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Genome-Wide Association Study For Disease Traits In Wheat And Its Wild Relatives

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Abstract

Wheat is the most widely grown crop in the world and as such, is an essential source of energy and nutrition. The challenges that breeders presently face is to increase production to feed the rising population of the world, while also accounting for climate change, pollution, water and environmental stresses. As genetic uniformity of modern cultivars has increased vulnerability to pests and diseases, the wild relatives of wheat offer a rich source of genetic diversity and stress tolerance traits, that can be harnessed and transferred in to modern wheat.

In this study, we used array-based genotyping to explore genetic diversity in 385 domesticated and non-domesticated lines of wheat and their wild relatives. Genetic characterization using the wheat 90K array, and subsequent filtering and validation mapped 9,570 single nucleotide polymorphic markers onto the wheat reference genome. Phylogenetic analyses illustrated four major clades, clearly separating the wild species from the domesticated, and the ancient *Triticum turgidum* species from modern *T. turgidum* cultivars.

Using this diverse germplasm, a genome-wide association study (GWAS) was performed for leaf rust, the most widespread rust disease of wheat. Identification of novel sources of resistance is necessary to maintain disease resistance and stay ahead in the plant-pathogen evolutionary arms race. GWAS was conducted using eight statistical models for infection types against six leaf rust isolates and leaf rust severity rated in field trials for 3-4 years at 2-3 locations in Canada. Functional annotation of genes containing significant quantitative trait nucleotides (QTNs) identified 96 disease-related nucleotide associated with leaf rust resistance. A total of 21 QTNs were in haplotype blocks or within flanking markers of at least 16 known leaf rust (*Lr*) resistance genes. The remaining significant QTNs were considered loci that putatively harbor new *Lr* resistance genes. Future efforts to validate these loci will help understand their role in disease resistance and promote their utility for marker-assisted selection in pre-breeding.

Résumé

Le blé est la plante la plus cultivée au monde, et représente une source essentielle d'énergie et d'aliment. Les cultivateurs doivent relever de gros défis en vue de nourrir une population toujours croissante, tels qu'une augmentation de la production tout en tenant compte des changements climatiques, de la pollution, de la sécheresse et des stress environnementaux. Comme l'uniformité génétique dans les cultivars modernes a causé une vulnérabilité contre les pestes et les maladies, ce sont les espèces sauvages apparentées au blé qui offrent une source riche en diversité génétique et en caractères de tolérance aux stress. Cette diversité retrouvée chez les espèces sauvages peut être ciblée et transférée dans le blé moderne.

Dans cette étude, nous utilisons du génotypage basé sur des bio-puces pour explorer la diversité génétique de 385 lignées de blé domestiqué et non-domestiqué ainsi que leurs espèces sauvages apparentées. La caractérisation génétique avec la bio-puce 90K du blé, suivi d'un filtrage et d'une validation, a cartographié 9570 marqueurs de polymorphisme à nucléotide unique (SNP) sur le génome de référence du blé. Des analyses phylogénétiques illustrent quatre clades majeurs qui démontrent clairement la démarcation qui sépare les cultivars modernes des cultivars anciens de T. turgidum, ainsi que les espèces domestiquées des espèces sauvages.

Avec ce matériel génétique aussi diversifié, une étude d'association pan-génomique (GWAS) a été menée pour identifier où se situe les gènes de résistance à la rouille brune, la rouille la plus répandue chez le blé. L'identification de nouvelles sources de résistance à cette maladie est primordiale afin de garder cette résistance et demeurer à la fine-pointe de la guerre entre plante et pathogène. Cette étude d'association pan-génomique a été produite avec l'utilisation de huit modèles statistiques pour les types d'infection contre six isolats de rouille brune et la mesure de sévérité telle qu'évaluée en champ pendant 3-4 années, à 2-3 sites au Canada. L'annotation fonctionnelle des gènes qui contiennent des nucléotides associés aux caractères quantitatifs (QTNs) significatifs a identifié 96 loci associés à la résistance à la rouille brune. En

tout, 21 QTNs se retrouvent à l'intérieur des blocs d'haplotype ou à proximité des marqueurs qui accompagnent 16 gènes connus de résistance à la rouille brune. Les QTNs significatifs qui restent sont considérés comme des loci qui pourraient contenir des nouveaux gènes de résistance contre la rouille. Des études futures envisagent de valider ces loci afin de mieux comprendre leurs rôles dans la résistance à la maladie, et à promouvoir leur utilité pour la sélection assistée par marqueurs dans des programmes d'amélioration génétique du blé.

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Dedications

This thesis is dedicated my 16-year-old self

who was too afraid to dream big

You are your only limit

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Acronyms

AAFC	Agriculture and Agri-Food Canada
APR	Adult plant resistance
B	Brittle
BLUP	Best linear unbiased predictors
CS	Chinese Spring
DAMPs	Damage-associated molecular patterns
DNA	Deoxyribonucleic acid
ETI	Effector-triggered immunity
FHB	*Fusarium* head blight
FT	Free-threshing
Gb	Giga bytes
GLM	Generalized linear model
GWAS	Genome-wide association study
H	Hulled
HR	Hypersensitive response
IT	Infection type
IWGSC	The International Wheat Genome Sequencing Consortium
LDB	Linkage disequilibrium block
LD	Linkage disequilibrium
LR	Leaf rust (disease)
Lr	Leaf rust (gene)
MAF	Minor allele frequency
MLM	Mixed linear model

mrMLM	Multi-locus random-SNP-effect mixed linear model
MTA	Marker-trait association
N	Northern
NB	Non-brittle
NGS	Next-generation sequencing
NLR	Nucleotide-binding domains and leucine-rich repeats
ORDC	Ottawa Research and Development Centre
PAMPs	Pathogen-associated molecular patterns
PTI	Pattern-triggered immunity
PB	Partially brittle
PRR	Pattern recognition receptor
RDC	Research and development centre
RFLP	Restriction fragment length polymorphism
RTM-GWAS	Restricted two-stage multi-locus genome wide association study
S	Southern
SHW	Synthetic hexaploid wheat
SNP	Single nucleotide polymorphism
SNPLDB	SNP linkage disequilibrium blocks
SSR	Simple sequence repeats
SW	Southwestern
TE	Transposable element
QTL	Quantitative trait loci
QTN	Quantitative trait nucleotide
WAK	Wall-associated kinase

1 General introduction

1.1 Agriculture of wheat

Wheat is a staple food crop cultivated worldwide for its grain products. Its economic importance and contribution to the diets of humans and livestock cannot be overlooked. It is in fact the second most cultivated food crop in the world, feeding approximately one-third of its population (FAO, 2018). In 2018, the global wheat production was 734 million tonnes, with China, India, Russia and the United States of America collectively providing 41% of the world's total wheat (FAO, 2018). In terms of nutrition, wheat accounts for 20% of the total human calories consumption, and is the highest source of protein than any other cereal crop, contributing to 20-21% of our needs (CGIAR, 2017). Apart from this, wheat is also a rich source of vitamins, dietary fibres and phytochemicals.

In recent years, wheat production has not met global demands, leading to price instability and food insecurity. By 2050, the world's population is predicted to rise to 9 billion and the demand of wheat is expected to increase by 60%; annual wheat yield gains must rise from the current sub-1% to at least 1.6% (Godfray et al., 2010; Tadesse et al., 2016). This, coupled with the challenges imposed by water scarcity, climate change, and constant outbreak of new pathogens, has delayed progress and hampered food security (Asseng et al., 2015; Chaves et al., 2013; Rasheed et al., 2018). Wheat producing countries must increase yield, tolerance to abiotic stresses, pathogens and pests, as well as improve agronomic practises to meet the rising demands of wheat production.

1.2 Evolution of wheat

Common or bread wheat (*Triticum aestivum*) is a hexaploid species (AABBDD genome, 2n=6x=42 chromosomes) that originated approximately 10,000 years ago as a result of two ancestral polyploidization events (**Figure 1.1**). Hybridization between *Triticum urartu* (AA,

2n=2x=14), commonly named red wild einkorn, and an unknown species (BB, 2n=2x=14), closely related to *Aegilops speltoides* (SS, 2n=2x=14) formed the allotetraploid *T. turgidum* ssp. *dicoccoides* (AABB, 2n=4x=28), commonly known as wild emmer (Blake et al., 1999; Dvorak et al., 1993; Dvorak and Zhang, 1990). Wild emmer was cultivated for several hundred years before being domesticated as emmer wheat (*T. turgidum* ssp. *dicoccum*), which eventually evolved into durum or pasta wheat (*T. turgidum durum*) (Dubcovsky and Dvorak, 2007). The second polyploidization event occurred between domesticated emmer wheat and the diploid wild species *Ae. tauschii* (DD, 2n=2x=14), commonly known as Tausch's goatgrass, to give rise to *T. aestivum* or bread wheat (McFadden and Sears, 1946). Through the course of wheat evolution, farmers have been selecting favorable traits such as non-brittle rachis and non-hulled glumes by repeatedly sowing and harvesting wheats that displayed these domestication traits which had been acquired through natural mutations; the non-brittle rachis phenotype prevents the shattering of seeds, and non-hulled glumes refers to the free-threshing ability of the grains.

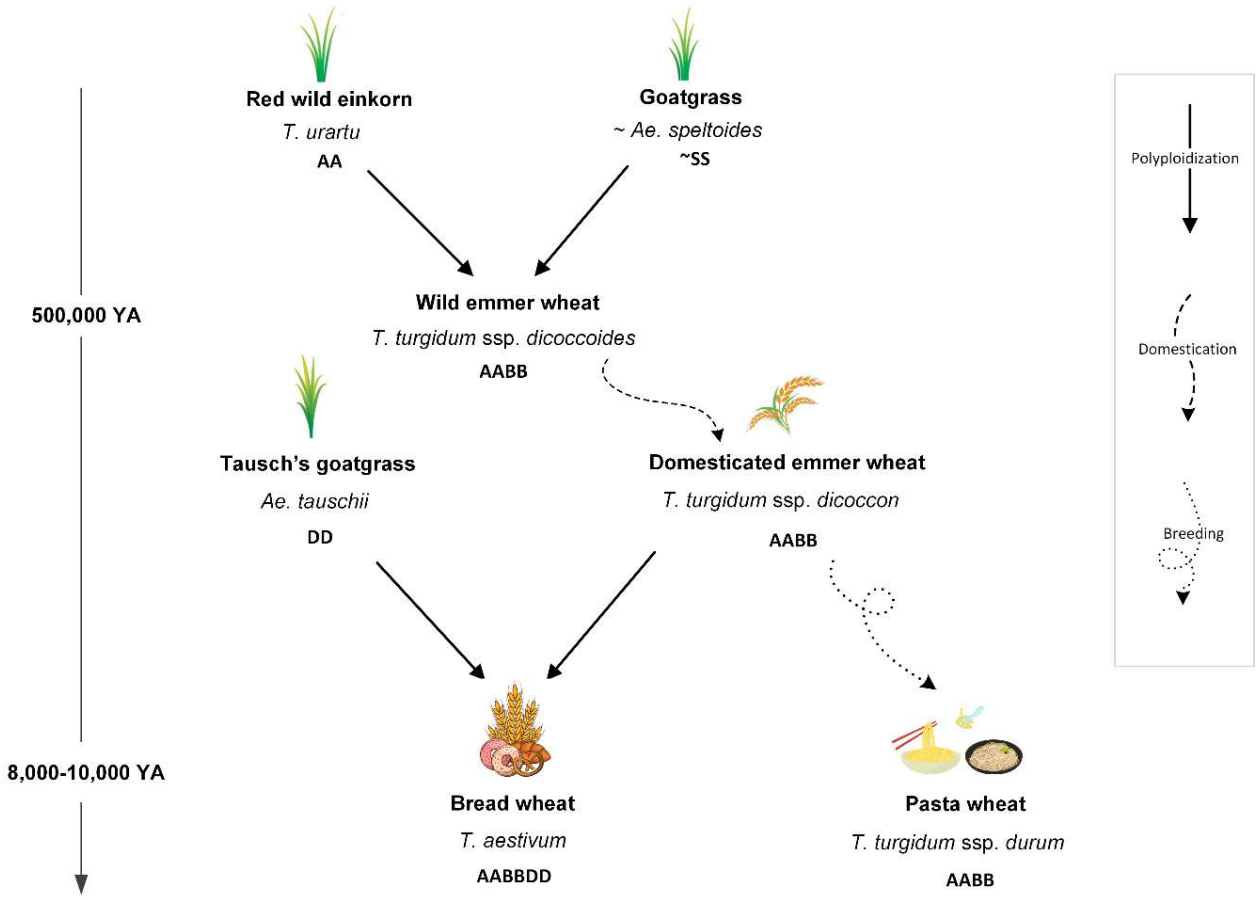

Figure 1.1 Overview of the evolution of wheat.
Timeline shows the estimated time points in number of years ago (YA) of the polyploidization events.

1.3 Wheat species

1.3.1 Cultivated species

Wheat belongs to the genus *Triticum* and the tribe Triticeae. The genus *Triticum* comprises several wheat species, of which bread wheat (*T. aestivum*) and pasta wheat (*T. turgidum durum*) are most widely cultivated commercially for food. Domesticated wheats are large-seeded, non-shattering and free-threshing.

Common or bread wheat, which accounts for 95% of all consumed wheat, is widely used for the production of baked products. The remaining 5% is *T. turgidum durum* which is used to make pasta, couscous and semolina flour. Other domesticated, but lesser-grown hexaploid

wheats, include compact (*T. aestivum compactum*), spelt (*T. aestivum spelta*), shot (*T. aestivum sphaerococcum)*, makha **(***T. aestivum macha*) and Vavilov's (*T. vavilovii*) wheats, which, except for the latter, are considered subspecies of bread wheat (*T. aestivum*). These subspecies differ in their morphology and geographical distribution (**Table 1.1**). For example, compact wheat, still grown in some parts of South America, in southern Europe and Southwestern Asia, has a more compact ear (or head) compared to common wheat, and spelt wheat, popular in the past and now considered a speciality crop, is hulled as opposed to free-threshing bread wheat. Similarly, aside from durum wheat, other lesser cultivated subspecies of tetraploid *T. turgidum* include persian (*T. turgidum carthlicum*), khorasan (*T. turgidum turanicum*), polish (*T. turgidum polonicum*) and rivet (*T. turgidum turgidum*) wheats (**Table 1.1**).

Table 1.1 Cultivated wheat species, their spike morphology and geographical distribution

Species name	Common name	Spike[1]	Geographical distribution[2]
Hexaploid (AABBDD)			
T. aestivum ssp**.** *aestivum*	Bread wheat	FT, NB	Widely cultivated
T. aestivum ssp. *compactum*	Compact wheat	FT, NB	S America, S Europe and SW Asia
T. aestivum ssp. *sphaerococcum*	Shot wheat	FT, NB	Middle East; Asia
T. aestivum ssp. *spelta*	Spelt wheat	H, PB	Iran, Europe
T. aestivum ssp. *macha*	Makha wheat	FT, NB	Georgia
T. vavilovii	Vavilov's wheat	H, PB	Armenia
Tetraploid (AABB)			
T. turgidum ssp. *carthlicum*	Persian wheat	FT, NB	Middle East, Armenia, Georgia
T. turgidum ssp. *turanicum*	Khorasan wheat	FT, NB	Iran, Iraq
T. turgidum ssp. *polonicum*	Polish wheat	FT, NB	S. Europe, Middle East, S Asia
T. turgidum ssp. *turgidum*	Rivet wheat	FT, NB	Middle East
T. turgidum ssp. *durum*	Durum wheat	FT, NB	Europe, Asia, N America
T. turgidum ssp. *dicoccum*	Emmer wheat	H, B	widely cultivated in ancient times

FT, Free-threshing; H, Hulled; NB, Non-brittle; PB, Partially brittle; B, Brittle; S, Southern; SW, Southwestern; N, Northern

[1]Spike morphology information obtained from (Dvorak, 2001)

[2]Geographical distribution obtained from the “Plants For A Future” Database (www.pfaf.org)

The planting and harvesting seasons of wheat depend on the variety of the cultivar. In Canada, spring wheats are planted in the spring and harvested in late summer or early fall, while

winter wheats are planted in the fall and harvested in the summer. Winter wheats, grown particularly in the northern hemisphere, must undergo a vernalization period when they are exposed to cold temperatures for several weeks in order to trigger flowering or heading, i.e., emergence of the ears. In many areas of the world, facultative varieties requiring shorter vernalization time and minimal cold exposure can be grown in either spring or winter. In countries which experience mild winters, such as those of South Asia and the Middle East, spring wheats, which do not require a vernalization period, can also be planted in the winter and harvested in late spring of the next year.

1.3.2 Wild relatives

The tribe Triticeae can be classified into 20-27 genera, of which the cultivated or edible species belong to the genera *Triticum* (wheat), *Hordeum* (Barley), *Secale* (Rye) and *Aegilops* (ancient food grains) (Kellogg, 2015; Soreng et al., 2015). The phylogenetic relationships between species within these genera are of interest because they constitute a gene pool of favorable traits for the improvement of modern wheat.

1.3.2.1 Progenitor species

Modern hexaploid wheat (2n= 6x= 42, AABBDD) was derived from three diploid wild species, that also originally diverged from a common ancestor. The A, B and D genome progenitors or their closely related species include the diploid *T. urartu* (A), *T. monococcum* (A^m), *Ae. tauschii* (D) and *Ae. speltoides* (S), and the non-domesticated forms of tetraploid wheat *T. turgidum* ssp. *dicoccon* and *dicoccoides* (AB) (**Figure 1.1**). *T. urartu,* the A genome donor, was never domesticated and is sparsely distributed across the Fertile Crescent (Brunazzi et al., 2018). However, its sister species, *T. monococcum*, available in domesticated (einkorn wheat) and wild forms, was a significant source of food thousands of years ago, before it was replaced by polyploid wheat. *Ae. speltoides*, the closest known relative to the B genome donor of wheat, is one of the five species

of the Sitopsis section of the *Aegilops* that possess an S-type of genome (van Slageren, 1994). *Ae. tauschii* the D genome donor, also known as Tausch's goatgrass, is one of the most well studied progenitors, and has been associated with important traits for adaptation and stress tolerance (Kishii, 2019).

Cultivated wheats have long been recognized to be able to naturally hybridize with their wild relatives, depending on species sympatry, concurrent flowering, and sexual compatibility (van Slageren, 1994). Wild species carrying the A, B and D genomes, along with domesticated polyploid wheats, are regarded as the primary sources of genes for improvement of modern wheat. Interspecific crossing of modern wheat with species from the primary gene pool occur as a consequence of direct hybridization, and, in this case, the progeny is not hindered by linkage drag (the undesirable effects of genes linked to the introgressed region) because crossing over is uninhibited (Mujeeb-Kazi and Rajaram, 2002).

1.3.2.2 Non-progenitor species

The non-progenitor wild relatives encompass all species of the tribe Triticeae that were not directly involved in the early evolution and domestication of wheat. However, the most studied relationships are those that belong to the *Aegilops* and *Triticum* genera (**Figure 1.2**).

The genus *Aegilops* comprises 23 species, of which 11 are diploids and 12 are allopolyploids. It can be divided into five sections (van Slageren, 1994):

(1) ***Aegilops***: diploid and allopolyploid species with the U genomes e.g. *Ae. umbellulata*

(2) ***Cylindropyrum***: diploid and allopolyploid species with the C and DC genomes e.g. *Ae. markgrafii*

(3) ***Vertebrata***: diploid and allopolyploid species with the D genomes e.g. *Ae. tauschii*, *Ae. crassa*

(4) ***Comopyrum***: diploid species with the M and N genomes e.g. *Ae. comosa*, *Ae. uniaristata*

(5) ***Sitopsis***: diploid species with the S genomes e.g. *Ae. bicornis*, *Ae. longissima*

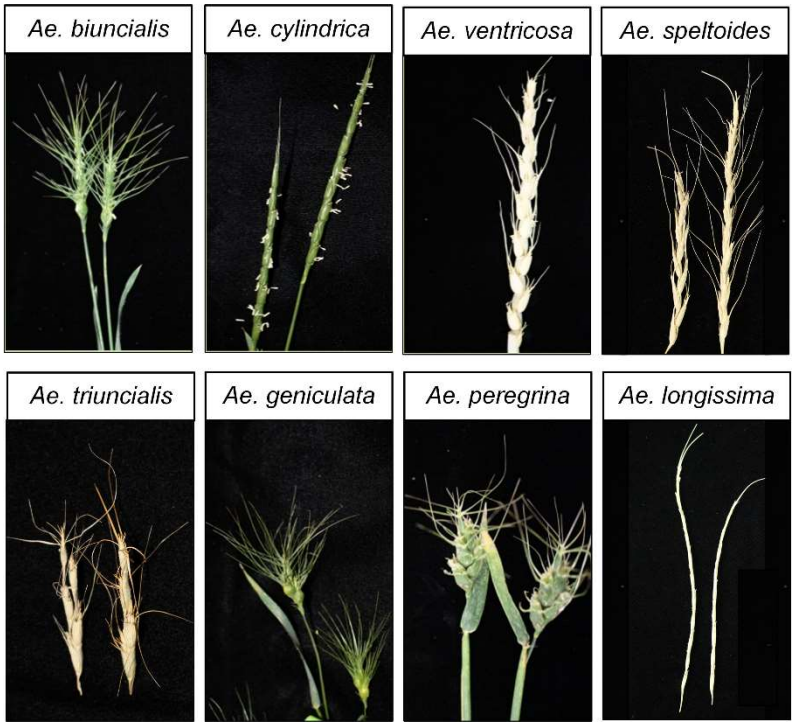

Figure 1.2 Spike morphology of some of the *Aegilops* species.
Photographs were taken by the Cloutier lab of the Ottawa Research and Development Centre.

Triticum species can be distinguished from *Aegilops* species by the presence of a well-developed keel on the glumes, creating a sharp outline around the glumes (Kilian et al., 2011). Apart from the previously mentioned *T. monococcum*, *T. urartu, T. turgidum*, *T. aestivum* and *T. vavilovii*, the genus *Triticum* also includes *T. timopheevii* and *T. zhukovskyi*. Hexaploid *T. zhukovskyi* originated through a natural interspecific hybridization between tetraploid *T. timopheevii* and diploid *T. monococcum* (Dvorak, 2001).

Natural hybridization between wheat and its wild relatives has been observed. Most hybrids were sterile, but some seeds were observed (Zaharieva and Monneveux, 2006). Artificial interspecific crossing between wheat and its wild relatives can be deployed to transfer useful traits into cultivated wheats. Species that share at least one genome with the A, B or D genomes of wheat e.g. *Ae. cylindrica* (DC) and *T. zhukovskyi* (GAA^m) belong to the secondary gene pool of wheat, while those which do not share any genome with wheat belong to the tertiary gene pool.

Introgression via the secondary and tertiary gene pools require special breeding protocols and manipulation strategies to recover fertile and viable seeds. In addition, the progeny often carry undesirable traits that can be difficult to breed-out as a consequence of linkage drag (Mujeeb-Kazi and Rajaram, 2002). Extensive crossing and backcrossing to elite varieties are often required prior to incorporation into breeding program.

1.4 The wheat genome

Bread wheat has a large and highly repetitive genome. Each of the A, B and D sub-genomes have seven pairs of homologous chromosomes, for a total of 42 chromosomes. The wheat genome also consists of homoeologous chromosomes, where each set of homoeologous chromosomes is made up of chromosomes from each sub-genome (**Figure 1.3**). Homoeologous chromosomes are considered duplicated chromosomes that are derived from different parental species, brought together in the same genome by allopolyploidization (Glover et al., 2016). Homoeologous chromosomes have largely similar gene content, but differ in their repetitive DNA which is mostly transposable elements. Therefore, as most genes have homoeo-alleles, there is functional redundancy. Chromosome pairing, however, is restricted to homologues during meiosis and the genome behaves as a diploid (Riley and Chapman, 1958). This can be altered by mutating the *Ph1* locus, that controls strict homologous chromosome pairing, to allow the creation of hybrids form wide crosses (Sears, 1976). As wheat is a self-pollinating (autogamous) plant, genotypes are largely homozygous, hence the homologs tend to have the same alleles at most loci (Dixon et al., 2018).

The International Wheat Genome Sequencing Consortium (IWGSC) recently released a fully annotated reference genome for bread wheat variety Chinese Spring, consisting of an assembly of 14.5Gb comprising 107,891 predicted high-confidence protein coding genes (IWGSC, 2018). The hexaploid genome comprises an estimated 17 billion nucleotides, i.e., five times the size of the human genome, of which more than 85% is repetitive (IWGSC, 2018). The

repetitive DNA is largely made up of major classes of transposable elements (TEs) i.e. 3,968,974 copies of TEs belonging to 505 families (IWGSC, 2018). The B sub-genome has the greatest assembly size (5.2Gb), followed by the A (4.9Gb) and the D (3.9Gb), however the distribution of high-confidence genes was relatively equal across all sub-genomes (35,345, 35,643 and 34,212, respectively) (IWGSC, 2018). Tetraploid and diploid wheat genome sizes are approximately 2/3 and 1/3 that of bread wheat. Until now, the genomes of durum wheat, (Maccaferri et al., 2019), wild emmer wheat (Avni et al., 2017), *Ae. tauschii* (Luo et al., 2017) and *T. urartu* (Ling et al., 2013) have also been sequenced. Overall, access to this sequence level information allows plant breeders to implement new strategies to improve wheat through genomics-assisted breeding.

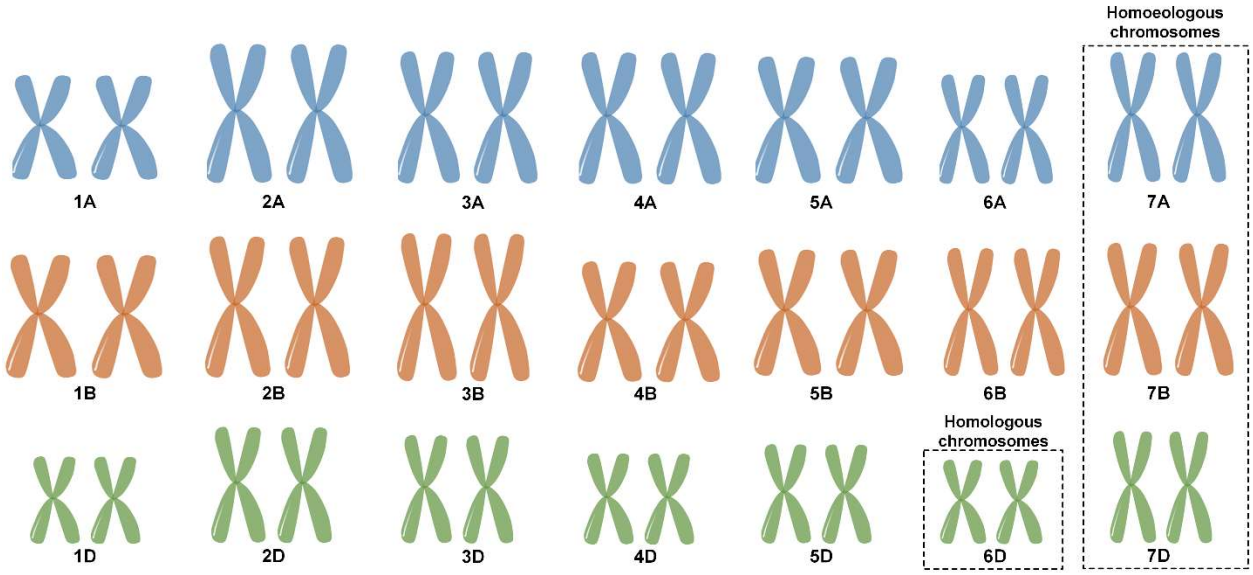

Figure 1.3 Structural organization of the hexaploid bread wheat chromosomes.
The size of the chromosomes are drawn to scale, based on the physical length (in base pairs) of each chromosome (IWGSC, 2018). The figure is adapted with permission from Haldar (2019).

1.4.1 Genetic diversity bottlenecks

The wheat genome has been subjected to a series of genetic diversity bottlenecks caused by polyploid speciation, domestication and, natural and artificial selections. The bottleneck of speciation is a founder effect where the genomes of a small number of individuals contributed to the formation of the newly formed polyploid species (Dubcovsky and Dvorak, 2007). For example,

as only a few *Ae. tauschii* participated in the origin of *T. aestivum*, the genetic diversity of the D sub-genome in modern wheat is only 15% of the *Ae. tauschii* gene pool diversity (Dvorak et al., 1998). Similarly, nucleotide diversity in the A and B genomes of *T. aestivum* was 31% that of wild emmer wheat (Haudry et al., 2007). In addition to natural selection caused by the diverse environments where these species grew, and long before genomic tools were available, farmers have been selecting for favorable traits by repeatedly sowing and harvesting wheats with desirable phenotypes. Modern day breeders now employ advanced husbandry techniques, coupled with genomic resources and biotechnological tools to artificially enhance important agronomic traits such as grain yield and quality, and resistance to biotic (disease) and abiotic stresses. These events of domestication and, environmental and artificial selections have further reduced genetic diversity, a fact that has in some cases and is forecasted to lead to improvement plateaus (Tanksley and McCouch, 1997).

1.4.2 New sources of genetic diversity

Modern wheat breeders have realized the importance of expanding diversity for successful crop improvement and are starting to use synthetic wheats, landraces and wild relatives in their breeding program. Synthetic hexaploid wheats (SHWs) are derived from recreating crosses between *Ae. tauschii* and *T. turgidum*, which allow breeders to explore novel genes in the tetraploid and diploid progenitors of wheat. They offer low reproduction barrier, producing fertile hybrids that may potentially carry alleles that are not present in modern wheat (Cox, 1997). Similarly, wheat landraces, evolved locally through a mixture of natural and artificial selections, are a source of putatively lost genetic diversity that can provide new genes or alleles for wheat improvement (Lopes et al., 2015).

Wild relatives of wheat, although lack adaptation traits for agriculture, have retained greater genetic diversity for many traits, such as abiotic and biotic stress tolerance, as they were

not subjected to domestication and artificial selection by breeders (Ceoloni et al., 2017). These relatives have evolved through separate paths allowing them to maintain certain genes or alleles that may no longer be present in cultivated bread or pasta wheats (Marcussen et al., 2014). For example, genes responsible for leaf rust resistance were identified in *Ae. tauschii* (Huang et al., 2003) and stem rust resistance in *Ae. sharonensis* (Nevo et al., 1986). Apart from these, numerous other genes from the wild gene pool have been identified for resistance to stripe rust (Helguera et al., 2003), powdery mildew (Weidner et al., 2012), *Fusarium* head blight (FHB) (Fedak et al., 2007), leaf rust (McCallum et al., 2012) and stem rust (Olivera et al., 2018). Resistance against pests such as greenbug and hessian fly (Gill and Raupp, 1987) and abiotic stresses such as freezing (Iriki et al., 2001), salinity (Colmer et al., 2006) and drought (Nevo and Chen, 2010) were also identified from wild relatives.

The traditional approach for introgressing the desired gene of interest into adapted germplasm is by interspecific crossing the wild relative with a high-crossability line. This is followed by crossing to a *ph1b* mutant line to break linkage drag and subsequent crossing and backcrossing to a recurrent parent to recover a desirable phenotype (Sears, 1976). However, this methodology requires special breeding protocols and is often impeded by sterility in the progeny and/or linkage drag resulting from the low recombination surrounding the introgressed alien fragment(s). Modern genome-assisted breeding strategies, such as gene cassettes and genome editing, have recently been proposed to overcome some of the disadvantages of the crossing method, facilitating the transfer of desirable genes/alleles from any germplasm in the secondary and tertiary gene pool (Keller et al., 2016; Wulff and Dhugga, 2018). Hence, breeders are showing an ever growing interest in crop wild relatives as a resource to harness beneficial traits. This can be achieved utilizing molecular markers such as single nucleotide polymorphism (SNP) genotyping and genome-wide association studies (GWAS).

1.5 SNP genotyping

SNPs are the most common type of genetic variation in plants and animals. A SNP is a substitution of a single DNA building block, called a nucleotide that occurs at specific positions in the genome. SNPs present within a gene or nearby a gene regulatory region may alter the gene's function and cause an altered phenotypic trait. They serve as useful molecular markers for investigating trait associations, drug response and creating genetic maps.

Molecular markers have gained increasing attention over the past couple of decades, due to their applications in crop genetics. Genotyping uses molecular markers such as SNP, simple sequence repeat (SSR) and restriction fragment length polymorphism (RFLP), to determine sequence variations at specific positions within a genome. SNP genotyping specifically identifies a set of SNPs or alternative alleles in an individual, allowing comparisons across individuals. It can be performed using three general allele discrimination methods: hybridization, primer extension and enzyme cleavage. SNP genotyping offers advantages over SSR and RFLP genotyping because SNPs are abundant, well-distributed across the genomes, cost-effective and offered in a range of sophisticated yet speedy genotyping platforms (Thomson, 2014).

1.5.1 SNP genotyping arrays

High-density SNP arrays, an application of the hybridization-based SNP genotyping method, have become increasingly popular. These SNP arrays follow the same principle as DNA microarrays, i.e., hybridization of single-stranded DNA fragments to thousands of allele-specific nucleotide probes. The ability of such arrays to interrogate variations between whole genomes simultaneously makes them an excellent tool for trait-association studies, gene discovery and linkage analysis. Over the past decade, several fixed SNP genotyping arrays have been developed for numerous crops, ranging from a 1,000 (1K) SNP array for pear to the high-density rice array with a million SNPs (Rasheed et al., 2017). Higher density arrays are accompanied with

higher genotyping costs per sample, whereas low-density array suffer from ascertainment bias and failure to capture rare alleles (Albrechtsen et al., 2010).

In wheat, the Illumina's Infinium and Affimetrix's Axiom array technologies enable the simultaneous genotyping of 9,000 to 819,571 SNP markers from seven custom SNP arrays (Rasheed et al., 2017). Illumina's Wheat 9K and 15K SNP arrays are a subset of their Wheat 90K SNP array, and Affimetrix's Wheat 35K SNP array and Wheat 55K SNP array are a subset of the Wheat 820K and Wheat 660K SNP arrays, respectively (Sun et al., 2020). The Infinium and Axiom arrays are based on two different technologies and each of their respective arrays are developed from distinctive sets of germplasm, catering to research objective and marker-assisted breeding programs. For example, the Wheat Breeders' 35K Axiom array provides breeder-oriented informative markers in bread wheat (Allen et al., 2017). On the other hand the 90K and 660K SNP arrays include markers from hexaploid and tetraploid wheat, emmer wheat and *Aegilops tauschii*, with the addition of some landraces, SHWs and wild relatives in the 820K SNP array, thereby offering a greater genetic diversity for different types of studies (Sun et al., 2020; Wang et al., 2014; Winfield et al., 2016).

1.6 Genome-wide association studies

Genome-wide association studies is a methodology which surveys hundreds and thousands of genetic variants across the genomes of many individuals to identify valuable marker-trait associations (MTAs). The study is performed using statistical models that requires at least two sets of data as input: genome-wide markers to account for genetic variation in the population and phenotypic scores of the population for the trait of interest (**Figure 1.4**). GWAS have typically been performed using genome-wide SNP markers, but association can also be identified using insertion/deletion and structural variants (Misra et al., 2017). For crops, the phenotypic trait can be any measurable trait, ranging from agronomic traits to biotic and abiotic stress tolerances.

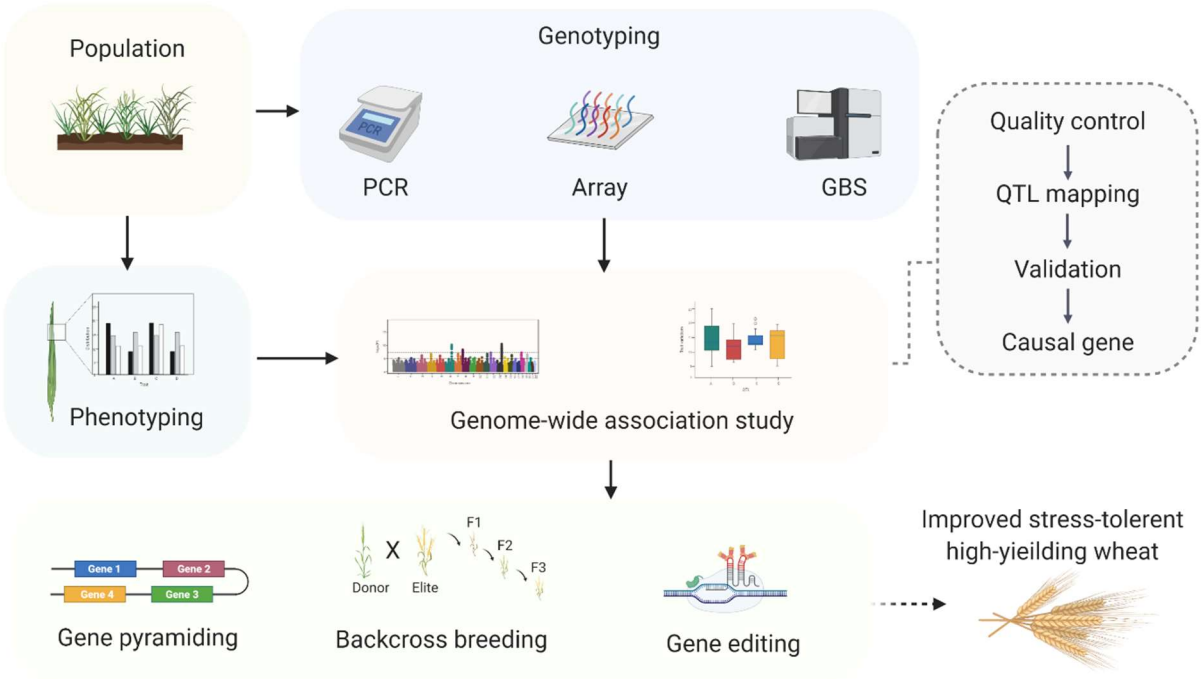

Figure 1.4 Workflow of genome-wide association studies and potential breeding applications. PCR; polymerase chain reaction, GBS, genotyping-by-sequencing; QTL, qualitative trait loci. Figure created with BioRender.com.

1.6.1 Basic principles of association analysis

Genome-wide association analysis has shown to be advantageous over linkage mapping experiments that also identify functional genetic variants (loci, alleles) linked to a trait of interest. They are both based on the ability of recombination to break up the genome into fragments that can be correlated with phenotypic trait of interest. The main difference, however, is the control over recombination (Myles et al., 2009). In linkage mapping individuals are crossed to create a mapping population. Here, relatedness is known and recombination breakpoints are few as there has not been enough time to shuffle the genome into small fragments. Phenotypic diversity may also be limited to that of the parental population. On the other hand, in GWAS, genotypic and phenotypic data is often collected from a diverse population, thereby taking advantage of all evolutionary historical recombination events that have occurred (Myles et al., 2009). The number of quantitative trait loci (QTL) or MTAs that can be mapped for a given trait are not limited to what

segregates between the parents of the cross, but rather by the number of real QTL underlying the trait (based on how well the mapping population captures genetic diversity available in nature) (Zhu et al., 2008). In addition association genetics is especially useful with organisms that are difficult to cross and develop mapping populations of, for example, when working with species from the secondary and tertiary gene pool of wheat.

Linkage disequilibrium, the non-random association between two markers or loci, also plays an important role in association genetics (Slatkin, 2008). Genotyped genetic markers that are in strong linkage disequilibrium (LD) with the functional variant(s) can be identified. This is useful when not all functional variant(s) were among the genotyped markers. Markers in LD can become proxies for the functional variant as their genotypes are highly correlated with the genotypes of the functional variant (Myles et al., 2009). Similarly, markers in high LD can also serve as proxies for each other; this is used to determine and optimize the number of non-redundant genetic markers required for association analysis. Linkage disequilibrium varies along the genome and is affected by population structure and size, recombination rates, mutation and inbreeding, among others (Flint-Garcia et al., 2003; Soto-Cerda and Cloutier, 2011). Similarly, for GWAS, the choice of germplasm, genotypic and phenotypic data quality, the use of appropriate statistical models and control for population structure are key for identifying reliable MTAs.

1.6.2 Statistical models

Over the past two decades, due to increased availability of cost-effective next-generation sequencing (NGS) and genotyping technologies, such as SNP arrays, MTAs identified in humans and plants through GWAS exponentially increased (Claussnitzer et al., 2020; Rasheed et al., 2017). GWAS have been historically based on single-locus models that performed one-dimensional genome scans, measuring the effect of one SNP marker at a time. Examples of such models include the general (GLM) (Price et al., 2006) and mixed (MLM) linear models (Yu et al., 2006). These models, however, have inherent limitations; they fail to capture complex traits which

are controlled by multiple loci, particularly those of small effects (Segura et al., 2012). Another problem with single-locus models is the multiple test corrections required for the critical value of a significance test. Here, Bonferroni correction is usually applied, but this type of correction is known to be too conservative; many important small effect loci may not pass the stringent correction (Segura et al., 2012; Zhang et al., 2018c).

To overcome these drawbacks, multi-locus GWAS methods such as restricted two-stage multi-locus GWAS (RTM-GWAS) (He et al., 2017) and multi-locus random-SNP-effect mixed linear model (mrMLM) (Wang et al., 2016) have been developed. Here, QTL or MTAs, are identified by multi-dimensional genome scans, measuring the effects of all SNPs simultaneously. These models follow a two-step algorithm: in the first step, a single-locus GWAS is applied, such as MLM, but a less stringent correction is used to select potential markers. In the second step, all potential markers associated with the trait are evaluated by a distinct multi-locus model. For example, in the first stage of mrMLM, the SNP-effect is treated as random and single-locus MLM GWAS is performed, makers selected from this step are simultaneously evaluated in a second model using an empirical Bayes approach (Wang et al., 2016). In the case of RTM, the model first groups SNPs into linkage disequilibrium blocks (SNPLDBs) and then uses a two-stage analysis for QTL identification, where markers are preselected by a single-locus model followed by multi-locus multi-allele model stepwise regression (He et al., 2017). These models do not require Bonferroni correction, have a higher power for QTN detection and were found superior to single-locus models in identifying small-effect loci for complex associations (Cui et al., 2018; Zhang et al., 2018b).

Candidate genes identified and validated from GWAS can be transferred into adapted germplasm through conventional backcross breeding using gene-specific markers or by modern approaches such as gene pyramiding (gene cassettes) and gene editing (Ahmad et al., 2020; Wulff and Moscou, 2014; Zhang et al., 2016) (**Figure 1.4**).

1.7 Diseases of wheat

Reduced genetic diversity, climate change, and decreased availability of suitable farmland has led to an unprecedented breakout of pathogens that continually threaten local and global wheat production. Biotic factors affecting wheat production include pathogens (fungi, bacteria, viruses), pests (nematodes, insects, mites) and weeds. Of the pathogens, fungi cause the greatest global losses in wheat, whereas bacterial and viral diseases are usually less problematic (Juroszek and von Tiedemann, 2013; Oerke, 2006). Diseases affecting the seed include FHB, common bunt, loose smut and *Stagonospora nodorum* blotch; these directly affect safety of the grain as well as its quality, size, yield, color and odor (Duveiller et al., 2012). Similarly, diseases affecting the leaves include rust (leaf, stem and stripe), powdery mildew, *Septoria* blotch and tan spot and, those affecting stems and roots include stem rust, common root rot and crown and foot rots (Wolf et al., 2011). These diseases can be further classified based on their symptoms, geographical distribution, economic importance and development conditions (humidity, temperature, etc.).

Disease management strategies include cultural, chemical and genetic control practices. Examples of cultural control include crop rotation, tillage and removal or eradication of alternative hosts, while chemical control involves usage of fungicides and pesticides. While chemical control may be costly and raise environmental and health concerns, genetic control to disease is considered more effective, sustainable and environmentally-friendly. The latter involves transferring disease resistance genes into wheat cultivars through conventional and modern breeding strategies as discussed above.

Systematic efforts have led to the identification of several hundreds of disease resistance genes in wheat, however, only a few of them have been isolated and cloned (McIntosh et al., 2017). To date, 32 disease resistance genes have been cloned in wheat, 24 of which are for rust diseases, while the remaining are for powdery mildew, *Septoria* and *Stagonospora nodorum* blotch, tan spot and FHB (Keller et al., 2016; Zhang et al., 2020). Cloning of a resistance gene

reveals its nucleotide sequence, exact chromosomal position and molecular function and enables its transfer for breeding through transgenesis, genome editing, or gene-specific marker-assisted crossing and selection.

1.7.1 Disease response mechanisms

Plant disease resistance is driven by complex mechanisms involving several layers of defense relying on pathogen detection, signal transduction and defence response. Detection of pathogen and damage associated molecular patterns (PAMPs and DAMPs) at the cell membrane leads to pattern-triggered immune (PTI) response and detection of pathogen effectors by intracellular receptors with nucleotide-binding domains and leucine-rich repeats (NLR) leads to effector-triggered immune response (ETI) (**Figure 1.5**) (Andersen et al., 2018). PRRs, WAKs, and NLRs activate a number of signalling cascades including mitogen-activated protein kinase cascades, G-proteins calcium ion signaling, hormone production and transcription factor activity that regulate expression of gene associated with defense response. PTI is often, but not always, achieved without the death of the affected plant cells, while ETI is often associated with programmed cell death of the affected cell, also known as hypersensitive response (HR) (Kanyuka and Rudd, 2019). Other defense responses include cell wall modifications, closure of stomata, or the production of anti-pathogen proteins, inhibits pathogen reproduction and further infection (Andersen et al., 2018).

The majority of plant disease resistance genes encode immune receptors that detect pathogen effectors. In the case of wheat, 23 (72%) of the 32 cloned wheat resistance genes encode NLR receptor proteins that either directly bind to pathogen effectors or indirectly recognize modifications triggered by the effector proteins, activating multiple defense signalling cascades (DeYoung and Innes, 2006; Keller et al., 2016; Zhang et al., 2020). Proteins encoded by other

wheat disease resistance genes include WAKs, protein kinases, transporter proteins and pore-forming toxin-like protein (Keller et al., 2016).

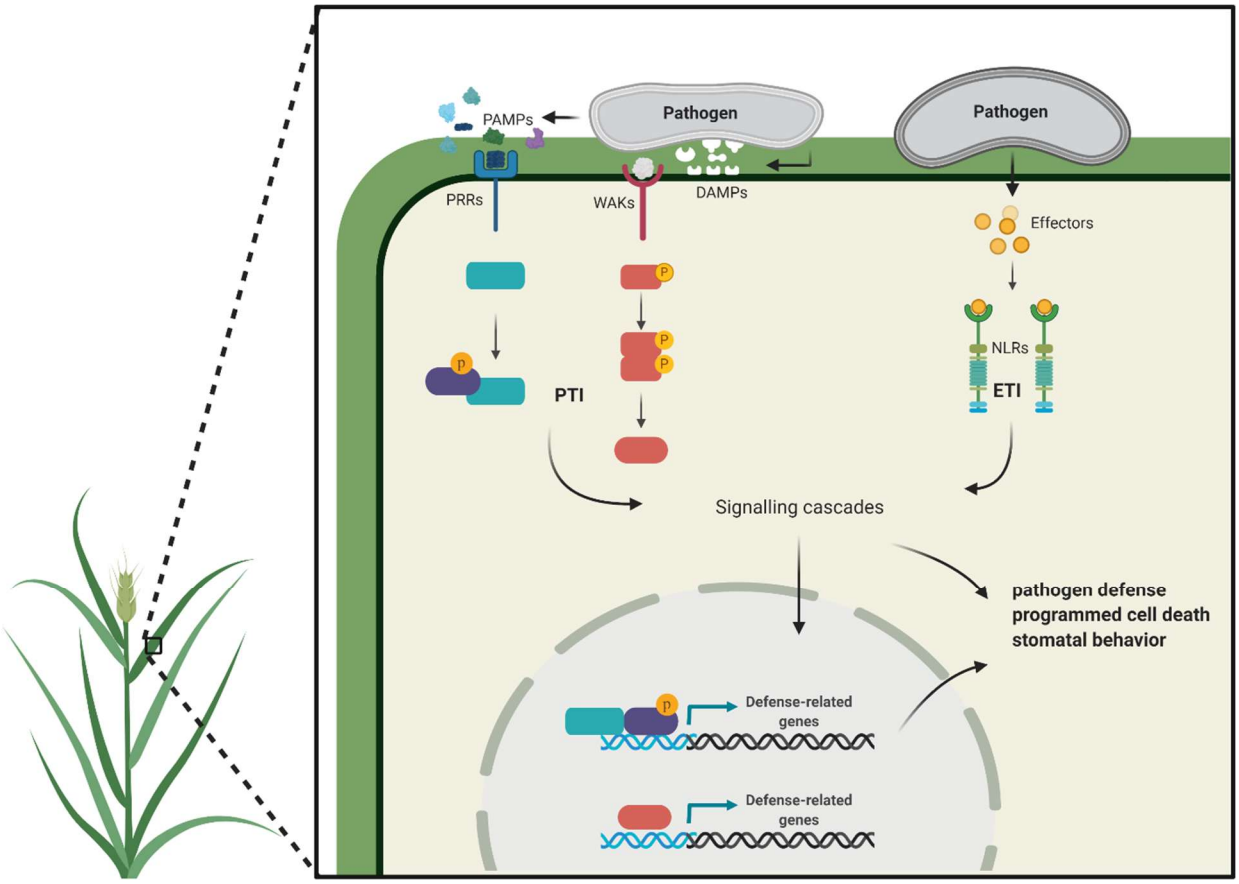

Figure 1.5 A simplified overview of the pathogen response mechanism in plants. PRRs: pattern recognition receptors, WAKs: wall-associated kinases, PAMPS: pathogen-associated molecular patterns, DAMPs: damage-associated molecular patterns, NLR: nucleotide-binding domains with leucine-rich repeats, PTI: pattern-triggered Immunity, ETI: effector-triggered Immunity. Figure created with BioRender.com.

