWWON-SA-215	73.16	55.91	14.98	80.65	56.94	17.99	83.00
20FAWWON-SA-222	78.92	53.12	14.36	75.12	55.19	17.92	80.49
20FAWWON-SA-223	65.70	52.15	13.50	73.40	54.65	18.07	79.42
20FAWWON-SA-224	65.94	52.49	13.86	74.48	54.11	17.17	78.26
20FAWWON-SA-226	72.33	53.82	13.98	76.05	55.62	17.97	80.82
20FAWWON-SA-227	75.69	53.93	14.18	76.40	55.45	18.22	80.46
20FAWWON-SA-232	75.18	54.74	14.69	77.36	55.15	17.06	79.45
20FAWWON-SA-236	75.11	55.31	16.09	80.91	55.99	18.12	81.93
20FAWWON-SA-237	72.29	55.83	15.67	80.45	56.68	18.06	82.23
20FAWWON-SA-241	81.41	52.69	15.25	77.31	55.99	18.51	82.64
20FAWWON-SA-243	77.89	50.42	14.34	73.00	54.32	18.06	80.10
20FAWWON-SA-244	68.54	48.28	14.25	71.30	52.81	18.16	78.43
20FAWWON-SA-249	68.00	49.97	15.49	74.49	53.51	18.69	79.79
20FAWWON-SA-251	68.22	54.17	15.80	79.43	56.38	19.40	83.12
20FAWWON-SA-252	79.41	53.65	16.00	78.97	55.62	19.18	82.27
20FAWWON-SA-254	75.07	50.10	14.52	73.04	54.39	18.41	80.37
20FAWWON-SA-256	75.00	47.44	14.85	70.19	52.97	18.42	78.84
20FAWWON-SA-257	65.44	50.29	14.15	72.88	54.13	17.60	79.14
20FAWWON-SA-258	76.29	50.05	15.03	73.82	53.64	18.47	79.51
20FAWWON-SA-259	70.48	51.65	15.42	75.73	54.65	17.69	79.79
21FAWWON-IRR-103	72.14	51.77	14.46	74.83	54.43	18.11	80.03
21FAWWON-IRR-14	61.80	46.17	15.18	70.43	51.21	18.32	76.83
21FAWWON-IRR-141	82.18	57.35	14.08	79.42	57.26	18.39	83.35
21FAWWON-IRR-143	81.39	53.61	14.31	75.87	55.62	17.92	80.67

21FAWWON-IRR-144	70.00	50.17	13.51	71.13	53.92	17.25	78.42
21FAWWON-IRR-150	77.64	54.07	14.51	76.45	56.41	19.34	83.39
21FAWWON-IRR-163	73.89	52.45	14.97	76.21	55.52	17.83	81.40
21FAWWON-IRR-43	67.41	49.89	14.09	71.79	53.63	17.83	78.93
21FAWWON-IRR-50	71.82	47.16	14.42	69.62	52.50	17.95	78.05
21FAWWON-IRR-7	70.63	48.04	13.56	69.30	52.75	17.35	78.06
21FAWWON-IRR-75	74.22	52.04	14.10	73.59	54.68	18.18	79.91
21FAWWON-IRR-83	81.39	51.69	14.19	73.58	54.62	18.40	80.25
21FAWWON-IRR-9	80.08	48.52	15.91	73.26	53.09	18.49	79.19
21FAWWON-IRR-95	82.84	57.21	15.21	81.52	58.04	18.98	84.98
21FAWWON-SA-202	69.18	54.48	15.12	78.20	56.00	18.24	81.81
21FAWWON-SA-207	76.94	53.79	14.94	77.56	55.13	18.04	80.77
21FAWWON-SA-210	75.40	48.81	14.95	72.75	53.56	17.75	79.12
21FAWWON-SA-211	72.41	49.54	14.07	71.09	53.39	17.16	77.94
21FAWWON-SA-227	71.05	43.45	14.54	65.86	50.71	18.27	76.42
21FAWWON-SA-228	70.83	53.15	15.33	77.72	55.34	17.64	80.47
21FAWWON-SA-234	68.53	49.02	14.47	71.47	53.05	17.76	77.92
21FAWWON-SA-243	76.25	53.24	13.60	74.64	55.54	18.16	81.11
21FAWWON-SA-247	81.46	53.97	14.07	76.48	56.19	18.16	82.20
21FAWWON-SA-261	81.19	48.07	14.08	69.85	52.94	17.37	78.22
21FAWWON-SA-281	67.83	45.27	14.99	69.32	51.27	18.31	77.15
21FAWWON-SA-286	74.61	44.95	14.76	67.97	51.54	18.87	77.82
21FAWWON-SA-287	87.80	45.68	15.15	70.11	51.98	19.33	79.12
21FAWWON-SA-292	77.40	47.51	14.00	69.63	52.66	18.34	78.36
Snowmass	84.35	54.77	13.85	76.73	55.64	17.21	80.29
Ripper	87.44	53.68	13.57	75.58	55.85	18.34	81.63
Antero	95.69	59.44	14.68	83.08	59.15	18.37	85.45
Denali	94.23	58.52	15.45	82.93	59.19	19.37	86.31
Byrd	85.51	56.14	14.41	79.20	56.85	17.98	82.46

Supplemental Table S5.17. Mean normalized difference vegetation indice (NDVI) values for Julesburg 2016.

	MEAN					
ID	VEG-R.NDVI	GF-R.NDVI	FULL-R.NDVI	VEG-G.NDVI	GF-G.NDVI	FULL-G.NDVI
22 FAWWON-IRR-85	0.53	0.39	0.47	0.55	0.51	0.53
22 FAWWON-IRR-53	0.58	0.41	0.50	0.58	0.51	0.54
22 FAWWON-IRR-87	0.57	0.43	0.50	0.58	0.53	0.55
22 FAWWON-IRR-71	0.55	0.43	0.49	0.56	0.52	0.54
22 FAWWON-IRR-48	0.56	0.42	0.49	0.57	0.52	0.55
22 FAWWON-IRR-10	0.59	0.43	0.51	0.59	0.51	0.55
22 FAWWON-SA-221	0.55	0.41	0.48	0.57	0.49	0.53
22 FAWWON-IRR-9	0.60	0.46	0.52	0.59	0.51	0.55
22 FAWWON-IRR-68	0.55	0.41	0.48	0.56	0.51	0.53
22 FAWWON-IRR-95	0.52	0.40	0.46	0.55	0.51	0.53
22 FAWWON-IRR-26	0.58	0.45	0.51	0.58	0.50	0.54
22 FAWWON-IRR-18	0.58	0.43	0.50	0.58	0.52	0.55
22 FAWWON-IRR-32	0.59	0.44	0.51	0.58	0.51	0.55
22 FAWWON-SA-232	0.57	0.42	0.49	0.57	0.50	0.53
22 FAWWON-SA-249	0.59	0.44	0.51	0.59	0.53	0.56
22 FAWWON-SA-235	0.57	0.42	0.50	0.57	0.52	0.55
22 FAWWON-IRR-103	0.56	0.42	0.49	0.57	0.51	0.54
22 FAWWON-SA-281	0.56	0.44	0.49	0.56	0.51	0.53
22 FAWWON-IRR-93	0.55	0.41	0.47	0.55	0.50	0.52
22 FAWWON-SA-214	0.59	0.46	0.52	0.59	0.53	0.56
22 FAWWON-SA-243	0.57	0.44	0.50	0.57	0.51	0.54
22 FAWWON-SA-260	0.57	0.42	0.50	0.58	0.53	0.56
22 FAWWON-IRR-21	0.57	0.43	0.50	0.58	0.53	0.55
22 FAWWON-SA-225	0.58	0.43	0.51	0.58	0.50	0.54
22 FAWWON-IRR-86	0.56	0.39	0.48	0.57	0.51	0.54
20FAWWON-SA-231	0.57	0.41	0.50	0.58	0.51	0.54
21FAWWON-IRR-137	0.59	0.42	0.51	0.59	0.51	0.55

22 FAWWON-SA-294	0.59	0.44	0.52	0.58	0.53	0.55
22 FAWWON-SA-263	0.59	0.45	0.52	0.58	0.52	0.55
22 FAWWON-IRR-98	0.59	0.42	0.51	0.59	0.52	0.55
22 FAWWON-SA-262	0.56	0.42	0.49	0.57	0.51	0.54
22 FAWWON-IRR-66	0.56	0.42	0.49	0.56	0.51	0.54
22 FAWWON-IRR-31	0.58	0.42	0.50	0.57	0.51	0.54
22 FAWWON-IRR-111	0.60	0.44	0.52	0.60	0.53	0.57
22 FAWWON-IRR-57	0.59	0.44	0.52	0.59	0.53	0.56
22 FAWWON-IRR-49	0.59	0.45	0.52	0.59	0.53	0.56
22 FAWWON-IRR-79	0.57	0.43	0.50	0.58	0.53	0.56
22 FAWWON-IRR-60	0.57	0.41	0.49	0.57	0.50	0.53
22 FAWWON-IRR-55	0.55	0.44	0.49	0.56	0.52	0.54
22 FAWWON-IRR-19	0.60	0.42	0.51	0.59	0.50	0.54
22 FAWWON-IRR-70	0.58	0.44	0.51	0.58	0.52	0.55
22 FAWWON-SA-239	0.60	0.45	0.52	0.60	0.53	0.57
22 FAWWON-SA-248	0.55	0.43	0.49	0.57	0.52	0.54