1.8 The scope and purpose of this study

In recent years, a number of GWAS have identified QTL associated with agronomic traits and disease resistance using elite cultivars and landraces of bread and durum wheats. However, these studies were based on traditional single-locus GWAS models whose inherent limitations are now widely recognized. As multi-locus association methodologies are recent, few have been reported in wheat and, the potential for multi-locus GWAS covering a diverse range of cultivated and wild wheat remains largely untested.

This study aims to use SNP array genotyping to explore the phylogenetic relationships within a diverse panel of various *Triticum* and *Aegilops* species and to investigate the genetic basis of disease resistance using SNP array genotyping and multi-locus GWAS. The outcomes of this research will guide decisions for the transfer of useful genetic traits for wheat improvement, a field of research referred to as pre-breeding.

1.8.1 Hypotheses

Genomic regions associated with quantitative phenotypic traits can be identified in a diverse panel of wheat, progenitors and wild relatives using SNP data generated by the wheat 90K array.

SNP data generated by the 90K array can be used to infer phylogenetic relationships between of diverse panel of wheat, progenitors and wild relatives.

1.8.2 Specific objectives

The specific objectives of this study include:

1. To genotype a diverse panel of cultivated wheat, progenitors and wild relatives;
2. To obtain a reliable SNP dataset by appropriate SNP filtering and validation;
3. To enhance our understanding of the evolutionary relationships between the *Triticum* and *Aegilops* species represented in the collection;
4. To perform association analysis for disease resistance traits using multiple GWAS models;
5. To annotate QTL identified for gene function using the wheat reference genome annotation;
6. To cross-check QTL identified against known genes previously reported in the literature;
7. To identify and map novel QTL in the germplasm;

The challenges and limitations of this study include ascertainment bias, genotyping complexities due to polyploidy, and lack of scientific literature available for some of the wild relatives included in the germplasm collection. Apart from *Ae. tauschii,* the majority of the accessions included in the development of the high-density 90K array were cultivars of bread and durum wheats (Wang et al., 2014). Ascertainment bias may exist when calling genotypes of the various wild relatives and progenitor species, resulting in failure to capture rare alleles and incorrect genotype calling. Genotyping is also complicated by the inherent complexities associated with the polyploid nature of wheat. Depending on the sequence similarities between probes and targets, a SNP probe may hybridize to the homoeologous and/or paralogous loci of the target, thereby affecting the allele-specific fluorescent signal ratios, and further complicating genotype clustering (Rasheed et al., 2017; Wang et al., 2014). Moreover, the majority of the GWAS studies reported in wheat are for cultivated varieties and their closely related progenitor species, and only a few such association and diversity analysis studies exist for its wild relatives. As 19 different species of wild wheat relatives are included in this study, research ambiguities and literature gaps are anticipated to constitute additional challenges for efficient and accurate germplasm data analysis.

Chapter 2

2 Identification of new leaf rust resistance loci in wheat and wild relatives by array-based SNP genotyping and association genetics

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Authors' contributions:

FF performed the data analysis and wrote the manuscript; FY provided bioinformatics and statistics guidance; BDM, SC and CP performed leaf rust severity phenotyping; BDM performed race-specific phenotyping; CM and CH produced the wheat 90K array data; GF co-developed the original experiment and provided some of the key germplasm; SC designed the experiment and co-wrote the manuscript.

Chapter 2

2.1 Abstract

Leaf rust caused by *Puccinia triticina* is the most widespread rust disease of wheat. As pathogen populations are constantly evolving, identification of novel sources of resistance is necessary to maintain disease resistance and stay ahead of this plant-pathogen evolutionary arms race. The wild genepool of wheat is a rich source of genetic diversity, accounting for 44% of the *Lr* genes identified. Here we performed a genome-wide association study (GWAS) on a diverse germplasm of 385 accessions, including 27 different *Triticum* and *Aegilops* species. Genetic characterization using the wheat 90K array and subsequent filtering identified a set of 20,501 single nucleotide polymorphic (SNP) markers. Of those, 9,570 were validated using exome capture and mapped onto the Chinese Spring reference sequence v1.0. Phylogenetic analyses defined four major clades, clearly separating the wild species from the *T. aestivum* and *T. turgidum* species. GWAS was conducted using eight statistical models for infection types against six leaf rust isolates and leaf rust severity rated in field trials for 3-4 years at 2-3 locations in Canada. Functional annotation of genes containing significant quantitative trait nucleotides (QTNs) identified 96 disease-related loci associated with leaf rust resistance. A total of 21 QTNs were in haplotype blocks or within flanking markers of at least 16 known *Lr* genes. The remaining significant QTNs were considered loci that putatively harbor new *Lr* resistance genes. Isolation of these candidate genes will contribute to elucidate their role in leaf rust resistance and promote their usefulness in marker-assisted selection and introgression.

Keywords: wheat, leaf rust, GWAS, QTN, genotyping array, single nucleotide polymorphism

2.2 Introduction

Triticum aestivum, commonly known as bread wheat, is an allohexaploid (AABBDD) species, created through the sequential hybridization of three grass species: *T. urartu* (AA), a species (BB) closely related to *Aegilops speltoides* (SS) and *Aegilops tauschii* (DD) (McFadden and Sears, 1946). Genetic diversity bottlenecks such as polyploidization, domestication, and natural and artificial selections have reduced diversity in modern wheat, and consequently increased its vulnerability to diseases, pests and environmental stresses (Tanksley and McCouch, 1997).

Leaf rust caused by *Puccinia triticina* is the most prevalent wheat rust disease, causing tremendous annual yield losses. *Puccinia triticina* attacks the foliage, covering its surface and thus causing loss of photosynthates, dehydration and early defoliation. Genetic resistance combatting yield losses can be categorized into seedling resistance and adult plant resistance (APR). Typically, seedling resistance is controlled by single major effect genes that confer hypersensitive and other responses, causing necrosis and preventing the pathogen from spreading (Dyck and Kerber, 1985). APR occurs at a post-seedling stage and confers either a race-specific or a quantitative race non-specific response (Dyck and Kerber, 1985; Samborski, 1985).

To date, 66 leaf rust resistance (*Lr*) genes have been characterized, six of which, namely *Lr1* (Cloutier et al., 2007), *Lr10* (Feuillet et al., 2003), *Lr21* (Huang et al., 2003), *Lr22a* (Thind et al., 2017), *Lr34* (Krattinger et al., 2009) and *Lr67* (Moore et al., 2015), have been isolated. The majority of the *Lr* genes described to date confer seedling-type resistance. Well-known APR genes include the race-specific *Lr12* (Dyck et al., 1966) and *Lr13* (Dyck et al., 1966) and the race non-specific *Lr34* (Dyck, 1977) and *Lr67* (Hiebert et al., 2010). Of the 66 *Lr* genes designated to date, 37 were identified in *T. aestivum* and *T. turgidum* and 29 originated from progenitors and other wild relative species such as *Ae. tauschii, Ae. speltoides, Ae. neglecta* and *Ae. peregrina*, among others (McCallum et al., 2012; USDA, 2017).

Chapter 2

The traditional approach for introgressing *Lr* genes into adapted germplasm is by interspecific crossing a donor line to an adapted line followed by backcrossing. Although many *Lr* genes have been described, few are utilized by present-day breeders because they have either been overcome by virulence changes in the pathogen populations, are not in an adapted background or suffer from linkage drag. Modern approaches, such as gene cassettes and genome editing may overcome some of the disadvantages of the crossing method and have been proposed to provide long-lasting broad spectrum resistance (Arora et al., 2019; Keller et al., 2016). However, commercialization of transgenic wheat has not received broad acceptance and introgression via crossing remains commonly used.

Identification of novel sources of resistance in the cultivated and the wild genepools of wheat is expected to contribute to broadening and maintaining the genetic base of leaf rust resistance. Array-based SNP genotyping platforms provide fast and cost-effective access to genetic variation in a diverse germplasm. In wheat, the Illumina's Infinium iSelect and Affimetrix's Axiom array technologies enable simultaneous genotyping of 9,000 to 819,571 SNP markers (Cavanagh et al., 2013; Winfield et al., 2016). Genome-wide association studies (GWAS) associate such genotypic data to phenotypic data to identify significant marker-trait associations. To date, numerous quantitative trait loci (QTL) associated with leaf rust resistance in elite cultivars and landraces of bread and durum wheats have been discovered (Aoun et al., 2016; Gao et al., 2016; Riaz et al., 2018). These QTL were identified based on traditional single-locus GWAS models whose inherent limitations, such as failure to capture complex traits controlled by multiple loci, are now widely recognized (Segura et al., 2012). Multi-locus GWAS models overcome these drawbacks by performing a multi-dimensional genome scan, and measuring the effects of multiple SNPs simultaneously to identify small-effect loci for complex traits (Wen et al., 2018). As multi-locus association methodologies are recent, few have been reported in wheat and the potential

for multi-locus GWAS covering a diverse range of cultivated wheat and wild relatives remains largely untested.

Here, we performed a GWAS for leaf rust severity and reaction types against six *P. triticina* isolates in a highly diverse germplasm of 385 accessions. The wheat 90K array was used to capture the genetic variation in cultivated wheats, progenitor species, synthetic hexaploid wheats (SHWs) and wild relatives (Wang et al., 2014). We used one single-locus and seven multi-locus models to identify quantitative trait nucleotides (QTNs) which were mapped on the reference genome, thus validating known loci and identifying new loci to be mined for novel candidate leaf rust resistance genes.

2.3 Materials and methods

2.3.1 Plant materials

A diverse collection of 385 accessions, encompassing 27 different species of cultivated wheats, SHWs, progenitor species and wild relatives were used in this study (**Appendix 1A**). The geographical origin of these accessions traverse 51 different countries (**Appendix 1B**). The AB and ABD genomes are represented by 170 accessions representing *T. vavilovii* and several subspecies of *T. turgidum* and *T. aestivum* as well as 65 primary SHWs. The A, B and D genome progenitors (or their closely related species) and the non-domesticated forms of tetraploid wheat comprised 93 accessions of *T. urartu* (A), *T. monococcum* (A^m), *Ae. tauschii* (D), *Ae. speltoides* (S), as well as *T. turgidum* ssp. *dicoccon* and *dicoccoides* (AB). Another 47 accessions belonged to the following *Aegilops* species: *Ae. bicornis* (S^b), *Ae. longissima* (S^l), *Ae. searsii* (S^s), *Ae. sharonensis* (S^{sh}), *Ae. markgrafii* (C), *Ae. comosa* (M), *Ae. umbellulata* (U), *Ae. geniculate* (MU), *Ae. peregrina* (SU), *Ae. triuncialis* (UC/CU), *Ae. columnaris* (UM), *Ae. cylindrica* (DC), *Ae. crassa* (DM/DDM), *Ae. juvenalis* (DMU), *Ae. biuncialis* and *Ae. neglecta* (UM/UMN). The collection also contained six accessions of *T. timopheevii* (A^tG), five of *T. zhukovskyi* (GAA^m), and one of

Haynaldia villosa (V), a related grass species. Overall, the germplasm consisted of 75 diploid, 136 tetraploid, 165 hexaploid and nine accessions that could be either tetraploid or hexaploid. The species names and genome symbols are according to (Kimber and Tsunewaki, 1988).

2.3.2 Seed increase

Seeds were planted and grown under controlled conditions at the Ottawa Research and Development Centre (RDC), Agriculture and Agri-Food Canada (AAFC) (Ottawa, Canada). Depending on their growth habit, the seeds were divided into a spring and a winter panel of 213 and 164 accessions, respectively . For the spring panel, the growth conditions were 20°C/16 hours light, and 16°C/8 hours dark. The winter panel was grown under the same conditions for approximately three weeks, i.e., the 4-5 leaf stage, at which time they were transferred to a vernalization cabinet (constant 2°C/12 hours photoperiod) for ten weeks to trigger meristem differentiation prior to being returned to the original growing conditions. Seeds harvested from all accessions were used for the greenhouse and field experiments described below.

2.3.3 Leaf rust race-specific response

Consecutive inoculations with six *P. triticina* isolates were performed for 360 of the 385 accessions of the panels (**Appendix 2**). The removed 25 accession consisted of those with >90% missing data or accessions removed from the collection due to ambiguities in their species classification. All tests were performed under controlled greenhouse conditions at the Morden RDC, AAFC (Morden, Canada). Briefly, test lines and the Thatcher and Emerson check lines were sown into fibre trays at a rate of approximately 5 seeds per clump and 3cm between clumps, which were inoculated with individual *P. triticina* isolates at the two-leaf stage (McCallum and Seto-Goh, 2006). The isolates tested were 12-3 MBDS, 128-1 MBRJ, 74-2 MGBJ, 11-180-1 TDBG, 06-1-1 TDBG, and 77-2 TJBJ, which represent the prevalent leaf rust race groups across Canada (McCallum et al., 2016). For simplicity, these will be referred to as MBDS, MBRJ, MGBJ,

TDBG1, TDBG2, and TJBJ, respectively. Infection type (IT) was rated 12 days post-inoculation using a 0–4 scale (Stakman et al., 1962), where ";" = hypersensitive flecks, "0" = no uredinia (reddish pustule like structure of hyphae and spores) or macroscopic sign of infection, "1" = small uredinia with necrosis, "2" = small to medium uredinia with chlorosis, "3" = medium uredinia without chlorosis or necrosis, "4" = large uredinia without chlorosis or necrosis. IT ";" and "0" to "2" were considered resistant, while "3" and "4" were considered susceptible (Long and Kolmer, 1989). The "+" or "-" IT qualifiers indicate larger or smaller than average uredinia, respectively. The "=" IT qualifier represents the lower size limit of the uredinia for the IT (Long and Kolmer, 1989). Plants with randomly distributed uredinia of variable sizes, or mesothetic (intermediate) response, were considered resistant and were rated with an "X" IT (Roelfs and Martens, 1988).

For downstream analysis, the IT scores were converted into a 1-9 linear scale, where "0/0;/;" = 1, ";1=/;1-" = 2, "1-/1/1+" = 3, ";12/1-2-" = 4, "2-/2/2+" = 5, "X" = 6, "3-/3/3+" = 7, "3+4/34" = 8, and "4" = 9 (**Appendix 2**). Scores 1-6 correspond to resistant reaction types while 7-9 are characteristic of susceptible reaction types, i.e., with medium to large uredinia.

2.3.4 Field leaf rust severity

Phenotyping of rust severity was performed in separate field trials for the spring and winter panels. The spring panel included 213 accessions, of which 20 were SHWs, while the remaining were subspecies of *T. aestivum* and *T. turgidum*. Trials for the spring panel were carried out in Morden, Manitoba, Canada (2016-2019), Ottawa, Ontario, Canada (2017-2019) and Saskatoon, Saskatchewan, Canada (2019). The winter panel comprised 164 diverse *Aegilops* and *Triticum* species, including 115 progenitors and wild relatives, 45 SHWs, and four winter wheat cultivars. Screening for the winter panel was performed in Morden (2017-2019) and in Ottawa (2017 & 2019).

For each panel, year and location, a completely randomized design with two replicates was used, except for the 2016 Morden field trial where a single replicate was used due to the limited seed availability in the first year. For the spring panel, 65 seeds/accession were planted in 1m-long rows with 20cm between rows. A mixture of *P. triticina* isolates was inoculated onto spreader rows of susceptible lines Thatcher, Morocco, and Little Club, planted every six test rows in Morden and every ten in Saskatoon. The mixture of isolates comprised more than 50 different virulence phenotypes representing the *P. triticina* population in western Canada identified during the annual virulence survey. In Ottawa, infection relied on natural inoculum but used the same interspersed spreader-row design as Morden with the Morocco spreader. Cultivars Thatcher, Roblin and Eurostar were used as checks and five plots of each were randomly distributed across each replicate.

For the winter panel, ten seeds/accession were planted indoors in early March at both Morden and Ottawa RDCs. At the 3-5 leaf stage, the plants were transferred into vernalization chambers as described above. Approximately ten days after planting the spreader-rows, the vernalized plantlets were transplanted as hills in the field. The cultivar Emerson served as a check. At peak infection and prior to senescence, the flag leaves were rated for leaf rust severity using a modified Cobb's scale (Peterson et al., 1948).

Leaf rust severity ratings across locations and years were modelled using the R package *Lme4* (Bates et al., 2014) with the following mixed linear model (MLM) equation:

$$Y_{ijk} = \mu + G_i + L_j + Y_k + GL_{ij} + GLY_{ijk} + e_{ijk}$$

where Y_{ijk} is the leaf rust severity measured, μ is the overall mean, G_i is the effect resulting from the i^{th} genotype, L_j is the effect resulting from the j^{th} location, Y_k is the effect resulting from the k^{th} year, GL_{ij} and GLY_{ijk} are the effects resulting from genotype × location and genotype × location x year interactions, respectively, and e_{ijk} is the residual error (effect resulting from

experimental error). In this model, location was considered a fixed effect, while year, genotype and interaction were considered random. The *lmerTest* package was used to generate an ANOVA-like table for the random effects and calculate *P*-values from the Satterthwaite's t-tests for the fixed effect (Kuznetsova et al., 2017). Best linear unbiased predictors (BLUP) estimates, also known as conditional means, were extracted for the random effects to account for environmental deviations and provide more precise estimates of phenotypic values (**Appendix 3**) (Mi et al., 2011; Wang et al., 2017).

2.3.5 Genotyping and SNP filtering

Young leaf tissue (75-100mg) from the germplasm grown in growth chambers was sampled at the 4-5 leaf stage. The DNA was extracted using the DNeasy Plant kit (Qiagen, Valencia, CA, USA) and quantified using the Quant-it PicoGreen kit (Thermo Fisher, Waltham, MA, USA). Genotyping was performed using the wheat 90K array (Illumina, San Diego, CA, USA) on the iScan instrument (Wang et al., 2014).

Genotype calling was performed for the entire collection using the default genotyping module, and separately for the different ploidy levels using the polyploidy module in GenomeStudio software v2.0.4 (Illumina). The tetraploid and hexaploid sets also included the nine accessions of unknown ploidy. The SNP markers with >20% missing data, <5% minor allele frequency (MAF), and >5% heterozygosity were removed. For the polyploid module, markers with >3 clusters were also removed (Hourcade et al., 2019).

2.3.6 SNP validation

To validate the filtered SNP dataset, we used an exome dataset obtained from 136 accessions of the panels. First, the position of the SNP markers in the protein coding regions of the Chinese Spring (CS) reference genome v1.0 was obtained by mapping the SNP probe sequences of the wheat Infinium array to the exome sequence of all the high-confidence annotated genes of the

CS reference sequence and their 5Kb upstream and downstream sequences (IWGSC, 2018; Wang et al., 2014). The SNP probes were aligned to the indexed exome reference sequence using the MEM-BWA algorithm (v0.7.12, http://bio-bwa.sourceforge.net/). Samtools (v1.3, http://samtools.sourceforge.net/) was used to generate and sort the BAM file alignment. The positions of the mapped SNPs were extracted using BBMap (v.38.43 https://sourceforge.net/projects/bbmap/). The mapped SNP probes were filtered using R to remove the misaligned probes and their coordinates were converted to their actual positions on the CS reference genome v1.0 (IWGSC, 2018).

Upon mapping of the SNP markers, the genotyping dataset was re-filtered with the following updated criteria: markers with <80% of χ_i missing data, <5% MAF, and >5% heterozygosity were removed, where χ_i is the proportion of each sub-genome represented in the germplasm. This less stringent criterion ensures retention of SNPs from underrepresented sub-genomes. The positions of the filtered SNPs from the wheat 90K array was compared to the variant call results of the exome-sequence data obtained from 136 of the 385 accessions (**Appendix 1A**). The exome sequencing data were obtained using the Nimblegen SeqCap EZ wheat exome design (120426_Wheat_WEC_D02, https://sequencing.roche.com/en/products-solutions/by-category/target-enrichment/shareddesigns.html). Raw reads were mapped to the same exome reference genome using the BWA-Samtools pipeline, and variant calling was performed using Bcftools (v1.3, https://samtools.github.io/bcftools/bcftools.html). SNPs common between the filtered wheat 90K array and the exome capture datasets were identified using Bcftools.

2.3.7 Phylogenetic relationships, population structure and kinship

To illustrate evolutionary relationships between the species in the collection, the filtered set of SNPs was used to perform a phylogenetic analysis. A maximum likelihood (ML) tree was generated with 1,000 bootstrap iterations using the default parameters of MEGA-CC (Nearest-Neighbor-Interchange heuristic and Tamura-Nei models) (Kumar et al., 2012). The tree was graphically displayed using iTol v3 (Letunic and Bork, 2016). PCAs were performed using the filtered set of SNPs for each ploidy level and the results were displayed using the R package *Scatterplot3d* (Ligges and Maechler, 2003).

Population structure analyses were carried out using the R packages *LEA* (Frichot and François, 2015) and *PCAdapt* (Luu et al., 2017), as well as the software Admixture v1.3 (Alexander et al., 2009). Both *LEA* and *PCAdapt* estimate structure using PCA-based methods. The proportion of variance explained by each PC was graphically illustrated in the form of scree plots. The “knee” in the scree plot (Cattell’s rule) was used to determine the number of sub-populations. Admixture is an ML-based approach which uses cross-validation to approximate the K number of sub-populations (Alexander and Lange, 2011). Cross-validation errors for K=2-30 were graphically illustrated using R and the value of K was selected using the rule described above. The approximate number of sub-populations was selected based on the congruity between the plots. The SNMF approach in *LEA* was used to visualize ancestry proportions in the Q matrix through structure plots. The kinship coefficient matrix was generated using Tassel v5.0 (Bradbury et al., 2007).

2.3.8 Genome-wide association analysis

GWAS was conducted for race-specific response and leaf rust severity rated in the field. For the race-specific response, the converted IT scores for each isolate were considered as individual

traits. For leaf rust severity, genotypic and location-specific BLUP estimates were used as phenotypic inputs, where the former summarizes the severity ratings across all locations and years, and the latter represents the severity ratings separately for each location.

GWAS was performed using one single-locus and seven multi-locus models. The MLM in Tassel v5.0 (Bradbury et al., 2007) was used for single-locus association analysis. Here, population structure and kinship were accounted for using K principle components and the Tassel-generated kinship matrix. The *P*-values were adjusted using the false discovery rate (FDR) (Benjamini and Hochberg, 1995). QTNs with FDR (False discovery rate) -adjusted *P*-values<0.05 were considered significant.

Of the seven multi-locus models, the six from the R package *mrMLM* (Wen et al., 2018) were mrMLM (Wang et al., 2016), FASTmrMLM (Tamba and Zhang, 2018), FASTmrEMMA (Wen et al., 2018), pLARmEB (Wang et al., 2016), pKWmEB (Ren et al., 2018) and ISIS EM-BLASSO (Tamba et al., 2017). The Q matrix generated by Admixture and the Tassel-generated kinship matrix were used to account for population structure and kinship. The seventh multi-locus model, RTM-GWAS, first grouped SNPs into linkage disequilibrium blocks (SNPLDBs) and then utilized a restricted two-stage multi-locus analysis for QTL identification (He et al., 2017). Here, population structure was accounted for by the RTM-generated covariate matrix and kinship and by the Tassel-generated kinship matrix. As with the single-locus MLM, the *P*-values of QTNs from all the multi-locus models used the same FDR-adjusted threshold. Allelic effect of QTNs was determined using the Kruskal–Wallis statistics to test the phenotypic variation of the associated traits between homozygous alleles.

2.3.9 *In silico* annotation of significant markers

Because only markers that aligned to the exome sequence of the CS reference genome v1.0 were used for the association analyses, all significant QTNs were within or close to high-

confidence annotated genes. Transcript IDs of the genes containing the significant QTNs were used to extract the protein products using EnsemblPlants (https://plants.ensembl.org/Triticum_aestivum/Info/Index) (IWGSC, 2018; Kersey et al., 2016). For significant SNPLDBs detected by RTM-GWAS that contained multiple SNPs, annotation was carried out for the first and last SNP marker of each SNPLDB.

2.3.10 Positioning *Lr* genes and QTNs onto the wheat reference sequence

Sequences coding for the six previously cloned *Lr* genes were retrieved from GenBank and mapped against the CS reference sequence v1.0 (IWGSC, 2018) using default BLASTn parameters (Expect threshold = 10, Word size = 15, Match/Mismatch scores =2,-3) on the Graingenes website (https://wheat.pw.usda.gov/cgi-bin/seqserve/blast_wheat.cgi). Through the same exercise, sequences of flanking or co-segregating markers were also mapped onto the reference genome so that a total of 55 of the 66 *Lr* genes were positioned (**Appendix 4**). A physical map of previously cloned or mapped *Lr* genes was constructed using the R package *KaryoploteR* (Gel and Serra, 2017). Linkage between the QTNs detected and known *Lr* genes, or their markers, was determined using haplotype block analysis. The SNP dataset was split into haplotype blocks using the R package *gpart* (Kim et al., 2019) and pairwise linkage disequilibrium between the SNPs was calculated using Tassel v5.0 (Bradbury et al., 2007). Known *Lr* genes and QTNs within the same haplotype block were considered linked, while the relationship between those in neighbouring blocks was determined by comparing *D'* statistics between the blocks.

2.4 Results

2.4.1 Race-specific resistance

IT response against six *P. triticina* isolates (MBDS, MBRJ, MGBJ, TDBG1, TDBG2, and TJBJ) was evaluated in the greenhouse for 360 accessions. Of these, 156, 171, 173, 177, 209 and 206 accessions were resistant (IT rating < 3, linear score < 7) to isolates MBDS, MBRJ, MGBJ, TJBJ, TDBG1 and TDBG2, respectively (**Appendix 2 and 5**). The resistant accessions included 85-131 SHW and cultivated species, 44-56 progenitors and 25-32 wild relatives. Overall, a total of 102 accessions were resistant to all six isolates, and another 153 to at least five isolates.

2.4.2 Field resistance

Phenotypic variation across the different environments was modelled. For both spring and winter panels, the year effect explained the smallest proportion of the variance with 2.1% and 0.31% for each panel, respectively, while the largest proportion was accounted for by the genotype effect with 43.0% and 60.2%, respectively (**Appendix 6**). The *P*-values from Satterthwaite's t-tests were <0.005 for all location effects and the genotype-location interaction explained 16.7% and 21.1% of the variation in the spring and winter panels, respectively. The genotypic and location-specific BLUP estimates were extracted from the models and compared to raw aggregate genotypic and location-specific mean values. A linear relationship was observed between the raw mean values and BLUP estimates (**Appendix 7 (a,b)**). However, due to the inherent nature of BLUP estimation to shrink outliers to the mean, the interquartile ranges (Q3-Q1) of location-specific BLUP estimates were smaller than the raw mean values (**Appendix 7 (c-f)**).

In the spring panel, 73 accessions were rated resistant (average severity <10%) and 70 were moderately resistant (11-30% average severity) (**Appendix 8 (a)**). The majority of the moderately resistant to resistant accessions belonged the subspecies of *T. turgidum* (**Appendix 3 (a)**). In the winter panel, respectively 90 and 38 accessions were rated resistant and moderately

resistant; these included 52 progenitors, 36 wild relatives and 12 SHWs (**Appendix 8 (b)**, **Appendix 3 (b)**). These distributions, however standardized, were also reflected in the genotypic BLUP estimates calculated for each panel (**Appendix 8 (c,d)**).

2.4.3 SNP filtering, mapping and validation

A total of 27,418 SNPs from the 385 accessions had a call rate >80%, of these, 20,501 had a MAF >5% and a maximum heterozygosity <5%. Genotype calling and filtering performed separately for the three ploidy levels yielded 34,614 SNPs in the hexaploid, 24,142 in the tetraploid and 15,364 in the diploid datasets. Of the 43,804 SNPs in the hexaploid and tetraploid accessions, 14,952 SNPs (34.13%) were shared (**Figure 2.1a**). A total of 7,243 SNPs (47.2%) in the diploid dataset were shared with the hexaploid, while only 3,877 SNPs were shared between the tetraploid and diploid datasets.

Mapping was performed to locate the position of the 81,587 SNPs of the wheat Infinium assay on the exome sequence of the CS reference genome v1.0 (IWGSC, 2018). A total of 52,550 SNP marker sequences were successfully mapped, of which 43,013 were retained after filtering out the misaligned probes (**Appendix 9**). Exome-capture sequencing and subsequent variant calling of 136 accessions identified a total of 142,181,095 SNPs, of which 27,852 were part of the 43,013 mapped SNPs from the array. Re-filtering of the genotyping dataset from the complete germplasm (call rate >80% of χ_i, MAF>5%, and heterozygosity <5%) positioned 12,627 SNPs on the exome reference genome, including 9,570 that were also called using exome capture. The chromosomal distribution of these 9,570 filtered and mapped SNP loci is illustrated (**Figure 2.1b)**.

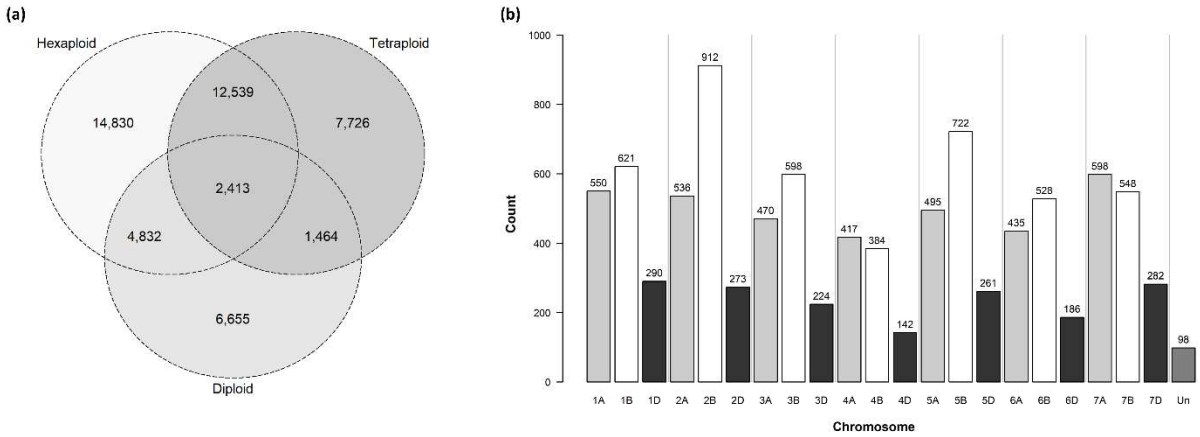

Figure 2.1 Filtered single nucleotide polymorphism (SNP) markers.
(a) Shared SNPs between the hexaploid, tetraploid and diploid datasets. (b) Distribution of 9,570 filtered and validated SNPs across the chromosomes of the CS reference genome v1.0 (IWGSC, 2018).

2.4.4 Phylogenetic relationships and principal component analysis

A ML phylogenetic tree was constructed to determine the relationships between the species in the collection (**Figure 2.2**). Four main clades were observed. The first consisted of all the *Aegilops* and non-domesticated *Triticum* species, where accessions clustered based on their shared sub-genomes. The second and largest clade comprised accessions with the ABD genome: SHWs, *T. vavilovii* and *T. aestivum* subspecies. The other two clades were primarily a mixture of *T. turgidum* subspecies and SHWs. Ancient tetraploid species *T. turgidum* ssp. *dicoccum* (emmer wheat) and the non-domesticated *T. turgidum* ssp. *dicoccoides* formed one clade, while modern cultivated species, such as *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *carthlicum*, formed the other. SHWs were distributed between these clades based on their tetraploid parent species. All *T. aestivum* ssp. *spelta* clustered with the ancient tetraploid species.

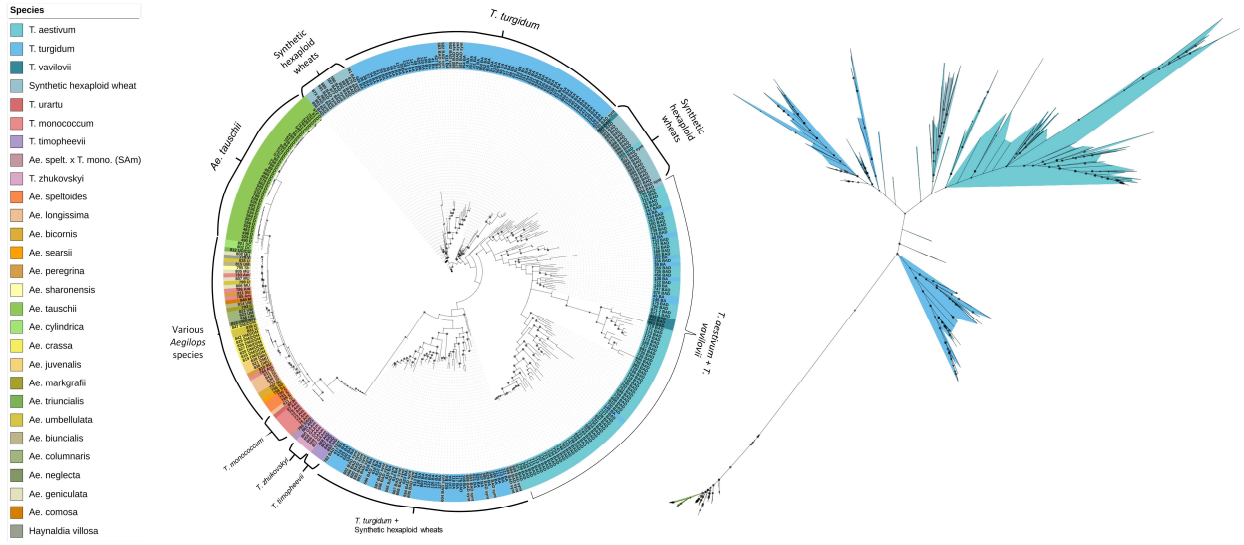

Figure 2.2 Phylogenetic trees illustrating the relationships between species.
The tree was generated using the maximum likelihood approach with 1,000 bootstrap iterations. Both rooted (left) and unrooted (right) trees are shown. The size of the internal node symbols reflects the bootstrap confidence level and the leaf node labels correspond to the identification number and genome of each accession. The species are color-coded as indicated in the legend.

PCA was performed to assess the genetic variation at different ploidy levels. In the hexaploid dataset, the first three PCs explained 29.0% of the variation (**Figure 1.3a**). Three to four main clusters were observed: the ABD genome species, *T. aestivum* and *T. vavilovii*, formed one cluster, *Ae. crassa* (DM/DDM) and *Ae. juvenalis* (DMU) formed a second closely related cluster, while *Ae. neglecta* (UM/UMN) and *T. zhukovskyi* (GAA^{m}) clustered into two distinct groups. Similarly, in the tetraploid dataset, the first three PCs explained 28.3% of the variation (**Figure 2.3b**). Here, *T. turgidum* subspecies clustered into three groups, while *T. timopheevii* ($A^{t}G$), *Ae. crassa* and *Ae. cylindrica* (DC) clustered into individual groups. Accessions belonging to species with the U or M sub-genome (*Ae. geniculata*, *Ae. peregrina*, *Ae. triuncialis*, *Ae. biuncialis*, *Ae. columnaris* and *Ae. neglecta*) clustered together. In the diploid dataset, the first three PCs explained 39.9% of the variation. *Ae. tauschii* (D) accessions clustered into two groups, *Ae. speltoides* (S) and *T. monococcum* (A^{m}) clustered separately, and nine other species, each

represented by few accessions, all clustered as individual groups (**Figure 2.3c**). Eight accessions did not cluster with other individuals of their respective species. They were assumed to have been mis-labeled and were removed from the datasets (**Appendix 10**).

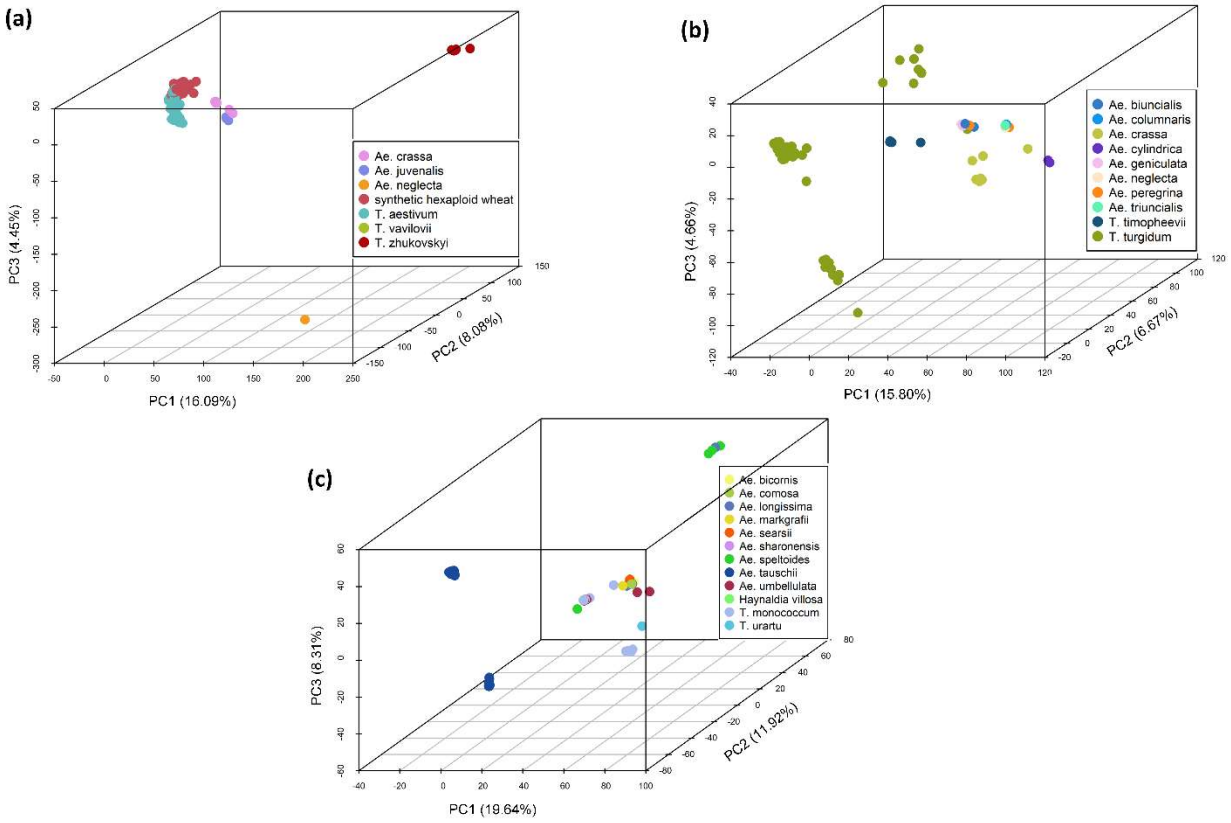

Figure 2.3 Scatter plots of the first three principal components at each ploidy level. Accessions in the (a) hexaploid, (b) tetraploid, and (c) diploid datasets are colored based on their species. The percentages of the variance explained by each principal component are in brackets on the axes.

2.4.5 Genome-wide association analysis

GWAS was performed using IT scores against six *P. triticina* isolates and the leaf rust severity measured in multiple field environments. The population structure was estimated using three tools and the optimal number of sub-populations was selected based on agreement between methods. For IT scores, K=8 was selected (**Appendix 11 (a)**) and ancestry proportions from Admixture

were used to survey the population structure. Here, the *T. aestivum* and *T. turgidum* subspecies were divided into two and four populations, respectively, while the wild relatives formed two separate populations. For the spring panel rated in the field, K=8 was also suggested (**Appendix 11 (b)**), where groupings on a subspecies level were observed for the *T. aestivum*, *T. turgidum* and SHWs of this panel. For the winter panel, K=6 was selected (**Appendix 11 (c)**). Here, the SHWs were grouped into three populations, *T. timopheevii* and *T. zhukovskyi* grouped together, while the remaining wild relatives formed two separate populations. The *LEA* structure plots for the three population structure analyses are shown in **Appendix 12**.

GWAS was conducted using one single-locus and seven multi-locus models, all of which accounted for kinship and population structure. For IT response, the single-locus MLM identified five QTNs for which the proportion of variance explained (r^2) ranged from 6-12% (**Appendix 13**). Of these, four QTNs were identified for response against the isolate MBDS. The six multi-locus models from *mrMLM* identified a total of 116 unique QTNs across the genome, of which 32 were identified by more than one model and 23 were associated to more than one isolate (**Appendix 13**). Of note, markers Tdurum_contig18471_456 and IAAV6025 associated with MBDS and Kukri_c12869_154 associated with TDBG1 had r^2 values >27%, while r^2 values ranged from 1-23% for the remaining QTNs. RTM, the seventh multi-locus model, grouped the SNPs into 7,607 SNPLDBs and identified 15 QTL with r^2 of 4-15%, including eight that had previously been detected by other multi-locus models (**Appendix 13**). Of the five QTNs identified by single-locus GWAS, four were identified by at least one of the seven multi-locus models.

Table 2.1 Number of QTNs or SNPLDBs identified by each statistical model
Table shows quantitative trait nucleotides (QTNs) and significant SNP linkage disequilibrium blocks (SNPLDBs) identified for both infection type (IT) and leaf rust (LR) severity.

Model	IT	LR severity spring panel	LR severity winter panel	Total
Single-locus				
MLM	5	1	4	10
Multi-locus				
FASTmrEMMA	14	14	1	29
FASTmrMLM	33	20	8	61
ISIS EM-BLASSO	30	22	14	66
mrMLM	54	36	10	100
pKWmEB	38	30	10	78
pLARmEB	41	25	13	79
RTM	15	21	16	52
Total	230 (124)	169 (104)	76 (53)	

Values in parentheses indicate the number of non-redundant loci i.e. loci identified by at least one statistical model

GWAS for leaf rust severity was conducted separately for the spring and winter panels. MLM identified five significant QTNs (r^2=18-24%), all of which were associated with leaf rust severity in Morden and located in the D sub-genome (**Appendix 14**). In the spring panel, *mrMLM* identified 85 unique QTNs (r^2=1-22%) associated with leaf rust severity, of which 30 were identified by more than one model and 57 were location-specific (**Appendix 14**). In the winter panel, 38 QTNs were identified including 10 by more than one model and one at both Morden and Ottawa locations (**Appendix 14**). Marker wsnp_Ex_c6548_11355524 on 5B explained the highest proportion of the variance (40%), while r^2 of the remaining QTNs ranged from 2-24%. RTM identified 37 QTL in the two panels, including seven that were also identified by other multi-locus models (**Appendix 14**). Overall, five QTNs associated with leaf rust severity were also associated with race-specific IT response against at least one isolate. The number of QTNs identified by each model, for both, IT response and leaf rust severity, are shown in **Table 2.1**. For each phenotypic dataset, the multi-locus model mrMLM identified the highest number of QTNs, while the single-locus model MLM identified the fewest.

2.4.6 Functional annotation

The transcript IDs of the genes within 5Kb of one or more QTN were extracted along with their functional annotation. Between 79-85% of the QTNs associated with race-specific IT response and leaf rust severity were annotated for gene function. These included genes involved in signaling pathways, metabolism, transport and DNA replication and repair. The complete annotation list of the QTNs within or nearby genes is compiled in **Appendix 15**.

A total of 46 loci associated with IT scores were within 5Kb of genes coding for known plant disease resistance proteins, including seven CC-NBS-LRR, nine F-box-like domain-containing proteins, seven proteins with kinase domains and three alcohol dehydrogenase domains among others (**Appendix 15**). Similarly, for leaf rust severity rated in the field, a total of 50 loci (37 in the spring panel and 13 in the winter panel), coded for proteins related to disease resistance: 11 CC-NBS-LRRs, eight kinases, four zinc finger-types and, three LRRs, among others (**Appendix 15**). Other disease-resistance-related proteins identified include ethylene receptor, alpha/beta hydrolase fold, ABC transporter and, WRKY and WD40 domain proteins. A combined total of 53 QTNs located within plant disease resistance genes explained more than 5% of the phenotypic variation observed (**Table 2.2**). For each of these, Kruskal–Wallis tests were performed to assay the difference in phenotypic values corresponding to the homozygous alleles. Results showed significant allele-phenotype differences (P-value<0.05) for 35 of the 53 QTNs (**Table 2.2**), where favorable alleles were detected in the domesticated *T. aestivum* and *T. turgidum* species, as well as the wild relative species (**Appendix 16**). Phenotypic variation for 11 of these significant QTNs present within CC-NBS-LRR, ABC-transporter and sereine/threonine protein kinase domains are illustrated (**Figure 2.4**). Of these, two QTNs represent non-synonymous substitutions, five synonymous substitutions, while the remaining were intronic or present upstream of the gene coding sequence. Such QTNs located within known classes of

resistance genes were considered high-confidence as their function and allelic-variation may add to their potential causation or correlation with leaf rust resistance.

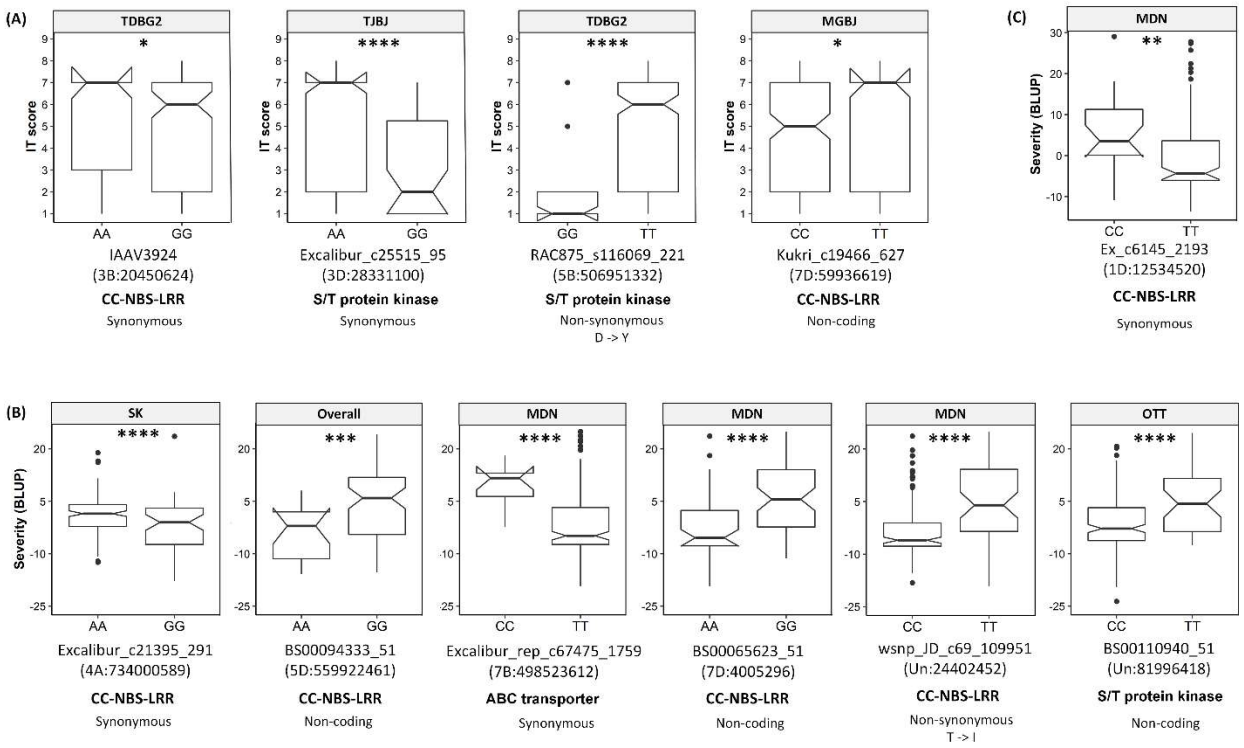

Figure 2.4 Boxplots showing significant allelic effects for a subset of the QTNs.

QTNs (quantitative trait nucleotides) associated with race-specific IT response. (b) QTNs associated with leaf rust severity in the winter panel. (c) QTNs associated with leaf rust severity in the spring panel. Labels at the top of each boxplot show the associated trait, i.e., the isolate for (a) and the location if the QTN was location-specific or overall, when severity was significant in all locations. For each QTN, figure also shows its annotated gene and its position relative to the gene's exons/introns and its amino acid change (synonymous vs. non-synonymous). Amino acid changes are represented by standard one-letter amino acid codes. Locations are Morden (MDN), Ottawa (OTT) and Saskatoon (SK). The level of significance was determined through Kruskal–Wallis tests and significance levels "*", "**", "***" and "****" correspond to *P*-value ≤ 0.05, 0.01, 0.001 and 0.0001, respectively.

2.4.7 Comparing associated loci with previously reported *Lr* genes

To identify novel putative disease resistance loci, the physical positions of the QTNs identified were compared to the positions of the 66 previously reported *Lr* genes (**Appendix 4**). All QTNs and *Lr* genes, except for *Lr10, Lr14 (a,b), Lr25, Lr26, Lr29, Lr30, Lr36, Lr44, Lr56*, *Lr59* and *Lr66,* were physically mapped on the CS reference genome v1.0 (IWGSC, 2018). The position of these mapped *Lr* genes and the IT and leaf rust severity QTNs identified herein by at least two models are illustrated (**Figure 2.5**).