22 FAWWON-SA-202	0.56	0.41	0.49	0.57	0.51	0.54
22 FAWWON-IRR-108	0.57	0.42	0.49	0.58	0.52	0.55
22 FAWWON-IRR-35	0.55	0.42	0.49	0.57	0.52	0.54
22 FAWWON-IRR-22	0.56	0.42	0.49	0.56	0.49	0.53
22 FAWWON-SA-282	0.56	0.41	0.48	0.57	0.50	0.53
22 FAWWON-IRR-41	0.54	0.42	0.48	0.55	0.50	0.52
22 FAWWON-SA-230	0.55	0.40	0.47	0.56	0.51	0.53
22 FAWWON-IRR-23	0.58	0.42	0.50	0.58	0.51	0.54
22 FAWWON-IRR-20	0.59	0.41	0.50	0.59	0.50	0.54
22 FAWWON-SA-223	0.58	0.43	0.51	0.58	0.52	0.56
22 FAWWON-IRR-14	0.57	0.42	0.49	0.58	0.51	0.54
22 FAWWON-SA-253	0.57	0.42	0.50	0.58	0.52	0.55
22 FAWWON-IRR-8	0.58	0.42	0.51	0.58	0.52	0.55
22 FAWWON-SA-237	0.61	0.44	0.52	0.60	0.52	0.56
22 FAWWON-IRR-42	0.58	0.44	0.51	0.57	0.52	0.54

22 FAWWON-IRR-25	0.59	0.43	0.51	0.58	0.52	0.55
22 FAWWON-IRR-34	0.57	0.43	0.50	0.57	0.51	0.54
22 FAWWON-IRR-27	0.61	0.44	0.53	0.59	0.51	0.55
22 FAWWON-SA-259	0.57	0.42	0.50	0.57	0.52	0.54
22 FAWWON-IRR-45	0.57	0.42	0.50	0.58	0.51	0.55
22 FAWWON-SA-231	0.56	0.43	0.49	0.56	0.50	0.53
22 FAWWON-SA-274	0.56	0.41	0.48	0.55	0.50	0.52
22 FAWWON-IRR-51	0.58	0.46	0.52	0.59	0.55	0.57
22 FAWWON-SA-277	0.56	0.41	0.48	0.56	0.49	0.52
22 FAWWON-IRR-84	0.54	0.41	0.48	0.55	0.51	0.52
22 FAWWON-SA-265	0.56	0.44	0.50	0.57	0.51	0.54
22 FAWWON-SA-269	0.56	0.42	0.49	0.56	0.51	0.53
22 FAWWON-IRR-69	0.63	0.43	0.53	0.62	0.54	0.58
22 FAWWON-SA-250	0.56	0.42	0.49	0.56	0.51	0.54
22 FAWWON-IRR-52	0.55	0.43	0.49	0.57	0.52	0.55
22 FAWWON-SA-270	0.58	0.43	0.51	0.58	0.54	0.56
22 FAWWON-SA-211	0.60	0.43	0.52	0.58	0.51	0.55
22 FAWWON-IRR-33	0.59	0.42	0.51	0.59	0.51	0.55
22 FAWWON-IRR-7	0.61	0.43	0.52	0.60	0.52	0.56
22 FAWWON-SA-217	0.56	0.42	0.49	0.57	0.50	0.53
22 FAWWON-SA-273	0.56	0.42	0.49	0.56	0.51	0.53
20FAWWON-IRR-100	0.58	0.41	0.50	0.58	0.51	0.55
20FAWWON-IRR-106	0.60	0.45	0.52	0.60	0.53	0.57
20FAWWON-IRR-11	0.58	0.42	0.50	0.57	0.52	0.54
20FAWWON-IRR-114	0.59	0.46	0.52	0.59	0.54	0.57
20FAWWON-IRR-115	0.58	0.42	0.50	0.59	0.52	0.55
20FAWWON-IRR-118	0.61	0.43	0.52	0.61	0.53	0.58
20FAWWON-IRR-12	0.57	0.41	0.49	0.58	0.51	0.54
20FAWWON-IRR-13	0.59	0.41	0.50	0.58	0.51	0.54
20FAWWON-IRR-143	0.58	0.44	0.51	0.58	0.51	0.54
20FAWWON-IRR-15	0.56	0.41	0.49	0.57	0.54	0.55

20FAWWON-IRR-18	0.56	0.43	0.50	0.57	0.52	0.54
20FAWWON-IRR-19	0.57	0.42	0.49	0.57	0.51	0.54
20FAWWON-IRR-21	0.56	0.41	0.49	0.57	0.51	0.54
20FAWWON-IRR-22	0.58	0.44	0.51	0.58	0.52	0.55
20FAWWON-IRR-23	0.58	0.44	0.51	0.58	0.51	0.55
20FAWWON-IRR-29	0.58	0.43	0.50	0.58	0.52	0.55
20FAWWON-IRR-31	0.55	0.43	0.50	0.57	0.53	0.55
20FAWWON-IRR-36	0.62	0.44	0.53	0.60	0.54	0.58
20FAWWON-IRR-37	0.58	0.45	0.52	0.59	0.56	0.58
20FAWWON-IRR-38	0.58	0.42	0.50	0.58	0.53	0.56
20FAWWON-IRR-39	0.58	0.45	0.52	0.58	0.53	0.56
20FAWWON-IRR-40	0.58	0.42	0.50	0.58	0.51	0.55
20FAWWON-IRR-41	0.59	0.44	0.52	0.58	0.53	0.56
20FAWWON-IRR-42	0.56	0.42	0.49	0.57	0.52	0.55
20FAWWON-IRR-44	0.60	0.43	0.52	0.60	0.53	0.57
20FAWWON-IRR-45	0.56	0.41	0.48	0.57	0.51	0.54
20FAWWON-IRR-46	0.57	0.42	0.50	0.58	0.50	0.54
20FAWWON-IRR-49	0.55	0.44	0.50	0.56	0.55	0.56
20FAWWON-IRR-55	0.58	0.42	0.49	0.58	0.51	0.55
20FAWWON-IRR-56	0.58	0.43	0.51	0.58	0.53	0.55
20FAWWON-IRR-57	0.56	0.41	0.49	0.58	0.52	0.55
20FAWWON-IRR-59	0.57	0.42	0.50	0.58	0.51	0.55
20FAWWON-IRR-7	0.55	0.42	0.48	0.56	0.51	0.53
20FAWWON-IRR-74	0.59	0.46	0.52	0.59	0.52	0.55
20FAWWON-IRR-86	0.58	0.42	0.50	0.58	0.51	0.55
20FAWWON-IRR-87	0.55	0.41	0.48	0.56	0.51	0.54
20FAWWON-IRR-88	0.59	0.42	0.51	0.58	0.52	0.55
20FAWWON-IRR-9	0.57	0.44	0.50	0.57	0.53	0.55
20FAWWON-IRR-95	0.58	0.43	0.50	0.58	0.51	0.54
20FAWWON-IRR-97	0.55	0.43	0.49	0.58	0.54	0.56
20FAWWON-IRR-98	0.57	0.45	0.51	0.58	0.53	0.55

20FAWWON-SA-206	0.57	0.42	0.50	0.57	0.50	0.54
20FAWWON-SA-209	0.59	0.44	0.51	0.59	0.52	0.55
20FAWWON-SA-210	0.54	0.43	0.48	0.55	0.52	0.54
20FAWWON-SA-212	0.57	0.42	0.49	0.57	0.51	0.54
20FAWWON-SA-213	0.53	0.41	0.47	0.54	0.50	0.52
20FAWWON-SA-214	0.60	0.45	0.52	0.59	0.53	0.56
20FAWWON-SA-215	0.60	0.43	0.52	0.59	0.51	0.55
20FAWWON-SA-222	0.58	0.42	0.50	0.58	0.51	0.55
20FAWWON-SA-223	0.57	0.39	0.49	0.58	0.51	0.55
20FAWWON-SA-224	0.59	0.40	0.50	0.57	0.49	0.53
20FAWWON-SA-226	0.60	0.41	0.51	0.59	0.51	0.55
20FAWWON-SA-227	0.59	0.41	0.51	0.59	0.52	0.55
20FAWWON-SA-232	0.58	0.43	0.50	0.57	0.49	0.52