Of the *Lr* genes mapped using both proximal and distal flanking markers, markers for *Lr12*, *Lr13*, *Lr15*, *Lr19*, *Lr27*, *Lr28*, *Lr49*, *Lr64* and *Lr75* co-located with 13 of the QTNs identified (**Appendix 17**). These include seven QTNs associated with leaf rust severity and six with IT response. Haplotype block analysis was used to evaluate the relationships between the QTNs detected and the *Lr* genes mapped using gene sequences or single genetic markers. A total of 2113 haplotype blocks (*D'* ≥0.5) were obtained, with an average block size of 4.9MB. Two QTNs, BS00094333_51, associated with leaf rust severity, and D_GDS7LZN02F1Q5F_180, with IT caused by isolates TDBG1, MGBJ and TJBJ, were in the same haplotype blocks as the cloned genes *Lr1* and *Lr34,* respectively, while three co-located in the same blocks as genetic markers of *Lr16*, *Lr32* and *Lr73* (**Appendix 17**). Apart from this, another three QTNs were in neighboring blocks of the markers linked to *Lr18* and *Lr54.* Pairwise linkage analysis between these blocks resulted in mean *D'* statistics ranging from 0.44 to 0.66. Overall, Kruskal–Wallis tests identified significant allele-phenotype differences (*P*-value<0.05) for 14 of the 21 QTNs mapping near positions of known *Lr* genes (**Table 2.2**, **Appendix 17**).

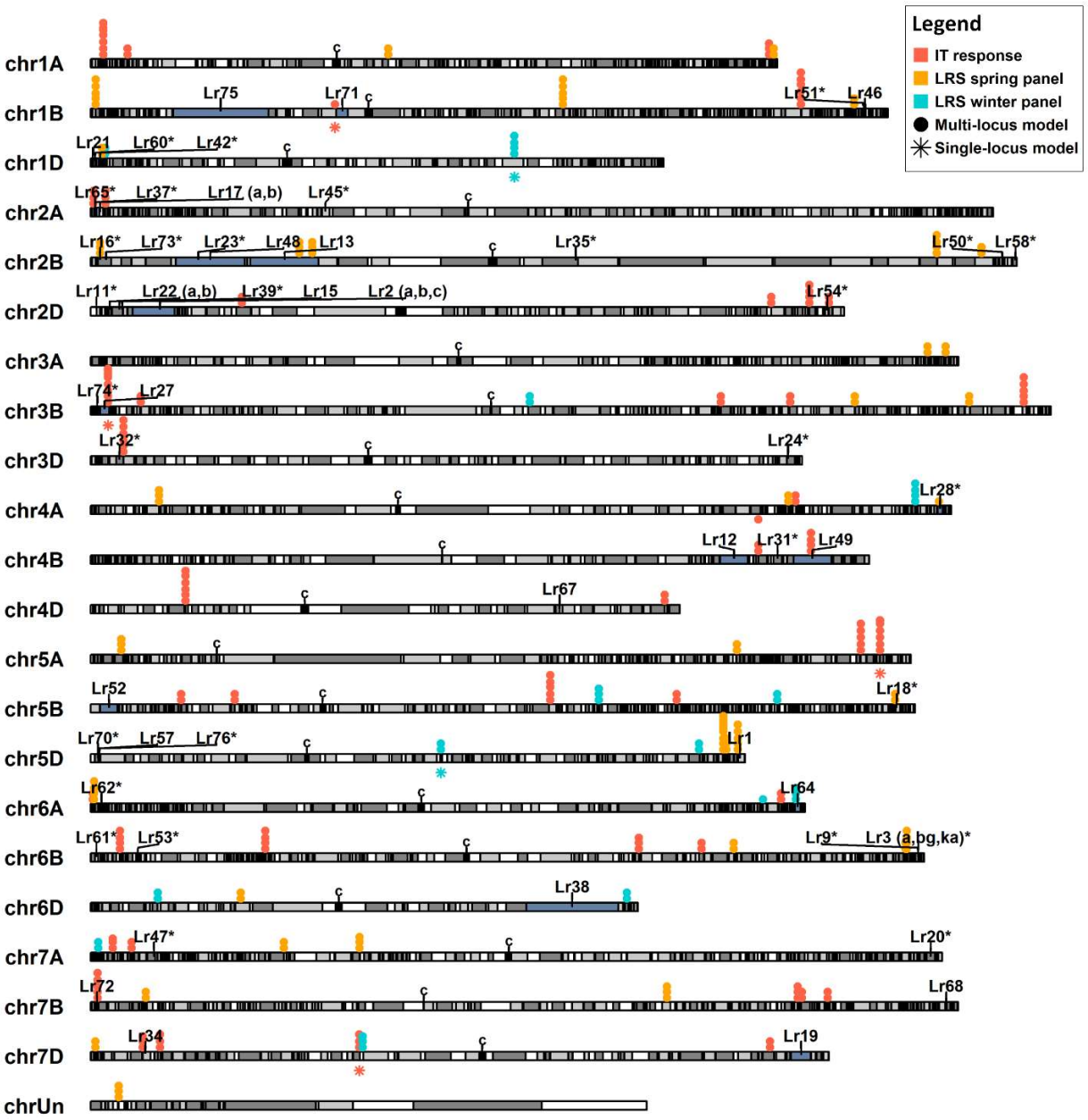

Figure 2.5 Physical map of known *Lr* genes and QTNs identified.

Map shows the position of known leaf rust resistance genes (*Lr*) and quantitative trait nucleotides (QTNs) associated with leaf rust severity (LRS) and infection type (IT) against six leaf rust races. The positions of the previously cloned *Lr* genes are indicated by a single vertical line on the chromosome. Regions shaded in grey indicate linkage disequilibrium blocks., while those shaded in blue indicate the location of the proximal and distal markers of mapped *Lr* genes. *Lr* genes previously mapped with a single marker are indicated with an asterix (*). For simplicity, QTNs associated with race-specific IT are shown in orange and those associated with LRS in the spring and winter panels are color-coded in yellow and blue, respectively. Solid dot (●) QTNs indicate association through a multi-locus model while star (✸) QTNs were identified with the single-locus model MLM. Centromeres are denoted with a “c” symbol. Only QTNs identified by more than one model are shown.

Table 2.2 Chromosomal location and functional annotation of significant loci.
For both, race-specific infection type and leaf rust severity, only quantitative trait nucleotides (QTNs) or linkage disequilibrium blocks (LDBs) located within disease resistance-related proteins explaining greater than 5% of the phenotypic variation are shown.

QTN/LDB	Chr	Position	Trait	Model	R^2	KW	R allele	Co-located *Lr* gene†	Gene annotation
Infection type									
IAAV6025	1B	211312483	MBDS	FASTmrEMMA	28.0	****	G		PC-Esterase, PMR5 N-terminal domain
				MLM	5.9				
Kukri_rep_c115699_270	2D	39829875	TDBG2	FASTmrEMMA	5.8	**	G	*Lr15*	Serpin superfamily
tplb0052b23_2493	2D	621964724	TDBG1	FASTmrEMMA	6.2	ns	-		LRR domain, NBS, CC domain
				pKWmEB	5.3				
RFL_Contig3121_1979	2D	648470008	MBDS	pKWmEB	5.8	ns	-	*Lr54*	LRR domain, S/T-protein kinase
Tdurum_contig18471_456	3A	75030422	MBDS	mrMLM	34.6	****	G		F-box-like domain
D_GCE8AKX02HMJXL_374	3B	15138756	MBDS	MLM	12.6	****	A	*Lr27*	Jacalin-like lectin domain
				pKWmEB	5.4				
IAAV3924	3B	20450624	TDBG2	pKWmEB	6.8	*	G		LRR domain, NBS, CC domain
Kukri_c12869_154	3B	130647769	TDBG1	mrMLM	27.9	***	C		F-box-like domain
Excalibur_c25515_95	3D	28331100	TJBJ	ISIS EM-BLASSO	7.7	****	G	*Lr32*	S/T-protein kinase
				pKWmEB	6.6				
				pLARmEB	5.2				
				FASTmrMLM	5.2				
D_contig10567_587	3D	141408492	MBDS	MLM	6.2	****	C		Glycoside hydrolase
D_contig29825_215	4D	82020798	TDBG1	FASTmrMLM	11.2	ns	-		LRR domain, NBS, CC domain
				pLARmEB	8.2				
			TDBG2	pKWmEB	11.0				
				pLARmEB	5.1				
RAC875_c9984_1003	5A	585458451	TDBG1	TDBG1	8.7	****	A		P-loop NTPase, Kinesin motor domain
wsnp_BJ224975A_Ta_2_2	5A	588737306	TDBG2	RTM	5.4	ns	-		Protein kinase, ATP binding site
Kukri_c17055_189	5A	588742167	TDBG2	RTM	5.4	****	T		P-loop NTPase, ABC transporter
RAC875_s116069_221	5B	506951332	TDBG2	pKWmEB	7.2	****	G		Serine/threonine-protein kinase
D_contig18780_204	5D	486259068	TDBG2	FASTmrEMMA	9.3	*	A		LRR domain, NBS, CC domain
wsnp_Ra_c3766_6947263	6B	151130562	MBDS	RTM	6.6	****	A		ZTL, PAS domain, beta-propeller, F-box-like

QTN/LDB	Chr	Position	Trait	Model	R^2	KW	R allele	Co-located *Lr* gene†	Gene annotation
Kukri_c39321_112	6B	151131531	TDBG2	pKWmEB	11.3	****	C		ZTL, PAS domain, beta-propeller, F-box-like
			TJBJ	pKWmEB	6.7				
			MBDS	RTM	6.6				
Kukri_c3664_1071	6D	10910854	MGBJ	mrMLM	6.8	*	G		P-loop NTPase, AAA+ ATPase domain
Ex_c54863_29	7B	561748617	TDBG2	RTM	14.7	****	C		Zinc finger, TAZ/ FYVE/PHD-type,
BS00063208_51	7B	637618402	MGBJ	mrMLM	5.4	**	T		LRR domain
Kukri_c19466_627	7D	59936619	MGBJ	pKWmEB	18.8	*	C		LRR domain, NBS, CC domain
Leaf rust severity in the spring panel									
wsnp_Ex_c3372_6195001	1A	257573729	SK	ISIS EM-BLASSO	6.4	***	T		LRR domain
				RTM	5.8				
Excalibur_c33567_363	1A	427819541	SK	mrMLM	17.6	ns	-		Zinc finger, FYVE/PHD-type
wsnp_Ex_rep_c67474_66076379	1A	591093391	OTT	pLARmEB	9.2	ns	-		P-loop NTPase, Armadillo-type fold
				FASTmrMLM	8.8				
Kukri_c55909_1109	2B	770681399	OTT	FASTmrMLM	7.9	****	C		WD40-repeat-containing domain
CAP8_c3568_256	3A	724200935	SK	mrMLM	10.0	ns	-		Alpha/Beta hydrolase fold
				pLARmEB	6.8				
Excalibur_c21395_291	4A	734000589	SK	FASTmrMLM	5.0	*	G	*Lr28*	LRR domain, NBS, CC domain
RAC875_c2099_2066	4B	670439103	Overall	pKWmEB	5.1	****	T		Zinc finger, FYVE/PHD-type
Tdurum_contig10128_593	5A	48464957	OTT	RTM	9.7	*	C		Papain-like cysteine peptidase
Excalibur_rep_c67473_320	5B	506789600	MDN	pKWmEB	5.1	ns	-		P-loop NTPase, AAA+ ATPase domain
BS00094333_51	5D	559922461	Overall	FASTmrMLM	9.6	***	A	*Lr1*	LRR domain, NBS, CC domain
				FASTmrEMMA	8.4				
				ISIS EM-BLASSO	8.4				
				pKWmEB	7.6				
				pLARmEB	6.5				
BS00037002_51	6A	2972683	MDN	FASTmrEMMA	5.8	ns	-		F-box-like domain
RAC875_c68525_284	6B	657946526	SK	mrMLM	13.3	*	G		Zinc finger, FYVE/PHD-type
BobWhite_rep_c66074_232	6B	706118869	Overall	FASTmrEMMA	5.1	ns	-		LRR domain
Kukri_c58096_480	6B	712390096	MDN	RTM	14.7	***	T		Papain-like cysteine peptidase
CAP7_c2923_366	6D	129784133	MDN	ISIS EM-BLASSO	11.8	***	T		Plant lipoxygenase, PLAT/LH2 domain

QTN/LDB	Chr	Position	Trait	Model	R^2	KW	R allele	Co-located *Lr* gene†	Gene annotation
				FASTmrEMMA	11.6				
CAP11_c5372_271	6D	465742757	MDN	RTM	10.4	ns	-		LRR domain, F-box-like domain
Excalibur_rep_c67475_1759	7B	498523612	MDN	mrMLM	5.9	****	T		P-loop NTPase, PDR ABC transporter
				ISIS EM-BLASSO	5.7				
tplb0021f14_1700	7B	653898244	Overall	mrMLM	9.5	ns	-		Serine/threonine-protein kinase
Excalibur_rep_c74234_183	7B	655037014	Overall	ISIS EM-BLASSO	5.1	ns	-		Serine/threonine-protein kinase
BS00065623_51	7D	4005296	MDN	pKWmEB	18.4	****	A		LRR domain, NBS, CC domain
				FASTmrEMMA	11.2				
D_GDS7LZN02FSYZC_227	7D	58491641	OTT	pLARmEB	5.1	ns	-		LRR domain, NBS, CC domain
wsnp_JD_c69_109951	Un	24402452	MDN	FASTmrMLM	13.5	****	C		LRR domain, NBS, CC domain
				pLARmEB	11.0				
				ISIS EM-BLASSO	6.4				
BS00110940_51	Un	81996418	OTT	pKWmEB	7.9	****	C		Serine/threonine-protein kinase
Leaf rust severity in the winter panel									
BS00067436_51	1A	578204373	MDN	FASTmrMLM	12.7	**	G		Glycoside hydrolase
Ex_c6145_2193	1D	12534520	MDN	RTM	6.5	**	T		LRR domain, NBS, CC domain
				mrMLM	7.8				
Kukri_c59403_339	2D	75001895	MDN	MLM	19.7	ns	-		WD40-repeat-containing domain
Excalibur_c3862_837	3B	245969143	MDN	FASTmrMLM	8.5	****	A		Peroxidase
BS00022555_51	5B	435769407	OTT	pKWmEB	14.0	ns	-		F-box-like domain, beta-propeller
wsnp_Ex_c6548_11355524	5B	439725143	MDN	ISIS EM-BLASSO	21.7	ns	-		WRKY domain
				pKWmEB	22.8				
				mrMLM	40.1				
Kukri_c855_2107	7A	708138675	MDN	ISIS EM-BLASSO	7.3	ns	-		Zinc finger, CCCH-type
D_contig28902_391	7D	456495802	Overall	ISIS EM-BLASSO	5.0	*	A		F-box-like domain

†*Lr* genes present within the same or neighbouring haplotype block, or *Lr* genes mapped using flanking markers

Chr, Chromosome; MDN, Morden; OTT, Ottawa; SK, Saskatoon; R allele, allele for resistance; KW, Kruskal–Wallis test significance level where "ns","*", "**", "***" and "****" correspond to not-significant and P-value ≤ 0.05, 0.01, 0.001 and 0.0001, respectively

2.5 Discussion

P. triticina populations are constantly evolving, as exemplified by the presence of more than 70 races detected in North America each year (Ellis et al., 2014). This can quickly render the deployed *Lr* genes ineffective. Identification of novel sources of disease resistance is necessary to stay ahead in this plant-pathogen evolutionary arms race and to maintain disease resistance in crops. The ability to detect novel *Lr* genes through marker-based association studies depends greatly on the phenotypic and genetic variation present in the germplasm. The majority of the GWAS in wheat are based on elite cultivars, breeding lines or landraces sourced from breeding programs, genebanks or private seed collections, mainly because introgression into adapted germplasm is easier and faster from the primary genepool as compared to more distant germplasm (Gao et al., 2016; Riaz et al., 2018). These collections, although geographically adapted, often provide limited genetic diversity due to the domestication and selective breeding bottlenecks. Conversely, ancestors and wild relatives of wheat lack adaptation traits for agriculture, but are a rich source of genetic variation, accounting for 44% of the *Lr* genes identified to date (McCallum et al., 2012; USDA, 2017). In the past century, research to identify and transfer resistance genes from wild relatives was laborious, lengthy and focused on one gene at the time. Recent development in genotyping technologies and the release of the wheat reference genome are enabling high throughput identification of new resistance genes regardless of the genepool, and thus accelerating their gene cloning (Arora et al., 2019; IWGSC, 2018). Here, we described an efficient method to identify new *Lr* gene loci and candidate genes from many *Triticum* and *Aegilops* species using an array-based SNP genotyping platform and eight GWAS models. Through this approach, we identified a total of 50 and 46 disease-related QTNs associated with field leaf rust severity and IT response against six *P. triticina* isolates, respectively, several of which near known *Lr* genes and others linked to putatively new ones. The QTNs identified in this

study provide the framework for investigating novel and effective *Lr* genes from this diverse germplasm and for cloning known *Lr* genes.

2.5.1 Genetic diversity

Bread wheat, an allohexaploid species, comprises an estimated 17 billion nucleotides, more than 85% of which is repetitive DNA (IWGSC, 2018). Array-based SNP genotyping platforms provide a quick and cost-effective opportunity to survey whole genomes of a large number of samples. We used the wheat 90K array to genotype a diverse collection of 385 accessions. A total of 34.1% of the SNPs were shared between the hexaploid and tetraploid datasets, similar to a previous report of 33.9% (Wang et al., 2014). The high percentage of shared SNPs is indicative of the extensive gene flow from the tetraploid ancestors to hexaploid wheat (Dvorak et al., 2006). Because nearly half of the diploid accessions were *Ae. tauschii*, the D genome donor of hexaploid wheat, the total of 7,243 (47.2%) of shared SNPs between the diploid and hexaploid datasets also agrees with the gene flow between these species.

The SNPs markers used to develop the wheat 90K array were generated from RNA-Seq data of *T. aestivum*, *T. turgidum* and *Ae. tauschii* (Wang et al., 2014). A total of 43,013 of the SNP markers from the array were physically mapped to the CS exome sequences, again similar to the 46,977 that were genetically mapped using eight *T. aestivum* mapping populations (Wang et al., 2014). Mapping against the CS exome sequence and subsequent comparison with exome capture data identified 9,570 SNPs, from which the B (45.1%), A (36.6%) and D (17.3%) sub-genome distribution compared to several previous reports (Daba et al., 2018; Pont et al., 2019; Wang et al., 2014).

2.5.2 Structure analysis

Relationships between the 27 species in the collection were explored using phylogenetic tree analysis. Four major clades were observed, clearly separating the wild species from the *T.*

aestivum and *T. turgidum* subspecies. *T. aestivum* ssp. *spelta*, hypothesized to have emerged from hybridization between *T. aestivum* and *T. turgidum* ssp. *dicoccum* (Blatter et al., 2004; Pont et al., 2019), was observed to cluster among the *T. aestivum* subspecies, separately from all *T. turgidum* ssp. *dicoccum* and *dicoccoides*. While some SHWs clustered with *T. aestivum*, the majority of them were distributed among their tetraploid donor. A population structure analysis showed similar clustering of SHWs on the basis of the origin and growth habit of the tetraploid parent (Bhatta et al., 2018).

The major clade of wild relatives was separately analysed to highlight the relationships between the species (**Appendix 18**). With the exception of *Ae. sharonensis,* clustering of the *Aegilops* species of the Sitopsis section was consistent with previous studies, where *Ae. speltoides* ssp. *speltoides* and *Ae. speltoides* ssp. *ligustica*, formed one clade and *Ae. longissima*, *Ae. bicornis* and *Ae. searsii* formed the other (Bahrman et al., 1988; Miki et al., 2019; Sasanuma et al., 1996). The majority of the *Triticum* species with an A genome also grouped together, where accessions of *T. zhukovskyi* were clustered closer to their tetraploid ancestor *T. timopheevii* (Dvorak et al., 1993). The unique amphiploid EKC22_RL5347 resulting from a cross between *Ae. speltoides* (S) and *T. monococcum* (A^m) also clustered with the A-genome species. The close relationship between *Ae. crassa* (DM or DDM) and *Ae. juvenalis* (DMU) species was also expected because they both share a D and an M genomes (Baum et al., 2012; Edet et al., 2018). Both genomes of *Ae. triuncialis* (UC or CU) are nearly identical to the diploid genomes of *Ae. umbellulata* (U) and *Ae. markgrafii* (C) (Badaeva et al., 2004) and, unsurprisingly, the *Ae. triuncialis* cluster located between the U and C genomes diploid accessions. With the exception of *Ae. juvenalis* (DMU), which clustered with its D genome progenitor, polyploid species carrying a U genome were closely related to one another and to *Ae. umbellulata* despite having different non-U genomes (Badaeva et al., 2004; Kilian et al., 2011). Some of the wild relative species were sparsely represented in our collection, somewhat limiting our ability to establish clear relationships

between the various genomes. Increasing the number of accessions representing these species is expected to create a more refined picture of their relationships, leading to a better understanding of the evolution of these genomes and species.

The relationships observed in the phylogenetic tree were also observed by PCA. Overall, clustering patterns hinted at possible ascertainment biases; species of the A, B or D sub-genomes segregated more clearly, with few to no outliers, compared to other species. As the 90K array consisted of SNPs previously discovered in cultivars of polyploid wheat, and its D genome progenitor *Ae. tauschii*, genotype calling may be limited to common alleles identified in the initial SNP discovery process (Albrechtsen et al., 2010; Rasheed et al., 2017). Although the genotyping data may not be sufficient to uncover novel ancestral relationships, it was nonetheless effective in revealing genetic variations at the species level and corroborating previously observed relationships (Badaeva et al., 2004; Bahrman et al., 1988).

2.5.3 Detection of previously reported *Lr* genes

A total of 13 QTNs identified were present within the mapped flanking markers of nine catalogued *Lr* genes. The QTN Excalibur_c21395_291 mapped between psr119 and mag3092, two markers tightly linked to *Lr28* (McIntosh et al., 1982; Younas Sohail et al., 2014). Similarly, the QTN Excalibur_rep_c68362_62, mapped 1.6Mb upstream, in a neighboring haplotype block of IWB41960, a marker tightly linked to the resistant gene *Lr18* (Carpenter et al., 2018; Dyck and Samborski, 1968). Both *Lr18* and *Lr28* loci QTNs were present within CC-NBS-LRR genes and showed significant allele-specific phenotypic differences, making them candidate genes.

Five QTNs were found to be in the same haplotype blocks as the cloned genes *Lr1* and *Lr34* and the genetic markers for *Lr16* (wmc764), *Lr32* (wmc43) and *Lr73* (wPt-4453) (Cloutier et al., 2007; Krattinger et al., 2009; McCartney et al., 2005; Park et al., 2014; Thomas, 2010). The QTNs close to *Lr1* and *Lr32* were present within CC-NBS-LRR and serine/threonine kinase

domains, while the others were located within a 3-ketoacyl-CoA synthase domain or within genes of unknown function. These QTNs identified had within-block D' statistics ranging from 0.54 to 0.85, where higher values suggest high linkage disequilibrium and similar association with phenotypic traits between pairs of SNPs the same block (Cuyabano et al., 2014). Moreover, four of these five QTNs showed significant allele-specific phenotypic variation.

Overall, the lack of cloned genes or tightly linked markers restrict the ability to pinpoint the precise physical position of some *Lr* genes. QTNs linked to or within flanking markers of known *Lr* genes may serve as novel markers for gene cloning, however fine-mapping, allelism tests, transformation genome editing (e.g. CRISPR) experiments must be performed to ascertain their identities.

2.5.4 Identification of novel sources of leaf rust resistance

The most prevalent class of known resistance genes encode intracellular immune receptors with NBS-LRR domains, many of which also possess a coiled-coil (CC) N-terminal motifs. These genes play an important role in pathogen recognition and initiation of downstream signaling cascades. In the wheat genome, as many as 661 to 1,560 full-length NBS-LRR genes have been reported, higher than any other plant species (Gu et al., 2015; Steuernagel et al., 2020). Four of the six *Lr* genes cloned to date encode CC-NBS-LRR proteins (Cloutier et al., 2007; Feuillet et al., 2003; Huang et al., 2003; Thind et al., 2017).

GWAS for race-specific IT response and leaf rust severity identified a total of 18 QTNs within genes encoding complete CC-NBS-LRR domains. Of these, 11 explained greater than 5% of the phenotypic variation, while the remaining were small-effect loci. As discussed above, QTNs close to *Lr1*, *Lr18*, *Lr28*, and *Lr54* were in CC-NBS-LRR genes but the remaining were located where no known *Lr* genes have been mapped to date. For IT response, the most prominent QTNs within CC-NBS-LRR genes included D_contig18780_204 and Kukri_c19466_627, where for the

former, all species in the U-genome group, SHWs and *Ae. tauschii* var. *strangulata* expressed the favorable allele, while for the latter, resistant accessions included wild relatives in the D-genome group and some SHWs, among others.

The highest number of QTNs within genes encoding CC-NBS-LRR proteins was identified in the spring panel rated for leaf rust severity. Of note is BS00065623_51 on the distal end of 7DS, where different subspecies of *T. aestivum*, such as *T. aestivum* ssp. *spelta*, was associated with the low-severity A allele, while most *T. aestivum* ssp. *aestivum* and all SHWs associated with the high-severity G allele. While the spring panel was made up of subspecies of *T. aestivum*, *T. turgidum* and SHWs, the winter panel was predominantly a collection of SHWs and wild relative species. The most notable *Lr* severity associated QTN identified in the winter panel may be Ex_c6145_2193. This QTN, present within a CC-NBS-LRR gene, was located on the distal end of the short arm of chromosome 1D. Here, all the wild relatives including *Ae. crassa*, *Ae. juvenalis* and *Ae. cylindrica* among others, associated with the low-severity T allele, but the high-severity C allele was only detected in some *Ae. tauschii* and SHW accessions. Candidate CC-NBS-LRR genes identified here, in the primary as well as the wild gene pool, are valuable sources of genetic resistance.

Plant disease resistance is driven by complex mechanisms involving several layers of defense. Not surprisingly, the classes of known disease resistance genes have expanded greatly in the past few years. For leaf rust, in addition to *Lr34* encoding an ABC transporter (Krattinger et al., 2009), the cloned *Lr67* gene codes for a hexose transporter (Moore et al., 2015). Other pathogen resistance genes cloned in wheat encode serine/threonine protein kinases and wall-associated kinases (Cao et al., 2011; Shi et al., 2016). Identification of these diverse resistance proteins supports the possibility of uncovering novel classes of disease resistance genes. Consequently, in addition to those in CC-NBS-LRR genes, we identified a number of QTNs present in genes coding for other known resistance proteins in wheat and other plant species. A

key QTN identified herein was Excalibur_rep_c67475_1759 on 7B. It was located within a pleiotropic drug resistance-type ABC transporter protein, which is known to be involved in the secretion of fungal defense-related metabolites, including resistance to DON accumulation in wheat *Fusarium* head blight infection (Jasiński et al., 2001; Shang, 2009). Similarly, QTN Kukri_c39321_112 on 6B was associated with IT responses against three isolates (TDBG2, MBDS, and TJBJ). It was found within a gene encoding a ZTL-type beta-propeller/F-box domain protein known to regulate plant flowering time and provide resistance against yellow rust in wheat and powdery mildew in barley (Bozkurt et al., 2007; Dagdas et al., 2009; Kim et al., 2005). Here, species with the favorable allele included modern *T. turgidum* cultivars, *Ae. speltoides*, *Ae. sharonensis* and *T. timopheevii*, among others. These loci, located in novel genomic regions, are also recognized as putative candidate leaf rust resistance genes, and some may potentially confer resistance against multiple leaf rust isolates.

Overall, twice as many QTNs were identified in the spring panel as compared to the winter panel. This imbalance may be due to the difference in the number of accessions in each panel or the nature of the germplasm within each one where the spring panel comprised mostly the species used to design the wheat 90K array, thereby providing higher quality genotyping. In addition, the potential for identifying novel disease resistance genes is also dependent on the mapping of the QTNs to the *T. aestivum* reference genome. As the reference only represents the A, B and D genomes of a single genotype, it may limit, but not prevent, our ability to identify rare resistance genes unique to the contrasting genomes of the wild relatives.

2.6 Conclusion

The GWAS described herein highlights the multi-genic and complex nature of pathogen disease resistance where multiple markers were associated with different field environments and pathogen races. We identified several QTNs located near known *Lr* resistance genes providing, at the very least, novel markers for the cloning of these genes. Some of them were located within

known resistance gene classes such as CC-NBS-LRR. As such, these become prime candidates for direct investigations. This study also identified novel leaf rust resistance loci from the domesticated *T. aestivum* and *T. turgidum* species that can be capitalized upon quickly but also others from wild relative species that may be harnessed to add to the leaf rust resistance repertoire of wheat. Once cloned, the novel *Lr* genes can be transferred into adapted germplasm using modern genome-assisted breeding strategies, such as gene cassettes and genome editing (Wang et al., 2018; Wulff and Moscou, 2014). Gene cassettes allow multiple cloned disease resistance genes to be transformed simultaneously into a single genome to provide durable and broad-spectrum resistance, because the closely linked genes will not segregate, will be easy to select for, and will essentially have the advantages of gene pyramiding (Arora et al., 2019; Kolmer et al., 2009). Gene-specific markers can also be developed to facilitate the transfer of these genes through conventional breeding. The recently introduced CRISPR-Cas9 system in wheat (Liang et al., 2017; Zhang et al., 2016) offers many advantages. It can facilitate the investigation of candidate genes in any germplasm, bypassing the laborious fine-mapping experiments and enabling their functional analyses. We believe that gene editing could also be capitalized upon to "transfer" resistance genes from wild relatives through the allelic conversion of the orthologous domesticated alleles, providing that sufficient sequence similarity exists between the wheat and the wild relative alleles. This "long-shot" strategy would eliminate the need for the long, laborious and difficult introgression via crossing, and eradicate its associated linkage drag drawbacks. In conclusion, we described a powerful approach to identify QTN markers and candidate genes for leaf rust resistance through combining a broad germplasm including cultivated species and wild relatives, array-based genotyping, field severity and IT phenotyping and, through the use of several GWAS models.

3 General discussion and conclusion

Wheat is arguably the most important crop in the world. For millennia it has been a symbol of harvest, prosperity and fertility. Before the advent of bread wheat, ancient wheats were cultivated in the Fertile Crescent (modern day Middle East) and spread from there towards Europe, Asia and onwards (Shewry, 2009). Wheat is now the most widely grown crop in the world, an essential source of energy and nutrients, and a major source of revenue to wheat producing and trading countries. The challenges that breeders currently face are to increase production to accommodate population growth and the increased consumption per capita, while also accounting for climate change, pollution, water scarcity and biotic and abiotic stresses (Curtis and Halford, 2014).

For various plant and animal species, access to a fully annotated reference genome has promoted the systematic development of approaches to study and select for important traits (Hickey et al., 2017). The genome of rice was sequenced in 2002 (Chen et al., 2002), soybean in 2008 (Schmutz et al., 2010) and maize in 2009 (Schnable et al., 2009). Wheat, while being one of the most important crops, has lagged behind in terms of genomic advances. The International Wheat Genome Sequencing Consortium (IWGSC) has been trying to decode the genome of wheat since 2005 and finally, after 14 years and a few incomplete drafts, in mid-2018, it released a fully sequenced and annotated reference genome of the Chinese Spring (CS) variety of bread wheat (IWGSC, 2018). This lag was largely due to the colossal size and highly repetitive nature of the polyploid genome. Approximately 113,653 (63%) of the total annotated genes in CS were present as homoeologous genes, i.e., were present as copies across the A, B and D sub-genomes. In addition, 15% of these had paralogous copies in at least one sub-genome, i.e., genes copied from tandem or segmental trans-duplication (IWGSC, 2018). This complicated the genome assembly process in terms of chromosome assignment and gene order. Nonetheless, availability of an annotated CS reference genome constitute a revolutionary milestone for wheat research,

giving researchers access to sequence-level information and facilitating the isolation of important genes, while also spurring the implementation of new strategies for genomics-assisted breeding.

The research project presented herein took advantage of this opportune time, leveraging positional and functional information from the newly available reference genome to identify novel genomic regions involved in leaf rust resistance. This reference sequence has served as a backbone to anchor all previously known disease resistance genes onto a single annotated reference, while also allowing comparison and validation of newly identified loci.

3.1 Highlights of the study

In this study, an array-based single nucleotide polymorphism (SNP) genotyping was used to characterize a diverse set of species and perform a genome-wide association study (GWAS) to map candidate leaf rust resistance genes. The germplasm consisted of 385 accessions, encompassing 27 different species of cultivated wheats, synthetic hexaploid wheats (SHWs) and wild relatives belonging to the primary, secondary and tertiary gene pools of wheat. Genetic diversity was captured using the wheat 90K array (Wang et al., 2014) and GWAS was conducted using eight statistical models for reaction ratings against six leaf rust isolates and for leaf rust severity rated in field in multiple year and location environments.

Genotyping using the 90K array allowed comparison of genetic diversity across different ploidy and species levels. Upon initial filtering, 20,501 SNP markers were retained from the complete germplasm. Using the sequences of the 81,587 SNP markers in the 90K array (Wang et al., 2014), one of the first physical map to position these markers on the protein coding regions of the CS reference genome was created. Knowledge of the chromosomal position of the makers provided the information necessary to perform SNP re-filtering to accommodate the differential genotype calls in the sub-genomes. For example, only 59% of all accessions carry the D sub-genome; an otherwise 80% call filter would have removed genome-specific SNPs will lower call

rates. This filtering resulted in 12,627 SNP markers, of which 9,570 were validated through exome-capture variant calling of a subset of 136 accessions.

Phylogenetic and population structure analysis illustrated the relationships between the *Aegilops* and *Triticum* species in the collection. Apart from eight accessions, the majority clustered based on their shared sub-genomes, species divergence and/or pedigree information. Ancient tetraploid species *T. turgidum* ssp. *dicoccum* (emmer wheat) and the non-domesticated *T. turgidum* ssp. *dicoccoides* formed one clade, while modern cultivated species, such as *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *carthlicum*, formed the other. These modern tetraploids wheats differentiated from wild emmer wheat due to selection pressures imposed by local environments and cultural practices across a larger distribution of areas (Bozzini et al., 2012). These recently differentiated species form a taxonomic subgroup separated from *T. turgidum* ssp. *dicoccum* and *dicoccoides,* as was observed through other phylogenetic studies of the *T. turgidum* subspecies (Laidò et al., 2013; Maccaferri et al., 2019; Marcotuli et al., 2016). Previous studies have shown a decrease in nucleotide diversity from wild emmer wheat (π=2.28), to domesticated emmer (π=1.17) and to durum wheat (π=0.87) (Akhunov et al., 2007).

Synthetic hexaploid wheats (SHWs) created by crossing tetraploid *T. turgidum* with diploid *Ae. tauschii*, were distributed between the two tetraploid clades based on the genetic characterization of their tetraploid parent. For example, 12 SHW accessions created by crossing the durum wheat cultivar ‘Langdon’ with different *Ae. tauschii* accessions, clustered with ‘Langdon’ in the modern tetraploids clade. Similarly, multiple SHWs created by crossing wild emmer wheat accessions PI113961 and PI355465 with *Ae. tauschii,* clustered with their tetraploid parents in the ancient tetraploid clade. Similar studies using SSR and AFLP markers have reported the genetic diversity of SHWs to clearly reflect the sub-species, geographical origin and morphological traits of their tetraploid parent, possibly due to the fact that it contributed to two-third of their genome (Dreisigacker et al., 2008; Lage et al., 2003; Szabo-Hever et al., 2018).

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All wild *Aegilops* and *Triticum* species clustered in one clade; however sub-clades were formed based on related species. In agreement with previous studies, genome-based grouping was observed for *Aegilops* species with the D, S, U, and C sub-genomes, and *Triticum* species with the A sub-genome (Badaeva et al., 2004; Bahrman et al., 1988; Baum et al., 2012; Dvorak et al., 1993). Clustering patterns observed in the phylogenetic tree were also reflected in principal component analyses and ancestry mix distributions of population structure. These analyses clearly illustrate the effectiveness of the 90K array filtered genotyping data set in differentiating the species and sub-species of the collection.

Using the filtered genotyping data, a GWAS was performed for leaf rust, the most widespread rust disease of wheat caused by the fungal pathogen *Puccinia triticina*. Two types of phenotypic data were collected, leaf rust infection type (IT) measured against six leaf rust isolates and multi-environment field leaf rust severity rated separately for the spring and winter panels. One single-locus and seven multi-locus statistical models were used, identifying 281 quantitative trait loci (QTL), some of which were unique to specific models but 53-68%, depending on the trait, were identified by more than one model. Multi-locus models, previously shown to have higher detection power because of their less stringent criteria for multiple test corrections, outperformed the single-locus model in identifying small-effect loci for complex associations (Cui et al., 2018; Segura et al., 2012; Zhang et al., 2018b). Indeed, in this study, the single locus model, MLM, identified the fewest QTL, with a maximum of five for race-specific IT, while multi-locus models identified up to 54 QTL for this same trait. The proportion of phenotypic variance explained, however, was higher for the single-locus model (average r^2=8-19%) compared to multi-locus models (average r^2=5-7%) which identified a large number of small-effect QTL. At the same time, of the total eleven QTL identified using MLM, six were also identified by multi-locus GWAS; comparison between five of these six QTL showed that the r^2 percentage for single-locus models was estimated to be 2-4 folds than that obtained from the multi-locus models.

Protein function of genes within 5kb of the QTL identified were extracted using the CS reference genome annotation v1.1. Between 79-85% of the QTL associated with race-specific IT and leaf rust severity were successfully annotated. Of these, a subset of 35 coding for known plant disease resistance proteins each explained greater than 5% of the phenotypic variation and showed significant allele-phenotype differences (*P*-value<0.05). The majority of the plant disease resistance genes classified encode immune receptors that detect pathogen effectors. In the case of wheat, 23 (72%) of the cloned disease resistance genes encode NLR receptor proteins (CC-NBS-LRR domains) (DeYoung and Innes, 2006; Keller et al., 2016; Zhang et al., 2020). Proteins encoded by other wheat disease resistance genes include protein kinases and transporter proteins (Keller et al., 2016). In this study, GWAS identified a total of 18 QTNs within genes encoding complete CC-NBS-LRR domains, while several other QTL encoded serine/threonine protein kinases, ABC transporter proteins and F-box domain containing proteins, among others. The favorable alleles associated with low severity and IT were present in the domesticated *T. aestivum* and *T. turgidum* species, as well as in the wild relatives of wheat.

Using gene sequences and sequences of flanking or co-segregating markers, the physical positions of 55 of the 66 previously reported *Lr* genes was determined on the CS reference genome v1.1 (McCallum et al., 2012; USDA, 2017). A total of 13 QTL identified were present within the mapped flanking markers of nine catalogued *Lr* genes, and an additional seven were within the same or neighboring haplotype block as six other *Lr* genes. The remaining significant QTLs, especially those which (1) were identified by multiple model, (2) encode disease related proteins and/or (3) explain high phenotypic variance, were considered loci that putatively harbor new *Lr* resistance genes. Examples of such loci in novel positions include Kukri_c19466_627 on 7D present within a CC-NBS-LRR domain (r^2=18.8) and Excalibur_rep_c67475_1759 present within a ABC-transporter domain (r^2=5-6%).

3.2 Practical and scientific implications of the results

In this study, not only were the markers from the 90K wheat array were mapped on the wheat reference genome, but also a compressive physical map of 55 of the 66 known *Lr* genes was created. This reference map will allow comparison and validation of newly identified loci from this and future association genetics studies. One of the strengths of this study was the diverse germplasm; through phylogenetic and clustering analyses, light was shed on to relationship between different *Aegilops* and *Triticum* species, their subspecies and synthetic crosses. Our analyses identified relationships hypothesized in the past from genetic diversity studies conducted using SNP, SSR and RFLP markers, and identified caveats to consider in future investigations. For example, the amphiploid resulting from a cross between *Ae. speltoides* (S) and *T. monococcum* (A^m) clustered with its A-genome progenitor, away from all the *Ae. speltoides* in the collection.

The QTNs identified by GWAS provide the framework for investigating novel *Lr* genes from this diverse germplasm and for cloning known *Lr* genes. Identification of novel sources of disease resistance is important to stay abreast of the plant-pathogen evolutionary arms race and to maintain disease resistance in crops. *P. triticina* populations are constantly evolving, which can quickly render the deployed *Lr* genes ineffective. For example, *Lr14a* and *Lr10*, once popular sources of resistance, are no longer effective against leaf rust races in Canada, while some genes such as *Lr13*, *Lr30* and *Lr34* still remain effective when used in combination with other *Lr* genes, a strategy referred to as gene pyramiding (McCallum et al., 2016).

Lr genes which bestow seedling-type resistance usually confer a race-specific response controlled by single major-effect genes, while adult plant resistance (APR) genes can also confer quantitative race non-specific responses. Of all the cloned *Lr* genes, seedling-type genes encode CC-NBS-LRR domains, while APR genes encode transport proteins. Candidate genes identified here, that were either associated with race-specific IT or leaf rust severity conferred by a mixture

of pathogen races, especially those which encode known classes of resistance proteins, are the prime targets for direct investigations. Functional validation of these loci can be performed using transformation (Cheng et al., 1997), CRISPR/Cas9 (Zhang et al., 2016), genomic selection strategies (Bassi et al., 2016), screening through KASP (Kompetitive Allele Specific PCR) assays (Rasheed et al., 2016) and mapping using bi-parental populations to select a donor parental line (Zhang et al., 2018a).

As wild relatives of wheat account for nearly half of the *Lr* genes identified to date, the cultivated and the wild gene pools in this study presents an excellent avenue for the identification of new sources of resistance to broaden and maintain the genetic base of leaf rust resistance. Novel leaf rust resistance loci such as BS00065623_51 and Excalibur_c21395_291 from the domesticated *T. aestivum* and *T. turgidum* species (**Appendix 16**, **Table 2.2**) can be capitalized upon quickly by standard breeding methods like hybridization, backcrossing and selection, using adapted germplasm. Resistant loci in *Ae. tauschii* can be transferred into hexaploid wheat through the creation of SHW lines or through direct hybridization with *T. aestivum*, which would be both followed by embryo rescue and backcrossing to *T. aestivum* to recover semi-adapted resistant genotypes (Cox et al., 2017). Lastly, resistant alleles such as Ex_c6145_2193 and D_contig28902_391, identified in the secondary and tertiary gene pools (**Appendix 16, Table 2.2**), can be transferred by interspecific crossing of the wild relative with an adapted cultivar followed by backcrossing to the recurrent parent (Kishii, 2019; Mujeeb-Kazi and Rajaram, 2002). This technique requires special breeding protocols and is plagued by sterility in the progeny and linkage drag resulting from the low recombination surrounding the introgressed alien fragment. On the other hand, modern genome-assisted breeding strategies, such as gene cassettes and CRISPR-Cas9 genome editing, offer an interesting alternative to bypass long and laborious introgression via crossing, allowing gene transfer and quick validation from any germplasm (Wulff and Moscou, 2014; Zhang et al., 2016).

Overall, novel candidate genes associated with leaf rust resistance were identified and several markers located near known *Lr* resistance genes were mapped. The outcomes of this research is expected to guide pre-breeding decisions for the transfer of useful *Lr* genes for wheat improvement. The genotyping data generated and the association analysis pipeline developed herein can also be further applied to perform GWAS and genomic selection strategies for the other disease-related and agronomic traits that were rated by our collaborators for this germplasm.

3.3 Limitations and suggested future studies

While this study provides insights into the population structure of various species and identifies candidate genes associated with leaf rust resistance, there are some limitations and gaps that must be acknowledged and taken into consideration.

SNP arrays, like the 90K wheat array, are made of a fixed set of SNPs identified from a discrete set of individuals. Inherent design biases from initial SNP discovery and array development hinder the capture of rare alleles during genotype calling, especially from the disparate germplasm used in this study. Genotyping was also complicated by the inherent complexities associated with the presence of homoeologous chromosomes in wheat. For some markers, genotype calls that were not specific to unique sub-genomes were observed, e.g., positive genotype calls for SNP markers aligning to the D sub-genome in species that did not carry a D sub-genome. This is because some SNP probes can not only hybridize to their target locus, but also to their homoeologous and/or paralogous loci, thereby affecting the allele-specific fluorescent signal ratios, complicating genotype calling and possibly resulting in false positives. Although, validation using exome-capture data and genome-specific filtering helped validate overall genotyping quality, it is likely that markers with some false positive calls were retained post-filtering and one must be mindful of error propagation when interpreting GWAS results from this subset of markers. To some extent, this limitation can be overcome by increasing the number

and diversity of individuals/SNPs used for array development and by combining fixed arrays with *de novo* NGS-based platforms, such as the exome capture used herein for cross-validation, genotyping by sequencing (GBS), and restriction site-associated DNA sequencing (RAD-seq), however, such approaches can be costly and carry their own complexities.

To perform GWAS, eight different statistical models were used, identifying a large number of QTL, some of which were unique while others were recurrent. Functional annotation and allelic tests using Kruskal–Wallis statistics were performed to shortlist effective candidate genes, however, there is still a need for further functional validation of the loci identified. A drawback of association analyses is that the statistical models used can identify many false positives (Ioannidis et al., 2009). Controlling for population structure and kinship, using more stringent criteria for multiple test corrections and performing cross-validation using multiple models are all practical ways to minimize this problem. The outcomes of GWAS in this study can be further studied by pinpointing the position of the QTL relative to the gene's exons/introns and its amino acid change (synonymous vs. non-synonymous). These QTL in high linkage disequilibrium with the functional variants as can become proxies or genetic markers as their genotypes are highly correlated with the genotypes of the functional variant (Myles et al., 2009). The biological role of candidate genes identified must also be further explored, i.e., their interaction networks, molecular pathways and contributions to disease resistance. For associated loci linked to or within flanking markers of known *Lr* genes additional fine-mapping, allelism tests, transformation or genome editing (e.g., CRISPR) experiments must be performed to ascertain their functional role(s). Moreover, reproducibility of the GWAS results can be further assessed using additional phenotypic or genotypic data. Strategies such as genomic selection can also be applied. Genomic selection uses genotypic and phenotypic data of a training population to predict the breeding value of each marker or QTN in a test population (Lorenz et al., 2011).

Other limitations of the study include unequal sample representation and missing phenotypic data. Our germplasm included 27 different species, but some of the wild relative species, such as *Ae. markgrafii*, *Ae. triuncialis*, and *Ae. comosa*, were sparsely represented. Increasing the number of accessions representing these species is expected to create a more refined picture of their relationships. This will also allow more in-depth analyses such as comparison of shared SNPs, allelic frequencies and nucleotide diversity (π) between the different species and historical groups (landraces, old cultivars and modern varieties). Association analysis studies are only as good as the weakest link which is often the phenotypic data. For some years/locations, the amount of missing data in the winter panel was substantial because some lines matured prior to the establishment of the infection for example. Although, using conditional means in the form of best linear unbiased predictors (BLUPs) provided extrapolated values, decreasing the amount of missing data can potentially improve this estimation.

3.4 Conclusions

Wheat is the most widely grown and consumed crop in the world. Changes in wheat production and utility over the past couple of centuries has clearly shown how farmers have progressively improved yield and quality through agronomic and genetic advances – conventional crop breeding combined with modern genomic and biotechnological tools now allows breeders to maximize genetic gains and improve grain quality and yield. However the broad use of single uniform varieties could lead to fast resistance breakdown. The wild relatives of wheat and other forms of non-adapted germplasm are a rich source of genetic diversity and stress tolerance traits. Pre-breeding identifies desirable genes from these non-adapted germplasm to transfer useful traits to adapted germplasm that breeders can use to produce new varieties.

Array-based genotyping was used to explore genetic diversity in various domesticated and non-domesticated species of wheat and their wild relatives. Phylogenetic analyses illustrated

four major clades, clearly separating the wild species from the domesticated and ancient *T. turgidum* species from modern *T. turgidum* cultivars. The clusters observed showed genetic differentiation between the various species and their sub-species, and reproduced relationships previously observed using genetic markers. Multiple statistical models combined this genotyping data to conduct a genome-wide association study for leaf rust resistance using scores for field leaf rust severity and IT against six leaf rust isolates. Several loci associated with race-specific IT and severity were identified, some of which were located near known leaf rust resistance genes and others linked to putatively new ones. A subset of 35 loci coding for known disease resistance proteins explained a substantial proportion of the phenotypic variation and showed significant allele-phenotype differences (r^2>5%, *P*-value<0.05). These were considered high-confidence candidate genes. Future efforts to validate these loci will help understand their role in disease resistance and promote their utility for marker-assisted selection in pre-breeding.

Overall, a powerful approach that combines a broad germplasm, array-based genotyping, multi-environment trait data and several GWAS models was described to identify candidate genes underlying leaf rust resistance in wheat and that could be applied to other traits such as other biotic and abiotic stress-related traits as well as agronomic traits in wheat.

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5 Appendix

Appendix 1 List of accessions included in this study

Appendix 1A For each accession table shows their respective genome, ploidy, growth habit, origin, and seed source.