20FAWWON-SA-236	0.61	0.46	0.53	0.59	0.52	0.55
20FAWWON-SA-237	0.60	0.45	0.52	0.59	0.51	0.55
20FAWWON-SA-241	0.60	0.44	0.52	0.60	0.53	0.56
20FAWWON-SA-243	0.56	0.42	0.49	0.57	0.51	0.54
20FAWWON-SA-244	0.56	0.41	0.49	0.57	0.52	0.54
20FAWWON-SA-249	0.57	0.45	0.51	0.57	0.53	0.55
20FAWWON-SA-251	0.60	0.46	0.53	0.60	0.55	0.58
20FAWWON-SA-252	0.58	0.46	0.52	0.58	0.55	0.56
20FAWWON-SA-254	0.57	0.42	0.50	0.58	0.52	0.55
20FAWWON-SA-256	0.54	0.43	0.48	0.57	0.53	0.55
20FAWWON-SA-257	0.57	0.41	0.49	0.58	0.50	0.54
20FAWWON-SA-258	0.58	0.44	0.51	0.58	0.53	0.55
20FAWWON-SA-259	0.56	0.45	0.50	0.57	0.50	0.53
21FAWWON-IRR-103	0.59	0.42	0.51	0.59	0.52	0.55
21FAWWON-IRR-14	0.56	0.43	0.50	0.56	0.52	0.54
21FAWWON-IRR-141	0.61	0.41	0.51	0.60	0.52	0.56
21FAWWON-IRR-143	0.58	0.41	0.50	0.59	0.51	0.55
21FAWWON-IRR-144	0.56	0.39	0.48	0.57	0.49	0.53

21FAWWON-IRR-150	0.58	0.42	0.50	0.59	0.55	0.57
21FAWWON-IRR-163	0.58	0.43	0.50	0.58	0.51	0.54
21FAWWON-IRR-43	0.55	0.41	0.47	0.56	0.51	0.54
21FAWWON-IRR-50	0.55	0.42	0.48	0.57	0.51	0.54
21FAWWON-IRR-7	0.54	0.40	0.46	0.56	0.49	0.53
21FAWWON-IRR-75	0.57	0.41	0.49	0.57	0.52	0.55
21FAWWON-IRR-83	0.57	0.41	0.49	0.58	0.53	0.55
21FAWWON-IRR-9	0.55	0.45	0.50	0.57	0.53	0.54
21FAWWON-IRR-95	0.61	0.44	0.53	0.61	0.54	0.58
21FAWWON-SA-202	0.61	0.43	0.52	0.60	0.52	0.56
21FAWWON-SA-207	0.59	0.43	0.51	0.58	0.51	0.54
21FAWWON-SA-210	0.57	0.43	0.50	0.58	0.51	0.54
21FAWWON-SA-211	0.54	0.41	0.47	0.55	0.49	0.52
21FAWWON-SA-227	0.54	0.42	0.48	0.56	0.52	0.54
21FAWWON-SA-228	0.58	0.44	0.51	0.58	0.50	0.54
21FAWWON-SA-234	0.54	0.42	0.48	0.55	0.50	0.53
21FAWWON-SA-243	0.59	0.39	0.49	0.59	0.52	0.55
21FAWWON-SA-247	0.60	0.41	0.51	0.60	0.52	0.56
21FAWWON-SA-261	0.55	0.40	0.47	0.56	0.49	0.53
21FAWWON-SA-281	0.54	0.43	0.49	0.55	0.52	0.54
21FAWWON-SA-286	0.53	0.43	0.48	0.56	0.54	0.55
21FAWWON-SA-287	0.54	0.44	0.49	0.57	0.55	0.56
21FAWWON-SA-292	0.56	0.41	0.49	0.57	0.52	0.55
Snowmass	0.60	0.40	0.50	0.58	0.49	0.54
Ripper	0.58	0.40	0.49	0.58	0.53	0.55
Antero	0.64	0.43	0.53	0.62	0.53	0.57
Denali	0.62	0.45	0.54	0.62	0.55	0.59
Byrd	0.61	0.42	0.51	0.60	0.51	0.55