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
796*	EKC111_RL5009	S[b]	*Ae. bicornis*	Wild	2X	W		AAFC
797*	EKC112_RL5301	S[b]	*Ae. bicornis*	Wild	2X	W		AAFC
814*	EKC171_RL5722	UM	*Ae. biuncialis*	Wild	4X	W		AAFC
815*	EKC186_RL5847	UM	*Ae. biuncialis*	Wild	4X	W		AAFC
823*	IPK-AE113	UM	*Ae. columnaris*	Wild	4X	W	Armenia	IPK
822	IPK-AE111	UM	*Ae. columnaris*	Wild	4X	W	Azerbaijan	IPK
848*	IPK-AE1607	UM	*Ae. columnaris*	Wild	4X	W	United Kingdom	IPK
840*	IPK-AE783	M	*Ae. comosa*	Wild	2X	W	Greece	IPK
819	IPK-AE8	DM/DDM	*Ae. crassa* ssp. *crassa*	Wild	4X/6X	W	Greece	IPK
842	IPK-AE899	DM/DDM	*Ae. crassa* ssp. *crassa*	Wild	4X/6X	W	Iraq	IPK
829	IPK-AE290	DM/DDM	*Ae. crassa* ssp. *crassa*	Wild	4X/6X	W	Turkmenistan	IPK
835*	IPK-AE467	DM/DDM	*Ae. crassa* ssp. *crassa*	Wild	4X/6X	W	USSR	IPK
847	IPK-AE1580	DM/DDM	*Ae. crassa* ssp. *vavilovii*	Wild	4X/6X	W	Morocco	IPK
820	IPK-AE30	DM/DDM	*Ae. crassa* ssp. *vavilovii*	Wild	4X/6X	W	Sweden	IPK
818*	IPK-AE1	DM/DDM	*Ae. crassa* ssp. *vavilovii*	Wild	4X/6X	W	USSR	IPK
827	IPK-AE162	DM/DDM	*Ae. crassa* ssp. *vavilovii*	Wild	4X/6X	W	Uzbekistan	IPK
802*	EKC130_RL5010	DC	*Ae. cylindrica*	Wild	4X	W		AAFC
801*	EKC135_RL5716	DC	*Ae. cylindrica*	Wild	4X	W		AAFC
805*	EKC154_RL5853	MU	*Ae. geniculata*	Wild	4X	W		AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
806	EKC158_RL5857	MU	*Ae. geniculata*	Wild	4X	W		AAFC
807	EKC159_RL5858	MU	*Ae. geniculata*	Wild	4X	W		AAFC
808*	EKC160_RL5859	MU	*Ae. geniculata*	Wild	4X	W		AAFC
821*	IPK-AE91	DMU	*Ae. juvenalis*	Wild	6X	W	United Kingdom	IPK
828*	IPK-AE182	DMU	*Ae. juvenalis*	Wild	6X	W	Uzbekistan	IPK
836	IPK-AE497	DMU	*Ae. juvenalis*	Wild	6X	W	Uzbekistan	IPK
794*	EKC110_RL5302	S^l	*Ae. longissima*	Wild	2X	W		AAFC
830	IPK-AE316	S^l	*Ae. longissima*	Wild	2X	W	Israel	IPK
833	IPK-AE409	S^l	*Ae. longissima*	Wild	2X	W	Israel	IPK
843	IPK-AE906	S^l	*Ae. longissima*	Wild	2X	W	Israel	IPK
831	IPK-AE346	S^l	*Ae. longissima*	Wild	2X	W	Turkey	IPK
793*	EKC105_RL5723	C	*Ae. markgrafii*	Wild	2X	W		AAFC
813*	EKC166_RL5012	UM/UMN	*Ae. neglecta*	Wild	4X/6X	W		AAFC
810*	EKC163_RL5017	SU	*Ae. peregrina*	Wild	4X	W		AAFC
811*	EKC164_RL5849	SU	*Ae. peregrina*	Wild	4X	W		AAFC
798*	EKC116_RL5706	S^s	*Ae. searsii*	Wild	2X	W		AAFC
795*	EKC108_RL5004	S^{sh}	*Ae. sharonensis*	Wild	2X	W		AAFC
789*	EKC101_RL5719	S	*Ae. speltoides*	Progenitor	2X	W		AAFC
788*	EKC97_RL5300	S	*Ae. speltoides*	Progenitor	2X	W		AAFC
790*	EKC102_RL5720	S	*Ae. speltoides ligustica*	Progenitor	2X	W		AAFC
791*	EKC103_RL5721	S	*Ae. speltoides ligustica*	Progenitor	2X	W		AAFC
493	RL5534	D	*Ae. tauschii*	Progenitor	2X	W	Azerbaijan	AAFC
494*	RL5536	D	*Ae. tauschii*	Progenitor	2X	W	Azerbaijan	AAFC
495*	RL5537	D	*Ae. tauschii*	Progenitor	2X	W	Azerbaijan	AAFC
491	RL5524	D	*Ae. tauschii*	Progenitor	2X	W	Azerbaijan	AAFC
90*	BW31221	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
91	BW31225	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
97	BW31261	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
757*	C23 (AS60)	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
529	RL5736	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
534	RL5741	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
535	RL5744	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
536	RL5745	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
539	RL5750	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
553	RL5772	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
556	RL5775	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
559	RL5778	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
562	RL5781	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
567	RL5786	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
538	RL5747	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
564	RL5783	D	*Ae. tauschii*	Progenitor	2X	W	Iran	AAFC
498	RL5554	D	*Ae. tauschii*	Progenitor	2X	W	Uzbekistan	AAFC
89	BW31215	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
94	BW31236	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
95	BW31260	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
758*	C24 (AS66)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
759*	C26 (AS2386)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
760*	C29 (AS2395)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
761*	C30 (AS2399)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
762*	C31 (AS2404)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
763*	C32 (AS2405)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
764*	C33 (AS2407)	D	*Ae. tauschii*	Progenitor	2X	W		AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
490	RL5499	D	*Ae. tauschii*	Progenitor	2X	W		AAFC
483*	RL5265	D	*Ae. tauschii* var. *anathera*	Progenitor	2X	W		AAFC
578*	RL5798	D	*Ae. tauschii* var. *mayeri*	Progenitor	2X	W		AAFC
521*	RL5686	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Azerbaijan	AAFC
527*	RL5695	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Azerbaijan	AAFC
528	RL5699	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Iran	AAFC
545	RL5761	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Iran	AAFC
549	RL5768	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Iran	AAFC
550	RL5769	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W	Iran	AAFC
572	RL5791	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W		AAFC
574	RL5793	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W		AAFC
575	RL5794	D	*Ae. tauschii* var. *strangulata*	Progenitor	2X	W		AAFC
812*	EKC165_RL5011	UC/CU	*Ae. triuncialis*	Wild	4X	W		AAFC
816	EKC169_RL5278	UC/CU	*Ae. triuncialis*	Wild	4X	W		AAFC
799	EKC119_RL5727	U	*Ae. umbellulata*	Wild	2X	W		AAFC
838*	IPK-AE714	U	*Ae. umbellulata*	Wild	2X	W	Bulgaria	IPK
839	IPK-AE740	U	*Ae. umbellulata*	Wild	2X	W	Turkey	IPK
841*	IPK-AE825	U	*Ae. umbellulata*	Wild	2X	W	Turkey	IPK
817	EKC193_RL5664	DMS	*Ae. vavilovii* (Zhuk.)	Wild	6X	W		AAFC
804*	EKC137_RL5650	DN	*Ae. ventricosa*	Wild	4X	W		AAFC
779*	EKC11_RL5477	V	*Haynaldia villosa*	Wild	2X	W		AAFC
592*	C48	ABD	*T. aestivum* (synt)	SHW	6X	W	AS2240/AS77	AAFC
583*	C38	ABD	*T. aestivum* (synt)	SHW	6X	S	AS2255/AS2393	AAFC
582*	C37	ABD	*T. aestivum* (synt)	SHW	6X	S	AS2255/AS2395	AAFC
579*	C34	ABD	*T. aestivum* (synt)	SHW	6X	S	AS2296/AS2388	AAFC
580*	C35	ABD	*T. aestivum* (synt)	SHW	6X	W	AS2313/AS2388	AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
581	C36	ABD	*T. aestivum* (synt)	SHW	6X	W	AS2382/AS2388	AAFC
605	C64	ABD	*T. aestivum* (synt)	SHW	6X	S	AS2399/PI355527	AAFC
584*	C39	ABD	*T. aestivum* (synt)	SHW	6X	S-W	AS285/AS2386	AAFC
585*	C40	ABD	*T. aestivum* (synt)	SHW	6X	W	AS285/AS2404	AAFC
587*	C42	ABD	*T. aestivum* (synt)	SHW	6X	W	AS286/AS2386	AAFC
588*	C43	ABD	*T. aestivum* (synt)	SHW	6X	S	AS286/AS2407	AAFC
586*	C41	ABD	*T. aestivum* (synt)	SHW	6X	W	AS286/AS66	AAFC
589*	C44	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/AS2386	AAFC
590*	C45	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/AS2399	AAFC
591*	C46	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/AS2404	AAFC
700	Synthetic W7984	ABD	*T. aestivum* (synt)	SHW	6X	S	Mexico	AAFC
601	C57	ABD	*T. aestivum* (synt)	SHW	6X	S	PI113961/AS2386	AAFC
600*	C56	ABD	*T. aestivum* (synt)	SHW	6X	S	PI113961/AS2404	AAFC
609*	C68	ABD	*T. aestivum* (synt)	SHW	6X	S	PI211681AS2386	AAFC
602*	C61	ABD	*T. aestivum* (synt)	SHW	6X	S	PI352335/AS2386	AAFC
603*	C62	ABD	*T. aestivum* (synt)	SHW	6X	W	PI355465/AS2405	AAFC
608*	C67	ABD	*T. aestivum* (synt)	SHW	6X	W	PI355465/AS60	AAFC
604*	C63	ABD	*T. aestivum* (synt)	SHW	6X	W	PI355476/AS2404	AAFC
607*	C66	ABD	*T. aestivum* (synt)	SHW	6X	S	PI377655/AS2386	AAFC
606*	C65	ABD	*T. aestivum* (synt)	SHW	6X	S	PI377655/AS2399	AAFC
594*	C50	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94627/AS2386	AAFC
595	C51	ABD	*T. aestivum* (synt)	SHW	6X	W	PI94650/AS2404	AAFC
596*	C52	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94655/AS2404	AAFC
597	C53	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94655/AS2407	AAFC
593*	C49	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94666/AS2405	AAFC
598*	C54	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94666/AS2407	AAFC

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Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
599*	C55	ABD	*T. aestivum* (synt)	SHW	6X	S	PI94675/AS2405	AAFC
781*	EKC24_RL5710	ABD	*T. aestivum* (synt)	SHW	6X	S		AAFC
782*	EKC25_RL5712	ABD	*T. aestivum* (synt)	SHW	6X	S-W		AAFC
886	17CAN-SYNT-15A	ABD	*T. aestivum* (synt)	SHW	6X	W	Aisberg/Ae.squarrosa(369)	CIMMYT
901	17CAN-SYNT-30A	ABD	*T. aestivum* (synt)	SHW	6X	W	Aisberg/Ae.squarrosa(511)	CIMMYT
887	17CAN-SYNT-16A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ig-126387	CIMMYT
892	17CAN-SYNT-21C	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ig-131606	CIMMYT
884	17CAN-SYNT-13B	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ig-48042	CIMMYT
877	17CAN-SYNT-06A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ku-2075	CIMMYT
882	17CAN-SYNT-11A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ku-20-9	CIMMYT
898	17CAN-SYNT-27A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ku-2092	CIMMYT
872	17CAN-SYNT-01A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ku-2096	CIMMYT
893	17CAN-SYNT-22A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/ku-2100	CIMMYT
875	17CAN-SYNT-04A	ABD	*T. aestivum* (synt)	SHW	6X	W	Langdon/pi 508262	CIMMYT
900	17CAN-SYNT-29A	ABD	*T. aestivum* (synt)	SHW	6X	W	leuc 84693/Ae.squarrosa(1026)	CIMMYT
873	17CAN-SYNT-02B	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
879	17CAN-SYNT-08B	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
885	17CAN-SYNT-14A	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
888	17CAN-SYNT-17B	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
890	17CAN-SYNT-19A	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
891	17CAN-SYNT-20A	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
896	17CAN-SYNT-25F	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(223)	CIMMYT
876	17CAN-SYNT-05A	ABD	*T. aestivum* (synt)	SHW	6X	W	Pandur/Ae.squarrosa(409)	CIMMYT
878	17CAN-SYNT-07A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 1530.94/Ae.squarrosa(1027)	CIMMYT

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
889	17CAN-SYNT-18A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 1530.94/Ae.squarrosa(1027)	CIMMYT
895	17CAN-SYNT-24A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 1530.94/Ae.squarrosa(1027)	CIMMYT
880	17CAN-SYNT-09A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 1530.94/Ae.squarrosa(458)	CIMMYT
897	17CAN-SYNT-26A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 1530.94/Ae.squarrosa(629)	CIMMYT
881	17CAN-SYNT-10A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 761.93/Ae.squarrosa(392)	CIMMYT
883	17CAN-SYNT-12A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 761.93/Ae.squarrosa(392)	CIMMYT
899	17CAN-SYNT-28A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 761.93/Ae.squarrosa(392)	CIMMYT
874	17CAN-SYNT-03A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 952.92/Ae.squarrosa(1031)	CIMMYT
894	17CAN-SYNT-23A	ABD	*T. aestivum* (synt)	SHW	6X	W	ukr-od 952.92/Ae.squarrosa(1031)	CIMMYT
610*	M321	ABD	*T. aestivum* (synt)	SHW	6X	S		
730*	BW779_Tezanos	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Argentina	AAFC
752	Wilgoyne	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Australia	AAFC
756	HC374	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
701*	RL4452	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
722	Selkirk	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
714	RL6050	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Iran	AAFC
729	BW31100	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
719	Lalbahadur	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
745	Pavon 76	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
749	Sonora 64	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
751	Weebill-1	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
696	BW278	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
707	RL6058	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
710	RL6069	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
711	RL6070	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
713	RL6077	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
708*	RL6091	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
712	RL6106	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
709	RL6159	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S		AAFC
728	Bluesky	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
720	AC Minto	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
738	Fieldstar BW365	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
705	Grandin	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
721*	Pasqua	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
746	Peace(PT416)	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
747	Regent	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
703	Roblin	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
694	Superb	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
704	AC Reed	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
871	Emerson-1	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	W	Canada	AAFC
718	Fielder-1	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	United States of America	AAFC
725	AC Barrie	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
698	AC Karma	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
726	AC Vista	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
742	LEADER (BW535)	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
743	Lillian = BW776	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
731*	Carberry BW874	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	AAFC
706	Foremost	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	AAFC
740	HARTOG	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Australia	AWCC
755	JANZ	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Australia	AWCC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
727	Aus30426_Otane	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	New Zealand	AWCC
754	AC Cora	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	CDC
702	AC Domain	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	CDC
750	Stanley	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	CDC
744	ND694=Parshall	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	United States of America	NDSU
715	Frontana	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Brazil	NSGC
717	PI58548	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	China	NSGC
695	Sumai3	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	China	NSGC
699	Opata	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Mexico	NSGC
739*	CN10112	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Australia	PGRC
723*	CN44011	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Brazil	PGRC
734	CN11189	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	PGRC
741*	CN38927	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	PGRC
735*	CN32076	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Japan	PGRC
736*	CN32077	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Japan	PGRC
732*	CN10719	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Kenya	PGRC
733*	CN11057	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Peru	PGRC
737*	CN9591_Bage	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Uruguay	PGRC
671	Thatcher	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	United States of America	PGRC
697	WhiteGlenlea	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Canada	PSD
724	01C0204206	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Australia	RICP,CZECH
693	Chinese Spring	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	China	USDA-ARS
748	Salamouni	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Lebanon	USDA-ARS
716	Terenzio	ABD	*T. aestivum* ssp. *aestivum*	Cultivated	6X	S	Portugal	USDA-ARS
168	CWI42787	ABD	*T. aestivum* ssp. *compactum*	Cultivated	6X	S	Denmark	AAFC
166	CN12213	ABD	*T. aestivum* ssp. *compactum*	Cultivated	6X	S		PGRC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
165*	CN2674	ABD	*T. aestivum* ssp. *compactum*	Cultivated	6X	S		PGRC
456*	01C0204206	ABD	*T. aestivum* ssp. *graecum*	Cultivated	6X	S	Australia	RICP,CZECH
455	01C0203832	ABD	*T. aestivum* ssp. *lutescense*	Cultivated	6X	S	Australia	RICP,CZECH
359	01C0203285	ABD	*T. aestivum* ssp. *lutescense*	Cultivated	6X	S	Czech	RICP,CZECH
365*	01C0105549	ABD	*T. aestivum* ssp. *lutescense*	Cultivated	6X	S	Yugoslavia	RICP,CZECH
176*	CN99032	ABD	*T. aestivum* ssp. *macha*	Cultivated	6X	S		PGRC
870	IPK-TRI19322	ABD	*T. aestivum* ssp. *Spelta*	Cultivated	6X	S	Germany	IPK
34*	AS11585	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S	Canada	PGRC
33	AS11527	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S	Czech	PGRC
162	CN12229	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S	Czech	PGRC
163*	CN12261	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S	Czech	PGRC
164	CN37599	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S	Sweden	PGRC
160	CN1849	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S		PGRC
161	CN2758	ABD	*T. aestivum* ssp. *spelta*	Cultivated	6X	S		PGRC
174*	G3893	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S		PGDC
171	CN33803	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S	Georgia	PGRC
169	CN11647	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S	Hungary	PGRC
170	CN11739	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S	Hungary	PGRC
173	CN33893	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S	India	PGRC
172	CN33892	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S	Pakistan	PGRC
175*	CWI42988	ABD	*T. aestivum* ssp. *spherococcum*	Cultivated	6X	S		PGRC
88	CWI16956	A^m	*T. monococcum*	Progenitor	2X	W	Russia	AAFC
87*	CWI19490_RL5444	A^m	*T. monococcum*	Progenitor	2X	W	Turkey	AAFC
786	EKC58_RL5216	A^m	*T. monococcum* ssp. *aegilopoides*	Progenitor	2X	W		AAFC
73	CN37617	A^m	*T. monococcum* ssp. *monococcum*	Progenitor	2X	W	Bulgaria	PGRC
74*	CN12440	A^m	*T. monococcum* ssp. *monococcum*	Progenitor	2X	W	France	PGRC

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Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
72	CN11649	A^m	*T. monococcum* ssp. *monococcum*	Progenitor	2X	W	Hungary	PGRC
78	CN37611	A^m	*T. monococcum* ssp. *monococcum*	Progenitor	2X	W	United Kingdom	PGRC
76	CN11756	A^m	*T. monococcum* ssp. *monococcum*	Progenitor	2X	W		PGRC
783*	EKC37_RL5247	A^m	*T. monococcum* var. *albo-hornemannii*	Progenitor	2X	W		AAFC
784	EKC47_RL5509	A^m	*T. monococcum* var. *albo-hornemannii*	Progenitor	2X	W		AAFC
785*	EKC48_RL5510	A^m	*T. monococcum* var. *hornemannii*	Progenitor	2X	W		AAFC
861	IPK-TRI7272	A^tG	*T. timopheevii*	Wild	4X	W	Ethiopia	IPK
867	IPK-TRI13604	A^tG	*T. timopheevii*	Wild	4X	W	Georgia	IPK
868*	IPK-TRI13606	A^tG	*T. timopheevii*	Wild	4X	W	Georgia	IPK
853	IPK-TRI4349	A^tG	*T. timopheevii*	Wild	4X	W	Hungary	IPK
849*	IPK-TRI677	A^tG	*T. timopheevii*	Wild	4X	W	USSR	IPK
862	IPK-TRI7301	A^tG	*T. timopheevii*	Wild	4X	W		IPK
627*	AS2255	AB	*T. turgidum*	Cultivated	4X	S	China	AAFC
104	DW7195	AB	*T. turgidum*	Cultivated	4X	S	Spain	AAFC
611*	AS2240	AB	*T. turgidum*	Cultivated	4X	S		AAFC
628*	AS285	AB	*T. turgidum*	Cultivated	4X	S		AAFC
629*	AS286	AB	*T. turgidum*	Cultivated	4X	S		AAFC
854	IPK-TRI4354	AB	*T. turgidum*	Cultivated	4X	S	Canada	IPK
40	CN10545	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
41	CN10547	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
42	CN11002	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
43	CN11003	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
44	CN11573	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
45	CN11579	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
47	CN12224	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
39	CN1748	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
53	CN51246	AB	*T. turgidum*	Cultivated	4X	S	Canada	PGRC
46	CN12222	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
35	CN12223	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
48	CN12225	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
49	CN12226	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
50	CN12227	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
51	CN12230	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
14	CN12232	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
52	CN12233	AB	*T. turgidum*	Cultivated	4X	S	Czech	PGRC
37	CN2644	AB	*T. turgidum*	Cultivated	4X	S	Portugal	PGRC
54	CN51253	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
38	CN51254	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
55	CN51255	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
56	CN51256	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
57	CN51257	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
58	CN51258	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
59	CN51259	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
60	CN51263	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
61	CN51265	AB	*T. turgidum*	Cultivated	4X	S	Russia	PGRC
36	CN32158	AB	*T. turgidum*	Cultivated	4X	S	United States of America	PGRC
62	CN51269	AB	*T. turgidum*	Cultivated	4X	S	United States of America	PGRC
780	EKC22_RL5347	SA^m	*T. turgidum* (amphiploid)	Wild	4X	S		AAFC
144	CWI44563	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Iran	AAFC
139	DW7196	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Jordan	AAFC

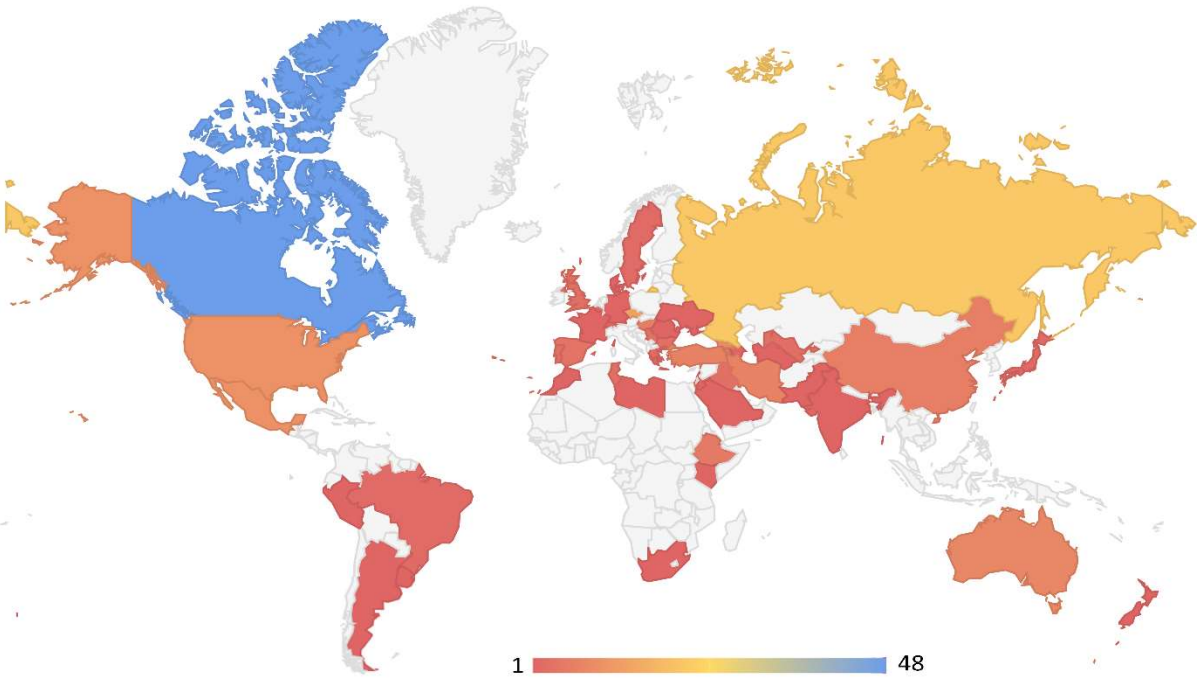
Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
142	CWI44453	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Russia	AAFC
145	CWI44464	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Russia	AAFC
143*	CWI44562	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Russia	AAFC
141	CWI44150	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S		AAFC
140	CWI5222	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S		AAFC
800*	EKC127_RL5577	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	W		AAFC
137	CN32502	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Armenia	PGRC
134	CN32496	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Georgia	PGRC
138	CN40686	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Georgia	PGRC
135	CN32498	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Hungary	PGRC
136	CN32500	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S	Iraq	PGRC
146	Blackbird	AB	*T. turgidum* ssp. *carthlicum*	Cultivated	4X	S		
851	IPK-TRI3241	AB	*T. turgidum* ssp. *compositum*	Cultivated	4X	S	Canada	IPK
110*	CWI18234	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Armenia	AAFC
117	5310	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Mexico	AAFC
118	5315	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Mexico	AAFC
112	CWI16984	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Spain	AAFC
113	CWI17128	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Spain	AAFC
116	CWI18902	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Turkey	AAFC
111	CWI15345	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S		AAFC
869*	IPK-TRI18539	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	W	Turkey	IPK
127	CN32486	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Ethiopia	PGRC
107	CN32494	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Hungary	PGRC
105	CN32492	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Israel	PGRC
106*	CN32493	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Spain	PGRC
108	CN32495	AB	*T. turgidum* ssp. *dicoccoides*	Progenitor	4X	S	Switzerland	PGRC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
131	CWI19155	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Ethiopia	AAFC
130	CWI36567	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S-W	Libya	AAFC
133	DW7191	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Tunisia	AAFC
132	DW7193	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Tunisia	AAFC
613*	PI94627	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Asia Minor	NSGC
621*	PI355465	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Belgium	NSGC
622*	PI355476	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S-W	Belgium	NSGC
615*	PI94655	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Bulgaria	NSGC
614*	PI94650	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Czech	NSGC
618*	PI113961	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Georgia	NSGC
619*	PI113963	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Georgia	NSGC
624	PI415152	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S-W	Israel	NSGC
616*	PI94666	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Russia	NSGC
623*	PI377655	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Serbia	NSGC
612	PI94614	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Ukraine	NSGC
620*	PI352335	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	United States of America	NSGC
617*	PI94675	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	United States of America	NSGC
125	CN32482	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Armenia	PGRC
124	CN2652	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Romania	PGRC
126*	CN32483	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Saudi Arabia	PGRC
128	CN32488	AB	*T. turgidum* ssp. *dicoccum*	Progenitor	4X	S	Serbia	PGRC
631	AC Morse	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
630	AC Avonlea	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
634	AC Pathfinder	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
635	Commander	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
636	DT 773 (Brigade)	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
638	Kyle	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
639	Strongfield	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
637*	DT 776 (Eurostar)	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	AAFC
632	AC Napoleon	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Canada	CDC
119	CN7773	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Israel	PGRC
121	CN10163	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	South Africa	PGRC
120	CN7786	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	Tunisia	PGRC
626*	Langdon	AB	*T. turgidum* ssp. *durum*	Cultivated	4X	S	United States of America	USDA-ARS
151	CN45831	AB	*T. turgidum* ssp. *polonicum*	Cultivated	4X	S		PGRC
152*	CN51900	AB	*T. turgidum* ssp. *polonicum*	Cultivated	4X	S		PGRC
153	CN51903	AB	*T. turgidum* ssp. *polonicum*	Cultivated	4X	S		PGRC
154	CN51933	AB	*T. turgidum* ssp. *polonicum*	Cultivated	4X	S		PGRC
625*	PI211691	AB	*T. turgidum* ssp. *turanicum*	Cultivated	4X	S	Turkey	NSGC
148*	CN10543	AB	*T. turgidum* ssp. *turanicum*	Cultivated	4X	S	Canada	PGRC
149	CN11587	AB	*T. turgidum* ssp. *turanicum*	Cultivated	4X	S		PGRC
147	CN1839	AB	*T. turgidum* ssp. *turanicum*	Cultivated	4X	S		PGRC
850	IPK-TRI2230	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S	United States of America	IPK
102	CN40845	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S	Ethiopia	PGRC
103	CN40848	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S	Ethiopia	PGRC
99	CN1837	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S	Portugal	PGRC
101	CN33858	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S	United States of America	PGRC
100	CN11761	AB	*T. turgidum* ssp. *turgidum*	Cultivated	4X	S		PGRC
852*	IPK-TRI3365	AB	*T. turgidum* var. *linnaeanum*	Cultivated	4X	W	China	IPK
856	IPK-TRI4653	AB	*T. turgidum* var. *linnaeanum*	Cultivated	4X	W	Australia	IPK
67*	CN38247	A	*T. urartu*	Progenitor	2X	W	Iraq	PGRC
863*	IPK-TRI7315	ABD	*T. vavilovii*	Cultivated	6X	W	Armenia	IPK

Entry[1]	Accession	Genome	Species	Category	Ploidy[2]	GH[3]	Origin/Pedigree	Seed Source
855*	IPK-TRI4630	ABD	*T. vavilovii*	Cultivated	6X	W	China	IPK
864*	IPK-TRI11555	ABD	*T. vavilovii*	Cultivated	6X	W	USSR	IPK
865	IPK-TRI11556	ABD	*T. vavilovii*	Cultivated	6X	W	USSR	IPK
858	IPK-TRI7258	GAA^m	*T. zhukovskyi*	Wild	6X	W	Georgia	IPK
860*	IPK-TRI7270	GAA^m	*T. zhukovskyi*	Wild	6X	W	Georgia	IPK
857*	IPK-TRI5416	GAA^m	*T. zhukovskyi*	Wild	6X	W	USSR	IPK
859	IPK-TRI7262	GAA^m	*T. zhukovskyi*	Wild	6X	W	USSR	IPK
866	IPK-TRI12094	GAA^m	*T. zhukovskyi*	Wild	6X	W		IPK

The species names and genome symbols are according to Kimber and Tsunewaki (Kimber and Tsunewaki, 1988)
[1] Entry numbers followed by a "*" symbol represents accessions that were a part of the 136 accession used for exome-capture variant calling
[2]2X, Diploid; 4X, Tetraploid; 6X, Hexaploid
[3]GH, Growth habit; S, Spring; W, Winter



Appendix 1B Geographical distribution of 217 of the 385 accessions in the collection.

Number of accessions originating in each country is represented by a gradient color scale, where the color red indicates the lowest number of accessions (one) and blue the highest number of accessions (48).

Chapter 5

Appendix 2 Infection type scores of accessions rated for response against leaf rust isolates

Accessions were scored using the Stakman scale (Stakman et al., 1962) and the linear conversion using a 1-9 scale is shown in brackets.

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
14	CN12232	; (1)	;1= (2)	;1=/3+ (NA)	X- (6)	X (6)	;/3+ (NA)
33	AS11527	3+ (7)	3 (7)	3+ (7)	3 (7)	3+ (7)	3+ (7)
34	AS11585	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
35	CN12223	; (1)	; (1)	; (1)	; (1)	NA	; (1)
36	CN32158	;1= (2)	;1- (2)	;1= (2)	;1= (2)	;1= (2)	;1= (2)
37	CN2644	3+ (7)	;1- (2)	1- (2)	1+ (3)	1- (2)	1- (2)
38	CN51254	3+ (7)	3- (7)	3 (7)	12 (4)	2 (5)	3 (7)
39	CN1748	3 (7)	3- (7)	3 (7)	;1= (2)	; (1)	3+ (7)
40	CN10545	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
41	CN10547	;1= (2)	;1= (2)	;1= (2)	; (1)	1- (2)	; (1)
42	CN11002	;1= (2)	;1= (2)	;1= (2)	;1= (2)	;1= (2)	; (1)
43	CN11003	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
44	CN11573	3+ (7)	3+ (7)	3+ (7)	X (6)	3+ (7)	X (6)
45	CN11579	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
46	CN12222	NA	1- (2)	3- (7)	3+ (7)	3 (7)	3 (7)
47	CN12224	3+ (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
48	CN12225	3+ (7)	X- (6)	X (6)	NA	NA	NA
50	CN12227	;1= (2)	;1= (2)	;1= (2)	1- (2)	X (6)	;1= (2)
51	CN12230	;1- (2)	1- (2)	;1= (2)	;1= (2)	X (6)	;1= (2)
52	CN12233	3+ (7)	1-/3+ (NA)	3+ (7)	3+ (7)	3 (7)	3+ (7)
53	CN51246	NA	NA	NA	NA	; (1)	; (1)
54	CN51253	2+ (5)	33- (7)	3+ (7)	X (6)	1+ (3)	3+ (7)
55	CN51255	1- (2)	;1- (2)	1- (2)	; (1)	1- (2)	1- (2)
56	CN51256	1- (2)	;1-1= (2)	;1- (2)	;1- (2)	;1- (2)	1- (2)
57	CN51257	;1- (2)	;1- (2)	;1- (2)	NA	;1- (2)	NA
58	CN51258	1+ (3)	;1- (2)	;1- (2)	;1- (2)	X- (6)	;1- (2)
59	CN51259	;1= (2)	3+ (7)	;1= (2)	;1- (2)	; (1)	;1= (2)
60	CN51263	3+ (7)	3+ (7)	3- (7)	NA	3- (7)	3+ (7)
61	CN51265	2- (5)	2+ (5)	23 (5)	1- (2)	2- (5)	3+ (7)
62	CN51269	2+ (5)	1+ (3)	2- (5)	;1- (2)	1+ (3)	1+ (3)
67	CN38247	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
73	CN37617	; (1)	; (1)	; (1)	; (1)	NA	; (1)
76	CN11756	;1= (2)	; (1)	; (1)	NA	NA	NA
78	CN37611	;1= (2)	; (1)	; (1)	; (1)	; (1)	; (1)
89	BW31215	2- (5)	;1= (2)	; (1)	; (1)	; (1)	; (1)
90	BW31221	3- (7)	NA	; (1)	;1= (2)	;1- (2)	;1- (2)
91	BW31225	3- (7)	3- (7)	; (1)	; (1)	NA	; (1)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
94	BW31236	; (1)	0; (1)	0 (1)	0 (1)	0; (1)	0 (1)
95	BW31260	2 (5)	11- (3)	1- (2)	2+ (5)	2+ (5)	2+ (5)
97	BW31261	1- (3)	0; (1)	; (1)	2- (5)	;1- (2)	;1- (2)
99	CN1837	;1= (2)	;1= (2)	;1= (2)	; (1)	;1- (2)	; (1)
100	CN11761	2+ (5)	2+ (5)	23 (5)	12 (4)	3+ (7)	3+ (7)
101	CN33858	;1= (2)	;1= (2)	;1= (2)	; (1)	;1= (2)	; (1)
102	CN40845	3+ (7)	3+/;1= (NA)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
103	CN40848	2- (5)	X (6)	;1- (2)	;1= (2)	; (1)	1- (2)
104	DW7195	;1- (2)	;1= (2)	;1= (2)	; (1)	; (1)	;1= (2)
106	CN32493	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	X (6)
107	CN32494	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3 (7)	3+ (7)
108	CN32495	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
110	CWI18234	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
111	CWI15345	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3 (7)
112	CWI16984	3+ (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
113	CWI17128	3+ (7)	3 (7)	3- (7)	X (6)	X (6)	X (6)
117	5310	;1= (2)	;1= (2)	;1= (2)	;1= (2)	;1= (2)	;1= (2)
118	5315	3+ (7)	3+ (7)	3+ (7)	3+ (7)	X (6)	3+ (7)
119	CN7773	1+3- (3)	1+ (3)	1+ (3)	1+ (3)	1+ (3)	1+ (3)
120	CN7786	;1= (2)	;1= (2)	;1= (2)	; (1)	; (1)	;1= (2)
121	CN10163	1+ (3)	1- (2)	1- (2)	;1- (2)	1- (2)	1- (2)
124	CN2652	3+ (7)	3- (7)	3- (7)	;1= (2)	;1= (2)	3- (7)
125	CN32482	;1= (2)	;1= (2)	1- (2)	; (1)	; (1)	; (1)
126	CN32483	2+ (5)	2 (5)	2 (5)	;1= (2)	1- (2)	1- (2)
127	CN32486	;1- (2)	;1= (2)	;1= (2)	;1= (2)	; (1)	;1= (2)
128	CN32488	2 (5)	3 (7)	2 (5)	;1- (2)	1- (2)	23 (5)
130	CWI36567	3+ (7)	3+ (7)	3 (7)	X (6)	X (6)	3+ (7)
131	CWI19155	3+ (7)	12 (4)	2 (5)	X- (6)	2- (5)	23 (5)
132	DW7193	;1= (2)	;1= (2)	;1= (2)	; (1)	; (1)	; (1)
133	DW7191	;1- (2)	;1= (2)	;1= (2)	;1=/3+ (NA)	;1= (2)	;1= (2)
134	CN32496	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
135	CN32498	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
136	CN32500	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
137	CN32502	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
138	CN40686	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
139	DW7196	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
140	CWI5222	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
141	CWI44150	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
142	CWI44453	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
143	CWI44562	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
144	CWI44563	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
145	CWI44464	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
146	Blackbird	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
147	CN1839	1- (2)	1- (2)	;1= (2)	1- (2)	1- (2)	1- (2)
148	CN10543	3+ (7)	;1= (2)	;1= (2)	;1= (2)	;1= (2)	;1= (2)
149	CN11587	3+ (7)	3+ (7)	3+ (7)	X (6)	;1=X (6)	3+ (7)
151	CN45831	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
152	CN51900	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
154	CN51933	;1= (2)	2 (5)	2- (5)	;1= (2)	;1- (2)	;1- (2)
160	CN1849	;1= (2)	3+ (7)	3+ (7)	3- (7)	3+ (7)	3+ (7)
161	CN2758	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
162	CN12229	;1- (2)	12 (4)	23 (5)	X (6)	X (6)	23 (5)
163	CN12261	3+ (7)	3 (7)	23 (5)	X (6)	X (6)	;1- (2)
164	CN37599	3+ (7)	3+ (7)	X (6)	X (6)	X (6)	X (6)
165	CN2674	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
166	CN12213	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
168	CWI42787	1- (2)	;1= (2)	;1= (2)	; (1)	0 (1)	; (1)
169	CN11647	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
170	CN11739	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
171	CN33803	3+ (7)	3+ (7)	3+ (7)	X (6)	3+ (7)	3+ (7)
172	CN33892	3+ (7)	3+ (7)	3+ (7)	3+ (7)	0/3+ (NA)	3+ (7)
173	CN33893	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
174	G3893	; (1)	; (1)	; (1)	3+ (7)	3+ (7)	3+ (7)
175	CWI42988	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
176	CN99032	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
359	01C0203285	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
365	01C0105549	;1= (2)	;1- (2)	; (1)	; (1)	; (1)	;1- (2)
455	01C0203832	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
456	01C0204206	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
483	RL5265	NA	3 (7)	3- (7)	3+ (7)	3+ (7)	3 (7)
490	RL5499	NA	NA	NA	3+ (7)	NA	NA
491	RL5524	0; (1)	0; (1)	0 (1)	0 (1)	0 (1)	0 (1)
493	RL5534	NA	NA	3 (7)	3 (7)	3- (7)	NA
494	RL5536	NA	;1= (2)	NA	; (1)	; (1)	; (1)
495	RL5537	NA	;1= (2)	; (1)	; (1)	;1= (2)	; (1)
498	RL5554	NA	NA	3- (7)	NA	3- (7)	3- (7)
521	RL5686	2- (5)	;1- (2)	; (1)	NA	;1- (2)	;1= (2)
527	RL5695	3 (7)	23 (5)	3- (7)	3+ (7)	3+ (7)	23 (5)
528	RL5699	3 (7)	1- (2)	; (1)	; (1)	; (1)	; (1)
529	RL5736	3+ (7)	3- (7)	3 (7)	3- (7)	3- (7)	3- (7)
534	RL5741	2 (5)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
535	RL5744	23 (5)	23 (5)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
536	RL5745	2+ (5)	NA	3+ (7)	NA	3+ (7)	3+ (7)
538	RL5747	3 (7)	3 (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)
539	RL5750	3 (7)	1- (2)	;1- (2)	NA	NA	;1- (2)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
545	RL5761	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
549	RL5768	; (1)	NA	0 (1)	; (1)	0 (1)	0 (1)
550	RL5769	NA	NA	1- (2)	;1- (2)	2- (5)	2 (5)
553	RL5772	3+ (7)	3 (7)	3 (7)	NA	NA	NA
556	RL5775	NA	NA	0 (1)	0 (1)	0 (1)	0 (1)
559	RL5778	NA	NA	; (1)	NA	; (1)	; (1)
562	RL5781	1- (2)	1- (2)	;1= (2)	1- (2)	2- (5)	;2- (5)
564	RL5783	2+ (5)	2+ (5)	2- (5)	2- (5)	3+ (7)	2- (5)
567	RL5786	NA	NA	2- (5)	3+ (7)	3+ (7)	3- (7)
572	RL5791	3+ (7)	;12 (4)	; (1)	; (1)	;1= (2)	;1- (2)
574	RL5793	; (1)	; (1)	; (1)	;1- (2)	; (1)	; (1)
575	RL5794	3+ (7)	3 (7)	3 (7)	3 (7)	3 (7)	3 (7)
578	RL5798	0; (1)	0; (1)	; (1)	;1- (2)	0 (1)	; (1)
579	C34	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
580	C35	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
581	C36	3+ (7)	4 (9)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
582	C37	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
583	C38	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
584	C39	3+ (7)	3+ (7)	3+ (7)	X (6)	3+ (7)	3+ (7)
585	C40	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3 (7)	3+ (7)
586	C41	3+ (7)	3+ (7)	3+ (7)	;1- (2)	;1- (2)	3+ (7)
587	C42	11+ (3)	1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
588	C43	3+ (7)	33+ (7)	3+ (7)	X (6)	X (6)	3 (7)
589	C44	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
590	C45	1- (2)	;1- (2)	;1- (2)	;1- (2)	;1= (2)	;1- (2)
591	C46	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
592	C48	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
593	C49	23 (5)	;1- (2)	1- (2)	;1= (2)	;1- (2)	;1- (2)
594	C50	3- (7)	1- (2)	; (1)	; (1)	; (1)	;1- (2)
595	C51	1- (2)	1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
596	C52	3+ (7)	3+ (7)	3+ (7)	; (1)	;1- (2)	3+ (7)
597	C53	3+ (7)	3+ (7)	3+ (7)	0 (1)	; (1)	NA
598	C54	NA	; (1)	;1- (2)	; (1)	; (1)	;1- (2)
599	C55	2- (5)	3+ (7)	;23- (5)	0 (1)	X (6)	1- (2)
600	C56	3 (7)	3- (7)	2- (5)	; (1)	;1= (2)	1- (2)
601	C57	3+ (7)	3+ (7)	3+ (7)	3+ (7)	X (6)	3+ (7)
602	C61	;1- (2)	;1= (2)	;1= (2)	; (1)	; (1)	;1- (2)
603	C62	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
604	C63	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
605	C64	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
606	C65	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
607	C66	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3 (7)
608	C67	3+ (7)	3+ (7)	3+ (7)	X/3+ (NA)	3+ (7)	3+4 (8)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
609	C68	;1- (2)	;1= (2)	;1- (2)	;1= (2)	;1- (2)	;1- (2)
610	M321	0 (1)	0 (1)	0 (1)	0 (1)	0 (1)	0; (1)
611	AS2240	3+ (7)	X+ (6)	3+ (7)	X (6)	X (6)	3- (7)
612	PI94614	1- (2)	;1- (2)	2- (5)	;1- (2)	;1- (2)	;1- (2)
613	PI94627	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
614	PI94650	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
615	PI94655	3- (7)	3=? (7)	3+ (7)	0; (1)	0 (1)	3 (7)
616	PI94666	2- (5)	3- (7)	3 (7)	; (1)	;1- (2)	;1= (2)
617	PI94675	1- (2)	;1- (2)	3 (7)	;1= (2)	0 (1)	;1- (2)
618	PI113961	2- (5)	12 (4)	2- (5)	; (1)	;1= (2)	2- (5)
619	PI113963	3+ (7)	3+ (7)	3+ (7)	NA	NA	NA
620	PI352335	3+ (7)	3- (7)	3+ (7)	; (1)	; (1)	3- (7)
621	PI355465	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
622	PI355476	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
623	PI377655	3+ (7)	3+ (7)	3+ (7)	0 (1)	X (6)	3+ (7)
624	PI415152	NA	2- (5)	NA	1- (2)	NA	NA
625	PI211691	3 (7)	3 (7)	3 (7)	3+ (7)	3+ (7)	3 (7)
626	Langdon	;1= (2)	;1- (2)	2- (5)	; (1)	; (1)	; (1)
627	AS2255	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
628	AS285	X (6)	;1- (2)	;1- (2)	;1= (2)	;1- (2)	;1- (2)
629	AS286	X (6)	X? (6)	X- (6)	; (1)	;1= (2)	;1- (2)
630	AC Avonlea	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
631	AC Morse	2- (5)	;1= (2)	;1- (2)	;1= (2)	;1= (2)	;1- (2)
632	AC Napoleon	2- (5)	1- (2)	2 (5)	1- (2)	12- (4)	1- (2)
634	AC Pathfinder	2- (5)	1- (2)	2 (5)	1- (2)	1- (2)	1- (2)
635	Commander	2 (5)	12 (4)	2- (5)	1- (2)	1- (2)	1- (2)
636	DT 773 (Brigade)	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
638	Kyle	;1- (2)	12- (4)	X- (6)	;1- (2)	;1- (2)	1- (2)
639	Strongfield	;1= (2)	;1= (2)	;1= (2)	; (1)	;1= (2)	; (1)
671	Thatcher	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
693	Chinese Spring	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
694	Superb	; (1)	; (1)	3+/; (NA)	3+ (7)	3+ (7)	3+ (7)
695	Sumai3	3+ (7)	3+ (7)	3+ (7)	3 (7)	3 (7)	3 (7)
696	BW278	1+ (3)	1- (2)	3- (7)	1+ (3)	1+ (3)	1+ (3)
697	WhiteGlenlea	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
698	AC Karma	1+ (3)	;1- (2)	3 (7)	1- (2)	1- (2)	1- (2)
699	Opata	3+ (7)	3+ (7)	3+ (7)	;1= (2)	;1= (2)	13 (3)
700	Synthetic W7984	3- (7)	X (6)	X (6)	1- (2)	3 (7)	;1- (2)
701	RL4452	3+ (7)	3+ (7)	3+4 (8)	3+ (7)	3+ (7)	3+ (7)
702	AC Domain	1+ (3)	1- (2)	3- (7)	1+ (3)	1+ (3)	1+ (3)
703	Roblin	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3 (7)
704	AC Reed	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
705	Grandin	0; (1)	; (1)	; (1)	1+ (3)	1+ (3)	1+ (3)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
706	Foremost	3 (7)	;1- (2)	1- (2)	;1- (2)	;1- (2)	;1- (2)
707	RL6058	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
708	RL6091	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
709	RL6159	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
710	RL6069	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
711	RL6070	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
712	RL6106	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
713	RL6077	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
714	RL6050	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3- (7)
715	Frontana	3+ (7)	X (6)	3+ (7)	; (1)	;1- (2)	X (6)
716	Terenzio	;1- (2)	;1- (2)	; (1)	0 (1)	;1= (2)	; (1)
717	PI58548	;1- (2)	;1= (2)	0; (1)	0 (1)	0; (1)	; (1)
718	Fielder-1	3+ (7)	3+ (7)	3+ (7)	; (1)	; (1)	3+ (7)
719	Lalbahadur (Pavon 1B)	3+ (7)	3+ (7)	3+ (7)	0 (1)	;1- (2)	3+ (7)
720	AC Minto	;1- (2)	X;12 (6)	;1= (2)	;1- (2)	;1- (2)	;1- (2)
721	Pasqua	; (1)	3+ (7)	; (1)	; (1)	; (1)	; (1)
722	Selkirk	1+ (3)	1+ (3)	2+ (5)	1- (2)	1+ (3)	1+ (3)
723	CN44011_Toropi	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
724	01C0204206_Sunbird	; (1)	; (1)	; (1)	3 (7)	3-? (7)	3 (7)
725	AC Barrie	1+ (3)	1- (2)	12 (4)	1- (2)	1- (2)	1- (2)
726	AC Vista	3+ (7)	2- (5)	2 (5)	2- (5)	2- (5)	;2- (5)
727	Aus30426_Otane	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
728	Bluesky	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
729	BW31100	;1- (2)	; (1)	;1= (2)	; (1)	; (1)	;1= (2)
730	BW779_	3- (7)	;1- (2)	X (6)	; (1)	; (1)	; (1)
731	Carberry BW874	0 (1)	0; (1)	0; (1)	1+ (3)	1+ (3)	1+ (3)
732	CN10719	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
733	CN11057	3+ (7)	X- (6)	X (6)	0 (1)	1- (2)	;1= (2)
734	CN11189	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
735	CN32076	3+ (7)	3+ (7)	3+4 (8)	3 (7)	3+ (7)	3+ (7)
736	CN32077_Nyu Bay	3+ (7)	3+ (7)	3+4 (8)	3+ (7)	3+ (7)	3+ (7)
737	CN9591_Bage	3+ (7)	3+/X (NA)	;1- (2)	X (6)	X (6)	;12 (4)
738	Fieldstar BW365	;1- (2)	;1= (2)	;1- (2)	13- (3)	;1- (2)	;1= (2)
739	CN10112_Gabo	3+ (7)	3+ (7)	3+ (7)	0? (1)	X (6)	3+ (7)
740	HARTOG	3+ (7)	3+ (7)	3+ (7)	3 (7)	3+ (7)	3+ (7)
741	CN38927_Katepwa	;1- (2)	3+ (7)	;1- (2)	; (1)	; (1)	;1= (2)
742	LEADER (BW535)	3+ (7)	3+ (7)	3+ (7)	NA	3+ (7)	3+ (7)
743	Lillian = BW776	;1- (2)	3+ (7)	X (6)	0 (1)	; (1)	;1= (2)
744	ND694=Parshall	0 (1)	; (1)	0; (1)	1+ (3)	1+ (3)	1+3- (3)
745	Pavon 76	3+ (7)	1+ (3)	3+ (7)	1+ (3)	X/3 (NA)	3- (7)
746	Peace(PT416)	3+ (7)	3+ (7)	3+ (7)	3 (7)	3+ (7)	3- (7)
747	Regent	3+ (7)	3+ (7)	3+ (7)	X- (6)	X (6)	3+ (7)
748	Salamouni	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
749	Sonora 64	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3 (7)
750	Stanley	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
751	Weebill-1	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
752	Wilgoyne	3- (7)	X- (6)	22- (5)	;1= (2)	; (1)	1- (2)
754	AC Cora	0 (1)	0; (1)	0 (1)	1- (2)	;1= (2)	; (1)
755	JANZ	; (1)	; (1)	0 (1)	0 (1)	X (6)	;1= (2)
756	HC374	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
757	C23 (AS60)	;1- (2)	; (1)	NA	NA	NA	NA
758	C24 (AA66)	3+ (7)	23 (5)	3 (7)	3+ (7)	NA	3 (7)
759	C26 (AS2386)	; (1)	; (1)	NA	; (1)	; (1)	; (1)
760	C29 (AS2395)	;1- (2)	;1= (2)	; (1)	; (1)	; (1)	; (1)
761	C30 (AS2399)	; (1)	1 (3)	; (1)	; (1)	; (1)	; (1)
762	C31 (AS2404)	23 (5)	22- (5)	; (1)	1- (2)	; (1)	3+ (7)
763	C32 (AS2405)	3- (7)	13 (3)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
764	C33 (AS2407)	;1= (2)	;1= (2)	; (1)	; (1)	; (1)	; (1)
779	EKC11_RL5477	2 (5)	; (1)	NA	NA	NA	;1- (2)
781	EKC24_RL5710	3+ (7)	3+ (7)	3+ (7)	X? (6)	3+ (7)	X (6)
782	EKC25_RL5712	3 (7)	23 (5)	23 (5)	3 (7)	3 (7)	23 (5)
783	EKC37_RL5247	0; (1)	1- (2)	;1= (2)	; (1)	;1- (2)	;1- (2)
784	EKC47_RL5509	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
785	EKC48_RL5510	; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
786	EKC58_RL5216	; (1)	; (1)	;1= (2)	;1- (2)	NA	;1- (2)
788	EKC97_RL5300	0; (1)	0; (1)	0 (1)	0 (1)	; (1)	0 (1)
789	EKC101_RL5719	0; (1)	NA	0 (1)	0 (1)	0 (1)	NA
790	EKC102_RL5720	; (1)	; (1)	;1= (2)	; (1)	; (1)	; (1)
791	EKC103_RL5721	; (1)	; (1)	; (1)	; (1)	0 (1)	0 (1)
793	EKC105_RL5723	3 (7)	3 (7)	NA	NA	3-? (7)	3+ (7)
794	EKC110_RL5302	;1- (2)	;1= (2)	3+ (7)	3 (7)	3 (7)	1- (2)
795	EKC108_RL5004	23 (5)	3+ (7)	;1- (2)	;1- (2)	;1- (2)	;1- (2)
796	EKC111_RL5009	3- (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
797	EKC112_RL5301	3 (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
798	EKC116_RL5706	NA	NA	3? (7)	3+ (7)	23 (5)	23? (5)
799	EKC119_RL5727	; (1)	; (1)	;1= (2)	; (1)	; (1)	0 (1)
800	EKC127_RL5577	1- (2)	1- (2)	2- (5)	2- (5)	2- (5)	1+ (3)
801	EKC135_RL5716	3+ (7)	1+3- (3)	NA	3+ (7)	3+ (7)	3+ (7)
802	EKC130_RL5010	; (1)	0 (1)	; (1)	; (1)	; (1)	; (1)
805	EKC154_RL5853	2- (5)	3-? (7)	;1= (2)	1- (2)	3- (7)	3 (7)
806	EKC158_RL5857	3-? (7)	NA	2- (5)	NA	; (1)	NA
807	EKC159_RL5858	2- (5)	;1= (2)	;1= (2)	NA	; (1)	; (1)
808	EKC160_RL5859	NA	NA	1- (2)	NA	NA	NA
810	EKC163_RL5017	11- (3)	1- (1-)	;1- (2)	; (1)	; (1)	;1- (2)
811	EKC164_RL5849	23 (5)	NA	3- (7)	NA	23 (5)	NA
812	EKC165_RL5011	2- (5)	2- (5)	;1- (2)	; (1)	; (1)	;1- (2)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
813	EKC166_RL5012	2- (5)	22+ (5)	2- (5)	1+ (3)	2- (5)	2- (5)
814	EKC171_RL5722	NA	NA	3- (7)	3+ (7)	3+ (7)	3+ (7)
815	EKC186_RL5847	3+ (7)	3+ (7)	23- (5)	3+ (7)	2- (5)	2- (5)
818	IPK-AE1	3 (7)	3+ (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)
819	IPK-AE8	3 (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
820	IPK-AE30	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
821	IPK-AE91	3+ (7)	3+ (7)	3+ (7)	X (6)	X (6)	3+ (7)
822	IPK-AE111	NA	; (1)	NA	; (1)	; (1)	; (1)
823	IPK-AE113	1- (2)	NA	NA	;1- (2)	2- (5)	NA
827	IPK-AE162	23 (5)	3 (7)	3+ (7)	3 (7)	3+ (7)	3+ (7)
828	IPK-AE182	3+ (7)	NA	34 (8)	X (6)	X (6)	3+ (7)
830	IPK-AE316	NA	; (1)	; (1)	; (1)	; (1)	;/3+ (NA)
831	IPK-AE346	1- (2)	13 (3)	;1- (2)	1- (2)	1- (2)	;1- (2)
835	IPK-AE467	3- (7)	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
838	IPK-AE714	23- (5)	2- (5)	NA	2+ (5)	2+ (5)	NA
841	IPK-AE825	11+ (3)	1- (2)	1- (2)	; (1)	NA	;1- (2)
842	IPK-AE899	23 (5)	23 (5)	3 (7)	23 (5)	3+ (7)	3+ (7)
843	IPK-AE906	;1- (2)	11+ (3)	2- (5)	2- (5)	2- (5)	2- (5)
847	IPK-AE1580	12 (4)	;1- (2)	2- (5)	2- (5)	3+ (7)	2+ (5)
848	IPK-AE1607	1- (2)	; (1)	; (1)	; (1)	; (1)	; (1)
849	IPK-TRI677	; (1)	0 (1)	; (1)	; (1)	; (1)	; (1)
852	IPK-TRI3365	11- (3)	11- (3)	2+ (5)	2+ (5)	3 (7)	2- (5)
853	IPK-TRI4349	0; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
855	IPK-TRI4630	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+4 (8)
856	IPK-TRI4653	11- (3)	11- (3)	2- (5)	2- (5)	2- (5)	1- (2)
857	IPK-TRI5416	0; (1)	0; (1)	0; (1)	; (1)	; (1)	; (1)
858	IPK-TRI7258	; (1)	NA	; (1)	; (1)	; (1)	; (1)
860	IPK-TRI7270	NA	; (1)	; (1)	; (1)	; (1)	; (1)
861	IPK-TRI7272	3+ (7)	NA	3+ (7)	; (1)	3+ (7)	3+ (7)
863	IPK-TRI7315	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+4 (8)
864	IPK-TRI11555	3+4 (8)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
865	IPK-TRI11556	3+ (7)	3+4 (8)	3+ (7)	3+ (7)	3+4 (8)	3+ (7)
866	IPK-TRI12094	0 (1)	0; (1)	; (1)	NA	; (1)	; (1)
867	IPK-TRI13604	0; (1)	0; (1)	; (1)	; (1)	; (1)	; (1)
868	IPK-TRI13606	0; (1)	; (1)	; (1)	; (1)	; (1)	; (1)
871	Emerson-1	3+ (7)	1- (2)	X (6)	3+ (7)	3+ (7)	3- (7)
872	17CAN-SYNT-01A	1- (2)	; (1)	;1- (2)	3 (7)	1- (2)	;1- (2)
873	17CAN-SYNT-02B	22+ (5)	;1- (2)	;1- (2)	3 (7)	;1- (2)	;1= (2)
874	17CAN-SYNT-03A	3 (7)	3+ (7)	3+ (7)	3+ (7)	3 (7)	3+ (7)
875	17CAN-SYNT-04A	3+ (7)	23 (5)	3+ (7)	3 (7)	3+ (7)	3 (7)
876	17CAN-SYNT-05A	3+ (7)	3+ (7)	1+ (3)	2+ (5)	3+ (7)	3+ (7)
877	17CAN-SYNT-06A	;1= (2)	;1- (2)	;1- (2)	;1- (2)	;1= (2)	;1= (2)

Entry	Accession	MBDS	MBRJ	MGBJ	TDBG1	TDBG2	TJBJ
878	17CAN-SYNT-07A	;1- (2)	;1- (2)	;1- (2)	1+3+ (3)	;1= (2)	1- (2)
879	17CAN-SYNT-08B	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
880	17CAN-SYNT-09A	4 (9)	4 (9)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
881	17CAN-SYNT-10A	3+4 (8)	4 (9)	3+ (7)	3+ (7)	3+4 (8)	3+4 (8)
882	17CAN-SYNT-11A	34 (8)	3- (7)	23 (5)	2+3 (7)	2+ (5)	2+ (5)
883	17CAN-SYNT-12A	4 (9)	3+ (7)	3+ (7)	3+ (7)	3+4 (8)	3+ (7)
884	17CAN-SYNT-13B	22+ (5)	2- (5)	23 (5)	2+ (5)	2+ (5)	2- (5)
885	17CAN-SYNT-14A	3+ (7)	3+ (7)	3+ (7)	;1-X (6)	;1-X (6)	3+ (7)
886	17CAN-SYNT-15A	3+4 (8)	34 (8)	23 (5)	3+ (7)	3+ (7)	3+ (7)
887	17CAN-SYNT-16A	3+ (7)	1+ (3)	2 (5)	2+ (5)	2+ (5)	2+ (5)
888	17CAN-SYNT-17B	4 (9)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
889	17CAN-SYNT-18A	11+ (3)	;1- (2)	;1= (2)	;1= (2)	; (1)	;1- (2)
890	17CAN-SYNT-19A	3+ (7)	3 (7)	3+ (7)	X- (6)	X (6)	2 (5)
891	17CAN-SYNT-20A	3- (7)	22- (5)	;1- (2)	;1- (2)	; (1)	2- (5)
892	17CAN-SYNT-21C	2- (5)	2- (5)	2+ (5)	2- (5)	2+ (5)	2- (5)
893	17CAN-SYNT-22A	2- (5)	;1- (2)	;1- (2)	3+ (7)	2- (5)	2- (5)
894	17CAN-SYNT-23A	3 (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
895	17CAN-SYNT-24A	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)	3+ (7)
896	17CAN-SYNT-25F	3 (7)	3 (7)	3+ (7)	; (1)	;1= (2)	;1- (2)
897	17CAN-SYNT-26A	3+ (7)	4 (9)	3+4 (8)	3+ (7)	3+ (7)	3+ (7)
898	17CAN-SYNT-27A	22- (5)	4 (9)	3+ (7)	3+ (7)	3+ (7)	3- (7)
899	17CAN-SYNT-28A	33- (7)	;1- (2)	3+ (7)	3/X (NA)	3/X (NA)	3+ (7)
900	17CAN-SYNT-29A	3+ (7)	3+ (7)	3 (7)	X (6)	X (6)	3+4 (8)
901	17CAN-SYNT-30A	2- (5)	1- (2)	X (6)	X (6)	; (1)	2+ (5)

The isolates tested were 12-3 MBDS, 128-1 MBRJ, 74-2 MGBJ, 11-180-1 TDBG, 06-1-1 TDBG, and 77-2 TJBJ. For simplicity, these were referred to as MBDS, MBRJ, MGBJ, TDBG1, TDBG2, and TJBJ, respectively.

IT scores were converted into a 1-9 linear scale using the following scale: “0/0;/;” = 1, “;1=/;1-” = 2, “1-/1/1+” = 3, “;12/1-2-” = 4, “2-/2/2+” = 5, “X” = 6, “3-/3/3+” = 7, “3+4/34” = 8, and “4” = 9

Chapter 5

Appendix 3 BLUP estimates and raw average score for leaf rust severity

Appendix 3A Overall and location-specific best linear unbiased predictors (BLUP) for leaf rust severity of the spring diversity panel (left of the vertical separator line). Table also shows raw average severity and infection type across all years and locations (right of the vertical separator line).

Entry	Accession	MDN	OTT	SK	Overall	Raw Average	Infection type[1]
132	DW7193	-5.21	-7.50	4.19	-15.23	1.50	R
850	IPK-TRI2230	NA	-6.70	-0.95	-12.83	1.50	R
52	CN12233	-4.23	-8.44	3.47	-17.56	1.54	R
127	CN32486	-5.15	-6.22	2.32	-17.50	1.83	R
35	CN12223	-5.02	-6.26	2.21	-17.34	2.00	R
62	CN51269	-5.13	-7.11	3.26	-17.44	2.60	R
58	CN51258	-5.66	-6.20	3.06	-17.07	3.07	R
46	CN12222	-6.53	-5.40	3.79	-16.07	3.08	R
56	CN51256	-5.94	-6.78	4.19	-16.38	3.14	R
151	CN45831	-7.64	-2.94	3.10	-13.78	3.27	R
103	CN40848	-6.03	-6.26	3.97	-16.26	3.50	R
639	Strongfield	-6.46	-5.41	3.76	-15.05	3.77	R
36	CN32158	-4.90	-6.02	2.72	-15.77	4.00	R
729	BW31100	-6.65	-7.15	6.12	-15.28	4.00	R
631	AC Morse	-6.03	-5.36	3.51	-14.72	4.31	R
48	CN12225	-6.60	-7.57	6.32	-15.45	4.33	R
55	CN51255	-6.38	-6.69	5.06	-15.65	4.33	R
38	CN51254	-6.03	-4.54	2.40	-15.60	4.36	R
61	CN51265	-7.36	-7.85	7.53	-15.25	4.40	R
37	CN2644	-7.11	-5.61	4.88	-15.20	4.43	R
121	CN10163	-6.37	-4.36	2.48	-16.01	4.47	R
630	AC Avonlea	-6.63	-4.11	3.18	-14.26	4.58	R
133	DW7191	-4.03	-10.93	7.41	-15.07	4.69	R
176	CN99032	-6.90	-3.28	2.20	-15.11	4.71	R
721	Pasqua	-7.09	-3.11	2.35	-15.15	4.79	R
131	CWI19155	-6.62	-4.87	4.25	-14.31	4.83	R
104	DW7195	-5.79	-5.87	4.34	-14.67	4.92	R
610	M321	-5.98	-3.51	1.30	-15.77	4.93	R
628	AS285	-7.92	-6.52	7.14	-14.47	5.07	R
636	DT 773 (Brigade)	-6.28	-5.72	4.65	-13.42	5.08	R
599	C55	-3.32	-6.79	2.17	-14.84	5.14	R
120	CN7786	-7.16	-4.08	3.43	-15.25	5.20	R
152	CN51900	-7.65	-5.60	5.84	-14.65	5.47	R
731	Carberry BW874	-3.46	-6.53	2.80	-12.63	5.73	R
41	CN10547	-7.94	-4.43	5.39	-14.17	5.77	R
110	CWI18234	-7.36	-5.64	5.72	-14.42	5.80	R
57	CN51257	-8.24	-1.54	2.69	-13.16	5.85	R
625	PI211691	-5.15	-4.85	2.80	-13.08	5.92	R
117	5310	-8.14	-5.53	6.75	-13.92	6.00	R
119	CN7773	-7.70	-5.90	6.72	-13.93	6.00	R
723	CN44011_Toropi	-7.27	-3.34	3.11	-14.66	6.00	R
147	CN1839	-6.33	-0.78	-0.47	-14.38	6.29	R
53	CN51246	-10.57	-11.42	16.53	-11.74	6.42	R

Entry	Accession	MDN	OTT	SK	Overall	Raw Average	Infection type[1]
126	CN32483	-8.03	-2.80	4.61	-12.72	6.58	R
614	PI94650	-7.46	-2.27	2.66	-13.78	6.64	R
54	CN51253	-8.67	-4.45	6.47	-13.29	7.00	R
154	CN51933	-6.83	-0.74	0.87	-12.62	7.15	R
612	PI94614	-6.71	-0.07	-0.09	-13.69	7.15	R
733	CN11057	-7.75	-0.01	0.97	-12.66	7.43	R
632	AC Napoleon	-5.77	-2.60	1.28	-13.64	7.53	R
49	CN12226	-4.40	-3.76	1.17	-12.91	7.75	R
626	Langdon	-8.93	3.26	-0.65	-12.76	7.77	R
602	C61	-7.20	-1.26	2.02	-11.88	7.92	R
47	CN12224	-8.67	-1.00	3.32	-11.70	8.00	R
60	CN51263	-7.96	-2.17	3.56	-12.80	8.00	R
609	C68	-6.86	-8.67	9.77	-11.48	8.33	R
693	Chinese Spring	-5.42	-0.56	-0.49	-11.90	8.38	R
620	PI352335	-4.68	-4.21	2.93	-11.39	8.42	R
720	AC Minto	-2.30	-6.65	2.27	-12.88	8.47	R
50	CN12227	-0.56	-10.55	4.75	-12.76	8.64	R
51	CN12230	-8.97	-2.48	5.62	-11.80	8.64	R
851	IPK-TRI3241	NA	-4.11	-0.90	-8.06	8.75	R
700	Synthetic W7984	0.71	-7.54	-0.06	-12.94	8.80	R
752	Wilgoyne	-2.12	-7.08	3.09	-11.68	8.85	R
137	CN32502	-3.61	-3.39	1.27	-10.43	8.91	R
624	PI415152	-1.51	-4.84	NA	-12.70	9.00	R
125	CN32482	-4.35	-3.78	1.85	-11.81	9.15	R
627	AS2255	-11.74	4.04	3.70	-7.34	9.18	R
623	PI377655	1.15	-7.64	-0.24	-12.27	9.33	R
728	Bluesky	-1.99	-7.37	3.17	-12.03	9.40	R
751	Weebill-1	-7.72	-7.58	10.35	-9.98	9.46	R
143	CWI44562	-1.50	-7.10	2.78	-10.17	10.00	R
635	Commander	-8.70	-1.68	5.07	-10.60	10.00	R
617	PI94675	-6.89	-1.85	3.54	-9.16	10.15	MR
59	CN51259	-4.31	-2.65	1.25	-11.22	10.23	MR
365	01C0105549	-9.08	2.67	0.97	-10.61	10.38	MR
42	CN11002	-7.50	-2.78	5.02	-10.26	10.73	MR
732	CN10719	-3.39	-4.86	2.60	-11.19	10.73	MR
118	5315	-6.56	-0.58	2.03	-9.51	10.85	MR
715	Frontana	-7.77	0.06	2.33	-10.44	11.13	MR
100	CN11761	-11.50	2.83	4.20	-9.51	11.57	MR
594	C50	0.24	-7.01	1.85	-8.32	11.60	MR
99	CN1837	-10.69	1.39	4.52	-9.83	11.77	MR
153	CN51903	-10.44	1.23	5.85	-5.95	11.78	MR
124	CN2652	-4.55	-0.56	0.31	-9.22	12.08	MR
621	PI355465	-4.64	-4.25	4.31	-9.03	12.15	MR
638	Kyle	-4.36	-0.18	-0.67	-9.93	12.36	MR
634	AC Pathfinder	-6.63	-6.44	9.21	-7.95	12.38	MR
101	CN33858	-8.30	3.50	0.15	-8.82	12.64	MR
107	CN32494	-10.82	5.76	3.08	-3.59	12.67	MR
146	Blackbird	1.75	-7.47	0.62	-9.70	12.67	MR
148	CN10543	-8.40	4.21	-0.85	-9.82	12.73	MR
629	AS286	-14.25	4.28	6.94	-7.32	12.85	MR

Entry	Accession	MDN	OTT	SK	Overall	Raw Average	Infection type[1]
746	Peace(PT416)	-2.15	-2.42	0.03	-8.75	13.64	MR
616	PI94666	-7.08	3.00	-0.22	-8.52	13.71	MR
854	IPK-TRI4354	NA	-1.78	-1.39	-4.78	13.75	MR
141	CWI44150	-4.80	0.18	0.06	-8.41	13.87	MR
136	CN32500	0.53	-4.75	-0.14	-7.17	14.31	MR
128	CN32488	-0.41	-1.30	-2.12	-7.10	14.44	MR
754	AC Cora	8.10	-13.06	0.92	-7.01	15.73	MR
173	CN33893	-5.93	3.43	-1.03	-6.22	15.77	MR
717	PI58548	-12.85	0.55	10.20	-4.82	16.40	MR
34	AS11585	-6.80	5.47	-2.31	-6.88	16.57	MR
611	AS2240	-10.93	5.60	2.49	-5.62	16.87	MR
134	CN32496	5.25	-7.25	-1.28	-5.69	17.08	MR
43	CN11003	-1.55	-3.34	2.27	-5.23	17.71	MR
14	CN12232	-7.81	4.12	0.97	-5.57	17.73	MR
781	EKC24_RL5710	6.54	-7.92	-1.59	-4.76	18.33	MR
142	CWI44453	0.37	-3.25	0.55	-3.63	19.00	MR
593	C49	-1.07	-4.43	3.27	-3.95	19.00	MR
703	Roblin	4.89	-6.33	-0.88	-4.49	19.23	MR
701	RL4452	6.02	-10.67	2.15	-3.94	19.46	MR
111	CWI15345	1.45	-1.55	-2.25	-4.25	19.62	MR
755	JANZ	-4.03	3.12	-1.15	-4.24	20.13	MR
716	Terenzio	-15.25	17.30	-2.66	-0.16	20.17	MR
738	Fieldstar BW365	5.59	-17.81	11.54	-1.51	21.21	MR
730	BW779	-10.49	15.45	-5.52	-0.62	21.23	MR
161	CN2758	-1.74	2.17	-1.83	-2.51	22.00	MR
697	WhiteGlenlea	0.52	-6.87	5.78	-1.36	22.07	MR
106	CN32493	-9.82	2.80	7.50	0.93	22.08	MR
33	AS11527	-5.42	4.07	0.46	-1.86	22.36	MR
113	CWI17128	-5.73	2.73	2.69	-1.79	22.50	MR
598	C54	3.40	-12.83	8.73	-0.11	23.00	MR
135	CN32498	6.94	-4.58	-3.50	-1.33	23.27	MR
743	Lillian = BW776	-3.82	6.28	-2.86	-1.21	23.57	MR
702	AC Domain	15.60	-11.71	-5.53	-2.03	24.07	MR
699	Opata	-7.41	12.02	-3.96	1.09	24.58	MR
705	Grandin	14.28	-15.38	0.34	-0.74	24.64	MR
694	Superb	16.48	-16.16	-1.77	-2.11	24.69	MR
140	CWI5222	7.46	-5.06	-2.83	-0.11	25.08	MR
740	HARTOG	0.90	1.33	-1.36	1.29	25.83	MR
162	CN12229	-1.18	0.73	1.39	1.70	26.67	MR
736	CN32077_Nyu Bay	-8.94	7.62	3.21	2.61	26.86	MR
706	Foremost	-6.55	7.34	0.75	3.35	26.93	MR
695	Sumai3	-12.10	7.95	6.04	3.07	26.93	MR
748	Salamouni	2.35	5.19	-7.40	0.85	27.40	MR
169	CN11647	-6.84	11.52	-2.62	4.35	27.92	MR
130	CWI36567	8.17	-8.33	NA	0.37	29.00	MR
724	01C0204206_Sunbird	-7.89	7.37	2.81	4.36	29.00	MR
714	RL6050	-2.53	10.35	-5.60	3.74	29.23	MR
737	CN9591_Bage	6.23	1.44	-6.22	2.48	29.62	MR
171	CN33803	-19.24	22.80	0.03	6.82	30.00	MR
870	IPK-TRI19322	NA	8.96	-6.18	5.91	30.00	MR

Entry	Accession	MDN	OTT	SK	Overall	Raw Average	Infection type[1]
144	CWI44563	4.59	-4.90	2.70	6.39	30.21	I
596	C52	6.35	2.98	-6.23	6.80	31.22	I
744	ND694=Parshall	24.97	-19.50	-4.40	1.97	31.43	I
698	AC Karma	-9.40	9.81	3.71	7.60	31.86	I
711	RL6070	-8.02	20.72	-8.78	7.64	32.31	I
735	CN32076	-18.17	24.54	-2.09	8.06	32.36	I
139	DW7196	7.69	-4.93	0.44	7.44	32.86	I
172	CN33892	-7.36	12.89	-1.67	7.95	32.86	I
622	PI355476	-15.52	20.23	NA	6.49	34.00	I
696	BW278	1.35	9.14	-6.96	7.29	34.29	I
174	G3893	3.21	4.32	-4.07	6.62	34.33	I
112	CWI16984	-1.25	9.27	-4.32	6.51	34.67	I
741	CN38927_Katepwa	15.80	-5.23	-7.69	6.20	35.00	I
727	Aus30426_Otane	-12.59	13.09	6.43	11.92	35.77	I
168	CWI42787	-0.77	13.15	-8.62	7.29	36.00	I
710	RL6069	-5.17	18.13	-8.22	8.81	36.43	I
359	01C0203285	-5.94	15.86	-5.29	9.25	36.80	I
163	CN12261	13.82	-6.86	-2.40	8.37	37.50	I
597	C53	16.03	-3.46	-8.72	7.15	38.00	I
726	AC Vista	-4.31	11.61	-1.18	11.86	38.21	I
40	CN10545	7.31	6.46	-8.64	8.16	38.64	I
725	AC Barrie	25.94	-14.68	-7.35	8.68	38.93	I
108	CN32495	-2.29	16.74	-8.98	11.11	39.00	I
712	RL6106	2.85	8.32	-5.93	10.02	39.00	I
44	CN11573	5.04	7.75	-7.44	10.78	39.29	I
780	EKC22_RL5347	NA	15.97	-10.32	11.63	40.00	I
582	C37	10.37	1.71	-6.39	11.20	40.67	MS
704	AC Reed	-1.46	17.66	-8.49	16.20	40.83	MS
742	LEADER (BW535)	-3.70	18.18	-7.62	13.65	41.43	MS
588	C43	12.08	3.68	-9.65	13.44	42.08	MS
713	RL6077	10.71	5.31	-9.78	11.68	42.50	MS
708	RL6091	4.74	10.20	-7.85	13.20	42.69	MS
455	01C0203832	-11.32	16.43	4.08	17.15	43.21	MS
745	Pavon 76	14.02	-1.80	-4.94	13.65	43.42	MS
734	CN11189_Neepawa	22.59	-8.83	-7.25	12.69	44.29	MS
160	CN1849	5.39	13.07	-11.03	14.12	45.67	MS
707	RL6058	8.10	3.76	-3.52	15.85	46.00	MS
718	Fielder-1	-2.33	-9.11	23.58	21.63	47.00	MS
613	PI94627	13.32	1.42	-6.37	16.28	47.08	MS
170	CN11739	-3.86	7.49	7.60	20.91	49.00	MS
722	Selkirk	24.80	-6.12	-9.76	17.57	50.71	MS
749	Sonora 64	6.08	-4.20	11.26	23.69	52.92	MS
138	CN40686	34.71	-18.01	-7.37	19.30	54.62	MS
579	C34	12.34	1.13	-0.19	24.10	57.14	MS
709	RL6159	20.83	2.49	-10.74	24.14	57.69	MS
164	CN37599	3.86	19.27	-9.26	26.81	58.08	MS
756	HC374	9.53	-3.56	9.17	27.78	58.67	MS
615	PI94655	19.64	-1.67	-5.25	25.28	58.75	MS
605	C64	31.31	-23.64	2.29	21.09	59.00	MS
166	CN12213	14.14	12.15	-12.26	27.20	60.42	S

Entry	Accession	MDN	OTT	SK	Overall	Raw Average	Infection type[1]
618	PI113961	3.19	-5.47	18.91	31.16	60.45	S
619	PI113963	19.69	5.09	-10.80	26.02	60.50	S
45	CN11579	11.83	8.15	-5.58	27.17	61.00	S
456	01C0204206	25.55	5.04	-17.91	25.02	61.43	S
606	C65	23.76	2.19	-12.09	26.54	62.50	S
102	CN40845	26.22	-3.25	-9.18	26.43	62.69	S
39	CN1748	28.50	-7.47	-6.81	26.89	62.86	S
149	CN11587	11.45	7.97	-3.22	29.97	63.85	S
583	C38	13.30	11.66	-8.81	30.54	65.00	S
719	Lalbahadur(Pavon1B)	-13.72	16.87	16.14	35.33	65.00	S
739	CN10112_Gabo	12.12	3.12	1.67	31.57	65.00	S
747	Regent	13.35	16.39	-14.02	30.52	65.71	S
600	C56	17.06	2.70	-3.40	29.00	65.83	S
750	Stanley	23.67	0.70	-8.52	30.12	66.00	S
165	CN2674	18.07	10.98	-12.98	30.74	67.33	S
607	C66	22.03	8.84	-14.60	31.89	67.50	S
175	CWI42988	18.00	11.32	-12.42	32.54	68.93	S
671	Thatcher	19.85	4.60	-5.79	34.39	70.77	S
145	CWI44464	9.01	9.19	1.55	36.85	71.07	S
601	C57	14.78	10.20	-0.53	45.74	83.21	S

MDN, Morden; OTT, Ottawa; SK, Saskatoon; Overall, all locations and years
[1]R, resistant; MR, moderately resistant; I, Intermediate; MS, moderately susceptible; S, susceptible.

Appendix 3B Overall and location-specific best linear unbiased predictors (BLUP) for leaf rust severity of the winter diversity panel (left of the vertical separator line). Table also shows raw average severity and infection type across all years and locations (right of the vertical separator line).

Entry	Accession	MDN	OTT	Overall	Raw average	Infection type
779	EKC11_RL5477	-6.034	0.674	-13.390	0.00	R
789	EKC101_RL5719	-6.034	0.674	-13.390	0.00	R
791	EKC103_RL5721	-6.034	0.674	-13.390	0.00	R
802	EKC130_RL5010	-6.034	0.674	-13.390	0.00	R
853	IPK-TRI4349	-6.034	0.674	-13.390	0.00	R
784	EKC47_RL5509	-5.919	0.604	-13.273	0.20	R
790	EKC102_RL5720	-5.919	0.604	-13.273	0.20	R
860	IPK-TRI7270	-5.919	0.604	-13.273	0.20	R
868	IPK-TRI13606	-5.919	0.604	-13.273	0.20	R
849	IPK-TRI677	-5.506	NA	-13.594	0.25	R
857	IPK-TRI5416	-5.553	0.384	-13.124	0.25	R
73	CN37617	-5.846	0.431	-13.307	0.30	R
786	EKC58_RL5216	-5.803	0.535	-13.157	0.40	R
840	IPK-AE783	-5.803	0.535	-13.157	0.40	R
867	IPK-TRI13604	-5.803	0.535	-13.157	0.40	R
74	CN12440	-5.664	0.235	-13.247	0.44	R
76	CN11756	-5.664	0.235	-13.247	0.44	R
783	EKC37_RL5247	-5.438	NA	-13.422	0.50	R

Entry	Accession	MDN	OTT	Overall	Raw average	Infection type
788	EKC97_RL5300	-5.438	NA	-13.422	0.50	R
858	IPK-TRI7258	-5.402	0.293	-12.989	0.50	R
760	C29 (AS2395)	-6.591	1.306	-12.971	0.56	R
764	C33 (AS2407)	-5.780	0.403	-13.090	0.56	R
807	EKC159_RL5858	-5.252	-0.171	-13.199	0.57	R
806	EKC158_RL5857	-5.163	-0.211	-13.176	0.60	R
574	RL5793	-6.504	1.248	-12.899	0.67	R
799	EKC119_RL5727	-5.205	NA	-13.181	0.67	R
812	EKC165_RL5011	-5.422	NA	-13.104	0.67	R
815	EKC186_RL5847	-4.269	-0.749	-12.317	0.67	R
87	CWI19490_RL5444	-6.433	1.201	-12.837	0.71	R
72	CN11649	-6.300	1.111	-12.831	0.75	R
877	17CAN-SYNT-06A	-5.572	0.395	-12.925	0.80	R
491	RL5524	-5.153	-0.235	-12.981	1.00	R
785	EKC48_RL5510	-5.302	NA	-13.080	1.00	R
822	IPK-AE111	-4.758	NA	-12.166	1.00	R
839	IPK-AE740	-4.383	NA	-11.457	1.00	R
841	IPK-AE825	-4.758	NA	-12.166	1.00	R
848	IPK-AE1607	-4.916	0.241	-11.965	1.00	R
89	BW31215	-7.085	2.087	-12.334	1.22	R
866	IPK-TRI12094	-6.945	1.979	-11.749	1.25	R
590	C45	-5.986	0.900	-12.465	1.33	R
763	C32 (AS2405)	-6.999	2.029	-12.262	1.33	R
762	C31 (AS2404)	-6.841	2.001	-11.702	1.43	R
759	C26 (AS2386)	-7.453	2.551	-12.049	1.50	R
761	C30 (AS2399)	-7.311	2.480	-11.728	1.50	R
805	EKC154_RL5853	-5.708	0.780	-12.018	1.50	R
78	CN37611	-8.586	4.253	-10.483	1.57	R
90	BW31221	-7.279	2.458	-11.723	1.57	R
856	IPK-TRI4653	-5.503	0.595	-12.255	1.60	R
585	C40	-5.727	0.726	-12.030	1.67	R
829	IPK-AE290	-4.936	NA	-12.352	1.67	R
808	EKC160_RL5859	-7.078	2.328	-11.521	1.86	R
794	EKC110_RL5302	-4.846	NA	-12.229	2.00	R
556	RL5775	-7.346	2.710	-11.613	2.13	R
587	C42	-4.959	0.210	-11.687	2.50	R
795	EKC108_RL5004	-4.893	NA	-12.054	2.50	R
549	RL5768	-5.035	0.261	-11.671	2.56	R
562	RL5781	-7.716	3.397	-10.486	2.75	R
852	IPK-TRI3365	-6.385	2.087	-10.740	2.80	R
494	RL5536	-3.989	-0.800	-11.779	2.86	R
603	C62	-4.776	0.086	-11.236	2.89	R
539	RL5750	-4.344	-0.204	-11.064	3.00	R
91	BW31225	-7.294	3.121	-10.102	3.38	R
810	EKC163_RL5017	-11.205	8.234	-7.156	3.43	R
843	IPK-AE906	-4.620	NA	-11.370	3.50	R
874	17CAN-SYNT-03A	-4.346	-0.102	-11.093	3.60	R
559	RL5778	-6.872	2.846	-9.717	4.00	R
572	RL5791	-4.839	0.577	-10.456	4.11	R
94	BW31236	-4.869	0.686	-10.227	4.33	R

Entry	Accession	MDN	OTT	Overall	Raw average	Infection type
876	17CAN-SYNT-05A	-3.767	-0.450	-10.512	4.60	R
528	RL5699	-2.583	-1.746	-10.418	4.67	R
545	RL5761	-8.488	4.912	-9.052	4.89	R
757	C23 (AS60)	-10.414	6.959	-8.472	5.20	R
67	CN38247	-6.218	2.829	-8.459	5.25	R
831	IPK-AE346	-10.793	8.347	-6.160	5.40	R
578	RL5798	-6.396	2.936	-8.250	5.50	R
896	17CAN-SYNT-25F	-2.612	-1.242	-9.577	5.50	R
608	C67	-7.681	4.280	-8.194	5.67	R
550	RL5769	-7.595	4.221	-8.558	5.78	R
553	RL5772	-8.521	5.292	-7.846	5.89	R
830	IPK-AE316	-3.801	NA	-9.317	6.50	R
838	IPK-AE714	-3.801	NA	-9.317	6.50	R
813	EKC166_RL5012	-2.263	-1.355	-9.002	7.20	R
890	17CAN-SYNT-19A	-9.173	7.372	-4.534	8.20	R
622	PI355476	-2.080	-0.503	-6.846	8.33	R
814	EKC171_RL5722	-3.144	NA	-7.825	8.33	R
823	IPK-AE113	0.031	-2.735	-7.224	8.67	R
575	RL5794	-3.163	0.423	-6.335	9.50	R
589	C44	-0.934	-2.395	-8.228	9.57	R
95	BW31260	-2.931	0.488	-5.815	9.70	R
888	17CAN-SYNT-17B	-8.132	6.746	-3.488	10.00	R
521	RL5686	1.501	-4.045	-5.952	11.22	MR
871	Emerson-1 (check)	0.764	-2.647	-4.354	12.10	MR
891	17CAN-SYNT-20A	-10.801	10.756	-0.164	12.20	MR
97	BW31261	0.113	-2.174	-4.846	12.88	MR
811	EKC164_RL5849	1.496	-3.273	-3.470	13.33	MR
878	17CAN-SYNT-07A	3.417	-5.181	-4.178	13.67	MR
873	17CAN-SYNT-02B	0.094	-1.811	-4.233	14.00	MR
879	17CAN-SYNT-08A	-13.585	14.836	3.044	14.20	MR
887	17CAN-SYNT-16A	1.902	-3.860	-4.819	14.40	MR
624	PI415152	2.222	-3.091	-2.723	15.00	MR
884	17CAN-SYNT-13B	0.712	-1.717	-2.415	15.00	MR
758	C24 (AS66)	2.467	-3.440	-2.029	16.11	MR
880	17CAN-SYNT-09A	2.943	-4.487	-3.773	16.20	MR
782	EKC24_RL5710	3.297	-3.738	-1.693	16.67	MR
595	C51	-7.876	8.997	3.121	16.83	MR
495	RL5537	5.357	-6.279	-1.932	17.22	MR
894	17CAN-SYNT-23A	-1.699	1.817	0.254	17.50	MR
898	17CAN-SYNT-27A	1.016	-1.163	-0.305	19.00	MR
889	17CAN-SYNT-18A	3.565	-3.899	-0.747	20.00	MR
892	17CAN-SYNT-21C	-2.347	3.265	2.322	20.00	MR
604	C63	-2.729	3.727	2.066	20.11	MR
893	17CAN-SYNT-22A	5.019	-4.530	1.441	20.83	MR
490	RL5499	8.588	-9.211	-0.452	21.38	MR
591	C46	0.709	0.430	3.022	21.67	MR
592	C48	-5.623	7.905	5.915	22.50	MR
527	RL5695	-0.170	2.365	5.221	24.44	MR
798	EKC116_RL5706	1.508	NA	3.109	25.00	MR
821	IPK-AE91	1.508	NA	3.109	25.00	MR

Entry	Accession	MDN	OTT	Overall	Raw average	Infection type
872	17CAN-SYNT-01A	4.487	-3.251	3.181	25.00	MR
875	17CAN-SYNT-04A	4.487	-3.251	3.181	25.00	MR
493	RL5534	3.185	-1.145	4.909	25.11	MR
899	17CAN-SYNT-28A	5.066	-3.599	3.762	26.00	MR
538	RL5747	-10.746	15.300	10.252	27.78	MR
564	RL5783	-12.486	17.610	12.793	27.86	MR
897	17CAN-SYNT-26A	6.223	-4.295	4.924	28.00	MR
885	17CAN-SYNT-14A	8.976	-6.331	6.916	28.50	MR
800	EKC127_RL5577	10.743	-9.420	3.459	29.00	MR
882	17CAN-SYNT-11A	-5.023	9.685	11.643	29.00	MR
130	CWI35567	18.314	-13.736	10.808	30.25	I
828	IPK-AE182	5.867	-1.677	9.775	31.67	I
796	EKC111_RL5009	4.772	NA	11.065	37.50	I
901	17CAN-SYNT-30A	15.671	-12.144	9.008	38.20	I
847	IPK-AE1580	2.498	5.161	19.195	42.00	MS
797	EKC112_RL5301	6.731	NA	15.838	45.00	MS
883	17CAN-SYNT-12A	21.281	-14.369	17.934	45.17	MS
534	RL5741	11.415	-3.224	21.019	45.83	MS
483	RL5265	17.368	-6.291	26.356	48.00	MS
863	IPK-TRI7315	5.969	3.072	22.681	48.00	MS
881	17CAN-SYNT-10A	20.342	-13.992	16.101	49.00	MS
529	RL5736	8.036	NA	19.020	50.00	MS
819	IPK-AE8	22.435	-14.049	19.650	50.00	MS
842	IPK-AE899	8.036	NA	19.020	50.00	MS
580	C35	11.018	-1.126	24.683	50.56	MS
567	RL5786	2.135	9.365	29.093	52.50	MS
581	C36	13.178	-2.578	26.489	53.33	MS
584	C39	29.065	-20.202	20.602	53.67	MS
498	RL5554	11.256	0.506	28.184	54.29	MS
536	RL5745	12.506	-1.326	28.435	55.00	MS
793	EKC105_RL5723	1.968	10.289	30.050	55.00	MS
864	IPK-TRI11555	18.088	-7.191	27.629	55.83	MS
535	RL5744	13.737	-2.129	29.536	56.67	MS
835	IPK-AE467	27.812	-17.283	24.803	58.33	MS
586	C41	15.756	-2.967	31.140	60.56	S
900	17CAN-SYNT-29A	5.607	8.100	34.326	61.00	S
895	17CAN-SYNT-24A	11.284	2.280	34.023	64.00	S
801	EKC135_RL5716	4.017	11.646	39.047	65.00	S
820	IPK-AE30	27.375	-14.616	30.387	65.00	S
886	17CAN-SYNT-15A	12.441	1.584	35.185	66.00	S
818	IPK-AE1	25.729	-13.625	30.557	66.25	S
855	IPK-TRI4630	18.696	-4.585	35.462	70.00	S
869	IPK-TRI18539	13.259	NA	31.749	70.00	S
861	IPK-TRI7272	12.079	6.612	46.829	79.00	S
827	IPK-AE162	15.870	NA	38.114	80.00	S
865	IPK-TRI11556	10.452	9.996	51.199	83.00	S

MDN, Morden; OTT, Ottawa; Overall, all locations and years

[1]R, resistant; MR, moderately resistant; I, Intermediate; MS, moderately susceptible; S, susceptible.

Appendix 4 Gene and marker position of known leaf rust resistance genes.

Table shows names of catalogued wheat leaf rust resistance (*Lr*) genes, their source and position on the Chinese Spring reference genome (IWGSC, 2018) mapped using gene sequences or flanking and linked markers.

Lr gene	Chr	Tester source	Marker[1]	Marker name	Marker start position	DNA marker reference
1	5DL	*T. aestivum*	GS	GenBank: EF439840.1	561644438	Cloutier et al. 2007. *Plant Mol Biol.* **65**:93-106
2a	2DS	*T. aestivum*	P & D	WPT-0330 & WMC453	63526415-56891826	Tsilo et al. 2014. *Phytopathology*. **104**:865-70.
2b	2DS	*T. aestivum*				
2c	2DS	*T. aestivum*				
3a	6BL	*T. aestivum*	P & Co	BCD1 & MWG798	685978679 & 716263614	Sacco et al. 1998. *Genome.* **41**: 686-690; Herrera-Foessel et al. 2007. Crop Sci. **47:**1450-66
3bg	6BL	*T. aestivum*				
3ka	6BL	*T. aestivum*				
9	6BL	*Ae. umbellulata*	P & Co	PSR546 & CMWG684	696145653 & 715599458	Schachermayr et al. 1994. *Theor Appl Genet.* **88**:110–15; Gupta et al. 2005. *Genome.* **48**:823–30.
10†	1AS	*T. aestivum*	GS	GenBank: AY270157.1	No hit	Nelson et al. 1997. *Crop Sci*. **37**:1928–35; Feuillet et al. 2003. *PNAS.* **100**:15253–8.
11	2DS	*T. aestivum*	P	WMC574	5053970	Darino et al. 2015. *Euphytica.* **206**:135–47
12	4BL	*T. aestivum*	P & D	WMS251-WMS149	568556214-544649745	Singh et al. 2010. *Mol Breeding.* **28**:137-42
13	2BS	*T. aestivum*	P & D	GPW1109 & KWH37	197349665-138117619	Zhang et al. 2016. *Theor Appl Genet.* **129**(3).
14a†	7BL	*T. aestivum*	D	WMS146 & WMS344	No hit	Herrera-Foessel et al. 2008. *Plant Dis.* **92**:469–73.
14b†	7BL	*T. aestivum*				
15	2DS	*T. aestivum*	P	GWM102	72660599	Dholakia et al. 2013. *Mol Breeding*. **31**:743–47
16	2BS	*T. aestivum*	P	WMC764	8228548	McCartney et al. 2005. *Mol Breeding.* **15:**329–37.
17a	2AS	*T. aestivum*	P & D	WMC407 & WMS636	7808699-4977228	Bremenkamp-Barrett et al. 2008. *Crop Sci.* **48**:1124–8.
17b	2AS	*T. aestivum*				
18	5BL	*T. aestivum*	Co	IWB41960	697682419	Carpenter et al. 2018. *J Plant Dis Biomark.* **1**:4-10.

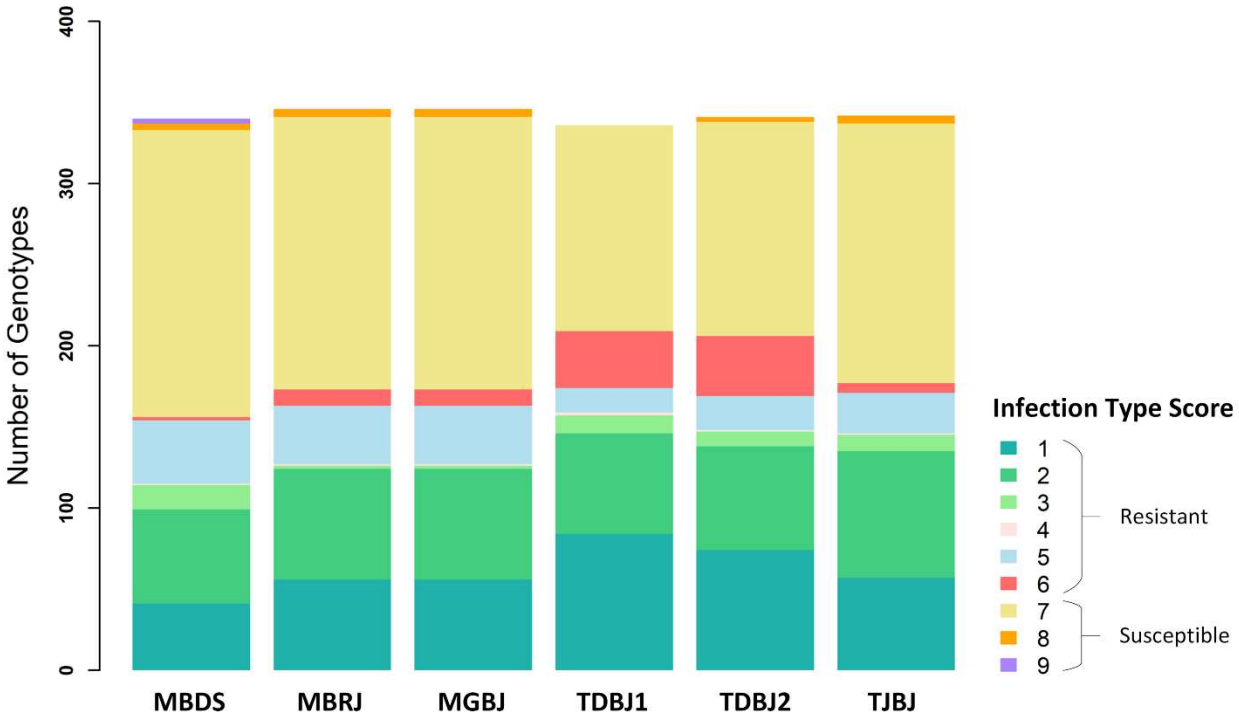
Chapter 5

Lr gene	Chr	Tester source	Marker[1]	Marker name	Marker start position	DNA marker reference
19	7DL	*Th. ponticum*	P & D	WG420 & S265512	608085674-623052562	Gupta et al. 2006. *Theor Appl Genet.* **113**:1027-36
20	7AL	*T. aestivum*	Co	PSR680 & PSR121	726815978 & 730504992	Neu et al. 2002. *Genome.* **45**:737-44.
21	1DS	*Ae. tauschii*	GS	GenBank: AH012974	2498320	Huang and Gill. 2001. *Theor Appl Genet.* **103**:1007–13.
22a	2DS	*Ae. tauschii*	GS	GenBank: KY064064.1	16355316	Thind et al. 2017. *Nat Biotechnol.* **35**:793-6.
22b	2DS	*T. aestivum*				
23	2BS	*T. turgidum*	Co	SUN471	93131233	Chhetri et al. 2017. *Mol Breeding*. **37**(3).
24	3DL	*Th. ponticum*	P & Co	PSR1203 & WMS114	600174068 & 603459606	Schachermayr et al. 1995. *Theor Appl Genet.* **90**:982–90; Bariana et al. 2016. *Mol Breeding*. **36**(7)
25†	4BS	*S. cereale*	Co	LR29F18	No hit	Procunier et al. 1995. *J. Genet. Breed.* **49**:87–92.
26†	1BL	*S. cereale*	Co	P6M12	No hit	Mago et al. 2005. *Theor Appl Genet.* **112**:41–50.
27	3BS	*T. aestivum*	P & D	CDO460 & KSUG53	16219598-8344499	Nelson et al. 1997. *Crop Sci.* **37**:1928–35.
28	4AL	*T. speltoides*	Co	PSR119 & MAG3092	732772100 & 737197805	Sohail et al. 2014. *Aust. J. Crop Sci.* **8**:1210-15
29†	7DS	*Th. ponticum*				Procunier et al. 1995. *J. Genet. Breed.* **49**:87–92.
30†	4AL	*T. aestivum*				
31	4BL	*T. aestivum*	Co	PTTKSUG10	594360521	Nelson et al. 1997. *Crop Sci*. **37**:1928–35.
32	3DS	*Ae. tauschii*	P	WMC43 & BARC135	25190590 & 25349688	Thomas et al. 2010. *Crop Sci*. **50**:2310–17.
33	1BL	*T. aestivum*	Co	RAC875_C51813_151	133113579	Che et al. 2019. *Euphytica.* **215**(29)
34	7DS	*T. aestivum*	GS	GenBank: ACN41354.1	47412062	Krattinger et al. 2009. *Science.* **323**:1360–63.
35	2BL	*T. speltoides*	Co	BCD260	419618016	Seyfarth et al. 1999. *Theor Appl Genet.* **99**:554-60.
36†	6BS	*T. speltoides*				
37	2AS	*Ae. ventricosa*	P & Co	GWM636 & CMWG682	4977228 & 3965433	Helguera et al. 2003. *Crop Sci.* **43**:1839–1847; Błaszczyk et al. 2004. *Cell Mol Biol Lett.* **9**:869-78
38	6DL	*Th. intermedum*	P & D	BARC273 & CFD5	376952741-456455789	Mebrate et al. 2008. *Euphytica.* **162**:457–466.
39	2DS	*Ae. tauschii*	P	WMS210 & GDM35	6637023 & 13754194	Raupp et al. 2001. *Theor Appl Genet.* 102:347–352.; Singh et al. 2004. *Theor Appl Genet.* **108:**586–591.

Lr gene	Chr	Tester source	Marker[1]	Marker name	Marker start position	DNA marker reference
42	1DS	*Ae. tauschii*	P	GDM33 & WMC432	No hit & 8474437	Sun et al. 2010. *Crop Sci.* **50:**59–66.; Liu et al. 2013. *Crop Sci.* **53**:1566-70
44[†]	1BL	*T. aestivum*	Co	GWM372 & G37294	203314435 & 203314888	
45	2AS	*S. cereale*				Naik et al. 2015. *Mol Breeding.* **35**:61
46	1BL	*T. aestivum*	P & D	BE518048 & STS1BL9F	669161515 & 670273696	Mateos- Hernandez et al. 2006. *Funct Integr Genomics*. **6**:122–131.
47	7AS	*Ae. speltoides*	Co	GWM60	54961993	Vanzetti et al. 2011. *Electron. J. Biotechnol.* **14**:9-9
48	2BS	*T. aestivum*	P & D	BARC55 & WMS429	133521485 & 73617950	Bansal. 2008. Theor Appl Genet. 117:307–312.
49	4BL	*T. aestivum*	P & D	BARC163 & WMS495	608252156-640976653	Bansal. 2008. Theor Appl Genet. 117:307–312.
50	2BL	*T. timopheevii*	D	WMS382 & WMS60	788537533 & No Hit	Brown-Guedira et al. 2003. *Phytopathology.* **93**:784–89.
51	1BL	*T. speltoides*	Co	AGA7-759R & S30-13L	668130688 & 668131472	Helguera et al. 2005. *Crop Sci.* **45**:728–734.
52	5BS	*T. aestivum*	P & D	WMC149 & WMS234	23332528 & 8189013	Hiebert et al. 2005. *Theor Appl Genet*. 110, 1453–1457; Obert et al. 2005. *Theor Appl Genet.* **110**:1439-44; Tar et al. 2008. *Cereal Res Commun.* **36**:409-15
53	6BS	*T. dicoccoides*	P	CFD1	41010308	Dadkhodaie et al. 2011. *Theor Appl Genet.* **122**:479-87
54	2DL	*Ae. kotschyi*	D	CFD50 & GDM6	637443897 & 599941000	Heyns et al. 2011. Open Plant Sci J. **5**(1)
56[†]	6AS	*Ae. sharonensis*	P	WMS427	No Reliable Hit	Marais et al. 2009. *Euphytica.* **171**:15-22
57	5DS	*Ae. geniculata*	P & D	BF474606 & BE606637	7413383 & 7013955	Kuraparthy et al. 2009. *Genome*. **52**:1025-36; Bansal et al. 2016. *Plant Pathol.* **66**:38-44
58	2BL	*Ae. triuncialis*	Co	BG123	800059744	Kuraparthy et al. 2007. *Crop Sci.* **47:**1995–2003.
59[†]	6BS	*Ae. peregrina*	P	S15-T3F	No Reliable Hit	Marais et al. 2010. *Plant Breed.* **129**:356-361; Pirseyedi et al. 2015. *Theor Appl Genet.* **128**:2403-14
60	1DS	*T. aestivum*	P	BARC149	4151474	Hiebert et al. 2008. *Crop Sci.* **48:**1020–1026.
61	6BS	*T. turgidum*	P & Co	SUN682 & SUN684	1573794 & 5075570	Qureshi et al. 2017. *Phytopathology.* **107**:1381-1387
62	6AS	*Ae. neglecta*	Co	WMS334	9249275	Marais et al. 2008. *Crop Sci.* **49**:871–879.
63	3AS	*T. monococcum*	D	BARC321 & BARC57	11685348 & 10312304	Kolmer et al. 2010. *Crop Sci.* **50**:2392–2395.

Lr gene	Chr	Tester source	Marker[1]	Marker name	Marker start position	DNA marker reference
64	6AL	*T. dicoccoides*	P & D	IWB59855 & K-IWB72197	614165744 & 609288614	Kolmer et al. 2019. *Theor Appl Genet.* ***132***:2809-2814
65	2AS	*T. aestivum*	Co	BARC124 & BARC212	3783829 & 1582819	Mohlner et al. 2012. *Plant Breeding.* **131**:252-257
66[†]	3AS	*Ae. speltoides*	Co	16-S13	No proper hit	Marais et al. 2010. **Euphytica 171**:71–85.
67	4DL	*T. aestivum*	GS	GenBank: KR604816.1	405774021	Hiebert et al. 2010. *Theor Appl Genet.* **121:**1083–1091.
68	7BL	*T. aestivum*	P & D	PSY-B1 & WMS146	739444514-WMS146	Herrera-Fossel et al. 2012. *Theor Appl Genet.* **124**:475-86.
70	5DS	*T. aestivum*	P	BARC130 &WMC233	6486408 & 5824923	Hiebert et al. 2014. *Theor Appl Genet.* **127:**2005–2009.
71	1B	*T. aestivum*	P & D	WMS18 & BARC187	222577675 & 212551802	Singh et al. 2013. *Euphytica.* **190**:131-136
72	7BS	*T. durum*	QTL	QTL1439	5195773-6009991	Herrera-Foessel et al. 2014. *Plant Dis.* **98**:631-635
73	2BS	*T. aestivum*	P	WPT-8235 & WPT-8235	No hit & 13481585	Park et al. 2014. *Theor Appl Genet.* **127**:2041-2049
74	3BS	*T. aestivum*	Co	CFB5006	6098344	Kolmner et al. 2018. *Crop Sci.* **58**:152-158.
75	1BS	*T. aestivum*	P & D	SWM271 & GWM604	153924534-71600965	Singla et al. 2017. *Theor. Appl. Genet.* **130**:1-12.
76	5DS	*Ae. umbellulata*	Co	XLr57/Yr40-MAS-CAPS16	7965692	Bansal et al. 2016. P*lant Pathol*. **66**:38-44.

[†]*Lr* genes that could not be mapped onto the reference genome.
[1]P, proximal; D, distal; Co, co-segregating; GS, gene sequence; QTL, quantitative trait loci



Appendix 5 Genotype distribution of infection type response against leaf rust isolates

Each bar represents the distribution of scores for a specific leaf rust isolate. Scores from the Stakman scale were converted to a linear 1-9 scale.

Appendix 6 Linear mixed model for leaf rust severity across years and locations.

Linear mixed model fit by REML. t-tests use Satterthwaite's method:
Formula: *Severity ~ Location + (1|Genotype) + (1|Year) + (1|Genotype:Location) + (1|Genotype:Year:Location)*

Spring Panel: Number of observations: 2818, groups: Genotype:Year:Location, 1569; Genotype:Location, 640; Genotype, 216; Year, 4

Random effects:

Groups	Variance	Standard deviation	Percentage variance
Genotype:Year:Location	127.26	11.28	19.19
Genotype:Location	110.91	10.53	16.72
Genotype	284.89	16.88	42.95
Year	13.92	3.73	2.10
Residual	126.27	11.24	19.04

Fixed effects:

Estimate	Std.	Error	df	t	value	Significance level
(Intercept)	24.03	2.37	6.47	10.15	3.27E-05	***
LocationOTT	7.76	1.32	327.61	5.90	9.28E-09	***
LocationSK	-5.54	1.60	665.70	-3.45	0.000591	***

Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Winter Panel: Number of obs: 978, groups: Genotype:Year:Location, 558; Genotype:Location, 310; Genotype, 167; Year, 3

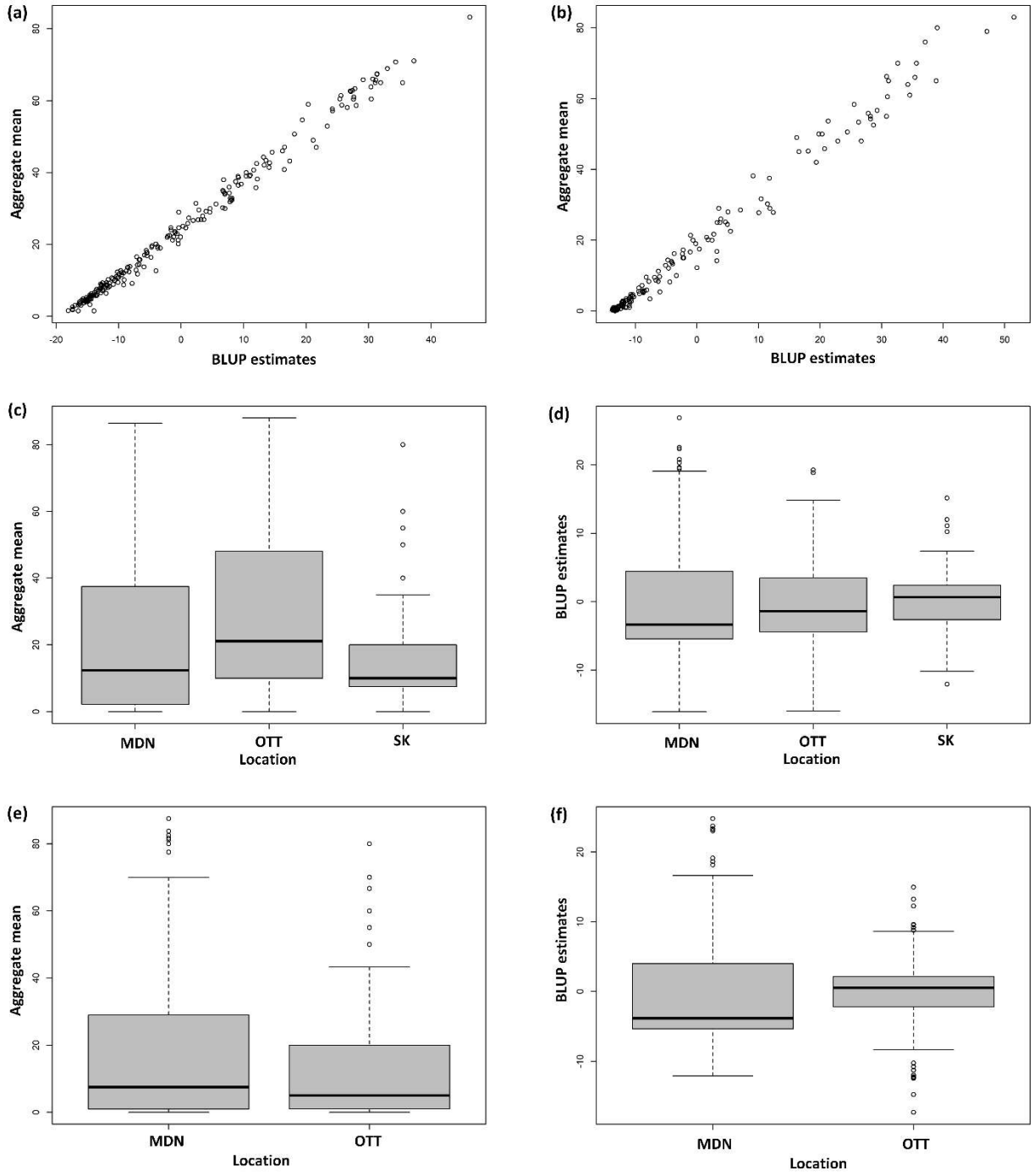
Random effects:

Groups	Variance	Standard deviation	Percentage variance
Genotype:Year:Location	37.91	6.16	6.82
Genotype:Location	117.29	10.83	21.11
Genotype	334.74	18.30	60.24
Year	1.76	1.33	0.32
Residual	63.95	8.00	11.51

Fixed effects:

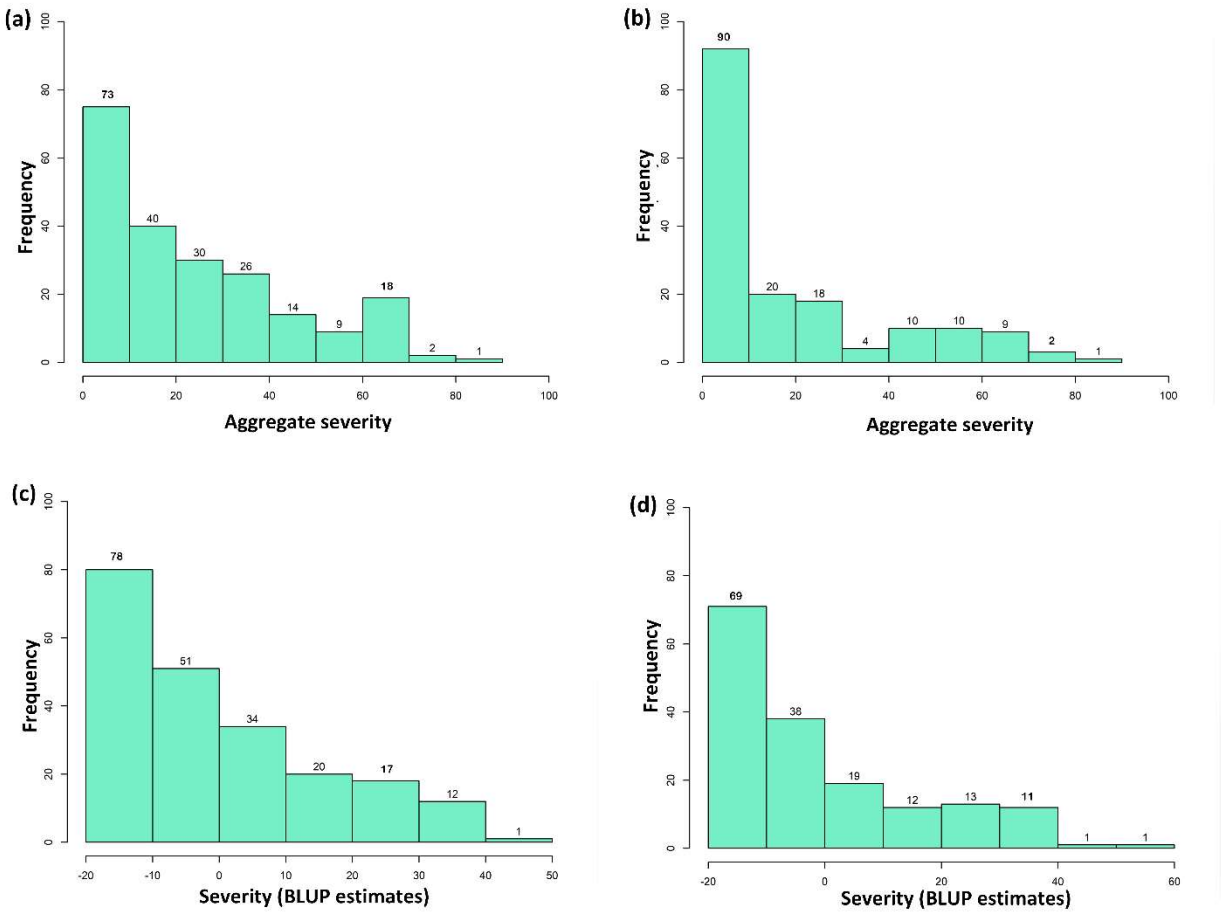
Estimate	Std.	Error	df	t	value	Significance level
(Intercept)	20.42	1.88	38.04	10.85	3.30E-13	***
LocationOTT	-7.10	1.56	137.39	-4.55	1.18E-05	***

Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1



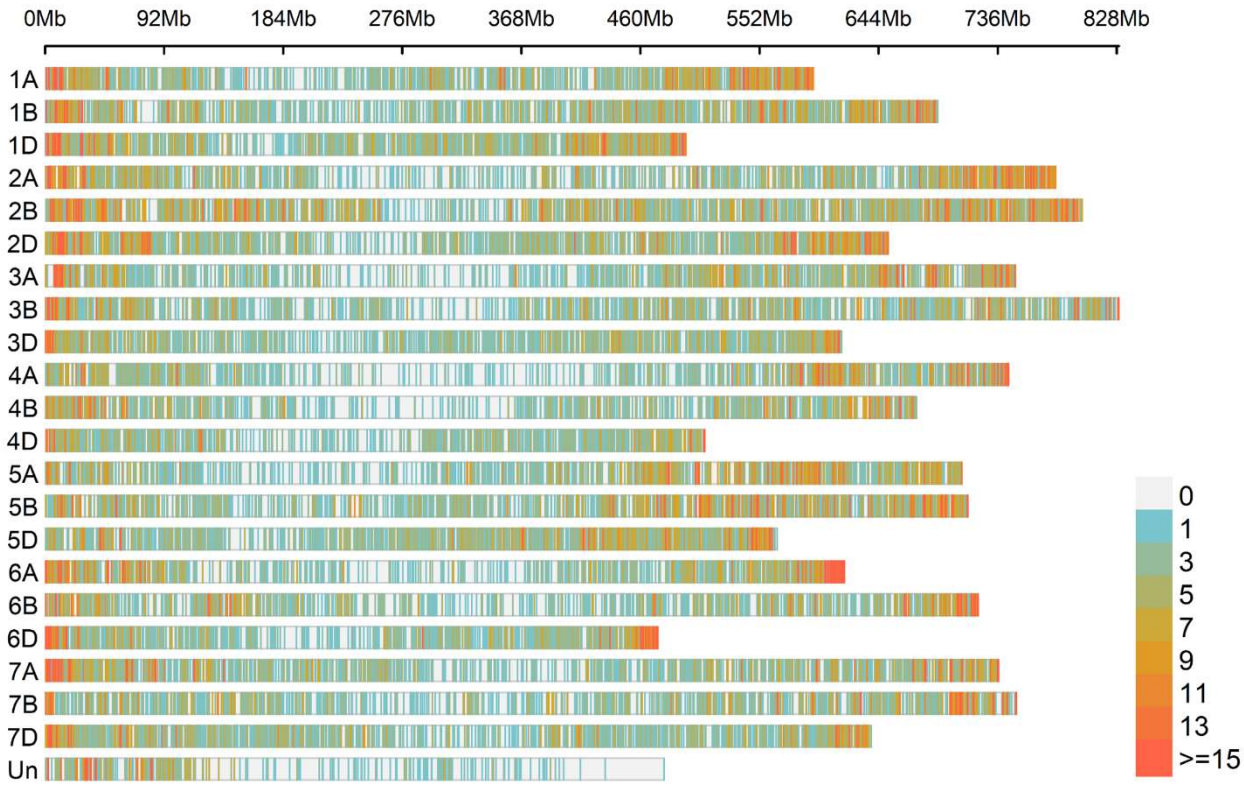
Appendix 7 Comparison between raw means and BLUP estimates for leaf rust severity.

Scatter plots show mean values (y-axis) vs. BLUP estimates (x-axis) for overall severity in the spring (a) and winter (b) diversity panels. Boxplots show the interquartile range and median severity calculated using aggregate means (c,e) and BLUP estimates (d,f) for Morden (MDN), Ottawa (OTT) and Saskatoon (SK) in the spring diversity panel, and MDN and OTT in the winter diversity panel.



Appendix 8 Distribution of severity scores in the spring and winter panels.

Raw mean values of the spring (a) and winter (b) diversity panels and genotypic best linear unbiased predictor (BLUP) estimates of the spring (c) and winter (d) diversity panels are illustrated. Genotypic BLUP estimates are conditional means which summarize phenotypic variation across all locations and years.

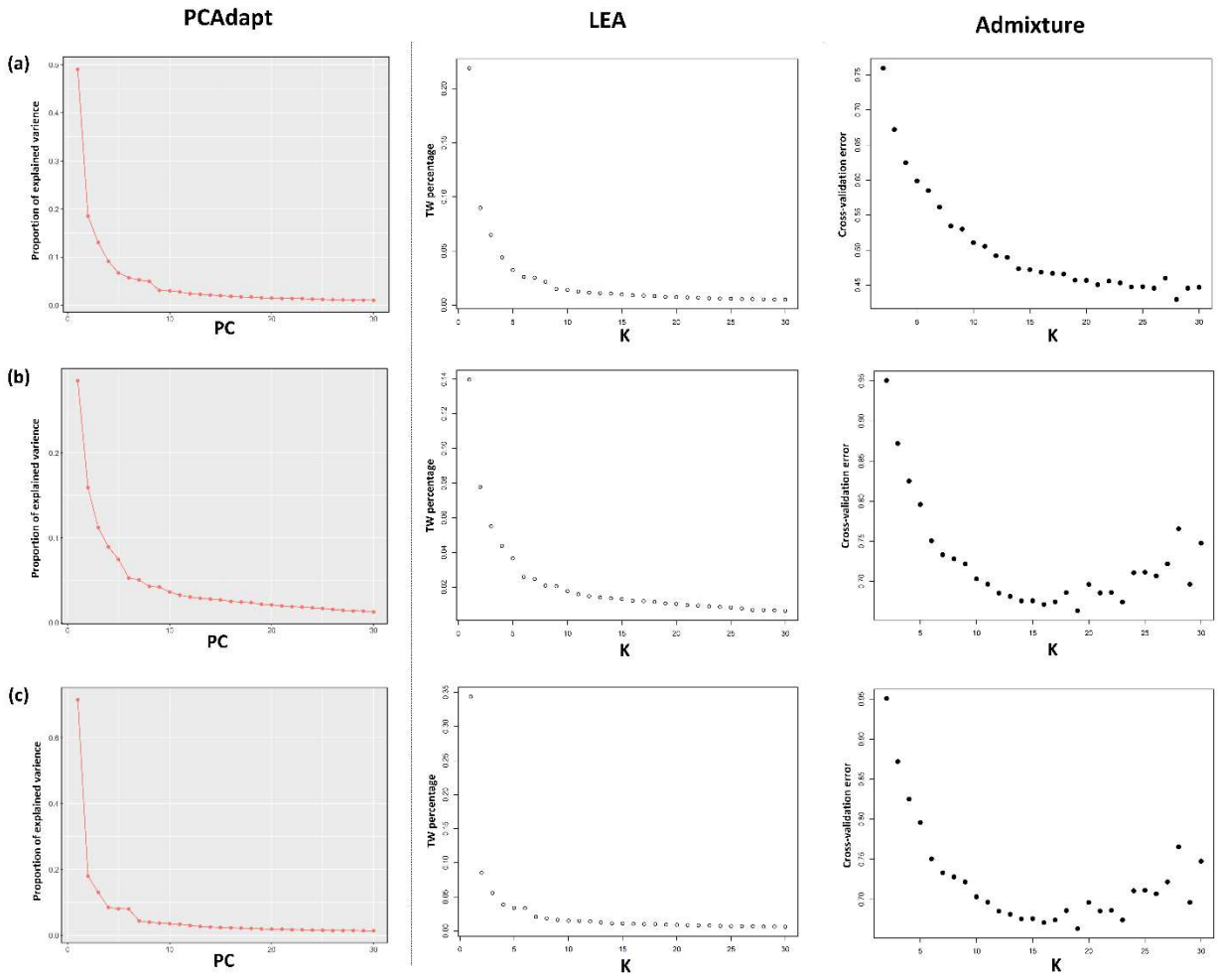


Appendix 9 Chromosomal distribution of markers from the wheat 90K array

A total of 43,804 markers were mapped. For each chromosome, the density plot shows the number of SNPs within one million base (Mb) window size.

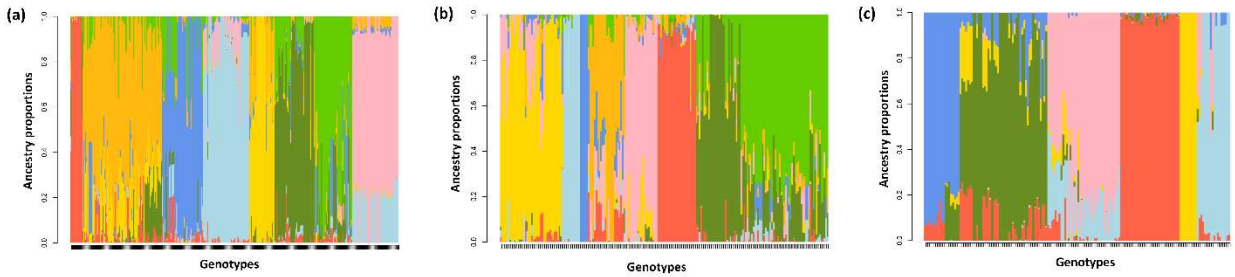
Appendix 10 Accessions that did not cluster with other individuals of the same species

Entry	Accession
88	CWI16956
105	CN32492
116	CWI18902
637	DT 776 (Eurostar)
804	EKC137_RL5650
816	EKC169_RL5278
817	EKC193_RL5664
862	IPK-TRI7301



Appendix 11 Scree plots for estimating the K number of sub-populations

K number of sub-populations was estimated using the SNP datasets for the race-specific infection type (a) and field leaf rust severity of the spring (b) and winter (c) diversity panels. PCAdapt and LEA, are both PCA-based methods, where PCAdapt plots the number of PCs vs. proportion of variance explained, and LEA plots the Tracy–Widom statistic vs. K. Admixture detects population structure through trends in cross-validation error vs. K.



Appendix 12 Structure plots illustrating the ancestry mix of the subpopulations

Ancestry mix shown for K=8 for the race-specific infection type (a), K=8 for leaf rust severity of the spring (b) and K=6 for the winter (c) diversity panels.

Appendix 13 Significant QTNs and LDBs for IT response against six leaf rust isolates

QTNs (Quantitative trait nucleotides) and LDBs (linkage disequilibrium blocks) for IT (infection type) response were identified by association mapping using one single-locus and seven multi-locus models.

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
Single-locus model							
35133-IAAV6025	1B	211312483	MBDS	MLM	6.56E-06	3.18E-02	5.874
18893-D_GCE8AKX02HMJXL_374	3B	15138756	MBDS	MLM	2.13E-07	2.07E-03	12.554
15576-D_contig10567_587	3D	141408492	MBDS	MLM	8.88E-06	2.87E-02	6.210
7730-BS00029462_51	5A	682898385	MBDS	MLM	1.42E-05	3.44E-02	7.778
15734-D_contig14443_745	7D	232496636	TDBG1	MLM	4.13E-06	4.01E-02	6.547
Multi-locus models							
59361-RAC875_c5831_1486	1A	10969929	TDBG2	FASTmrEMMA	8.54E-06	2.76E-02	3.779
				pKWmEB	1.04E-06	2.02E-03	4.535
			MBRJ	FASTmrEMMA	3.84E-08	3.72E-04	6.081
				FASTmrMLM	0.00001	1.62E-02	3.000
				ISIS EM-BLASSO	3.50E-07	3.40E-03	3.839
				pLARmEB	1.73E-07	3.35E-04	1.762
31602-GENE-0002_856	1A	32087536	MGBJ	ISIS EM-BLASSO	1.01E-06	2.46E-03	3.488
				pLARmEB	1.07E-08	3.48E-05	3.817
10214-BS00068036_51	1A	268932276	MBDS	mrMLM	5.47E-08	1.06E-04	1.360
45449-Kukri_c44500_315	1A	586952125	TDBG1	ISIS EM-BLASSO	6.47E-08	6.28E-04	5.542
				mrMLM	1.35E-05	2.63E-02	3.984
			MGBJ	mrMLM	2.76E-05	2.68E-02	2.401
79341-wsnp_Ex_rep_c67474_66076379	1A	591093391	MGBJ	ISIS EM-BLASSO	3.71E-06	7.21E-03	2.659
7236-BS00022745_51	1B	70711155	MBDS	mrMLM	2.85E-06	3.46E-03	16.344
26303-Excalibur_c4215_1327	1B	95323618	TDBG2	mrMLM	5.61E-07	1.82E-03	23.731
35133-IAAV6025	1B	211312483	MBDS	FASTmrEMMA	4.04E-06	9.79E-03	28.027
50495-Kukri_rep_c91496_1320	1B	331420168	TDBG2	mrMLM	4.28E-06	8.30E-03	1.459
73768-Tdurum_contig9164_233	1B	533863925	MBRJ	mrMLM	5.32E-05	3.97E-02	1.744
42096-Kukri_c19247_711	1B	614455731	MBDS	FASTmrMLM	5.05E-06	4.90E-02	4.125
3634-BobWhite_c48071_144	1B	614455863	MBDS	ISIS EM-BLASSO	5.42E-07	5.26E-03	3.947
				mrMLM	4.75E-08	1.15E-04	3.485
				pKWmEB	1.58E-06	5.10E-03	5.942

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
				pLARmEB	1.11E-05	1.19E-02	2.035
			MBRJ	FASTmrMLM	1.69E-05	2.34E-02	2.451
				pLARmEB	1.37E-05	1.90E-02	1.142
19295-D_GDS7LZN01C3204_275	1D	101139746	MBRJ	mrMLM	2.18E-05	2.12E-02	1.699
7344-BS00022962_51	1D	206101173	MBRJ	mrMLM	2.07E-06	3.35E-03	4.397
19196-D_GDRF1KQ02F3JLT_66	1D	273812413	MGBJ	mrMLM	5.88E-06	9.52E-03	2.767
34680-IAAV32	2A	2485710	MGBJ	FASTmrMLM	9.72E-06	2.36E-02	2.996
				ISIS EM-BLASSO	3.66E-08	1.77E-04	5.780
				pLARmEB	1.81E-05	1.95E-02	2.384
28816-Excalibur_c7682_652	2A	4951004	MBDS	mrMLM	1.42E-08	4.61E-05	9.403
17360-D_F1BEJMU02HXD1T_170	2A	12985497	MGBJ	FASTmrEMMA	1.68E-06	1.63E-02	5.001
				FASTmrMLM	1.11E-06	5.39E-03	3.639
				pLARmEB	9.60E-06	1.55E-02	2.308
79083-wsnp_Ex_rep_c103167_88182254	2A	33044691	TDBG1	mrMLM	1.02E-05	2.46E-02	2.805
69592-Tdurum_contig28682_120	2A	101381504	MBRJ	pKWmEB	5.25E-06	1.02E-02	6.799
80648-wsnp_Ku_c6826_11860405	2A	104876095	TJBJ	pKWmEB	6.55E-08	3.18E-04	4.637
21864-Excalibur_c11398_913	2A	118446604	MGBJ	mrMLM	4.53E-05	4.00E-02	4.363
9450-BS00065105_51	2B	69648893	MGBJ	mrMLM	1.12E-05	1.36E-02	5.571
23783-Excalibur_c22285_762	2B	493986458	MBDS	mrMLM	5.80E-08	9.38E-05	3.235
34658-IAAV3067	2B	699173434	TJBJ	pKWmEB	1.57E-06	2.54E-03	2.604
1208-BobWhite_c18678_95	2B	751257597	TJBJ	pKWmEB	1.69E-07	4.11E-04	9.045
32025-GENE-0674_105	2D	13773809	TDBG1	pLARmEB	3.64E-05	4.42E-02	5.448
49685-Kukri_rep_c115699_270	2D	39829875	TDBG2	FASTmrEMMA	2.37E-06	1.15E-02	5.780
15256-D_contig03226_643	2D	130822442	MBRJ	FASTmrMLM	3.40E-05	4.13E-02	1.370
				pLARmEB	4.23E-05	4.56E-02	0.634
36072-IACX5941	2D	588793333	MGBJ	pKWmEB	6.36E-08	1.23E-04	6.229
				pLARmEB	1.77E-05	2.15E-02	1.902
75000-tplb0052b23_2493	2D	621964724	TDBG1	FASTmrEMMA	3.94E-07	1.91E-03	6.233
				pKWmEB	9.57E-09	9.29E-05	5.256
				pLARmEB	2.25E-07	2.18E-03	2.990
23770-Excalibur_c22201_907	2D	638613120	TDBG1	ISIS EM-BLASSO	2.07E-06	5.03E-03	3.925
				pKWmEB	9.59E-06	1.55E-02	6.159
64223-RFL_Contig3121_1979	2D	648470008	MBDS	pKWmEB	2.02E-05	3.91E-02	5.850
68735-Tdurum_contig18471_456	3A	75030422	MBDS	mrMLM	2.34E-07	3.24E-04	34.645
66940-Tdurum_contig11121_997	3A	532448246	MBRJ	mrMLM	6.92E-07	2.24E-03	4.583

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
45125-Kukri_c41296_172	3A	576209128	MBRJ	mrMLM	7.88E-07	1.91E-03	2.268
18893-D_GCE8AKX02HMJXL_374	3B	15138756	MBDS	FASTmrEMMA	2.13E-06	6.90E-03	4.007
				ISIS EM-BLASSO	8.31E-06	2.69E-02	2.912
				mrMLM	7.76E-09	3.76E-05	1.864
				pKWmEB	2.53E-10	2.46E-06	5.437
				pLARmEB	2.16E-07	2.62E-04	2.474
			MBRJ	ISIS EM-BLASSO	2.08E-06	6.73E-03	2.976
				pKWmEB	4.18E-07	1.35E-03	3.016
			MGBJ	pKWmEB	2.35E-05	2.53E-02	1.529
34803-IAAV3924	3B	20450624	TDBG2	pKWmEB	5.41E-07	1.31E-03	6.790
3061-BobWhite_c39480_122	3B	43274832	MBDS	mrMLM	3.66E-06	3.95E-03	2.089
			TJBJ	mrMLM	1.19E-05	2.31E-02	4.603
40913-Kukri_c12869_154	3B	130647769	TDBG1	mrMLM	1.57E-09	1.53E-05	27.900
54100-RAC875_c15509_436	3B	283604560	MGBJ	FASTmrMLM	2.08E-06	6.72E-03	4.838
63403-RAC875_s108395_60	3B	605267456	TDBG2	mrMLM	1.50E-07	1.45E-03	3.716
			TJBJ	mrMLM	2.79E-06	9.03E-03	2.520
7087-BS00022441_51	3B	807288990	MBRJ	FASTmrMLM	2.19E-06	4.24E-03	5.165
				pLARmEB	2.38E-06	3.86E-03	2.364
			MGBJ	pKWmEB	8.51E-06	1.18E-02	3.873
			TJBJ	pLARmEB	6.69E-07	3.25E-03	5.227
24328-Excalibur_c25515_95	3D	28331100	MBDS	FASTmrEMMA	4.13E-09	4.01E-05	4.823
			TJBJ	FASTmrEMMA	3.00E-06	2.91E-02	4.475
				FASTmrMLM	3.73E-06	9.06E-03	5.214
				ISIS EM-BLASSO	1.08E-08	1.05E-04	7.690
				pKWmEB	1.56E-07	5.05E-04	6.575
				pLARmEB	2.26E-07	2.20E-03	5.241
12255-BS00105800_51	3D	611558374	MBRJ	pKWmEB	2.58E-07	1.25E-03	11.193
27771-Excalibur_c57945_355	4A	94765437	TDBG1	pKWmEB	4.87E-07	1.58E-03	8.185
72073-Tdurum_contig50388_343	4A	499345041	TDBG1	mrMLM	5.22E-06	1.69E-02	2.271
7448-BS00023151_51	4A	606586747	MGBJ	ISIS EM-BLASSO	3.70E-05	3.59E-02	2.768
76797-wsnp_Ex_c16175_24619793	4A	609805169	TDBG1	ISIS EM-BLASSO	6.91E-07	3.35E-03	3.736
			MBDS	pKWmEB	1.01E-06	4.92E-03	4.127
71854-Tdurum_contig47858_908	4A	625249359	MGBJ	mrMLM	3.81E-06	9.24E-03	1.493
59451-RAC875_c59673_500	4A	681670895	TDBG2	mrMLM	2.50E-06	6.06E-03	3.317
57805-RAC875_c42019_60	4B	538268580	MBRJ	mrMLM	1.18E-10	1.15E-06	14.468

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
11789-BS00093089_51	4B	552827949	TDBG1	FASTmrEMMA	7.23E-09	7.01E-05	13.823
40320-Kukri_c10321_228	4B	577655390	MBDS	FASTmrEMMA	2.32E-08	1.12E-04	9.940
				mrMLM	4.36E-09	4.24E-05	6.956
			TJBJ	mrMLM	2.29E-07	1.11E-03	9.128
38863-Ku_c2346_1339	4B	623066948	TDBG2	mrMLM	6.91E-06	1.12E-02	4.788
			TJBJ	FASTmrMLM	4.39E-06	8.53E-03	6.105
				pKWmEB	9.73E-11	9.44E-07	10.463
				pLARmEB	1.88E-05	3.66E-02	4.564
16427-D_contig29825_215	4D	82020798	TDBG2	pKWmEB	1.98E-08	6.40E-05	10.951
				pLARmEB	2.16E-06	6.99E-03	5.066
			TDBG1	FASTmrMLM	2.28E-08	2.22E-04	11.152
				pLARmEB	2.95E-07	1.43E-03	8.172
			MBRJ	pLARmEB	1.68E-05	2.04E-02	3.830
28179-Excalibur_c63208_105	4D	358039232	MGBJ	mrMLM	5.98E-05	4.46E-02	4.388
17554-D_F5XZDLF01DBHUA_161	4D	496649455	TDBG2	pKWmEB	2.49E-05	4.02E-02	3.031
				pLARmEB	1.28E-07	1.24E-03	2.552
36264-IACX8002	5A	485201265	TDBG2	mrMLM	1.56E-05	2.16E-02	3.611
61301-RAC875_c9984_1003	5A	585458451	TDBG1	pKWmEB	6.80E-07	1.65E-03	8.719
59300-RAC875_c57603_144	5A	666228776	MBRJ	FASTmrEMMA	2.30E-06	1.12E-02	3.773
				FASTmrMLM	1.43E-08	6.94E-05	5.128
				ISIS EM-BLASSO	5.53E-07	2.68E-03	4.307
				pLARmEB	3.77E-08	1.83E-04	2.218
4426-BobWhite_c8115_648	5A	682712749	MGBJ	pKWmEB	8.95E-08	1.45E-04	5.794
7730-BS00029462_51	5A	682898385	MGBJ	FASTmrEMMA	5.84E-06	2.84E-02	3.286
				FASTmrMLM	1.73E-05	3.35E-02	2.745
				ISIS EM-BLASSO	4.79E-09	4.65E-05	4.470
				pKWmEB	4.27E-08	1.04E-04	4.371
				pLARmEB	2.42E-13	2.35E-09	4.739
			TJBJ	mrMLM	5.37E-06	1.30E-02	2.398
9144-BS00063855_51	5A	685964650	MBRJ	mrMLM	2.85E-05	2.51E-02	0.663
69406-Tdurum_contig28001_110	5A	700619759	MBRJ	mrMLM	4.77E-06	5.79E-03	3.664
51347-Ra_c19198_137	5B	26916277	MGBJ	ISIS EM-BLASSO	7.46E-07	2.41E-03	3.086
1854-BobWhite_c2479_214	5B	78420589	TDBG1	ISIS EM-BLASSO	1.03E-06	3.32E-03	6.231
				pLARmEB	4.79E-06	9.29E-03	4.447
72519-Tdurum_contig56538_337	5B	124636878	TDBG1	FASTmrMLM	1.72E-05	2.08E-02	3.224

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
			TJBJ	FASTmrMLM	1.90E-06	6.13E-03	4.953
35222-IAAV6616	5B	397673282	MBRJ	mrMLM	5.22E-05	4.23E-02	1.216
			MGBJ	ISIS EM-BLASSO	4.44E-05	3.91E-02	1.398
				mrMLM	6.47E-05	4.49E-02	2.343
				pKWmEB	3.52E-08	1.14E-04	3.064
				pLARmEB	9.21E-08	2.23E-04	2.020
34690-IAAV3268	5B	488107093	MBRJ	mrMLM	2.56E-06	3.55E-03	1.784
63448-RAC875_s116069_221	5B	506951332	TDBG2	pKWmEB	2.96E-11	2.88E-07	7.183
			MGBJ	pKWmEB	1.19E-05	1.44E-02	2.693
81257-wsnp_Ra_c8465_14340896	5B	539293955	TJBJ	mrMLM	1.48E-10	1.43E-06	6.507
34530-IAAV2296	5B	566686138	TJBJ	ISIS EM-BLASSO	1.83E-05	4.43E-02	3.552
74020-Tdurum_contig97942_163	5B	701174382	TDBG1	ISIS EM-BLASSO	9.73E-06	1.89E-02	2.837
18809-D_GCE8AKX01CE518_452	5D	302353075	MGBJ	mrMLM	3.64E-07	1.77E-03	1.018
48181-Kukri_c8949_906	5D	354938992	MBRJ	mrMLM	8.14E-07	1.58E-03	NA
15938-D_contig18780_204	5D	486259068	TDBG2	FASTmrEMMA	1.81E-10	1.76E-06	9.263
10557-BS00071571_51	6A	1879563	MGBJ	ISIS EM-BLASSO	2.43E-05	2.62E-02	2.744
				pLARmEB	9.78E-06	1.36E-02	2.253
78974-wsnp_Ex_c965_1845676	6A	581747079	MGBJ	mrMLM	1.86E-05	2.00E-02	3.085
63713-RFL_Contig1715_631	6A	597292476	MBRJ	FASTmrMLM	1.03E-06	2.50E-03	2.740
				pLARmEB	7.23E-08	1.75E-04	1.498
14865-CAP8_c6448_265	6A	604882706	MBDS	pKWmEB	1.35E-05	3.27E-02	6.210
18412-D_GBF1XID01EGI95_65	6B	25279886	TDBG2	FASTmrMLM	1.39E-05	4.50E-02	6.093
				pLARmEB	1.78E-05	3.45E-02	3.534
			TJBJ	FASTmrMLM	8.29E-07	8.05E-03	5.470
				ISIS EM-BLASSO	1.46E-05	4.72E-02	3.959
				pLARmEB	2.56E-06	8.28E-03	4.035
44910-Kukri_c39321_112	6B	151131531	TDBG2	pKWmEB	1.01E-08	4.91E-05	11.323
			MBDS	pLARmEB	4.05E-05	3.58E-02	3.759
			TJBJ	pKWmEB	4.48E-07	8.70E-04	6.713
5404-BobWhite_rep_c63804_353	6B	451926960	TDBG2	pLARmEB	8.32E-07	4.04E-03	4.686
76118-wsnp_CD452643B_Ta_2_1	6B	474177746	TDBG2	ISIS EM-BLASSO	3.89E-06	3.77E-02	4.155
				mrMLM	3.16E-07	1.54E-03	4.758
			TDBG1	FASTmrMLM	2.51E-07	1.22E-03	3.858
20105-Ex_c20946_574	6B	481863585	MBRJ	mrMLM	1.38E-05	1.48E-02	3.186
28858-Excalibur_c7785_123	6B	526481172	MBRJ	ISIS EM-BLASSO	3.56E-06	8.65E-03	2.537

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
404-BobWhite_c12770_158	6B	528622948	MBRJ	FASTmrMLM	5.25E-09	5.10E-05	5.487
				pLARmEB	4.59E-08	1.48E-04	2.237
8425-BS00046264_51	6B	704974282	TDBG1	FASTmrMLM	1.29E-06	2.50E-03	3.080
48184-Kukri_c89555_57	6D	3917522	MGBJ	ISIS EM-BLASSO	4.46E-06	7.21E-03	4.420
44590-Kukri_c3664_1071	6D	10910854	MGBJ	mrMLM	5.88E-10	5.71E-06	6.823
9598-BS00065628_51	6D	40773214	MBRJ	pKWmEB	3.02E-06	7.32E-03	2.880
14891-CAP8_c6799_93	6D	462632139	MBRJ	pKWmEB	2.50E-08	2.43E-04	10.703
62295-RAC875_rep_c114991_493	7A	19006634	MBRJ	FASTmrMLM	1.80E-08	5.83E-05	4.930
				ISIS EM-BLASSO	5.54E-06	1.08E-02	2.847
				pLARmEB	3.00E-08	2.92E-04	2.221
25092-Excalibur_c31383_82	7A	31879084	TDBG2	FASTmrMLM	2.22E-06	1.08E-02	7.983
28748-Excalibur_c7538_2718	7A	35602223	TDBG1	FASTmrMLM	3.53E-05	3.43E-02	1.096
			MGBJ	mrMLM	1.11E-05	1.54E-02	1.214
55491-RAC875_c23339_236	7A	48094405	TDBG1	pKWmEB	5.40E-06	1.05E-02	7.429
60067-RAC875_c67063_703	7A	112265416	MBDS	pLARmEB	2.95E-05	2.86E-02	2.566
60997-RAC875_c90330_82	7A	721224063	TJBJ	ISIS EM-BLASSO	1.22E-06	5.92E-03	4.028
23174-Excalibur_c18631_169	7A	733332972	TDBG1	FASTmrMLM	2.56E-06	3.55E-03	2.386
27109-Excalibur_c50044_749	7B	6179392	TDBG2	FASTmrMLM	1.63E-06	1.59E-02	7.118
			TDBG1	FASTmrMLM	5.60E-07	1.36E-03	7.493
				pLARmEB	9.97E-07	3.23E-03	4.741
			TJBJ	FASTmrMLM	1.72E-06	8.34E-03	6.426
				pLARmEB	1.16E-05	2.83E-02	4.127
10797-BS00075332_51	7B	611615637	MGBJ	pKWmEB	5.71E-09	2.77E-05	4.877
3028-BobWhite_c39053_78	7B	611743356	MBRJ	mrMLM	8.56E-08	4.16E-04	3.570
			MGBJ	ISIS EM-BLASSO	1.38E-05	1.91E-02	2.311
				pLARmEB	5.40E-10	2.62E-06	3.648
5025-BobWhite_rep_c52876_72	7B	612257379	TDBG1	FASTmrMLM	3.53E-05	3.81E-02	3.644
				pLARmEB	1.22E-05	1.98E-02	3.623
56081-RAC875_c27548_417	7B	626239007	TDBG2	pLARmEB	3.68E-06	8.93E-03	3.225
9018-BS00063208_51	7B	637618402	MGBJ	ISIS EM-BLASSO	1.46E-05	1.77E-02	3.498
				mrMLM	5.64E-05	4.56E-02	5.410
73054-Tdurum_contig67161_99	7B	703310984	TJBJ	pLARmEB	2.64E-05	4.27E-02	1.852
19354-D_GDS7LZN02F1Q5F_180	7D	45129712	TDBG1	mrMLM	1.79E-05	2.90E-02	9.146
			MGBJ	FASTmrMLM	3.55E-07	3.45E-03	9.326
				mrMLM	3.78E-06	1.22E-02	14.270

QTN or LDB	Chr	Position	Trait	Model	P-value	FDR	r^2 (%)
			TJBJ	pKWmEB	6.48E-06	8.99E-03	14.019
42140-Kukri_c19466_627	7D	59936619	MGBJ	pKWmEB	3.77E-15	3.66E-11	18.808
				pLARmEB	6.76E-06	1.31E-02	4.775
55515-RAC875_c23473_165	7D	70126657	MGBJ	mrMLM	5.10E-06	9.90E-03	6.877
52752-Ra_c8680_450	7D	101475229	TDBG1	mrMLM	2.86E-06	1.39E-02	15.987
15734-D_contig14443_745	7D	232496636	TDBG1	FASTmrMLM	3.86E-07	1.25E-03	2.467
				pKWmEB	2.05E-07	9.94E-04	4.571
				pLARmEB	1.53E-06	3.71E-03	1.936
72568-Tdurum_contig5724_344	7D	587733069	TDBG1	FASTmrMLM	1.66E-06	2.69E-03	3.711
				pLARmEB	1.29E-05	1.79E-02	2.427
18377-D_GBF1XID01CATV7_146	7D	600701805	TJBJ	ISIS EM-BLASSO	1.96E-05	3.80E-02	6.279
15958-D_contig19288_196	7D	619884620	MBRJ	FASTmrMLM	3.55E-05	3.83E-02	3.621
24279-Excalibur_c25224_202	Un	51205798	MBDS	ISIS EM-BLASSO	8.12E-06	3.94E-02	2.154
Multi-locus model RTM[1]							
59361-RAC875_c5831_1486	1A	10969929	MBRJ	RTM	3.25E-08	2.47E-04	7.891
35133-IAAV6025	1B	211312483	MBRJ	RTM	1.89E-05	2.88E-02	3.727
59043-RAC875_c54588_191	2A	393113820	TJBJ	RTM	1.79E-06	6.80E-03	NA
75000-tplb0052b23_2493	2D	621964724	TDBG2	RTM	2.25E-05	5.70E-02	4.671
8908-BS00062734_51	3B	545069001	MGBJ	RTM	2.17E-09	1.65E-05	8.519
			TDBG1	RTM	8.79E-13	6.68E-09	12.340
7087-BS00022441_51	3B	807288990	MBRJ	RTM	2.73E-05	3.46E-02	3.829
16427-D_contig29825_215	4D	82020798	MBRJ	RTM	1.63E-05	4.14E-02	4.833
75749 - 41702	5A	588737306-588742167	TDBG2	RTM	4.39E-06	1.67E-02	5.415
59300-RAC875_c57603_144	5A	666228776	MBRJ	RTM	9.60E-07	3.65E-03	5.796
75518 - 45559	5B	479388707-479716557	MBRJ	RTM	4.31E-05	4.68E-02	6.550
81123 - 44910	6B	151130562-479716557	MBDS	RTM	8.93E-07	6.79E-03	6.595
72452 - 72450	6B	582823808-582824969	TJBJ	RTM	1.12E-09	8.52E-06	11.148
18070-D_GB5Y7FA02G6KBX_382	6D	339399173	MBRJ	RTM	1.69E-05	3.22E-02	3.614
79153 - 20908	7B	561748617-561748617	TDBG2	RTM	5.26E-12	4.00E-08	14.722
42140-Kukri_c19466_627	7D	59936619	MGBJ	RTM	7.71E-06	2.93E-02	4.344

Appendix 14 Significant QTNs and LDBs for leaf rust severity in spring and winter panels

QTNs (Quantitative trait nucleotides) and LDBs (linkage disequilibrium blocks) for leaf rust severity in the spring and winter diversity panels response were identified by association mapping using one single-locus and seven multi-locus models.

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
SPRING DIVERSITY PANEL							
Single-locus model							
33585-GENE-3735_720	6D	462275413	MDN	MLM	5.48E-06	4.65E-02	11.233
Multi-locus models							
77798-wsnp_Ex_c3372_6195001	1A	257573729	SK	ISIS EM-BLASSO	1.24E-07	1.05E-03	6.383
25356-Excalibur_c33567_363	1A	427819541	SK	mrMLM	3.70E-05	4.49E-02	17.615
45449-Kukri_c44500_315	1A	586952125	All locations	mrMLM	1.20E-05	1.28E-02	7.428
79341-wsnp_Ex_rep_c67474_66076379	1A	591093391	OTT	FASTmrMLM	7.72E-08	6.55E-04	8.812
				pLARmEB	4.72E-10	4.01E-06	9.203
7123-BS00022505_51	1B	4347120	All locations	ISIS EM-BLASSO	8.27E-06	1.00E-02	4.943
				FASTmrEMMA	2.03E-06	5.74E-03	5.067
				pLARmEB	1.23E-10	5.21E-07	6.835
				FASTmrMLM	3.52E-09	9.95E-06	7.220
				pKWmEB	2.19E-07	9.31E-04	8.463
47637-Kukri_c75399_226	1B	408656937	All locations	FASTmrMLM	1.64E-10	6.94E-07	7.217
			MDN	FASTmrMLM	8.99E-07	1.91E-03	5.084
				mrMLM	2.72E-05	2.56E-02	2.708
				pKWmEB	4.87E-09	1.38E-05	6.243
				pLARmEB	8.20E-06	1.39E-02	3.214
6619-BS00015519_51	1B	660528121	All locations	ISIS EM-BLASSO	8.61E-07	1.83E-03	2.900
				pKWmEB	1.78E-05	1.89E-02	3.936
28820-Excalibur_c7684_54	1B	660531484	All locations	ISIS EM-BLASSO	5.25E-06	8.92E-03	2.355
47907-Kukri_c8211_159	1D	9875153	MDN	mrMLM	4.66E-05	3.30E-02	2.335
				pLARmEB	2.78E-08	7.85E-05	4.767
57419-RAC875_c38580_350	1D	460254487	All locations	FASTmrMLM	4.94E-09	1.05E-05	17.013
31871-GENE-0416_480	1D	476257353	MDN	pKWmEB	1.09E-05	1.03E-02	2.331
14845-CAP8_c607_659	2A	504711045	OTT	mrMLM	3.76E-06	1.06E-02	2.309
55821-RAC875_c25628_180	2B	8273044	SK	ISIS EM-BLASSO	1.28E-05	2.72E-02	3.943
				mrMLM	1.81E-06	3.84E-03	4.247

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
				pLARmEB	3.77E-05	2.91E-02	2.648
24825-Excalibur_c2933_1350	2B	8290437	All locations	pKWmEB	8.99E-06	1.09E-02	6.758
36726-Jagger_c7188_67	2B	180561127	MDN	ISIS EM-BLASSO	2.65E-05	3.75E-02	2.868
				pKWmEB	1.09E-08	2.31E-05	8.663
				pLARmEB	2.86E-05	4.04E-02	2.257
76662-wsnp_Ex_c14771_22883575	2B	191734319	SK	FASTmrMLM	1.28E-05	3.63E-02	2.818
				mrMLM	8.81E-06	1.25E-02	5.248
				pKWmEB	1.84E-05	3.12E-02	5.622
				pLARmEB	4.44E-06	5.39E-03	3.647
45381-Kukri_c43745_1935	2B	578601210	MDN	mrMLM	2.27E-05	2.76E-02	2.447
4154-BobWhite_c6365_385	2B	731895391	MDN	FASTmrEMMA	1.16E-06	1.97E-03	3.818
				ISIS EM-BLASSO	4.58E-08	1.95E-04	4.414
				mrMLM	6.67E-05	4.04E-02	3.478
				pKWmEB	6.41E-08	1.09E-04	6.144
73196-Tdurum_contig71365_233	2B	738410414	All locations	pKWmEB	1.55E-06	3.28E-03	4.693
14959-CAP8_c8516_542	2B	749028333	OTT	mrMLM	1.49E-05	3.16E-02	12.275
46560-Kukri_c55909_1109	2B	770681399	OTT	FASTmrMLM	9.00E-07	3.82E-03	7.921
				pLARmEB	1.16E-05	1.64E-02	4.793
29707-Excalibur_rep_c101288_130	2D	17169662	OTT	ISIS EM-BLASSO	1.37E-07	5.84E-04	7.566
74411-tplb0030j08_1960	2D	27928724	MDN	mrMLM	2.56E-07	7.23E-04	22.105
66898-Tdurum_contig11028_533	2D	87406015	MDN	pKWmEB	4.60E-05	3.90E-02	3.650
5774-BS00000905_51	2D	369762241	All locations	pKWmEB	6.68E-07	1.89E-03	5.030
66206-Tdurum_contig10048_447	2D	635229168	OTT	pKWmEB	2.98E-06	8.42E-03	3.447
7692-BS00028660_51	3A	507467861	All locations	mrMLM	2.87E-05	2.21E-02	1.104
37081-JD_c1636_113	3A	672556342	MDN	mrMLM	1.20E-06	2.54E-03	7.970
14695-CAP8_c3568_256	3A	724200935	SK	mrMLM	2.80E-08	2.37E-04	9.982
				pLARmEB	4.02E-06	5.69E-03	6.797
50704-Kukri_s117946_404	3A	739734944	OTT	FASTmrMLM	2.73E-06	7.71E-03	4.882
				pLARmEB	3.53E-07	1.50E-03	4.599
75559-wsnp_BE499016B_Ta_2_1	3B	661016320	All locations	mrMLM	3.32E-08	1.41E-04	11.942
			MDN	mrMLM	5.52E-05	3.60E-02	2.306
28781-Excalibur_c76110_101	3B	760137269	All locations	FASTmrMLM	4.68E-06	7.95E-03	3.796
				mrMLM	9.30E-06	1.13E-02	5.093
4262-BobWhite_c6974_329	3D	460250774	All locations	mrMLM	6.45E-06	1.09E-02	2.687
35630-IACX1049	3D	551981733	MDN	mrMLM	9.97E-08	4.23E-04	3.753

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
67877-Tdurum_contig13140_69	4A	59321657	SK	FASTmrMLM	1.86E-05	3.95E-02	3.114
				pKWmEB	4.37E-07	1.24E-03	7.759
				pLARmEB	1.61E-05	1.36E-02	2.492
47419-Kukri_c67793_237	4A	595821093	SK	mrMLM	5.90E-06	1.00E-02	4.030
54888-RAC875_c19718_551	4A	603453604	All locations	mrMLM	1.34E-05	1.26E-02	3.320
			MDN	mrMLM	2.75E-06	4.67E-03	4.446
58552-RAC875_c49370_327	4A	629917691	All locations	mrMLM	1.43E-05	1.22E-02	1.118
23633-Excalibur_c21395_291	4A	734000589	SK	FASTmrMLM	3.15E-07	2.68E-03	4.967
53152-RAC875_c10704_67	4B	154114340	MDN	ISIS EM-BLASSO	4.51E-09	3.83E-05	7.783
62918-RAC875_rep_c72961_977	4B	616999234	OTT	mrMLM	4.59E-08	3.90E-04	6.058
58215-RAC875_c46098_110	4B	669559717	All locations	mrMLM	7.37E-06	1.04E-02	3.259
55110-RAC875_c2099_2066	4B	670439103	All locations	pKWmEB	5.53E-05	4.27E-02	5.065
24829-Excalibur_c29380_255	5A	26469747	OTT	FASTmrEMMA	5.95E-07	2.52E-03	8.322
				pKWmEB	4.08E-06	8.66E-03	12.401
				pLARmEB	1.45E-06	3.08E-03	6.300
46209-Kukri_c52_225	5A	559070986	OTT	FASTmrEMMA	2.21E-05	3.75E-02	5.340
				ISIS EM-BLASSO	2.26E-05	4.79E-02	5.410
27236-Excalibur_c51589_200	5A	561660942	All locations	mrMLM	1.08E-12	9.21E-09	11.293
45725-Kukri_c47057_758	5B	447840598	SK	mrMLM	9.51E-07	2.69E-03	4.220
30867-Excalibur_rep_c67473_320	5B	506789600	MDN	pKWmEB	9.31E-07	1.32E-03	5.051
30952-Excalibur_rep_c68362_62	5B	695992792	SK	ISIS EM-BLASSO	1.61E-06	4.56E-03	4.319
				pLARmEB	6.35E-06	6.74E-03	2.744
1281-BobWhite_c19443_131	5D	442701407	OTT	mrMLM	3.12E-07	1.33E-03	6.952
14533-CAP8_c145_89	5D	547273518	All locations	FASTmrMLM	1.62E-05	2.29E-02	3.332
				pKWmEB	1.86E-06	2.63E-03	5.528
				pLARmEB	1.36E-05	1.92E-02	2.810
			MDN	FASTmrEMMA	1.55E-08	4.37E-05	5.864
				pKWmEB	4.70E-10	2.00E-06	8.722
			SK	ISIS EM-BLASSO	4.10E-07	1.74E-03	6.325
				pLARmEB	1.50E-05	1.41E-02	3.343
49205-Kukri_rep_c106820_591	5D	548880858	MDN	mrMLM	2.55E-05	2.70E-02	8.590
4362-BobWhite_c7604_254	5D	550206088	All locations	mrMLM	1.68E-07	3.56E-04	5.237
4361-BobWhite_c7604_181	5D	550206161	MDN	FASTmrMLM	5.42E-12	2.30E-08	14.135
				ISIS EM-BLASSO	6.44E-07	1.09E-03	6.726
				pLARmEB	1.88E-11	7.97E-08	11.048

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
11863-BS00094333_51	5D	559922461	All locations	FASTmrEMMA	5.43E-09	4.61E-05	8.391
				FASTmrMLM	1.22E-15	1.04E-11	9.563
				ISIS EM-BLASSO	2.69E-14	2.28E-10	8.382
				pKWmEB	3.50E-09	2.97E-05	7.613
				pLARmEB	7.73E-12	6.56E-08	6.525
8077-BS00037002_51	6A	2972683	MDN	FASTmrEMMA	5.69E-07	1.21E-03	5.804
				FASTmrMLM	8.68E-06	1.47E-02	3.740
				pKWmEB	1.21E-06	1.47E-03	3.791
				pLARmEB	6.43E-07	1.37E-03	4.237
10105-BS00067630_51	6A	5221726	SK	pKWmEB	4.88E-06	1.04E-02	7.721
2064-BobWhite_c27145_318	6A	598635853	OTT	pKWmEB	8.91E-09	7.56E-05	6.431
47927-Kukri_c8239_987	6B	25914950	MDN	mrMLM	1.47E-08	1.25E-04	4.612
31558-Excalibur_s113695_111	6B	556491270	All locations	FASTmrEMMA	8.68E-06	1.84E-02	3.982
				ISIS EM-BLASSO	1.54E-07	4.36E-04	4.454
60190-RAC875_c68525_284	6B	657946526	SK	mrMLM	3.47E-07	1.47E-03	13.261
8425-BS00046264_51	6B	704974282	OTT	FASTmrMLM	1.83E-05	3.10E-02	3.009
				pLARmEB	1.41E-05	1.71E-02	2.338
5593-BobWhite_rep_c66074_232	6B	706118869	All locations	FASTmrEMMA	7.44E-07	3.16E-03	5.113
				ISIS EM-BLASSO	6.71E-06	9.49E-03	3.555
				pKWmEB	5.50E-05	4.67E-02	4.366
				pLARmEB	1.15E-05	1.96E-02	2.095
13973-CAP7_c2923_366	6D	129784133	OTT	FASTmrEMMA	8.35E-07	2.36E-03	11.562
				ISIS EM-BLASSO	1.03E-07	8.74E-04	11.835
50713-Kukri_s118416_65	7A	167271145	MDN	FASTmrEMMA	2.48E-09	1.05E-05	19.597
26882-Excalibur_c4759_564	7A	232751332	OTT	FASTmrEMMA	2.42E-07	2.06E-03	7.343
				ISIS EM-BLASSO	1.24E-05	3.50E-02	4.366
				pLARmEB	1.11E-06	3.14E-03	6.361
687-BobWhite_c1469_112	7A	515009750	All locations	pLARmEB	2.71E-07	7.66E-04	5.129
65210-RFL_Contig6074_1058	7A	691535765	MDN	mrMLM	2.89E-05	2.45E-02	2.173
25155-Excalibur_c3188_1352	7A	692879432	SK	pKWmEB	1.93E-09	1.64E-05	15.549
81116-wsnp_Ra_c35321_43882919	7A	692880572	SK	FASTmrMLM	4.17E-06	1.77E-02	10.369
30143-Excalibur_rep_c105674_315	7A	712307419	All locations	ISIS EM-BLASSO	2.47E-05	2.62E-02	1.963
71429-Tdurum_contig43523_1458	7B	47742258	OTT	FASTmrEMMA	1.34E-05	2.85E-02	4.432
				FASTmrMLM	8.00E-06	1.70E-02	4.825

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
30869-Excalibur_rep_c67475_1759	7B	498523612	MDN	FASTmrMLM	5.23E-07	1.48E-03	4.839
				ISIS EM-BLASSO	7.39E-08	2.09E-04	5.736
				mrMLM	2.98E-05	2.30E-02	5.931
80349-wsnp_Ku_c29256_39161320	7B	539232386	All locations	pKWmEB	1.82E-06	3.09E-03	5.229
7573-BS00025286_51	7B	636508176	All locations	pKWmEB	1.79E-05	1.69E-02	2.295
74097-tplb0021f14_1700	7B	653898244	All locations	mrMLM	4.84E-08	1.37E-04	9.459
31227-Excalibur_rep_c74234_183	7B	655037014	All locations	ISIS EM-BLASSO	5.41E-08	2.30E-04	5.104
75603-wsnp_BE605194B_Ta_2_1	7B	657932119	All locations	pLARmEB	6.97E-06	1.48E-02	4.236
79099-wsnp_Ex_rep_c104090_88891443	7B	687803644	SK	pKWmEB	8.57E-09	3.64E-05	12.520
9595-BS00065623_51	7D	4005296	MDN	FASTmrEMMA	2.96E-10	2.51E-06	11.173
				pKWmEB	1.25E-11	1.06E-07	18.396
22812-Excalibur_c16580_388	7D	18438257	MDN	pKWmEB	1.09E-05	1.15E-02	7.233
19377-D_GDS7LZN02FSYZC_227	7D	58491641	OTT	pLARmEB	4.26E-06	7.23E-03	5.070
33938-GENE-4375_382	7D	465165900	MDN	mrMLM	7.64E-06	1.08E-02	5.730
79862-wsnp_JD_c69_109951	Un	24402452	MDN	FASTmrMLM	2.34E-13	1.99E-09	13.464
				ISIS EM-BLASSO	2.56E-07	5.42E-04	6.436
				pLARmEB	5.28E-13	4.48E-09	10.958
12610-BS00110940_51	Un	81996418	OTT	pKWmEB	1.34E-08	5.70E-05	7.927
Multi-locus model RTM[2]							
77798-wsnp_Ex_c3372_6195001	1A	257573729	SK	RTM	1.41E-05	0.0296	5.791
9566 - 7076	1B	8559397-8559748	All locations	RTM	6.86E-05	0.0433	3.179
2192-BobWhite_c28341_51	1D	204295576	SK	RTM	1.41E-05	0.0222	NA
9578-BS00065548_51	2A	148866377	All locations	RTM	9.72E-07	0.00204	3.878
51049-Ra_c13247_528	2A	675079920	All locations	RTM	5.01E-05	0.0395	1.905
26314-Excalibur_c42248_663	2B	6715740	All locations	RTM	2.49E-05	0.0224	3.073
65093-RFL_Contig5709_3312	3B	66581492	All locations	RTM	1.33E-05	0.014	2.631
5332-BobWhite_rep_c63085_120	3B	9780568	All locations	RTM	6.66E-05	0.0467	2.036
48662-Kukri_rep_c101532_1046	3D	591985403	SK	RTM	4.93E-05	0.0623	4.657
22324-Excalibur_c13811_1086	4A	723810464	SK	RTM	2.16E-06	0.0136	7.580
66289 - 8437	5A	48464957-49956315	OTT	RTM	6.16E-06	0.0194	9.717
38458-Ku_c1454_984	5D	22378179	MDN	RTM	4.89E-07	0.00154	7.201

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
14533-CAP8_c145_89	5D	547273518	All locations	RTM	1.77E-07	0.000559	8.116
			MDN	RTM	3.12E-06	0.00656	5.295
72401-Tdurum_contig5486_177	6B	90280258	SK	RTM	3.31E-06	0.0105	9.281
46716-Kukri_c58096_480	6B	712390096	OTT	RTM	5.11E-09	3.22E-05	14.671
12939 - 12245	6D	465742757-465959637	MDN	RTM	1.51E-07	0.000956	10.351
50713-Kukri_s118416_65	7A	167271145	MDN	RTM	5.23E-06	0.00825	4.369
8051 - 78361	7A	275545643-275920469	All locations	RTM	1.23E-10	7.77E-07	13.048
36277 - 73863	7B	457383441-457401612	All locations	RTM	2.34E-06	0.00296	5.302
58340-RAC875_c4732_1672	7B	533774856	SK	RTM	7.31E-05	0.0769	2.960
72089-Tdurum_contig50574_304	7B	597463583	All locations	RTM	1.54E-06	0.00243	4.786
WINTER DIVERSITY PANEL							
Single-locus model							
18025-D_GB5Y7FA01EE4DJ_242	1D	361914448	MDN	MLM	9.54E-07	2.65E-03	24.366
16342-D_contig28058_60	1D	366674212	MDN	MLM	2.03E-07	1.70E-03	18.460
46794-Kukri_c59403_339	2D	75001895	MDN	MLM	5.68E-07	2.37E-03	19.716
19215-D_GDRF1KQ02GC5EV_278	5D	301127151	MDN	MLM	1.81E-06	3.78E-03	18.991
Multi-locus models							
10050-BS00067436_51	1A	578204373	MDN	FASTmrMLM	3.15E-06	1.31E-02	12.716
38236-Ku_c11394_862	1B	339908061	All locations	ISIS EM-BLASSO	2.13E-05	4.44E-02	17.360
24999-Excalibur_c30667_102	1B	360517459	MDN	pLARmEB	2.15E-07	5.98E-04	6.205
8318-BS00042340_51	1B	630700832	All locations	mrMLM	2.12E-07	1.77E-03	4.567
21002-Ex_c6145_2193	1D	12534520	MDN	mrMLM	1.27E-05	5.30E-02	7.761
16342-D_contig28058_60	1D	366674212	MDN	ISIS EM-BLASSO	1.40E-07	5.84E-04	7.446
				pLARmEB	2.96E-06	4.94E-03	5.994
			OTT	ISIS EM-BLASSO	3.83E-05	5.33E-02	4.872
				pLARmEB	3.07E-05	5.12E-02	5.693
27190-Excalibur_c50934_159	2A	85289098	OTT	mrMLM	1.97E-09	1.64E-05	14.080
15473-D_contig08350_924	2B	394098064	MDN	FASTmrEMMA	1.27E-06	1.06E-02	15.788
19356-D_GDS7LZN02F3V0T_214	2D	14117424	MDN	pKWmEB	1.27E-06	2.12E-03	10.437
27281-Excalibur_c5199_423	2D	593270920	MDN	FASTmrMLM	3.30E-06	9.18E-03	4.875
30442-Excalibur_rep_c109863_383	3A	9854380	All locations	mrMLM	2.53E-05	5.28E-02	5.871

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
25955-Excalibur_c3862_837	3B	245969143	MDN	FASTmrMLM	5.51E-08	4.60E-04	8.550
79515-wsnp_Ex_rep_c69783_68742690	3B	379995020	MDN	pLARmEB	1.59E-07	6.63E-04	6.667
52937-RAC875_c101793_136	3D	547625537	All locations	ISIS EM-BLASSO	1.69E-05	4.70E-02	3.086
74685-tplb0040j04_1007	4A	708613278	MDN	pKWmEB	5.42E-08	4.52E-04	11.522
37657-JD_c581_466	4A	713519525	OTT	FASTmrMLM	3.28E-09	2.74E-05	19.326
				pKWmEB	9.07E-10	3.78E-06	12.206
				pLARmEB	4.46E-06	9.30E-03	9.445
74800-tplb0044j06_689	5A	596013562	OTT	mrMLM	1.71E-05	3.57E-02	13.047
7154-BS00022555_51	5B	435769407	OTT	pKWmEB	1.87E-06	3.90E-03	13.992
78640-wsnp_Ex_c6548_11355524	5B	439725143	MDN	ISIS EM-BLASSO	3.49E-10	2.91E-06	21.739
				mrMLM	1.63E-12	1.36E-08	40.130
				pKWmEB	4.18E-07	1.16E-03	22.773
6745-BS00021735_51	5B	593943053	OTT	ISIS EM-BLASSO	4.56E-11	3.80E-07	15.407
				pLARmEB	1.46E-12	1.22E-08	24.295
69972-Tdurum_contig30194_256	5B	653230498	OTT	mrMLM	1.91E-07	7.97E-04	12.813
53681-RAC875_c13208_684	5B	680352542	OTT	pKWmEB	4.43E-12	3.70E-08	18.076
77355-wsnp_Ex_c24031_33277856	5B	707133745	All locations	pLARmEB	8.71E-10	7.27E-06	7.686
19215-D_GDRF1KQ02GC5EV_278	5D	301127151	All locations	pLARmEB	1.53E-06	4.25E-03	8.187
78974-wsnp_Ex_c965_1845676	6A	581747079	All locations	FASTmrMLM	6.19E-07	5.16E-03	7.902
				ISIS EM-BLASSO	1.69E-09	1.41E-05	8.931
				pKWmEB	1.39E-06	1.16E-02	13.320
				pLARmEB	2.34E-08	9.76E-05	4.609
60427-RAC875_c76675_372	6A	610199793	MDN	FASTmrMLM	1.28E-05	2.67E-02	2.916
				pKWmEB	3.10E-07	1.29E-03	3.583
				pLARmEB	2.14E-08	1.79E-04	4.134
17318-D_F1BEJMU01DYWUS_134	6D	58096323	OTT	FASTmrMLM	2.76E-06	1.15E-02	3.439
				pLARmEB	1.82E-06	7.59E-03	3.559
15945-D_contig18907_85	6D	463870710	OTT	FASTmrMLM	6.83E-06	1.90E-02	8.525
				ISIS EM-BLASSO	2.27E-07	6.31E-04	11.874
24038-Excalibur_c23756_1461	7A	6485654	OTT	ISIS EM-BLASSO	3.56E-06	7.43E-03	8.881
				pLARmEB	2.00E-06	5.56E-03	7.969
25650-Excalibur_c35919_107	7A	259562231	All locations	mrMLM	9.97E-06	2.77E-02	12.109
34228-GENE-4898_208	7A	572869014	OTT	ISIS EM-BLASSO	1.13E-07	4.71E-04	11.094
48036-Kukri_c855_2107	7A	708138675	MDN	ISIS EM-BLASSO	1.32E-05	2.75E-02	7.273

QTN or LDB	Chr	CS position	Trait[1]	Method	P-value	FDR	r^2 (%)
52617-Ra_c73849_639	7B	1255228	OTT	pKWmEB	4.43E-09	1.23E-05	17.735
34569-IAAV2530	7D	102541074	OTT	mrMLM	5.44E-06	1.51E-02	8.369
15734-D_contig14443_745	7D	232496636	MDN	ISIS EM-BLASSO	5.07E-06	1.41E-02	3.295
				pKWmEB	1.08E-06	2.25E-03	9.821
				pLARmEB	1.84E-06	3.84E-03	3.493
8614-BS00052386_51	7D	289257907	All locations	mrMLM	3.73E-07	1.56E-03	18.834
16386-D_contig28902_391	7D	456495802	All locations	ISIS EM-BLASSO	1.02E-05	4.25E-02	5.036
23018-Excalibur_c17808_478	7D	609277272	OTT	ISIS EM-BLASSO	3.30E-05	5.51E-02	3.885
Multi-locus model RTM[2]							
12157-BS00100994_51	1B	9936518	MDN	RTM	4.38E-09	1.57E-05	13.610
21002-Ex_c6145_2193	1D	12534520	MDN	RTM	4.70E-06	0.0056	6.504
76918-wsnp_Ex_c17852_26612172	2A	197559361	All locations	RTM	2.39E-08	0.000171	13.796
74910 - 56694	2B	622904989-624539187	All locations	RTM	2.63E-05	0.0376	8.130
17812-D_GA8KES401EQTMF_68	2D	446313187	MDN	RTM	4.23E-05	0.0302	3.189
38473 - 76298	3A	497649774-497655032	MDN	RTM	9.92E-07	0.00177	2.551
75655-wsnp_BF429272A_Ta_2_1	3A	498774691	MDN	RTM	9.92E-07	0.00142	NA
27648 - 2309	3A	651627266-651627599	All locations	RTM	8.31E-06	0.0198	7.305
73056 - 71662	3A	662940157-663181023	All locations	RTM	1.95E-05	0.0349	8.947
79515-wsnp_Ex_rep_c69783_68742690	3B	379995020	MDN	RTM	4.36E-05	0.0283	2.047
37657 - 1382	4A	713519525-713523112	OTT	RTM	1.14E-10	8.15E-07	33.768
61163-RAC875_c96615_107	5A	403876844	MDN	RTM	2.43E-05	0.0193	1.555
19215-D_GDRF1KQ02GC5EV_278	5D	301127151	MDN	RTM	5.97E-06	0.0061	6.110
15609-D_contig11260_295	5D	526292356	All locations	RTM	4.08E-06	0.0146	9.036
			MDN	RTM	7.84E-11	5.60E-07	21.596
39827 - 4395	7B	181035062-181036896	MDN	RTM	2.44E-07	0.000581	5.761
5616-BobWhite_rep_c66630_331	7B	624351237	MDN	RTM	6.23E-06	0.00557	3.265

[1] MDN, Mordern; OTT, Ottawa; SK, Saskatoon

[2] For significant SNP LDBs identified by RTM, only the SNP index are shown.

Appendix 15 Functional annotation of genes located within 5KB of associated loci

Table shows quantitative trait nucleotides (QTNs) or peak single nucleotide polymorphism (SNP) markers of linkage disequilibrium blocks (LDBs) associated with infection type response against six leaf rust isolates and leaf rust (LR) severity of the spring and winter diversity panels.

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
INFECTION TYPE							
59361-RAC875_c5831_1486	1A	10969929	TraesCS1A02G022500	TDBG2	M1		
				TDBG2	M2		
				MBRJ	M3		
				MBRJ	M2		
				MBRJ	M4		
				MBRJ	M5		
				MBRJ	M6		
31602-GENE-0002_856	1A	32087536	TraesCS1A02G050100	MGBJ	M6	1	ADH, GroES-like
				MGBJ	M4	1	ADH, GroES-like
10214-BS00068036_51	1A	268932276	TraesCS1A02G154400	MBDS	M7		Put_SAM_MeTrfase
45449-Kukri_c44500_315	1A	586952125	TraesCS1A02G437400	TDBG1	M4		
				TDBG1	M7		
				MGBJ	M7		
79341-wsnp_Ex_rep_c67474_66076379	1A	591093391	TraesCS1A02G442400	MGBJ	M4	1	ARM-type, Helicase ATP-bd
7236-BS00022745_51	1B	70711155	TraesCS1B02G086200	MBDS	M7		
26303-Excalibur_c4215_1327	1B	95323618	TraesCS1B02G093900	TDBG2	M7		WH-like-DNA-bd_sf, RPC62
35133-IAAV6025	1B	211312483	TraesCS1B02G147300	MBDS	M2	1	PC-Esterase-PMR5, TBL
				MBDS	M8	1	PC-Esterase-PMR5, TBL
				MBRJ	M3	1	PC-Esterase-PMR5, TBL
50495-Kukri_rep_c91496_1320	1B	331420168	TraesCS1B02G184700	TDBG2	M7		DNA ligase, ATP-dependent
73768-Tdurum_contig9164_233	1B	533863925	TraesCS1B02G310800	MBRJ	M7		
42096-Kukri_c19247_711	1B	614455731	TraesCS1B02G382000	MBDS	M5		JAMM/MPN domain, BRCC36_C
3634-BobWhite_c48071_144	1B	614455863	TraesCS1B02G382000	MBDS	M1		JAMM/MPN domain, BRCC36_C
				MBDS	M4		JAMM/MPN domain, BRCC36_C
				MBDS	M7		JAMM/MPN domain, BRCC36_C
				MBDS	M6		JAMM/MPN domain, BRCC36_C
				MBRJ	M5		JAMM/MPN domain, BRCC36_C
				MBRJ	M6		JAMM/MPN domain, BRCC36_C
19295-D_GDS7LZN01C3204_275	1D	101139746	TraesCS1D02G108500	MBRJ	M7		4Fe4S_Fe_S_CS

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
7344-BS00022962_51	1D	206101173	TraesCS1D02G149700	MBRJ	M7		RNase_T2-like
19196-D_GDRF1KQ02F3JLT_66	1D	273812413	TraesCS1D02G195000	MGBJ	M7		Ribo/fructo_kinase
34680-IAAV32	2A	2485710	TraesCS2A02G004800	MGBJ	M4		tRNA(m1A58)MTase
				MGBJ	M5		tRNA(m1A58)MTase
				MGBJ	M6		tRNA(m1A58)MTase
28816-Excalibur_c7682_652	2A	4951004	TraesCS2A02G012600	MBDS	M7		GlycoTrans_28_N
17360-D_F1BEJMU02HXD1T_170	2A	12985497	TraesCS2A02G028300	MGBJ	M2		AGD
				MGBJ	M5		AGD
				MGBJ	M6		AGD
79083-wsnp_Ex_rep_c103167_88182254	2A	33044691	TraesCS2A02G074700	TDBG1	M7		E2p-PDH
69592-Tdurum_contig28682_120	2A	101381504	TraesCS2A02G153400	MBRJ	M1		Ltv1
80648-wsnp_Ku_c6826_11860405	2A	104876095	TraesCS2A02G157900	TJBJ	M1		TPR-like,PPR
21864-Excalibur_c11398_913	2A	118446604	TraesCS2A02G165800	MGBJ	M7	1	Ser/Thr_kinase_AS
59043-RAC875_c54588_191	2A	393113820	TraesCS2A02G256400	TJBJ	M3	1	Uncharacterized At1g61900-lke
9450-BS00065105_51	2B	69648893	TraesCS2B02G109100	MGBJ	M7		
23783-Excalibur_c22285_762	2B	493986458	TraesCS2B02G347100	MBDS	M7		RdRP
34658-IAAV3067	2B	699173434	TraesCS2B02G505000	TJBJ	M1		CutA Nitrogen regulatory PII-like
1208-BobWhite_c18678_95	2B	751257597	TraesCS2B02G556100	TJBJ	M1		DNA_pol_palm, RNHL
32025-GENE-0674_105	2D	13773809	TraesCS2D02G037000	TDBG1	M6		
49685-Kukri_rep_c115699_270	2D	39829875	TraesCS2D02G090100	TDBG2	M2	1	Serpin_fam
15256-D_contig03226_643	2D	130822442	TraesCS2D02G185600	MBRJ	M5		Epimerase_deHydtase
				MBRJ	M6		Epimerase_deHydtase
36072-IACX5941	2D	588793333	TraesCS2D02G489900	MGBJ	M1		AHCY
				MGBJ	M6		AHCY
75000-tplb0052b23_2493	2D	621964724	TraesCS2D02G545300	TDBG2	M3	1	CC-NB-ARC-LRR domain
				TDBG1	M2	1	CC-NB-ARC-LRR domain
				TDBG1	M1	1	CC-NB-ARC-LRR domain
				TDBG1	M6	1	CC-NB-ARC-LRR domain
23770-Excalibur_c22201_907	2D	638613120	TraesCS2D02G573500	TDBG1	M1		
				TDBG1	M4		
64223-RFL_Contig3121_1979	2D	648470008	TraesCS2D02G595000	MBDS	M1	1	LRR domain, PKinase-like
68735-Tdurum_contig18471_456	3A	75030422	TraesCS3A02G109100	MBDS	M7	1	F-box-like domain
66940-Tdurum_contig11121_997	3A	532448246	TraesCS3A02G297700	MBRJ	M7		Lipoyl synthase, Aldolase TIM
45125-Kukri_c41296_172	3A	576209128	TraesCS3A02G331500	MBRJ	M7	1	Prot_inh_cystat_CS
18893-D_GCE8AKX02HMJXL_374	3B	15138756	TraesCS3B02G032600	MBDS	M8	1	Jacalin-like_lectin_dom

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				MBDS	M1	1	Jacalin-like_lectin_dom
				MBDS	M2	1	Jacalin-like_lectin_dom
				MBDS	M4	1	Jacalin-like_lectin_dom
				MBDS	M6	1	Jacalin-like_lectin_dom
				MBDS	M7	1	Jacalin-like_lectin_dom
				MBRJ	M1	1	Jacalin-like_lectin_dom
				MBRJ	M4	1	Jacalin-like_lectin_dom
				MGBJ	M1	1	Jacalin-like_lectin_dom
34803-IAAV3924	3B	20450624	TraesCS3B02G041300	TDBG2	M1	1	CC-NB-ARC-LRR domain
3061-BobWhite_c39480_122	3B	43274832	TraesCS3B02G071700	MBDS	M7		MAM33
				TJBJ	M7		MAM33
40913-Kukri_c12869_154	3B	130647769	TraesCS3B02G142700	TDBG1	M7	1	F-box-like domain
54100-RAC875_c15509_436	3B	283604560	TraesCS3B02G222400	MGBJ	M5		RNA-binding, CRM domain
8908-BS00062734_51	3B	545069001	TraesCS3B02G339000	TDBG1	M3		Lipoyl synthase, Aldolase TIM
				MGBJ	M3		Lipoyl synthase, Aldolase TIM
63403-RAC875_s108395_60	3B	605267456	TraesCS3B02G385100	TDBG2	M7		IQ motif, EF-hand binding site
				TJBJ	M7		IQ motif, EF-hand binding site
7087-BS00022441_51	3B	807288990	TraesCS3B02G577200	MBRJ	M5		t-SNARE-Syntaxin-6
				MBRJ	M3		t-SNARE-Syntaxin-6
				MBRJ	M6		t-SNARE-Syntaxin-6
				MGBJ	M1		t-SNARE-Syntaxin-6
				TJBJ	M6		t-SNARE-Syntaxin-6
24328-Excalibur_c25515_95	3D	28331100	TraesCS3D02G064200	MBDS	M2	1	Ser/Thr_kinase
				TJBJ	M4	1	Ser/Thr_kinase
				TJBJ	M1	1	Ser/Thr_kinase
				TJBJ	M6	1	Ser/Thr_kinase
				TJBJ	M5	1	Ser/Thr_kinase
				TJBJ	M2	1	Ser/Thr_kinase
15576-D_contig10567_587	3D	141408492	TraesCS3D02G167100	MBDS	M8	1	GH, β-amylase
12255-BS00105800_51	3D	611558374	TraesCS3D02G539900	MBRJ	M1		PPase
27771-Excalibur_c57945_355	4A	94765437	TraesCS4A02G088800	TDBG1	M1		E3 Ubiquitin-protein Ligase
72073-Tdurum_contig50388_343	4A	499345041	TraesCS4A02G206200	TDBG1	M7	1	Ser/Thr_kinase
7448-BS00023151_51	4A	606586747	TraesCS4A02G316900	MGBJ	M4		
76797-wsnp_Ex_c16175_24619793	4A	609805169	TraesCS4A02G321300	TDBG1	M4		RST domain, PARP
				MBDS	M1		RST domain, PARP

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
71854-Tdurum_contig47858_908	4A	625249359	TraesCS4A02G346600	MGBJ	M7	1	F-box-like, LRR domain
59451-RAC875_c59673_500	4A	681670895	TraesCS4A02G408900	TDBG2	M7		Cytoplasmic FMR1-interacting
57805-RAC875_c42019_60	4B	538268580	TraesCS4B02G266300	MBRJ	M7		
11789-BS00093089_51	4B	552827949	TraesCS4B02G274900	TDBG1	M2		S8pro/Inhibitor_I9, subtilisin peptidase
40320-Kukri_c10321_228	4B	577655390	TraesCS4B02G292100	MBDS	M2		C-N_Hydrolase
				MBDS	M7		C-N_Hydrolase
				TJBJ	M7		C-N_Hydrolase
38863-Ku_c2346_1339	4B	623066948	TraesCS4B02G332500	TDBG2	M7		FA hydroxylase
				TJBJ	M1		FA hydroxylase
				TJBJ	M5		FA hydroxylase
				TJBJ	M6		FA hydroxylase
16427-D_contig29825_215	4D	82020798	TraesCS4D02G103400	TDBG2	M1	1	CC-NB-ARC-LRR domain
				TDBG2	M6	1	CC-NB-ARC-LRR domain
				TDBG1	M5	1	CC-NB-ARC-LRR domain
				TDBG1	M6	1	CC-NB-ARC-LRR domain
				MBRJ	M3	1	CC-NB-ARC-LRR domain
				MBRJ	M6	1	CC-NB-ARC-LRR domain
28179-Excalibur_c63208_105	4D	358039232	TraesCS4D02G208000	MGBJ	M7		E3 Ubiquitin Ligase
17554-D_F5XZDLF01DBHUA_161	4D	496649455	TraesCS4D02G338700	TDBG2	M1	1	Aspartic peptidase, Xylanase inhibitor
				TDBG2	M6	1	Aspartic peptidase, Xylanase inhibitor
36264-IACX8002	5A	485201265	TraesCS5A02G275800	TDBG2	M7		
61301-RAC875_c9984_1003	5A	585458451	TraesCS5A02G390000	TDBG1	M1	1	P-loop NTPase, Kinesin motor
75749-wsnp_BJ224975A_Ta_2_2	5A	588737306	TraesCS5A02G392500	TDBG2	M3	1	Pkinase, ATP binding
41702-Kukri_c17055_189	5A	588742167	TraesCS5A02G392600	TDBG2	M3	1	ABC transporter type 1, P-loop NTPase
59300-RAC875_c57603_144	5A	666228776	TraesCS5A02G499900	MBRJ	M3		EF-hand-dom_pair, FNR
				MBRJ	M5		EF-hand-dom_pair, FNR
				MBRJ	M4		EF-hand-dom_pair, FNR
				MBRJ	M2		EF-hand-dom_pair, FNR
				MBRJ	M6		EF-hand-dom_pair, FNR
4426-BobWhite_c8115_648	5A	682712749	TraesCS5A02G521500	MGBJ	M1		UAA transporter
7730-BS00029462_51	5A	682898385	TraesCS5A02G521600	MBDS	M8		Terpenoid_cyclase/PrenylTrfase
				MGBJ	M6		Terpenoid_cyclase/PrenylTrfase
				MGBJ	M4		Terpenoid_cyclase/PrenylTrfase
				MGBJ	M1		Terpenoid_cyclase/PrenylTrfase

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				MGBJ	M2		Terpenoid_cyclase/PrenylTrfase
				MGBJ	M5		Terpenoid_cyclase/PrenylTrfase
				TJBJ	M7		Terpenoid_cyclase/PrenylTrfase
9144-BS00063855_51	5B	685964650	TraesCS5A02G525700	MBRJ	M7	1	F-box-like domain
69406-Tdurum_contig28001_110	5A	700619759	TraesCS5A02G546500	MBRJ	M7		CAAX_protease_2
51347-Ra_c19198_137	5B	26916277	TraesCS5B02G027800	MGBJ	M4		
1854-BobWhite_c2479_214	5B	78420589	TraesCS5B02G068700	TDBG1	M4		Cbl_biosynth_CbiX
				TDBG1	M6		Cbl_biosynth_CbiX
72519-Tdurum_contig56538_337	5B	124636878	TraesCS5B02G094700	TDBG1	M5		
				TJBJ	M5		
35222-IAAV6616	5B	397673282	TraesCS5B02G222600	MBRJ	M7	1	P-loop NTPase, Kinesin motor
				MGBJ	M1	1	P-loop NTPase, Kinesin motor
				MGBJ	M7	1	P-loop NTPase, Kinesin motor
				MGBJ	M6	1	P-loop NTPase, Kinesin motor
				MGBJ	M4	1	P-loop NTPase, Kinesin motor
75518-wsnp_BE495277B_Ta_2_5	5B	479388707	TraesCS5B02G295600	MBRJ	M3		
45559-Kukri_c45713_151	5B	479716557	TraesCS5B02G296500	MBRJ	M3		S35F6
34690-IAAV3268	5B	488107093	TraesCS5B02G303800	MBRJ	M7	1	ADH, GroES-like
63448-RAC875_s116069_221	5B	506951332	TraesCS5B02G321900	TDBG2	M1	1	Ser/Thr_kinase
				MGBJ	M1	1	Ser/Thr_kinase
81257-wsnp_Ra_c8465_14340896	5B	539293955	TraesCS5B02G359500	TJBJ	M7		TPR-like, PB1 domain
34530-IAAV2296	5B	566686138	TraesCS5B02G387600	TJBJ	M4		TPR-like, PB1 domain
74020-Tdurum_contig97942_163	5B	701174382	TraesCS5B02G549200	TDBG1	M4		Mitochondrial_sb/sol_carrier
18809-D_GCE8AKX01CE518_452	5D	302353075	TraesCS5D02G199800	MGBJ	M7		MOCS2B
48181-Kukri_c8949_906	5D	354938992	TraesCS5D02G247600	MBRJ	M7		Zinc finger, Sec23/Sec24-type
15938-D_contig18780_204	5D	486259068	TraesCS5D02G429000	TDBG2	M2	1	CC-NB-ARC-LRR domain
10557-BS00071571_51	6A	1879563	TraesCS6A02G004500	MGBJ	M4	1	Ser/Thr_kinase
				MGBJ	M6	1	Ser/Thr_kinase
78974-wsnp_Ex_c965_1845676	6A	581747079	TraesCS6A02G349200	MGBJ	M7		cNMP-bd, RmlC-like
63713-RFL_Contig1715_631	6A	597292476	TraesCS6A02G374500	MBRJ	M5		GNAT domain, NAT
				MBRJ	M6		GNAT domain, NAT
14865-CAP8_c6448_265	6A	604882706	TraesCS6A02G389200	MBDS	M1		
18412-D_GBF1XID01EGI95_65	6B	25279886	TraesCS6B02G040900	TDBG2	M5		S8pro/Inhibitor_I9, subtilisin Peptidase
				TDBG2	M6		S8pro/Inhibitor_I9, subtilisin Peptidase
				TJBJ	M5		S8pro/Inhibitor_I9, subtilisin Peptidase

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				TJBJ	M6		S8pro/Inhibitor_I9, subtilisin Peptidase
				TJBJ	M4		S8pro/Inhibitor_I9, subtilisin Peptidase
81123-wsnp_Ra_c3766_6947263	6B	151130562	TraesCS6B02G149800	MBDS	M3	1	PAS domain, b-propeller
44910-Kukri_c39321_112	6B	151131531	TraesCS6B02G149800	TDBG2	M1	1	PAS domain, b-propeller
				MBDS	M3	1	PAS domain, b-propeller
				MBDS	M6	1	PAS domain, b-propeller
				TJBJ	M1	1	PAS domain, b-propeller
5404-BobWhite_rep_c63804_353	6B	451926960	TraesCS6B02G251800	TDBG2	M6		
76118-wsnp_CD452643B_Ta_2_1	6B	474177746	TraesCS6B02G263200	TDBG2	M7	1	ADH, GroES-like
				TDBG2	M4	1	ADH, GroES-like
				TDBG1	M5	1	ADH, GroES-like
20105-Ex_c20946_574	6B	481863585	TraesCS6B02G268200	MBRJ	M7	1	Zinc finger, CCHC/RING/FYVE-type
28858-Excalibur_c7785_123	6B	526481172	TraesCS6B02G292700	MBRJ	M4	1	F-box-like domain
404-BobWhite_c12770_158	6B	528622948	TraesCS6B02G294500	MBRJ	M5		
				MBRJ	M6		
72452-Tdurum_contig55473_989	6B	582823808	TraesCS6B02G331400	TJBJ	M3		CRAL-TRIO_dom_sf
72450-Tdurum_contig55473_381	6B	582824969	TraesCS6B02G331400	TJBJ	M3		CRAL-TRIO_dom_sf
8425-BS00046264_51	6B	704974282	TraesCS6B02G439600	TDBG1	M5	1	Ethylene receptor
48184-Kukri_c89555_57	6D	3917522	TraesCS6D02G010200	MGBJ	M4		
44590-Kukri_c3664_1071	6D	10910854	TraesCS6D02G028200	MGBJ	M7	1	WH-like_DNA-bd, P-loop NTPase
9598-BS00065628_51	6D	40773214	TraesCS6D02G076300	MBRJ	M1	1	F-box-like domain
18070-D_GB5Y7FA02G6KBX_382	6D	339399173	TraesCS6D02G239000	MBRJ	M3		
14891-CAP8_c6799_93	6D	462632139	TraesCS6D02G384200	MBRJ	M1		Acoase/IPM_deHydtase_lsu
62295-RAC875_rep_c114991_493	7A	19006634	TraesCS7A02G040900	MBRJ	M5		Sucrose_synth
				MBRJ	M4		Sucrose_synth
				MBRJ	M6		Sucrose_synth
25092-Excalibur_c31383_82	7A	31879084	TraesCS7A02G063700	TDBG2	M5		MFS transporter, SPX domain
28748-Excalibur_c7538_2718	7A	35602223	TraesCS7A02G069600	TDBG1	M5	1	CC-NB-ARC-LRR domain
				MGBJ	M7	1	CC-NB-ARC-LRR domain
55491-RAC875_c23339_236	7A	48094405	TraesCS7A02G083400	TDBG1	M1		LCMT1
60067-RAC875_c67063_703	7A	112265416	TraesCS7A02G158000	MBDS	M6	1	AP2/ERF domain
60997-RAC875_c90330_82	7A	721224063	TraesCS7A02G545200	TJBJ	M4		Rhodanese-like domain
23174-Excalibur_c18631_169	7A	733332972	TraesCS7A02G562600	TDBG1	M5	1	Peptidase S9A, A/B hydrolase
27109-Excalibur_c50044_749	7B	6179392	TraesCS7B02G010100	TDBG2	M5		Q motif, EF-hand binding site
				TDBG1	M5		Q motif, EF-hand binding site

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				TDBG1	M6		Q motif, EF-hand binding site
				TJBJ	M5		Q motif, EF-hand binding site
				TJBJ	M6		Q motif, EF-hand binding site
79153-wsnp_Ex_rep_c109138_92064554	7B	560531289	TraesCS7B02G313700	TDBG2	M3		CHP01589
20908-Ex_c54863_29	7B	561748617	TraesCS7B02G314400	TDBG2	M3	1	Zinc finger, TAZ/ZZ/FYVE/PHD-type
10797-BS00075332_51	7B	611615637	TraesCS7B02G353800	MGBJ	M1	1	CC-LRR domain, PKinase-like
3028-BobWhite_c39053_78	7B	611743356	TraesCS7B02G354000	MBRJ	M7		Ub-like domain
				MGBJ	M6		Ub-like domain
				MGBJ	M4		Ub-like domain
5025-BobWhite_rep_c52876_72	7B	612257379	TraesCS7B02G354200	TDBG1	M5		Ub-like domain
				TDBG1	M6		Ub-like domain
56081-RAC875_c27548_417	7B	626239007	TraesCS7B02G363900	TDBG2	M6	1	Zinc finger, RING-CH/FYVE/PHD-type
9018-BS00063208_51	7B	637618402	TraesCS7B02G371600	MGBJ	M7	1	LRR, F-box-like domain
				MGBJ	M4	1	LRR domain
73054-Tdurum_contig67161_99	7B	703310984	TraesCS7B02G437100	TJBJ	M6	1	LRR domain
19354-D_GDS7LZN02F1Q5F_180	7D	45129712	TraesCS7D02G076400	TDBG1	M7		KCS-1, ACP synthase III
				MGBJ	M7		KCS-1, ACP synthase III
				MGBJ	M5		KCS-1, ACP synthase III
				TJBJ	M1		KCS-1, ACP synthase III
42140-Kukri_c19466_627	7D	59936619	TraesCS7D02G099900	MGBJ	M1	1	CC-NB-ARC-LRR domain
				MGBJ	M6	1	CC-NB-ARC-LRR domain
				MGBJ	M3	1	CC-NB-ARC-LRR domain
55515-RAC875_c23473_165	7D	70126657	TraesCS7D02G114700	MGBJ	M7		
52752-Ra_c8680_450	7D	101475229	TraesCS7D02G153000	TDBG1	M7		Nucleoporin
15734-D_contig14443_745	7D	232496636	TraesCS7D02G257100	TDBG1	M8		Ribosomal_L32e
				TDBG1	M1		Ribosomal_L32e
				TDBG1	M5		Ribosomal_L32e
				TDBG1	M6		Ribosomal_L32e
72568-Tdurum_contig5724_344	7D	587733069	TraesCS7D02G475600	TDBG1	M5	1	Aspartic peptidase, Xylanase inhibitor
				TDBG1	M6	1	Aspartic peptidase, Xylanase inhibitor
18377-D_GBF1XID01CATV7_146	7D	600701805	TraesCS7D02G491200	TJBJ	M4		Acyl_Trfase/lysoPLipase
15958-D_contig19288_196	7D	619884620	TraesCS7D02G523200	MBRJ	M5	1	EDR2-START-like domain
24279-Excalibur_c25224_202	Un	51205798	TraesCSU02G065800	MBDS	M4		PPPDE

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
LR SEVERITY - SPRING DIVERSITY PANEL							
77798-wsnp_Ex_c3372_6195001	1A	257573729	TraesCS1A02G150100	SK	M4	1	LRR domain
				SK	M3	1	LRR domain
25356-Excalibur_c33567_363	1A	427819541	TraesCS1A02G240600	SK	M7	1	Zinc finger, FYVE/PHD-type
45449-Kukri_c44500_315	1A	586952125	TraesCS1A02G437400	All	M7		
79341-wsnp_Ex_rep_c67474_66076379	1A	591093391	TraesCS1A02G442400	OTT	M5	1	ARM-type, Helicase ATP-bd
				OTT	M6	1	ARM-type, Helicase ATP-bd
7123-BS00022505_51	1B	4347120	TraesCS1B02G008000	All	M4		RRM3, Nucleotide-bd_a/b_plait_sf
				All	M1		RRM3, Nucleotide-bd_a/b_plait_sf
				All	M5		RRM3, Nucleotide-bd_a/b_plait_sf
				All	M6		RRM3, Nucleotide-bd_a/b_plait_sf
				All	M2		RRM3, Nucleotide-bd_a/b_plait_sf
9566-BS00065487_51	1B	8559397	TraesCS1B02G017600	All	M3	1	CC-NB-ARC-LRR domain
7076-BS00022429_51	1B	8559748	TraesCS1B02G017600	All	M3	1	CC-NB-ARC-LRR domain
47637-Kukri_c75399_226	1B	408656937	TraesCS1B02G227400	All	M5		6-blade_b-propeller
				MDN	M7		6-blade_b-propeller
				MDN	M1		6-blade_b-propeller
				MDN	M5		6-blade_b-propeller
				MDN	M6		6-blade_b-propeller
6619-BS00015519_51	1B	660528121	TraesCS1B02G438100	All	M1	1	LRR domain
				All	M4	1	LRR domain
28820-Excalibur_c7684_54	1B	660531484	TraesCS1B02G438100	All	M4	1	LRR domain
47907-Kukri_c8211_159	1D	9875153	TraesCS1D02G023400	MDN	M7		Rab-GTPase_TBC
				MDN	M6		Rab-GTPase_TBC
2192-BobWhite_c28341_51	1D	204295576	TraesCS1D02G148400	SK	M3		CDK inhibitor
57419-RAC875_c38580_350	1D	460254487	TraesCS1D02G388100	All	M5		
31871-GENE-0416_480	1D	476257353	TraesCS1D02G419300	MDN	M1		
9578-BS00065548_51	2A	148866377	TraesCS2A02G187200	All	M3		Chloro_AB-bd_pln
14845-CAP8_c607_659	2A	504711045	TraesCS2A02G293700	OTT	M7		ATP_synth_dsu
51049-Ra_c13247_528	2A	675079920	TraesCS2A02G419500	All	M3		PAZ_dom, RNaseH_dom
26314-Excalibur_c42248_663	2B	6715740	TraesCS2B02G013500	All	M3		
55821-RAC875_c25628_180	2B	8273044	TraesCS2B02G017800	SK	M6		
				SK	M7		
				SK	M4		

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
24825-Excalibur_c2933_1350	2B	8290437	TraesCS2B02G018100	All	M1		Terpenoid_cyclase/PrenylTrfase
36726-Jagger_c7188_67	2B	180561127	TraesCS2B02G201400	MDN	M6		COBRA-like protein
				MDN	M1		COBRA-like protein
				MDN	M4		COBRA-like protein
76662-wsnp_Ex_c14771_22883575	2B	191734319	TraesCS2B02G209400	SK	M5		
				SK	M1		
				SK	M7		
				SK	M6		
45381-Kukri_c43745_1935	2B	578601210	TraesCS2B02G407500	MDN	M7		NAD/diacylglycerol_kinase
4154-BobWhite_c6365_385	2B	731895391	TraesCS2B02G536100	MDN	M7		S04_transporter, STAS domain
				MDN	M1		S04_transporter, STAS domain
				MDN	M4		S04_transporter, STAS domain
				MDN	M2		S04_transporter, STAS domain
73196-Tdurum_contig71365_233	2B	738410414	TraesCS2B02G542000	All	M1		
14959-CAP8_c8516_542	2B	749028333	TraesCS2B02G553600	OTT	M7		Chloro_AB-bd
46560-Kukri_c55909_1109	2B	770681399	TraesCS2B02G583300	OTT	M6	1	WD40-repeat, TPR
				OTT	M5	1	WD40-repeat, TPR
29707-Excalibur_rep_c101288_130	2D	17169662	TraesCS2D02G046800	OTT	M4		
74411-tplb0030j08_1960	2D	27928724	TraesCS2D02G066100	MDN	M7		G6PD
66898-Tdurum_contig11028_533	2D	87406015	TraesCS2D02G145500	MDN	M1	1	Ankyrin_rpt-contain
5774-BS00000905_51	2D	369762241	TraesCS2D02G288600	All	M1		
66206-Tdurum_contig10048_447	2D	635229168	TraesCS2D02G565200	OTT	M1		P-loop NTPase,DNA_repair_MutS
7692-BS00028660_51	3A	507467861	TraesCS3A02G277800	All	M7		ENTH domain
37081-JD_c1636_113	3A	672556342	TraesCS3A02G429800	MDN	M7		TPR-like_helical_dom, TOM20
14695-CAP8_c3568_256	3A	724200935	TraesCS3A02G498700	SK	M6	1	Alpha/Beta hydrolase fold
				SK	M7	1	Alpha/Beta hydrolase fold
50704-Kukri_s117946_404	3A	739734944	TraesCS3A02G526000	OTT	M6		FLC EXPRESSOR/FLX-like
				OTT	M5		FLC EXPRESSOR/FLX-like
65093-RFL_Contig5709_3312	3B	9780568	TraesCS3B02G022500	All	M3		GRDP1
5332-BobWhite_rep_c63085_120	3B	66581492	TraesCS3B02G099400	All	M3		Peptidase M48
				All	M7		T_SNARE_dom
75559-wsnp_BE499016B_Ta_2_1	3B	661016320	TraesCS3B02G423500	MDN	M7		T_SNARE_dom
28781-Excalibur_c76110_101	3B	760137269	TraesCS3B02G517100	All	M5		RRM_dom
				All	M7		RRM_dom
4262-BobWhite_c6974_329	3D	460250774	TraesCS3D02G348500	All	M7		GPR107/GPR108-like

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
35630-IACX1049	3D	551981733	TraesCS3D02G441600	MDN	M7		
48662-Kukri_rep_c101532_1046	3D	591985403	TraesCS3D02G504500	SK	M3	1	Papain-like_cys_pep
67877-Tdurum_contig13140_69	4A	59321657	TraesCS4A02G062800	SK	M6		WH-like_DNA-bd, HSF-type
				SK	M1		WH-like_DNA-bd, HSF-type
				SK	M5		WH-like_DNA-bd, HSF-type
47419-Kukri_c67793_237	4A	595821093	TraesCS4A02G294400	SK	M7	1	Ankyrin_rpt
54888-RAC875_c19718_551	4A	603453604	TraesCS4A02G311200	All	M7	1	Zinc finger, RING/FYVE/PHD-type
				MDN	M7	1	Zinc finger, RING/FYVE/PHD-type
58552-RAC875_c49370_327	4A	629917691	TraesCS4A02G356400	All	M7		Kelch-typ_b-propeller, ACBP
22324-Excalibur_c13811_1086	4A	723810464	TraesCS4A02G458600	SK	M3		Nucleotide-bd_a/b_plait
23633-Excalibur_c21395_291	4A	734000589	TraesCS4A02G474900	SK	M5	1	CC-NB-ARC-LRR domain
53152-RAC875_c10704_67	4B	154114340	TraesCS4B02G125200	MDN	M4		
62918-RAC875_rep_c72961_977	4B	616999234	TraesCS4B02G325900	OTT	M7		Ub-like domain
58215-RAC875_c46098_110	4B	669559717	TraesCS4B02G395300	All	M7		
55110-RAC875_c2099_2066	4B	670439103	TraesCS4B02G395800	All	M1	1	Zinc finger, RING/FYVE/PHD-type
24829-Excalibur_c29380_255	5A	26469747	TraesCS5A02G030500	OTT	M6		Tubulin-specific chaperone A
				OTT	M1		Tubulin-specific chaperone A
				OTT	M2		Tubulin-specific chaperone A
66289-Tdurum_contig10128_593	5A	48464957	TraesCS5A02G053400	OTT	M3	1	Papain-like_cys_pep
8437-BS00046773_51	5A	49956315	TraesCS5A02G054000	OTT	M3		
46209-Kukri_c52_225	5A	559070986	TraesCS5A02G357000	OTT	M2		TPR
				OTT	M4		TPR
27236-Excalibur_c51589_200	5A	561660942	TraesCS5A02G359900	All	M7		PPM-type phosphatase
45725-Kukri_c47057_758	5B	447840598	TraesCS5B02G263200	SK	M7		
30867-Excalibur_rep_c67473_320	5B	506789600	TraesCS5B02G321800	MDN	M1	1	ClpA/ClpB, P-loop NTPase
30952-Excalibur_rep_c68362_62	5B	695992792	TraesCS5B02G541500	SK	M6	1	CC-NB-ARC-LRR domain
				SK	M4	1	CC-NB-ARC-LRR domain
38458-Ku_c1454_984	5D	22378179	TraesCS5D02G025000	MDN	M3		NOC2L
1281-BobWhite_c19443_131	5D	442701407	TraesCS5D02G365600	OTT	M7		PDZ, ClpP/crotonase-like_dom
14533-CAP8_c145_89	5D	547273518	TraesCS5D02G532100	All	M6		NA-bd_OB-fold, SRBD1
				All	M3		NA-bd_OB-fold, SRBD1
				All	M1		NA-bd_OB-fold, SRBD1
				All	M5		NA-bd_OB-fold, SRBD1
				MDN	M3		NA-bd_OB-fold, SRBD1
				MDN	M1		NA-bd_OB-fold, SRBD1

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				MDN	M2		NA-bd_OB-fold, SRBD1
				SK	M4		NA-bd_OB-fold, SRBD1
				SK	M6		NA-bd_OB-fold, SRBD1
49205-Kukri_rep_c106820_591	5D	548880858	TraesCS5D02G534600	MDN	M7		AKiii-LysC-EC, A/G/U kinase
4362-BobWhite_c7604_254	5D	550206088	TraesCS5D02G537700	All	M7		DUF2301
4361-BobWhite_c7604_181	5D	550206161	TraesCS5D02G537700	MDN	M4		DUF2301
				MDN	M5		DUF2301
				MDN	M6		DUF2301
11863-BS00094333_51	5D	559922461	TraesCS5D02G557600	All	M6	1	CC-NB-ARC-LRR domain
				All	M5	1	CC-NB-ARC-LRR domain
				All	M2	1	CC-NB-ARC-LRR domain
				All	M4	1	CC-NB-ARC-LRR domain
				All	M1	1	CC-NB-ARC-LRR domain
8077-BS00037002_51	6A	2972683	TraesCS6A02G007500	MDN	M5	1	F-box-like domain
				MDN	M2	1	F-box-like domain
				MDN	M6	1	F-box-like domain
				MDN	M1	1	F-box-like domain
10105-BS00067630_51	6A	5221726	TraesCS6A02G011200	SK	M1		
2064-BobWhite_c27145_318	6A	598635853	TraesCS6A02G377400	OTT	M1		SAP-like BP-7
47927-Kukri_c8239_987	6B	25914950	TraesCS6B02G041900	MDN	M7	1	CC-NB-ARC-LRR domain
72401-Tdurum_contig5486_177	6B	90280258	TraesCS6B02G109400	SK	M3		START-like domain
31558-Excalibur_s113695_111	6B	556491270	TraesCS6B02G310700	All	M2		Thr-tRNA-ligase_lia
				All	M4		Thr-tRNA-ligase_lia
60190-RAC875_c68525_284	6B	657946526	TraesCS6B02G382800	SK	M7	1	Zinc finger, RING/FYVE/PHD-type
8425-BS00046264_51	6B	704974282	TraesCS6B02G439600	OTT	M5	1	Ethylene receptor
				OTT	M6	1	Ethylene receptor
5593-BobWhite_rep_c66074_232	6B	706118869	TraesCS6B02G442600	All	M6	1	LRR domain
				All	M2	1	LRR domain
				All	M1	1	LRR domain
				All	M4	1	LRR domain
46716-Kukri_c58096_480	6B	712390096	TraesCS6B02G456100	OTT	M3	1	Papain-like_cys_pep
13973-CAP7_c2923_366	6D	129784133	TraesCS6D02G154600	OTT	M2	1	PLAT/LH2 domain
				OTT	M4	1	PLAT/LH2 domain
33585-GENE-3735_720	6D	462275413	TraesCS6D02G382700	MDN	M8		
12939-CAP11_c5372_271	6D	465742757	TraesCS6D02G390600	MDN	M3	1	LRR, F-box-like domain

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
12245-BS00105522_51	6D	465959637	TraesCS6D02G390700	MDN	M3		
50713-Kukri_s118416_65	7A	167271145	TraesCS7A02G205200	MDN	M3		DUF1537
50713-Kukri_s118416_65	7A	167271145	TraesCS7A02G205200	MDN	M2		DUF1537
26882-Excalibur_c4759_564	7A	232751332	TraesCS7A02G250700	OTT	M4		
				OTT	M2		
				OTT	M6		
8051-BS00036422_51	7A	275545643	TraesCS7A02G269600	All	M3		Ub-like domain
78361-wsnp_Ex_c5330_9422106	7A	275920469	TraesCS7A02G269800	All	M3		Ub-like domain
687-BobWhite_c1469_112	7A	515009750	TraesCS7A02G351800	All	M6		
65210-RFL_Contig6074_1058	7A	691535765	TraesCS7A02G502600	MDN	M7		NAD(P)-bd_dom
25155-Excalibur_c3188_1352	7A	692879432	TraesCS7A02G504800	SK	M1		PPM-type phosphatase
81116-wsnp_Ra_c35321_43882919	7A	692880572	TraesCS7A02G504800	SK	M5		PPM-type phosphatase
30143-Excalibur_rep_c105674_315	7A	712307419	TraesCS7A02G533900	All	M4		SWEET sugar transporter
71429-Tdurum_contig43523_1458	7B	47742258	TraesCS7B02G048100	OTT	M2	1	AP2/ERF domain
				OTT	M5	1	AP2/ERF domain
36277-IACX82	7B	457383441	TraesCS7B02G247000	All	M3		ATX1
73863-Tdurum_contig93324_764	7B	457401612	TraesCS7B02G247100	All	M3		Protein RETICULATA-related
30869-Excalibur_rep_c67475_1759	7B	498523612	TraesCS7B02G271600	MDN	M5	1	PDR ABC transporter
				MDN	M7	1	PDR ABC transporter
				MDN	M4	1	PDR ABC transporter
58340-RAC875_c4732_1672	7B	533774856	TraesCS7B02G297000	SK	M3	1	Ser/Thr_kinase_AS
80349-wsnp_Ku_c29256_39161320	7B	539232386	TraesCS7B02G302400	All	M1		MetRS_core
72089-Tdurum_contig50574_304	7B	597463583	TraesCS7B02G342500	All	M3		RBD
7573-BS00025286_51	7B	636508176	TraesCS7B02G370700	All	M1	1	Lysozyme-like, Glyco_hydro_19
74097-tplb0021f14_1700	7B	653898244	TraesCS7B02G388000	All	M7	1	Ser/Thr_kinase_AS
31227-Excalibur_rep_c74234_183	7B	655037014	TraesCS7B02G388800	All	M4	1	Ser/Thr_kinase_AS
75603-wsnp_BE605194B_Ta_2_1	7B	657932119	TraesCS7B02G391300	All	M6	1	Ser/Thr_kinase_AS
79099-wsnp_Ex_rep_c104090_88891443	7B	687803644	TraesCS7B02G419100	SK	M1		
9595-BS00065623_51	7D	4005296	TraesCS7D02G008200	MDN	M2	1	CC-NB-ARC-LRR domain
				MDN	M1	1	CC-NB-ARC-LRR domain
22812-Excalibur_c16580_388	7D	18438257	TraesCS7D02G036100	MDN	M1		RNaseH-like, PAZ domain
19377-D_GDS7LZN02FSYZC_227	7D	58491641	TraesCS7D02G096000	OTT	M6	1	CC-NB-ARC-LRR domain
33938-GENE-4375_382	7D	465165900	TraesCS7D02G362100	MDN	M7		Zinc/iron permease
79862-wsnp_JD_c69_109951	Un	24402452	TraesCSU02G024000	MDN	M4	1	CC-NB-ARC-LRR domain
				MDN	M5	1	CC-NB-ARC-LRR domain

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
				MDN	M6	1	CC-NB-ARC-LRR domain
12610-BS00110940_51	Un	81996418	TraesCSU02G092400	OTT	M1	1	Ser/Thr_kinase_AS
LR SEVERITY - WINTER DIVERSITY PANEL							
10050-BS00067436_51	1A	578204373	TraesCS1A02G422900	MDN	M5	1	GH, X8 domain
12157-BS00100994_51	1B	9936518	TraesCS1B02G021700	MDN	M3		DUF247
38236-Ku_c11394_862	1B	339908061	TraesCS1B02G189500	All	M4		
24999-Excalibur_c30667_102	1B	360517459	TraesCS1B02G201300	MDN	M6		
8318-BS00042340_51	1B	630700832	TraesCS1B02G399600	All	M7		rSAM_horseshoe
21002-Ex_c6145_2193	1D	12534520	TraesCS1D02G032200	MDN	M7	1	CC-NB-ARC-LRR domain
				MDN	M3	1	CC-NB-ARC-LRR domain
18025-D_GB5Y7FA01EE4DJ_242	1D	361914448	TraesCS1D02G266100	MDN	M8		Prot_inh_BBI
16342-D_contig28058_60	1D	366674212	TraesCS1D02G272700	MDN	M4		Palmitoyltrfase_DHHC
				MDN	M6		Palmitoyltrfase_DHHC
				MDN	M8		Palmitoyltrfase_DHHC
				OTT	M4		Palmitoyltrfase_DHHC
				OTT	M6		Palmitoyltrfase_DHHC
27190-Excalibur_c50934_159	2A	85289098	TraesCS2A02G140100	OTT	M7		BSD domain
76918-wsnp_Ex_c17852_26612172	2A	197559361	TraesCS2A02G212800	All	M3		Peptidase C65, otubain
15473-D_contig08350_924	2B	394098064	TraesCS2B02G286100	MDN	M2		At1g61900-lke
74910-tplb0048g05_866	2B	622904989	TraesCS2B02G433600	All	M3		
56694-RAC875_c32066_684	2B	624539187	TraesCS2B02G434600	All	M3		Peptidase T2, asparaginase 2
19356-D_GDS7LZN02F3V0T_214	2D	14117424	TraesCS2D02G038300	MDN	M1		
46794-Kukri_c59403_339	2D	75001895	TraesCS2D02G129200	MDN	M8	1	WD40/YVTN repeat-like
17812-D_GA8KES401EQTMF_68	2D	446313187	TraesCS2D02G348400	MDN	M3		MFS transporter
27281-Excalibur_c5199_423	2D	593270920	TraesCS2D02G497400	MDN	M5		MoeA_C_domain_IV
30442-Excalibur_rep_c109863_383	3A	9854380	TraesCS3A02G013800	All	M7		Fatty acyl-CoA reductase
38473-Ku_c14982_168	3A	497649774	TraesCS3A02G270400	MDN	M3		PRONE domain
76298-wsnp_Ex_c11397_18400400	3A	497655032	TraesCS3A02G270500	MDN	M3	1	LRR, Ser-Thr/Tyr_kinase
75655-wsnp_BF429272A_Ta_2_1	3A	498774691	TraesCS3A02G271100	MDN	M3	1	Ser/Thr_kinase_AS
27648-Excalibur_c56240_200	3A	651627266	TraesCS3A02G406700	All	M3		
2309-BobWhite_c29826_602	3A	651627599	TraesCS3A02G406700	All	M3		
73056-Tdurum_contig67196_285	3A	662940157	TraesCS3A02G421500	All	M3		Clathrin_sm-chain_CS
71662-Tdurum_contig4598_502	3A	663181023	TraesCS3A02G421700	All	M3		P-loop NTPase, Small_GTPase

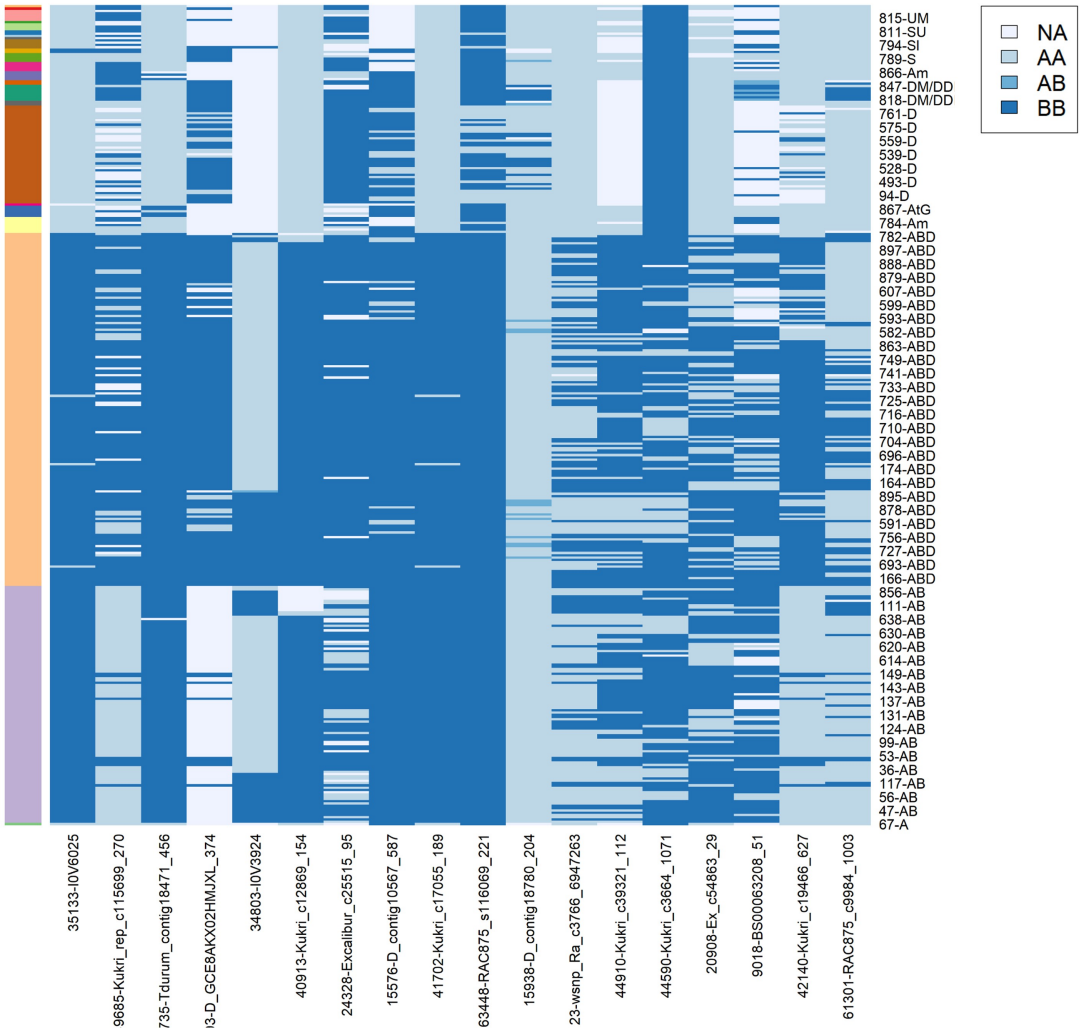
QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
25955-Excalibur_c3862_837	3B	245969143	TraesCS3B02G209800	MDN	M5	1	Peroxidase
79515-wsnp_Ex_rep_c69783_68742690	3B	379995020	TraesCS3B02G240900	MDN	M6		ARM-type fold, SIT4
				MDN	M3		ARM-type fold, SIT5
52937-RAC875_c101793_136	3D	547625537	TraesCS3D02G435400	All	M4	1	WD40/YVTN repeat-like, QPCT
74685-tplb0040j04_1007	4A	708613278	TraesCS4A02G439000	MDN	M1		peptide transporter, OPT1/isp4
37657-JD_c581_466	4A	713519525	TraesCS4A02G445600	OTT	M1		Cytochrome P450
				OTT	M6		Cytochrome P450
				OTT	M5		Cytochrome P450
				OTT	M3		Cytochrome P450
1382-BobWhite_c20322_559	4A	713523112	TraesCS4A02G445600	OTT	M3		Cytochrome P450
61163-RAC875_c96615_107	5A	403876844	TraesCS5A02G199000	MDN	M3		
74800-tplb0044j06_689	5A	596013562	TraesCS5A02G403700	OTT	M7		Cold-regulated 413 protein
7154-BS00022555_51	5B	435769407	TraesCS5B02G252700	OTT	M1	1	F-box-like domain, b-propeller
78640-wsnp_Ex_c6548_11355524	5B	439725143	TraesCS5B02G257300	MDN	M7	1	WRKY domain
				MDN	M4	1	WRKY domain
				MDN	M1	1	WRKY domain
6745-BS00021735_51	5B	593943053	TraesCS5B02G418200	OTT	M6		eEF1a1
				OTT	M4		eEF1a2
69972-Tdurum_contig30194_256	5B	653230498	TraesCS5B02G480700	OTT	M7		Ribosomal protein L24e
53681-RAC875_c13208_684	5B	680352542	TraesCS5B02G515900	OTT	M1		Kelch-type beta propeller
77355-wsnp_Ex_c24031_33277856	5B	707133745	TraesCS5B02G560400	All	M6		PGR5-like protein 1
19215-D_GDRF1KQ02GC5EV_278	5D	301127151	TraesCS5D02G198300	All	M6		Agmatine deiminase
				MDN	M8		Agmatine deiminase
				MDN	M3		Agmatine deiminase
15609-D_contig11260_295	5D	526292356	TraesCS5D02G493600	All	M3		TPR-like_helical_dom
				MDN	M3		TPR-like_helical_dom
78974-wsnp_Ex_c965_1845676	6A	581747079	TraesCS6A02G349200	All	M4		cNMP-bd-like
				All	M6		cNMP-bd-like
				All	M5		cNMP-bd-like
				All	M1		cNMP-bd-like
60427-RAC875_c76675_372	6A	610199793	TraesCS6A02G401900	MDN	M6		
				MDN	M5		
				MDN	M1		
17318-D_F1BEJMU01DYWUS_134	6D	58096323	TraesCS6D02G093100	OTT	M6	1	F-box-like domain
				OTT	M5	1	F-box-like domain

QTN or LDB	Chr	position	Gene ID	Trait[1]	Model[2]	DR	Gene annotation
15945-D_contig18907_85	6D	463870710	TraesCS6D02G386600	OTT	M4		Ribonuclease H-like
				OTT	M5		Ribonuclease H-like
24038-Excalibur_c23756_1461	7A	6485654	TraesCS7A02G014500	OTT	M6		
				OTT	M4		
25650-Excalibur_c35919_107	7A	259562231	TraesCS7A02G262700	All	M7		
34228-GENE-4898_208	7A	572869014	TraesCS7A02G394500	OTT	M4		Peptidase M16, N-terminal
48036-Kukri_c855_2107	7A	708138675	TraesCS7A02G525900	MDN	M4	1	Zinc finger, CCCH-type
52617-Ra_c73849_639	7B	1255228	TraesCS7B02G003000	OTT	M1		
39827-Ku_c68626_1054	7B	181035062	TraesCS7B02G142200	MDN	M3		SBP domain
4395-BobWhite_c7907_657	7B	181036896	TraesCS7B02G142200	MDN	M3		SBP domain
5616-BobWhite_rep_c66630_331	7B	624351237	TraesCS7B02G362600	MDN	M3		GTP-binding, Transl_B-barrel
34569-IAAV2530	7D	102541074	TraesCS7D02G154500	OTT	M7		
15734-D_contig14443_745	7D	232496636	TraesCS7D02G257100	MDN	M1		Ribosomal_L32e_sf
				MDN	M4		Ribosomal_L32e_sf
				MDN	M6		Ribosomal_L32e_sf
8614-BS00052386_51	7D	289257907	TraesCS7D02G282700	All	M7		COG_su3
16386-D_contig28902_391	7D	456495802	TraesCS7D02G353200	All	M4	1	F-box-like domain
23018-Excalibur_c17808_478	7D	609277272	TraesCS7D02G503700	OTT	M4	1	Ser/Thr_kinase_AS

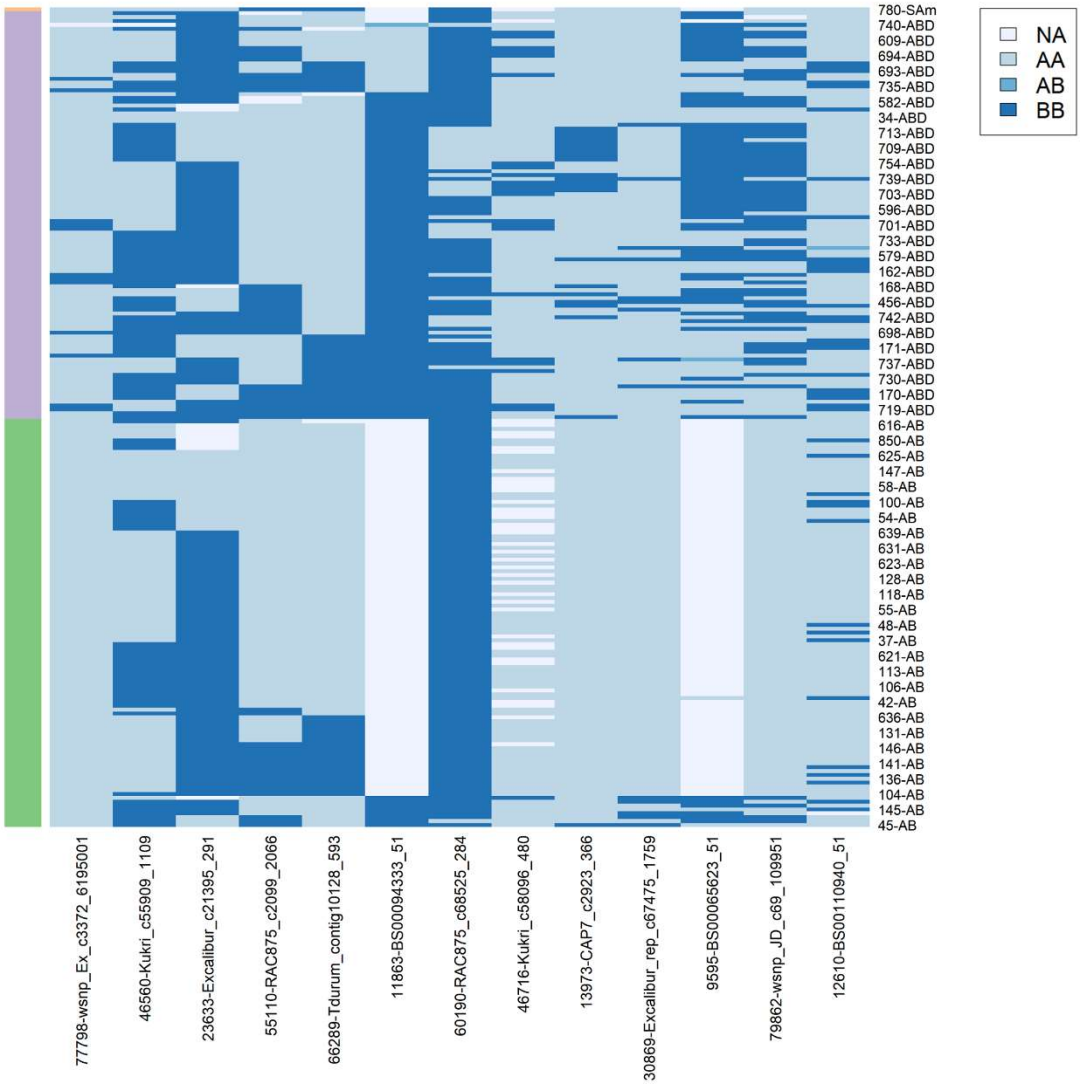
[1] MDN, Morden; OTT, Ottawa; SK, Saskatoon; All, all locations

[2] M1, pLARmEB; M2, FASTmrEMMA ; M3, RTM; M4, ISIS-EM-BLASSO; M5, FASTmrMLM; M6, pLARmEB; M7, mrMLM; M8, MLM

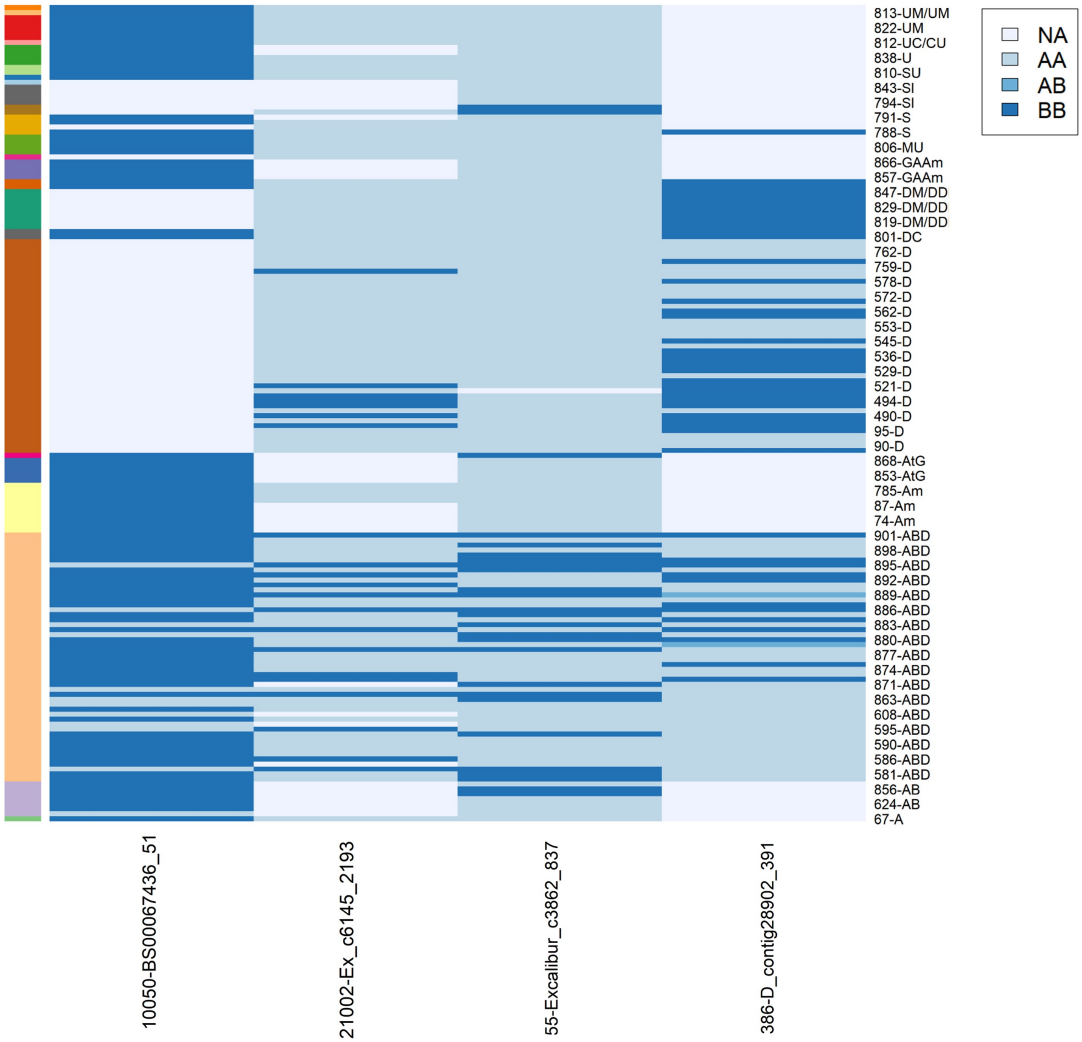
Appendix 16 Genotypes for QTNs showing significant allele-specific phenotype differences



Appendix 16A Heatmap showing genotype calls for quantitative trait nucleotides (QTNs) that displayed significant allele-specific phenotype differences for infection type against six leaf rust isolates. Rows represent the entry number and genome symbol of the accessions in the germplasm and columns represent the QTNs. Genotypes AA and BB represent homozygous alleles associated with low and high infection type scores, respectively. Genotype AB and NA represent heterozygous alleles and no genotype calls, respectively. Different colors in the left panel represent the different groups of species in the germplasm.



Appendix 16B Heatmap showing genotype calls for quantitative trait nucleotides (QTNs) that displayed significant allele-specific phenotype differences for leaf rust severity in the spring diversity panel. Rows represent the entry number and genome symbol of the accessions in the germplasm and columns represent the QTNs. Genotypes AA and BB represent homozygous alleles associated with low and high leaf rust severity scores, respectively. Genotype AB and NA represent heterozygous alleles and no genotype calls, respectively. Different colors in the left panel represent the different groups of species in the germplasm.



Appendix 16C Heatmap showing genotype calls for quantitative trait nucleotides (QTNs) that displayed significant allele-specific phenotype differences for leaf rust severity in the winter diversity panel. Rows represent the entry number and genome symbol of the accessions in the germplasm and columns represent the QTNs. Genotypes AA and BB represent homozygous alleles associated with low and high leaf rust severity scores, respectively. Genotype AB and NA represent heterozygous alleles and no genotype calls, respectively. Different colors in the left panel represent the different groups of species in the germplasm.

Appendix 17 QTNs located within flanking markers of *Lr* resistance genes

Appendix 17A Quantitative trait nucleotides (QTNs) located within flanking markers of leaf rust (*Lr*) resistance genes positioned onto the Chinese Spring reference genome sequence v1.0 (IWGSC 2018).

Lr gene	flanking region	QTN	position	Trait[1]	Model[2]	r^2 (%)	KW[3]	Gene ID
Lr75	71600965-153924534	Excalibur_c4215_1327	1B:95323618	IT TDBG2	M1	23.731	ns	TraesCS1B02G093900
Lr13	138117619-197349665	Jagger_c7188_67	2B:180561127	LRS SP MDN	M2	2.257	****	TraesCS2B02G201400
					M3	2.868		
					M4	8.663		
		wsnp_Ex_c14771_22883575	2B:191734319	LRS SP SK	M4	2.818	****	TraesCS2B02G209400
					M1	5.248		
					M4	5.622		
					M2	3.647		
Lr15	36439202-72660599	Kukri_rep_c115699_270	2D:39829875	IT TDBG2	M6	5.780	**	TraesCS2D02G090100
Lr27	8344499-16219598	D_GCE8AKX02HMJXL_374	3B:15138756	IT MBDS	M7	12.554	****	TraesCS3B02G032600
					M4	5.437		
					M6	4.007		
					M3	2.912		
					M2	2.474		
					M1	1.864		
				IT MBRJ	M4	3.016	****	
					M3	2.976		
				IT MGBJ	M4	1.529	****	

Lr gene	flanking region	QTN	position	Trait[1]	Model[2]	r^2 (%)	KW[3]	Gene ID
		RFL_Contig5709_3312	3B:9780568	LRS SP SK	M8	2.036	ns	TraesCS3B02G022500
lr28	732772923-737197805	Excalibur_c21395_291	4A:734000589	LRS SP SK	M4	4.967	*	TraesCS4A02G474900
Lr12	544649745-568556214	BS00093089_51	4B:552827949	IT TDBG1	M6	13.823	****	TraesCS4B02G274900
Lr49	608252156-640976653	Ku_c2346_1339	4B:623066948	IT TDBG2	M1	4.788	**	TraesCS4B02G332500
				IT TJBJ	M4	10.463	**	
					M4	6.105		
					M2	4.564		
		RAC875_rep_c72961_977	4B:616999234	LRS SP OTT	M1	6.058	**	TraesCS4B02G325900
Lr64	609288614-614165744	RAC875_c76675_372	6A:610199793	LRS WP MDN	M2	4.134	ns	TraesCS6A02G401900
					M4	2.916		
					M4	3.583		
Lr19	605875095-623052562	D_contig19288_196	7D:619884620	IT MBRJ	M4	3.621	ns	TraesCS7D02G523200
		Excalibur_c17808_478	7D:609277272	LRS WP OTT	M3	3.885	ns	TraesCS7D02G503700

[1] IT, infection type; LRS, leaf rust severity; SP, spring panel; WP, winter panel; MDN, Morden; OTT, Ottawa; SK, Saskatoon

[2] M1, mrMLM; M2, pLARmEB; M3, ISIS EM-BLASSO; M4, pKWmEB; M4; M5, FASTmrMLM; M6, FASTmrMLM; M7, MLM; M8, RTM

[3] KW, Kruskal–Wallis statistical test; significance levels “ns”,“*”, “**”, “***” and “****” correspond to not significant and P-values ≤ 0.05, 0.01, 0.001 and 0.0001, respectively

Appendix 17B Quantitative trait nucleotides (QTNs) located within the same linkage disequilibrium block (LDB) as leaf rust (*Lr*) resistance genes positioned onto the Chinese Spring reference genome sequence v1.0 (IWGSC 2018).

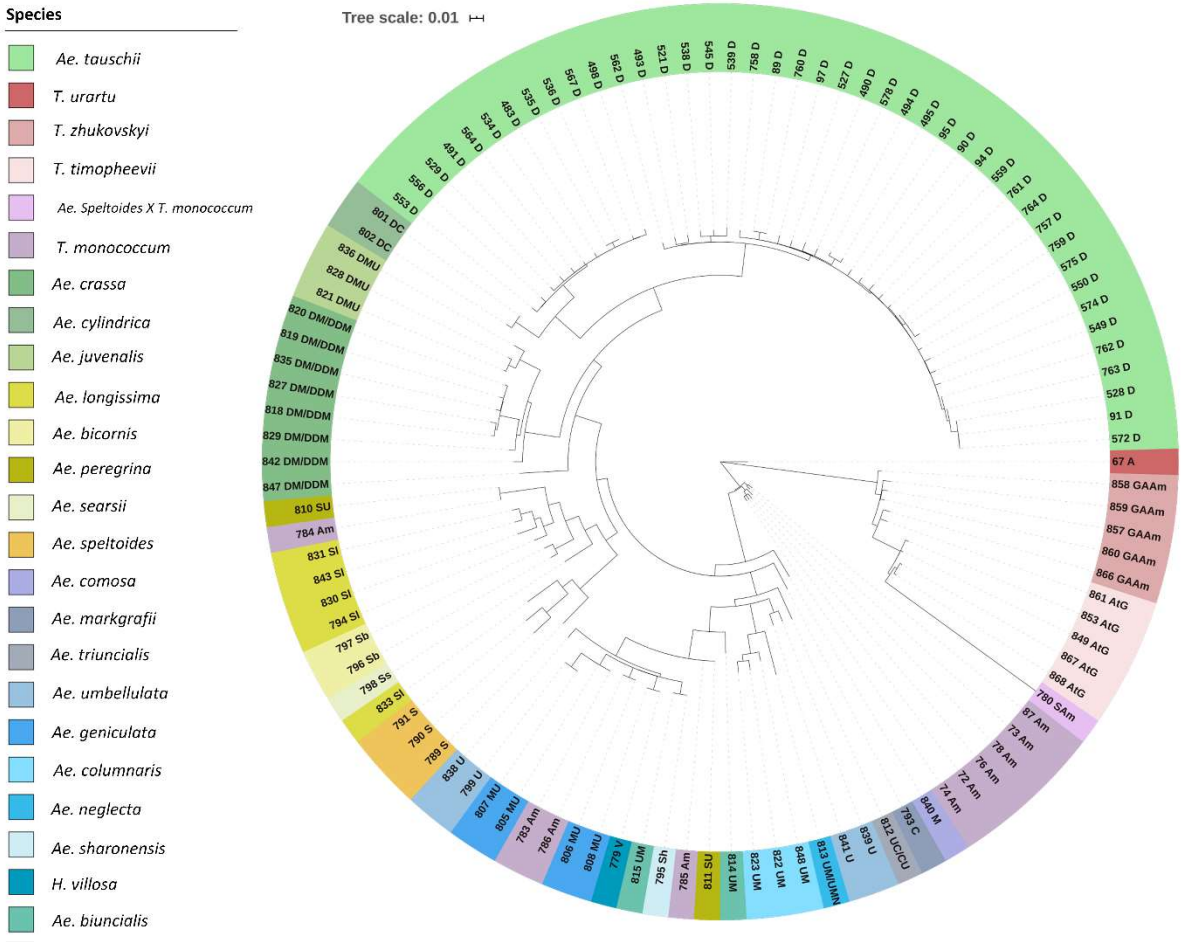
Lr gene	QTN	LDB Position	LDB D'[1]	Trait[2]	Model[3]	r^2 (%)	KW[4]	Gene ID
Lr1	BS00094333_51	5D:559922461-561795330	0.858	LRS SP AL	M1	6.52	***	TraesCS5D02G557600
					M2	9.56		
					M3	8.39		
					M4	8.38		
					M5	7.61		
Lr34	D_GDS7LZN02F1Q5F_180	7D:45129712-51781960	0.536	IT TDBG1	M6	9.15	***	TraesCS7D02G076400
				IT MGBJ	M6	14.27	****	
					M2	9.33		
				IT TJBJ	M5	14.02	****	
Lr16, Lr75	Excalibur_c42248_663	2B:6210157-17783697	0.567	LRS SP AL	M7	3.07	****	TraesCS2B02G013500
	RAC875_c25628_180	2B:6210157-17783697	0.567	LRS SP SK	M1	2.65	ns	TraesCS2B02G017800
					M6	4.25		
					M4	3.94		
Lr32	Excalibur_c25515_95	3D:22087639-28331100	0.848	IT MBDS	M3	4.82	****	TraesCS3D02G064200
				IT TJBJ	M4	7.69	****	
					M5	6.57		
					M1	5.24		
					M2	5.21		
					M3	4.48		

[1] Intra-block D' were calculated by taking the average of all pairwise D' in a haplotype block
[2] IT, infection type; LRS, leaf rust severity; SP, spring panel; SK, Saskatoon; AL, all locations
[3] M1, pLARmEB; M2, FASTmrMLM; M3, FASTmrEMMA; M4, ISIS EM-BLASSO; M5, pKWmEB; M6, MLM; M7, RTM
[4] KW, Kruskal–Wallis statistical test; significance levels “ns”,“*”, “**”, “***” and “****” correspond to not significant and P-values ≤ 0.05, 0.01, 0.001 and 0.0001, respectively

Appendix 17C Quantitative trait nucleotides (QTNs) located within a neighboring linkage disequilibrium block (LDB) of one containing a leaf rust (*Lr*) resistance gene positioned onto the Chinese Spring reference genome sequence v1.0 (IWGSC 2018).

Lr gene	QTN	Gene-QTN LDBs[1]	Inter-block D'[2]	Trait[3]	Model[4]	r^2 (%)	KW[5]	Gene ID
Lr54	Excalibur_c22201_907	2D:638613120:641603488 2D:635595000:638141003	0.626	IT TDBG1	M1 M2	6.16 3.93	**	TraesCS2D02G573500
	RFL_Contig3121_1979	2D:641963416:649147452 2D:635595000:638141003	0.666	IT MBDS	M1	5.85	ns	TraesCS2D02G595000
Lr18	Excalibur_rep_c68362_62	5B:695705144-696189453 5B:696490959-700236129	0.44	LRS SP SK	M3 M2	2.74 4.32	*	TraesCS5B02G541500

[1] Neighboring linkage disequilibrium blocks containing the QTN and mapped *Lr* genes
[2] Inter-block D' were calculated by taking the average of all pairwise D' between the two haplotype blocks
[3] IT, infection type; LRS, leaf rust severity; SP, spring panel; SK, Saskatoon
[4] M1, pKWmEB; M2, ISIS EM-BLASSO; M3, pLARmEB
[5] KW, Kruskal–Wallis statistical test; significance levels “ns”,“*” and “**” correspond to not significant and P-values ≤ 0.05 and 0.01, respectively



Appendix 18 Phylogenetic tree illustrating the relationships between the wild species.

The leaf node labels are the entry number and genome symbol of the *Aegilops*, *Triticum* and *Haynaldia* accessions in the germplasm.